SEQUENCE LISTING

<110> Halozyme, Inc.
Christopher Thanos
Lin Wang
H. Michael Shepard

<120> COMPOSITIONS OF ADENOSINE DEAMINASE-2
(ADA2), VARIANTS THEREOF AND METHODS OF USING SAME

<130> 33320.03121.WO02/3121PC

<140> Not Yet Assigned
<141> Herewith

<150> 62/063,936
<151> 2014-10-14

<160> 931

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Homo sapiens

<220>
<223> Adenosine deaminase 2 precursor

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<212> PRT
<213> Homo sapiens

<220>
<223> Adenosine deaminase 2 precursor

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
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<309> 2002-04-16

<400> 2

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        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
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Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
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465                 470                 475                 480
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Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
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<210> 3
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> ADA1-linker-Strep


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            20                  25                  30
Arg Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn
        35                  40                  45
Val Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys
    50                  55                  60
Phe Asp Tyr Tyr Met Pro Ala Ile Ala Gly Cys Arg Glu Ala Ile Lys
65                  70                  75                  80
Arg Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val
                85                  90                  95
Tyr Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val
            100                 105                 110
Glu Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu
        115                 120                 125
Val Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe
    130                 135                 140
Gly Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn
145                 150                 155                 160
Trp Ser Pro Lys Val Val Glu Leu Cys Lys Tyr Gln Gln Gln Thr
                165                 170                 175
Val Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser
            180                 185                 190
Leu Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly
        195                 200                 205
Ile His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val
    210                 215                 220
Lys Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr
225                 230                 235                 240
His Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn
                245                 250                 255
Met His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp
            260                 265                 270
Lys Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala
        275                 280                 285
Asn Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu
    290                 295                 300
Asp Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu
305                 310                 315                 320
Glu Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro
                325                 330                 335
Glu Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly
            340                 345                 350
Met Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu Ser Gly Ser Gly Ser
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Trp Ser His Pro Gln Phe Glu Lys
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<210> 4
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<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> ADA2 crystal structure sequence

<400> 4

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Ala Asn Glu Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala
        35                  40                  45
Met Arg Thr Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys
    50                  55                  60
His Leu Ile Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro
65                  70                  75                  80
Lys Gly Ala Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp
                85                  90                  95
Trp Leu Val Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe
            100                 105                 110
Thr Pro Arg Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg
        115                 120                 125
Pro Ser Glu Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys
    130                 135                 140
Arg Val Gln Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe
145                 150                 155                 160
Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val
                165                 170                 175
Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile
            180                 185                 190
His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu
        195                 200                 205
Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu
    210                 215                 220
Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val
225                 230                 235                 240
Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu
                245                 250                 255
Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val
            260                 265                 270
Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys
        275                 280                 285
Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr
    290                 295                 300
Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys
305                 310                 315                 320
Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp
                325                 330                 335
Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn
            340                 345                 350
Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val
        355                 360                 365
Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile
    370                 375                 380
Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val
385                 390                 395                 400
Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp
                405                 410                 415
Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val
            420                 425                 430
Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln
        435                 440                 445
Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys
    450                 455                 460
Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala
465                 470                 475                 480
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Asp Val Ala Thr Lys Gly Ser Leu His His Ile Leu Asp Ala Gln Lys
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Met Val Trp Asn His Arg His His His His His His
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<211> 482
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 mature protein

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Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
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Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
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Thr Lys

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<212> DNA
<213> Aritificial Sequence

<220>
<223> pCMV-Script

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cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga ctttccattg 180
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<210> 7
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<212> PRT
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<223> ADA2-FLAG

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<222> (483)...(490)
<223> FLAG tag

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            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
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Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
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His Leu Asp Gly Ser Ile Lys Pro Glu Thr Ile Leu Tyr Tyr Gly Arg
            20   25   30
Arg Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn
        35   40   45
Val Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys
    50   55   60
Phe Asp Tyr Tyr Met Pro Ala Ile Ala Gly Cys Arg Glu Ala Ile Lys
65   70   75   80
Arg Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val
                85   90   95
Tyr Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val
            100   105   110
Glu Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu
        115   120   125
Val Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe
    130   135   140
Gly Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn
145   150   155   160
Trp Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr Gln Gln Gln Thr
                165   170   175
Val Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser
            180   185   190
Leu Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly
        195   200   205
Ile His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val
    210   215   220

```
Lys Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr
225                 230                 235                 240
His Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn
                245                 250                 255
Met His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp
            260                 265                 270
Lys Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala
        275                 280                 285
Asn Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu
    290                 295                 300
Asp Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu
305                 310                 315                 320
Glu Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro
                325                 330                 335
Glu Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly
            340                 345                 350
Met Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu
        355                 360


<210> 13
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11A, mature numbering


<400> 13
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
```

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 14
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11D, mature numbering

<400> 14
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Asp Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 15
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11E, mature numbering

<400> 15

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Glu Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
```

Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 16
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K13A, mature numbering

<400> 16
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Ala Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 17
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K13D, mature numbering

<400> 17

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Asp Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 18
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K13E, mature numbering

<400> 18

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Glu Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 19
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371A, mature numbering

<400> 19

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
```

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 20
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 K371D, mature numbering

<400> 20
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 21
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371E, mature numbering

<400> 21
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 22
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K372A, mature numbering

<400> 22
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Ala Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 23
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K372D, mature numbering

<400> 23
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

Ser Trp Lys Asp Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 24
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K372E, mature numbering

<400> 24
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Glu Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 25
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K452A, mature numbering

<400> 25

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Ala Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 26
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K452D, mature numbering

<400> 26

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
```

```
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Asp Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 27
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K452E, mature numbering

<400> 27

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
```

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Glu Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 28
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R20A, mature numbering

<400> 28

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

```
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 29
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R20D, mature numbering

<400> 29

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Asp Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 30
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R20E, mature numbering

<400> 30

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 31
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R366A, mature numbering

<400> 31
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Ala Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 32
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R366D, mature numbering

<400> 32

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Asp Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 33
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R366E, mature numbering

<400> 33
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Glu Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 34
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264A, mature numbering

<400> 34
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Ala Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 35
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264Q, mature numbering

<400> 35
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Gln Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

```
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 36
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264N, mature numbering

<400> 36

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp Asn Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
```

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 37
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264G, mature numbering

<400> 37

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Gly Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 38
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219K, mature numbering

<400> 38
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Lys Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 39
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q, mature numbering

<400> 39

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 40
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219N, mature numbering

<400> 40

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
```

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Asn Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 41
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219A, mature numbering

<400> 41

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ala Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 42
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221A, mature numbering

<400> 42

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Ala Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 43
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221V, mature numbering

<400> 43
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Val Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 44
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221G, mature numbering

<400> 44
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Gly Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 45
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179D, mature numbering

<400> 45
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Asp Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 46
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179A, mature numbering

<400> 46
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Ala Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 47
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179S, mature numbering

<400> 47

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Ser Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
```

290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 48
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179T, mature numbering

<400> 48
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Thr Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly

```
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 49
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179V, mature numbering

<400> 49

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Val Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

```
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 50
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179G, mature numbering

<400> 50

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
```

145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Gly Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 51
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262A, mature numbering

<400> 51
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg

```
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ala Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 52
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262V, mature numbering

<400> 52

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
```

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Val Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 53
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262M, mature numbering

<400> 53
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg

```
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Met Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 54
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N, mature numbering

<400> 54

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 55
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11A/R20A, mature numbering

<400> 55
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe

450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 56
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11A/R20A/K371A, mature numbering

<400> 56
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 57
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R20A/K371A, mature numbering

<400> 57
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 58
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K11A/K371A, mature numbering

<400> 58

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
```

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 59
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/K371D, mature numbering

<400> 59
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 60
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/K371E, mature numbering

<400> 60
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 61
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/R20E, mature numbering

<400> 61
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser

```
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 62
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/R20E/K371D, mature numbering

<400> 62

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
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        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 63
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/R20E/K371E, mature numbering

<400> 63

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> SGSGS Linker

<400> 64
Ser Gly Ser Gly Ser
1 5

<210> 65
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Strep tag

<400> 65
Trp Ser His Pro Gln Phe Glu Lys
 1   5

<210> 66
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<223> mature ADA1 protein

<400> 66
Ala Gln Thr Pro Ala Phe Asp Lys Pro Lys Val Glu Leu His Val His
 1   5   10   15
Leu Asp Gly Ser Ile Lys Pro Glu Thr Ile Leu Tyr Tyr Gly Arg Arg
            20   25   30
Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn Val
        35   40   45
Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys Phe
    50   55   60
Asp Tyr Tyr Met Pro Ala Ile Ala Gly Cys Arg Glu Ala Ile Lys Arg
65   70   75   80
Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val Tyr
                85   90   95
Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val Glu
            100   105   110
Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu Val
        115   120   125
Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe Gly
    130   135   140
Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn Trp
145   150   155   160
Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr Gln Gln Gln Thr Val
                165   170   175
Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser Leu
            180   185   190
Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly Ile
        195   200   205
His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val Lys
    210   215   220
Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr His
225   230   235   240
Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn Met
                245   250   255
His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp Lys
            260   265   270
Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala Asn
        275   280   285
Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu Asp
    290   295   300
Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu Glu
305   310   315   320
Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro Glu
                325   330   335
Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly Met
            340   345   350
Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu
        355   360

<210> 67
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> mature ADA1-linker-Strep

<400> 67
Ala Gln Thr Pro Ala Phe Asp Lys Pro Lys Val Glu Leu His Val His
 1   5   10   15
Leu Asp Gly Ser Ile Lys Pro Glu Thr Ile Leu Tyr Tyr Gly Arg Arg
            20   25   30
Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn Val
        35   40   45
Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys Phe
    50   55   60
Asp Tyr Tyr Met Pro Ala Ile Ala Gly Cys Arg Glu Ala Ile Lys Arg
65   70   75   80
Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val Tyr
                85   90   95
Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val Glu
            100   105   110
Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu Val
        115   120   125
Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe Gly
    130   135   140
Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn Trp
145   150   155   160
Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr Gln Gln Gln Thr Val
                165   170   175
Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser Leu
            180   185   190
Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly Ile
        195   200   205
His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val Lys
    210   215   220
Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr His
225   230   235   240
Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn Met
                245   250   255
His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp Lys
            260   265   270
Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala Asn
        275   280   285
Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu Asp
    290   295   300
Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu Glu
305   310   315   320
Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro Glu
                325   330   335
Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly Met
            340   345   350
Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu Ser Gly Ser Gly Ser Trp
        355   360   365
Ser His Pro Gln Phe Glu Lys
    370   375

<210> 68
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> ADA2 protein isoform 2

<300>
<308> Uniprot Q9NZK5-2
<309> 2002-04-16

<400> 68
Met Asp Ser Leu Glu Trp Asn Trp Ala Leu Val Tyr Glu Leu Ser Gly
 1   5   10   15
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
            20   25   30
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
        35   40   45
Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
    50   55   60
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
65   70   75   80
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
                85   90   95
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
            100   105   110
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
        115   120   125
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
    130   135   140
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys
145   150   155   160
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
                165   170   175
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
            180   185   190
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
        195   200   205
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
    210   215   220
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
225   230   235   240
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
                245   250   255
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            260   265   270

<210> 69
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> mature ADA1 C74S

<400> 69
Ala Gln Thr Pro Ala Phe Asp Lys Pro Lys Val Glu Leu His Val His
 1   5   10   15
Leu Asp Gly Ser Ile Lys Pro Glu Thr Ile Leu Tyr Tyr Gly Arg Arg
            20   25   30
Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn Val
        35   40   45
Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys Phe
    50   55   60
Asp Tyr Tyr Met Pro Ala Ile Ala Gly Ser Arg Glu Ala Ile Lys Arg
65   70   75   80
Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val Tyr
                85   90   95
Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val Glu
            100   105   110
Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu Val

```
        115                 120                 125
Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe Gly
    130                 135                 140
Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn Trp
145                 150                 155                 160
Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr Gln Gln Gln Thr Val
                165                 170                 175
Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser Leu
            180                 185                 190
Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly Ile
        195                 200                 205
His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val Lys
    210                 215                 220
Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr His
225                 230                 235                 240
Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn Met
                245                 250                 255
His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp Lys
            260                 265                 270
Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala Asn
        275                 280                 285
Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu Asp
    290                 295                 300
Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu Glu
305                 310                 315                 320
Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro Glu
                325                 330                 335
Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly Met
            340                 345                 350
Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu
        355                 360


<210> 70
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> mature ADA1-linker-Strep

<400> 70
Ala Gln Thr Pro Ala Phe Asp Lys Pro Lys Val Glu Leu His Val His
 1               5                  10                  15
Leu Asp Gly Ser Ile Lys Pro Glu Thr Ile Leu Tyr Tyr Gly Arg Arg
            20                  25                  30
Arg Gly Ile Ala Leu Pro Ala Asn Thr Ala Glu Gly Leu Leu Asn Val
        35                  40                  45
Ile Gly Met Asp Lys Pro Leu Thr Leu Pro Asp Phe Leu Ala Lys Phe
    50                  55                  60
Asp Tyr Tyr Met Pro Ala Ile Ala Gly Ser Arg Glu Ala Ile Lys Arg
65                  70                  75                  80
Ile Ala Tyr Glu Phe Val Glu Met Lys Ala Lys Glu Gly Val Val Tyr
                85                  90                  95
Val Glu Val Arg Tyr Ser Pro His Leu Leu Ala Asn Ser Lys Val Glu
            100                 105                 110
Pro Ile Pro Trp Asn Gln Ala Glu Gly Asp Leu Thr Pro Asp Glu Val
        115                 120                 125
Val Ala Leu Val Gly Gln Gly Leu Gln Glu Gly Glu Arg Asp Phe Gly
    130                 135                 140
Val Lys Ala Arg Ser Ile Leu Cys Cys Met Arg His Gln Pro Asn Trp
145                 150                 155                 160
Ser Pro Lys Val Val Glu Leu Cys Lys Lys Tyr Gln Gln Gln Thr Val
                165                 170                 175
Val Ala Ile Asp Leu Ala Gly Asp Glu Thr Ile Pro Gly Ser Ser Leu
            180                 185                 190
Leu Pro Gly His Val Gln Ala Tyr Gln Glu Ala Val Lys Ser Gly Ile
        195                 200                 205
```

```
His Arg Thr Val His Ala Gly Glu Val Gly Ser Ala Glu Val Val Lys
    210                 215                 220
Glu Ala Val Asp Ile Leu Lys Thr Glu Arg Leu Gly His Gly Tyr His
225                 230                 235                 240
Thr Leu Glu Asp Gln Ala Leu Tyr Asn Arg Leu Arg Gln Glu Asn Met
                245                 250                 255
His Phe Glu Ile Cys Pro Trp Ser Ser Tyr Leu Thr Gly Ala Trp Lys
            260                 265                 270
Pro Asp Thr Glu His Ala Val Ile Arg Leu Lys Asn Asp Gln Ala Asn
        275                 280                 285
Tyr Ser Leu Asn Thr Asp Asp Pro Leu Ile Phe Lys Ser Thr Leu Asp
    290                 295                 300
Thr Asp Tyr Gln Met Thr Lys Arg Asp Met Gly Phe Thr Glu Glu Glu
305                 310                 315                 320
Phe Lys Arg Leu Asn Ile Asn Ala Ala Lys Ser Ser Phe Leu Pro Glu
                325                 330                 335
Asp Glu Lys Arg Glu Leu Leu Asp Leu Leu Tyr Lys Ala Tyr Gly Met
            340                 345                 350
Pro Pro Ser Ala Ser Ala Gly Gln Asn Leu Ser Gly Ser Gly Ser Trp
        355                 360                 365
Ser His Pro Gln Phe Glu Lys
    370                 375


<210> 71
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K26A, mature numbering


<400> 71
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Ala Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 72
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K26D, mature numbering

<400> 72

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Asp Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
```

```
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 73
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K26E, mature numbering

<400> 73

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Glu Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
```

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 74
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R217A, mature numbering

<400> 74

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Ala Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 75
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R217D, mature numbering

<400> 75
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Asp Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 76
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R217E, mature numbering

<400> 76

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Glu Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 77
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K258A, mature numbering

<400> 77
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Ala Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 78
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K258D, mature numbering

<400> 78

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Asp Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 79
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K258E, mature numbering

<400> 79
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Glu Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 80
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R277A, mature numbering

<400> 80
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Ala Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 81
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R277D, mature numbering

<400> 81
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Asp Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 82
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R277E, mature numbering

<400> 82
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Glu Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 83
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R283A, mature numbering

<400> 83

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Ala Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 84
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R283D, mature numbering

<400> 84

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
```

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Asp Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 85
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R283E, mature numbering

<400> 85

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Glu Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 86
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K309A, mature numbering

<400> 86

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
```

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Ala Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 87
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K309D, mature numbering

<400> 87

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Asp Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 88
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K309E, mature numbering

<400> 88

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Glu Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 89
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K317A, mature numbering

<400> 89
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Ala Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 90
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K317D, mature numbering

<400> 90
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Asp Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 91
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K317E, mature numbering

<400> 91
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Glu Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 92
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K321A, mature numbering

<400> 92
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Ala Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 93
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K321D, mature numbering

<400> 93

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
```

```
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Asp Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 94
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K321E, mature numbering

<400> 94

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
```

```
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Glu Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 95
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R352A, mature numbering

<400> 95

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
```

```
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Ala
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 96
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R352D, mature numbering

<400> 96

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
```

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Asp
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 97
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R352E, mature numbering

<400> 97

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Glu
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 98
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R441A, mature numbering

<400> 98

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Ala Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 99
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R441D, mature numbering

<400> 99

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
```

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Asp Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 100
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 R441E, mature numbering

<400> 100
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Glu Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 101
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K444A, mature numbering

<400> 101
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Ala Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 102
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K444D, mature numbering

<400> 102
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Asp Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 103
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K444E, mature numbering

<400> 103
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Glu Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 104
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K461A, mature numbering

<400> 104

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Ala Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 105
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K461D, mature numbering

<400> 105

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Asp Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 106
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K461E, mature numbering

<400> 106

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
```

```
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Glu Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 107
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K469A, mature numbering

<400> 107

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
```

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Ala Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 108
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K469D, mature numbering

<400> 108

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

```
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Asp Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 109
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K469E, mature numbering

<400> 109

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Glu Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 110
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K470A, mature numbering

<400> 110

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Ala Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 111
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K470D, mature numbering

<400> 111
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Asp Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 112
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K470E, mature numbering

<400> 112
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Glu Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480

Thr Lys

<210> 113
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86A, mature numbering

<400> 113
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Ala Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 114
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86C, mature numbering

<400> 114
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Cys Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 115
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86E, mature numbering

<400> 115
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Glu Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

```
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 116
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86F, mature numbering

<400> 116

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Phe Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
```

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 117
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86G, mature numbering

<400> 117

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Gly Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 118
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86H, mature numbering

<400> 118

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His His Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
```

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 119
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86I, mature numbering

<400> 119

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Ile Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 120
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86K, mature numbering

<400> 120

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Lys Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
```

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 121
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86L, mature numbering

<400> 121

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Leu Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 122
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86M, mature numbering

<400> 122

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Met Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 123
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86N, mature numbering

<400> 123
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asn Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 124
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86P, mature numbering

<400> 124
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Pro Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

```
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 125
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86Q, mature numbering

<400> 125

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Gln Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
```

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 126
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86R, mature numbering

<400> 126
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Arg Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 127
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86S, mature numbering

<400> 127

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Ser Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
```

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 128
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86T, mature numbering

<400> 128
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Thr Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 129
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86V, mature numbering

<400> 129

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Val Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
```

Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 130
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86W, mature numbering

<400> 130
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Trp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 131
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 D86Y, mature numbering

<400> 131

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Tyr Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 132
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179C, mature numbering

<400> 132

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Cys Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 133
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179F, mature numbering

<400> 133

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
```

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Phe Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 134
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 E179H, mature numbering

<400> 134
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe His Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 135
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179I, mature numbering

<400> 135
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Ile Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

```
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 136
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179K, mature numbering

<400> 136

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Lys Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
```

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 137
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179L, mature numbering

<400> 137
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Leu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 138
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179M, mature numbering

<400> 138

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Met Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 139
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179N, mature numbering

<400> 139

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Asn Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 140
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179P, mature numbering

<400> 140

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Pro Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
```

Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 141
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179Q, mature numbering

<400> 141
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175

```
Lys Phe Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 142
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179R, mature numbering

<400> 142

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

```
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Arg Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 143
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179W, mature numbering

<400> 143

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Trp Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 144
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E179Y, mature numbering

<400> 144

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Tyr Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 145
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219C, mature numbering

<400> 145
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Cys Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 146
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219D, mature numbering

<400> 146

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Asp Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 147
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219E, mature numbering

<400> 147
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Glu Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 148
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219F, mature numbering

<400> 148
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Phe Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 149
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219G, mature numbering

<400> 149
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gly Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 150
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219H, mature numbering

<400> 150
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala His Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 151
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219I, mature numbering

<400> 151
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ile Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 152
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219L, mature numbering

<400> 152

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
```

Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Leu Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 153
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219M, mature numbering

<400> 153
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Met Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 154
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219P, mature numbering

<400> 154

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
```

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Pro Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 155
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219S, mature numbering

<400> 155

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ser Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 156
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219T, mature numbering

<400> 156

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Thr Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 157
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219V, mature numbering

<400> 157
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Val Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 158
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219W, mature numbering

<400> 158
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Trp Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 159
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Y, mature numbering

<400> 159
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Tyr Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 160
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221C, mature numbering

<400> 160
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Cys Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 161
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221D, mature numbering

<400> 161

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Asp Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
```

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 162
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221E, mature numbering

<400> 162
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Glu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 163
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221F, mature numbering

<400> 163

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
```

```
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Phe Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 164
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221H, mature numbering

<400> 164

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
```

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu His Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 165
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221I, mature numbering

<400> 165

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Ile Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 166
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221K, mature numbering

<400> 166

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Lys Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 167
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221M, mature numbering

<400> 167

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
```

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Met Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 168
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 L221N, mature numbering

<400> 168
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Asn Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 169
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221P, mature numbering

<400> 169

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Pro Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
```

```
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 170
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221Q, mature numbering

<400> 170

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Gln Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
```

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 171
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221R, mature numbering

<400> 171
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Arg Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 172
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221S, mature numbering

<400> 172

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Ser Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 173
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221T, mature numbering

<400> 173

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Thr Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 174
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221W, mature numbering

<400> 174

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Trp Pro Val Tyr
    210                 215                 220
```

Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 175
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 L221Y, mature numbering

<400> 175
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Tyr Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 176
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262C, mature numbering

<400> 176

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

```
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Cys Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 177
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262D, mature numbering

<400> 177

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asp Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 178
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262E, mature numbering

<400> 178

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Glu Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 179
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262F, mature numbering

<400> 179
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Phe Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 180
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262G, mature numbering

<400> 180
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Gly Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480

Thr Lys

<210> 181
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262H, mature numbering

<400> 181

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr His Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
```

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 182
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262I, mature numbering

<400> 182
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ile Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 183
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262K, mature numbering

<400> 183
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Lys Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 184
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262L, mature numbering

<400> 184
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Leu Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr

275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 185
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262P, mature numbering

<400> 185
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Pro Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 186
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262Q, mature numbering

<400> 186
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

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            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Gln Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 187
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262R, mature numbering

<400> 187

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
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130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Arg Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 188
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262T, mature numbering

<400> 188
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

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                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Thr Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 189
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262W, mature numbering

<400> 189

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Trp Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 190
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262Y, mature numbering

<400> 190
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Tyr Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 191
<211> 482
<212> PRT

<213> Artificial Sequence

<220>
<223> human ADA2 H264C, mature numbering

<400> 191
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp Cys Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 192
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264D, mature numbering

<400> 192
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp Asp Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met

```
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 193
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264E, mature numbering

<400> 193

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp Glu Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
```

385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 194
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264F, mature numbering

<400> 194
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Phe Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg

340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 195
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264I, mature numbering

<400> 195
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Ile Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser

290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 196
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264K, mature numbering

<400> 196
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly

245 250 255
Ile Lys Ile Ile Tyr Ser Asp Lys Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 197
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264L, mature numbering

<400> 197
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu

195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Leu Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 198
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264M, mature numbering

<400> 198
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val

145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Met Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 199
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264P, mature numbering

<400> 199
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg

```
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp Pro Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 200
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264R, mature numbering

<400> 200

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
```

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Arg Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 201
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264S, mature numbering

<400> 201
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg

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 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp Ser Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 202
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264T, mature numbering

<400> 202

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp Thr Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 203
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264V, mature numbering

<400> 203
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp Val Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe

450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 204
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264W, mature numbering

<400> 204
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Trp Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 205
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 H264Y, mature numbering

<400> 205
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp Tyr Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 206
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266A, mature numbering

<400> 206
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ala Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 207
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266C, mature numbering

<400> 207
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Cys Lys Asp Val Ala Val Ile

```
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 208
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266D, mature numbering

<400> 208

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
```

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Asp Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 209
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266E, mature numbering

<400> 209
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser

```
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Glu Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 210
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266F, mature numbering

<400> 210

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
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        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Phe Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 211
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266G, mature numbering

<400> 211

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Gly Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 212
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266H, mature numbering

<400> 212
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg His Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 213
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266I, mature numbering

<400> 213
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ile Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 214

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266K, mature numbering

<400> 214

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Lys Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 215
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266L, mature numbering

<400> 215
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Leu Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly

420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 216
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266M, mature numbering

<400> 216
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Met Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln

370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 217
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266N, mature numbering

<400> 217
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Asn Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 218
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266P, mature numbering

<400> 218
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Pro Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr

275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 219
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266Q, mature numbering

<400> 219
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Gln Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 220
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266R, mature numbering

<400> 220
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Arg Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 221
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266T, mature numbering

<400> 221
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln

130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Thr Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 222
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266V, mature numbering

<400> 222
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

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                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Val Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 223
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266W, mature numbering

<400> 223

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Trp Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 224
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S266Y, mature numbering

<400> 224
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Tyr Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 225
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267A, mature numbering

<400> 225

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Ala Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
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Thr Lys

<210> 226
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267C, mature numbering

<400> 226
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Cys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 227
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267D, mature numbering

<400> 227
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Asp Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 228
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267E, mature numbering

<400> 228
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Glu Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 229
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267F, mature numbering

<400> 229
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Phe Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 230
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267G, mature numbering

<400> 230
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Gly Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 231
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267H, mature numbering

<400> 231
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190

Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser His Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 232
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267I, mature numbering

<400> 232
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140

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Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Ile Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 233
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267L, mature numbering

<400> 233

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
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Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Leu Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 234
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267M, mature numbering

<400> 234

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
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Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Met Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 235
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267N, mature numbering

<400> 235

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Asn Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 236
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267P, mature numbering

<400> 236
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Pro Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 237
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267Q, mature numbering

<400> 237
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Gln Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 238
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267R, mature numbering

<400> 238
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Arg Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 239
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267S, mature numbering

<400> 239
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Ser Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 240
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267T, mature numbering

<400> 240

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Thr Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
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Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 241
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267V, mature numbering

<400> 241
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Val Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 242
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267W, mature numbering

<400> 242

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
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Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Trp Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 243
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K267Y, mature numbering

<400> 243
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Tyr Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 244
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296A, mature numbering

<400> 244

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Ala Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 245
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296C, mature numbering

<400> 245

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Cys Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 246
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296D, mature numbering

<400> 246

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
```

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Asp Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 247
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 V296E, mature numbering

<400> 247
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Glu Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 248
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296F, mature numbering

<400> 248

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Phe Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
```

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 249
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296G, mature numbering

<400> 249
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Gly Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 250
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296H, mature numbering

<400> 250
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu His Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 251
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296I, mature numbering

<400> 251

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Ile Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 252
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296K, mature numbering

<400> 252

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
```

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Lys Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 253
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296L, mature numbering

<400> 253

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
```

```
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Leu Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 254
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296M, mature numbering

<400> 254

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
```

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Met Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 255
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296N, mature numbering

<400> 255

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Asn Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 256
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296P, mature numbering

<400> 256
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Pro Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 257
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296Q, mature numbering

<400> 257

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
```

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Gln Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 258
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296R, mature numbering

<400> 258
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Arg Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 259
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296S, mature numbering

<400> 259
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Ser Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480

Thr Lys

<210> 260
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296T, mature numbering

<400> 260

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Thr Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
```

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 261
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296W, mature numbering

<400> 261
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Trp Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 262
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V296Y, mature numbering

<400> 262
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Tyr Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

```
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 263
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K371E, mature numbering

<400> 263

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
```

Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 264
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K371D, mature numbering

<400> 264
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 265
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/R20E, mature numbering

<400> 265

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
```

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 266
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K371E/R20E, mature numbering

<400> 266

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 267
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K371D/R20E, mature numbering

<400> 267

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
```

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 268
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371E, mature numbering

<400> 268

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 269
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D, mature numbering

<400> 269

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 270
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R20E, mature numbering

<400> 270
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 271
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371E/R20E, mature numbering

<400> 271
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met

435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 272
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/R20E, mature numbering

<400> 272
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Glu Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 273
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N, mature numbering

<400> 273
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

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Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 274
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 I1insNAS, mature numbering

<400> 274

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Asn Ala Ser Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys
 1               5                  10                  15
Met Met Arg Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu
            20                  25                  30
Ala Asn Glu Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala
        35                  40                  45
Met Arg Thr Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys
    50                  55                  60
His Leu Ile Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro
65                  70                  75                  80
Lys Gly Ala Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp
                85                  90                  95
Trp Leu Val Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe
            100                 105                 110
Thr Pro Arg Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg
        115                 120                 125
Pro Ser Glu Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys
    130                 135                 140
Arg Val Gln Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe
145                 150                 155                 160
Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val
                165                 170                 175
Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile
            180                 185                 190
His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu
        195                 200                 205
Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu
    210                 215                 220
Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val
225                 230                 235                 240
Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu
                245                 250                 255
Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val
            260                 265                 270
Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys
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275 280 285
Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr
290 295 300
Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys
305 310 315 320
Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp
325 330 335
Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn
340 345 350
Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val
355 360 365
Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile
370 375 380
Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val
385 390 395 400
Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp
405 410 415
Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val
420 425 430
Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln
435 440 445
Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys
450 455 460
Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala
465 470 475 480
Asp Val Ala Thr Lys
485

<210> 275
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R20N/V22S, mature numbering

<400> 275
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Asn Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 276
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371N/D373S, mature numbering

<400> 276
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Asn Lys Ser Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 277
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K372N/I374S, mature numbering

<400> 277
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln

130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Asn Asp Ser Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 278
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 T403N/H405S, mature numbering

<400> 278
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

```
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Asn Gly Ser Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 279
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 G404N/P406S, mature numbering

<400> 279

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Asn His Ser Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 280
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)n, mature numbering,
where n = 2 to 20

<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
14, 15, 16, 17, 18, 19 or 20 times

<400> 280
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
100 105 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
115 120 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
130 135 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145 150 155 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
165 170 175
Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
180 185 190
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
195 200 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser
210 215 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu
225 230 235 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
245 250 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
260 265 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
275 280 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
290 295 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305 310 315 320
Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val
325 330 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
340 345 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
355 360 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
370 375 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385 390 395 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
405 410 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
420 425 430
Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 281
<211> 454

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)15, mature numbering

<400> 281

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Gly Gly Gly Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn
        115                 120                 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
    130                 135                 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145                 150                 155                 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
                165                 170                 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
            180                 185                 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
        195                 200                 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210                 215                 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
225                 230                 235                 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245                 250                 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260                 265                 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445
Ala Asp Val Ala Thr Lys
    450
```

<210> 282
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)10, mature numbering

<400> 282

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195                 200                 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210                 215                 220
Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225                 230                 235                 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245                 250                 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260                 265                 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275                 280                 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290                 295                 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305                 310                 315                 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325                 330                 335
Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340                 345                 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355                 360                 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370                 375                 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385                 390                 395                 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405                 410                 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
            420                 425                 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
        435                 440                 445
Lys
```

<210> 283
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)7, mature numbering

<400> 283
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Glu
            100   105   110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115   120   125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130   135   140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145   150   155   160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165   170   175
Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180   185   190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195   200   205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210   215   220
Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225   230   235   240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245   250   255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260   265   270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275   280   285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290   295   300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305   310   315   320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys
                325   330   335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340   345   350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355   360   365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370   375   380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385   390   395   400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405   410   415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420   425   430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440   445

<210> 284
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)5, mature numbering

<400> 284
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Glu Phe Asp
            100   105   110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115   120   125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130   135   140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145   150   155   160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165   170   175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180   185   190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195   200   205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
    210   215   220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225   230   235   240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245   250   255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260   265   270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275   280   285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290   295   300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305   310   315   320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325   330   335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340   345   350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355   360   365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370   375   380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385   390   395   400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405   410   415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420   425   430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440

<210> 285
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(Gly)3, mature numbering

<400> 285
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Glu Phe Asp Asp Ser
            100                 105                 110
Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr
        115                 120                 125
Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr
    130                 135                 140
Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe
145                 150                 155                 160
Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile
                165                 170                 175
Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp
            180                 185                 190
Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val
        195                 200                 205
Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His
    210                 215                 220
Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met
225                 230                 235                 240
Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val
                245                 250                 255
Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu
            260                 265                 270
Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala
        275                 280                 285
Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp
    290                 295                 300
Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser
305                 310                 315                 320
Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile
                325                 330                 335
Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu
            340                 345                 350
Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val
        355                 360                 365
Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr
    370                 375                 380
Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu
385                 390                 395                 400
Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu
                405                 410                 415
Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp
            420                 425                 430
Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
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<210> 286
<211> 511
<212> PRT
<213> Pan troglodytes

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI XP_003317127.1
<309> 2012-10-05

<400> 286
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Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Val Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Ser Arg Ile Gly His
    370                 375                 380
```

Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385 390 395 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
405 410 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
420 425 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
435 440 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
450 455 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465 470 475 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
485 490 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
500 505 510

<210> 287
<211> 511
<212> PRT
<213> Gorilla gorilla

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI XP_004063024.1
<309> 2012-12-03

<400> 287
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Arg Phe Leu Leu
1 5 10 15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
20 25 30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
35 40 45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
50 55 60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65 70 75 80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
85 90 95
Gln Val Phe Asn Val Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
100 105 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
115 120 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
130 135 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser
145 150 155 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Gln Val Gln Asn Val Thr
165 170 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
180 185 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
195 200 205
Asn Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
210 215 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225 230 235 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
245 250 255

```
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510


<210> 288
<211> 511
<212> PRT
<213> Pan paniscus

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI XP_003828345.1
<309> 2014-09-02

<400> 288
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Ser Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
```

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    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Val Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Ala Ser Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Glu
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510


<210> 289
<211> 511
<212> PRT
<213> Pongo abelii

<220>
<223> ADA2 (CECR1)


<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI NP_001125360.1
<309> 2014-09-28

<400> 289
Met Leu Val Asp Gly Pro Ser Glu Trp Pro Ala Leu Arg Phe Leu Leu
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 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met
    50                  55                  60
Met Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Lys Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Gln Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly Arg Glu Asp Thr Gly His Ser Leu Gln Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Gly Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Ala Tyr Ser Trp Lys
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Ile Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Ala Leu Leu Glu Ile Glu Lys Asn Thr Phe Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510
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<210> 290
<211> 504
<212> PRT

<213> Nomascus leucogenys

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<220>
<221> UNSURE
<222> (230)...(230)
<223> Xaa = unknown

<300>
<308> NCBI: XP_004088517.1
<309> 2013-02-15

<400> 290

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Met Leu Val Asp Gly Pro Ser Glu Trp Pro Ala Leu Arg Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Ser Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Thr Glu Met Lys Glu Ala Met Lys Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Lys Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Xaa Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
225                 230                 235                 240
Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
                245                 250                 255
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
            260                 265                 270
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser
        275                 280                 285
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Thr Ala Met Gly Leu
    290                 295                 300
Arg Ala Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
305                 310                 315                 320
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
                325                 330                 335
Pro Thr Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
            340                 345                 350
Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn Ile Leu Asp Ala Leu
        355                 360                 365
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
    370                 375                 380
Pro Ala Val Arg Ala Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val
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385 390 395 400
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
405 410 415
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
420 425 430
Ser Asp Asp Pro Ala Ile Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
435 440 445
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
450 455 460
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
465 470 475 480
Thr Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
485 490 495
Phe Ile Ala Asp Val Ala Thr Lys
500

<210> 291
<211> 509
<212> PRT
<213> Macaca fascicularis

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI XP_005568111.1
<309> 2013-09-19

<400> 291
Met Leu Val Asp Gly Pro Ser Glu Trp Pro Ala Leu Arg Phe Leu Leu
1 5 10 15
Leu Ala Val Ala Met Ser Phe Phe Arg Ser Ala Leu Ser Ile Asp Glu
20 25 30
Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly Pro Leu
35 40 45
Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met Thr Leu
50 55 60
Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile Phe Pro Pro
65 70 75 80
Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser Gln Val
85 90 95
Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His Leu His
100 105 110
Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val Thr Tyr
115 120 125
Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile Met Gln Phe
130 135 140
Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser Lys Trp
145 150 155 160
Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr Glu Phe
165 170 175
Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu
180 185 190
Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Gln Thr Ile
195 200 205
Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val Phe Arg Asp
210 215 220
Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr
225 230 235 240
Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu
245 250 255
His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln
260 265 270

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Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr
        275                 280                 285
Ser Asp Asp Arg Ser Lys Asp Val Thr Val Ile Ala Glu Ser Ile Arg
    290                 295                 300
Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala Gly Phe
305                 310                 315                 320
Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Tyr Tyr Lys
                325                 330                 335
Glu Ala Leu Met Ile Pro Ala Arg Asp Gly Gly Lys Leu Pro Tyr Phe
            340                 345                 350
Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn
        355                 360                 365
Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe
    370                 375                 380
Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp Glu Lys Asp
385                 390                 395                 400
Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val
                405                 410                 415
Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala Ile Gly His
            420                 425                 430
Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly
        435                 440                 445
Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly Gly Met Lys
    450                 455                 460
Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Arg Tyr
465                 470                 475                 480
Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu Ile Trp Lys
                485                 490                 495
Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505


<210> 292
<211> 509
<212> PRT
<213> Chlorocebus sabaeus

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI: XP_007972990.1
<309> 2014-05-14

<400> 292
Met Ser Ala Asp Gly Pro Ser Glu Trp Pro Ser Leu Arg Phe Leu Leu
 1                  5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Arg Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly Pro Leu
        35                  40                  45
Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met Arg Leu
    50                  55                  60
Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile Phe Pro Pro
65                  70                  75                  80
Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser Gln Val
                85                  90                  95
Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His Leu His
            100                 105                 110
Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val Thr Tyr
        115                 120                 125
Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile Met Gln Phe
    130                 135                 140
Lys Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser Lys Trp
```

```
145                 150                 155                 160
Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr Glu Phe
                165                 170                 175
Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu
            180                 185                 190
Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Arg Phe Gln Thr Ile
        195                 200                 205
Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val Phe Arg Asp
    210                 215                 220
Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr
225                 230                 235                 240
Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu
                245                 250                 255
His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln
            260                 265                 270
Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr
        275                 280                 285
Ser Asp Asp Arg Phe Lys Asp Val Thr Val Ile Ala Glu Ser Ile Arg
    290                 295                 300
Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala Gly Phe
305                 310                 315                 320
Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys
                325                 330                 335
Asp Ala Leu Met Ile Pro Ala Arg Asp Gly Val Lys Leu Pro Tyr Phe
            340                 345                 350
Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn
        355                 360                 365
Ile Leu Asp Ala Leu Met Leu Asn Thr Ser Arg Ile Gly His Gly Phe
    370                 375                 380
Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp Glu Lys Asp
385                 390                 395                 400
Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val
                405                 410                 415
Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala Ile Gly His
            420                 425                 430
Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly
        435                 440                 445
Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly Gly Met Lys
    450                 455                 460
Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Arg Tyr
465                 470                 475                 480
Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu Ile Trp Lys
                485                 490                 495
Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505


<210> 293
<211> 509
<212> PRT
<213> Macaca mulatta

<220>
<223> ADA2 (CECR1)


<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> GenBank: AFH32795.1
<309> 2012-04-30

<400> 293
Met Leu Val Asp Gly Pro Ser Glu Trp Pro Ala Leu Arg Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Arg Ser Ala Leu Ser Ile Asp Glu
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            20                  25                  30
Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly Pro Leu
        35                  40                  45
Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met Thr Leu
    50                  55                  60
Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile Phe Pro Pro
65                  70                  75                  80
Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser Gln Val
                85                  90                  95
Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His Leu His
            100                 105                 110
Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val Thr Tyr
        115                 120                 125
Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile Met Gln Phe
    130                 135                 140
Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser Lys Trp
145                 150                 155                 160
Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr Glu Phe
                165                 170                 175
Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu
            180                 185                 190
Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Gln Thr Ile
        195                 200                 205
Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val Phe Arg Asp
    210                 215                 220
Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr
225                 230                 235                 240
Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu
                245                 250                 255
His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln
            260                 265                 270
Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr
        275                 280                 285
Ser Asp Asp Arg Ser Lys Asp Val Thr Val Ile Ala Glu Ser Ile Arg
    290                 295                 300
Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala Gly Phe
305                 310                 315                 320
Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Tyr Tyr Lys
                325                 330                 335
Glu Ala Leu Met Ile Pro Ala Arg Asp Gly Gly Lys Leu Pro Tyr Phe
            340                 345                 350
Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn
        355                 360                 365
Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe
    370                 375                 380
Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp Glu Lys Asp
385                 390                 395                 400
Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val
                405                 410                 415
Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala Ile Gly His
            420                 425                 430
Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly
        435                 440                 445
Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly Gly Met Lys
    450                 455                 460
Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Arg Tyr
465                 470                 475                 480
Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu Ile Trp Lys
                485                 490                 495
Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505
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<210> 294
<211> 511
<212> PRT
<213> Callithrix jacchus

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> NCBI: XP_009004591.1
<309> 2014-09-02

<400> 294

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Met Leu Gly Asn Gly Pro Ser Gly Trp Ser Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Ala Ala Val Ser Phe Phe Gly Ser Ala Leu Ser Met Asp Glu
            20                  25                  30
Thr Arg Glu His Leu Leu Thr Lys Glu Lys Met Met Gln Leu Gly Gly
        35                  40                  45
Gln Leu Val Leu Asn Ile Lys Glu Glu Arg Ala Asn Glu Lys Leu Met
    50                  55                  60
Thr Leu Lys Val Thr Glu Met Lys Glu Ala Met Lys Thr Leu Leu Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Arg Ala Lys His Leu Ile Asp Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Thr Lys Gly Ile Val
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Glu Cys Pro
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg Val Gln Asn Val Thr
                165                 170                 175
Asp Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asp Gln Asn Ala Val Trp Ser Lys Phe Lys
        195                 200                 205
Thr Ile Phe Ser Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Gln Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu Gln His Asp Leu Gln Trp Ser Val Lys Gly Tyr Gln Glu Val
            260                 265                 270
Ala Glu Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Thr Val Ile Ala Gly Ser
    290                 295                 300
Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly Arg Glu Asp Thr Gly His Ser Leu His Tyr
                325                 330                 335
His Asn Arg Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Asn Lys His Pro Ala Leu Arg Ala Tyr Ser Arg Lys
385                 390                 395                 400
Lys Asp Val Pro Val Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Ala Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Ile Phe Gly Ala
```

```
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Ile Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Ser Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Ala Val
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala His Val Ala Thr Asp
            500                 505                 510


<210> 295
<211> 510
<212> PRT
<213> Xenopus laevis

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(19)

<300>
<308> NCBI: NP_001090531.1
<309> 2014-05-14

<400> 295
Met Ala Cys Val Ser His Trp Leu Leu Leu Leu Ser Leu Ala Ser Ala
 1               5                  10                  15
Thr Leu Ser Arg Pro Leu Trp Ser Glu Arg Asn Gly Leu Ile Glu Met
            20                  25                  30
Glu Asn Ser Ile Arg Leu Gly Gly Asn Ile Ile Leu Thr Pro Ser Glu
        35                  40                  45
Ala Thr Ala Asn Gln Lys Leu Met Thr Val Lys Gly Ala Glu Phe Lys
    50                  55                  60
Glu Ala Glu Ser Thr Gly Leu Phe Pro Pro Ser Met His Phe Phe Lys
65                  70                  75                  80
Ala Arg Pro Leu Ile Gln Gln Ser His Val Phe Ser Ile Leu Arg Gln
                85                  90                  95
Met Pro Lys Gly Gly Ala Leu His Leu His Asp Phe Ala Ile Leu Ser
            100                 105                 110
Val Asp Trp Leu Val Lys Asn Ala Ser Tyr Met Ala Asp Cys Tyr Met
        115                 120                 125
Cys Leu Thr Arg Asp Gly Gly Val Arg Phe Leu Phe Ala Lys Pro Ala
    130                 135                 140
Pro Val Gly Met Leu Pro Pro Gly Cys Ser Glu Trp Ile Leu Leu Glu
145                 150                 155                 160
Thr Tyr Arg Lys Lys Leu Gly Asp Val Thr Glu Phe Asp Lys Gly Leu
                165                 170                 175
Ile Arg Asn Leu Thr Leu Leu Thr Asp Ser Pro Glu Pro His Ile Pro
            180                 185                 190
Ser Gln Asp Glu Ile Trp Arg Arg Phe Glu Gly Ala Phe Ile Thr Ala
        195                 200                 205
Ser Gly Leu Ile Cys Tyr Ala Pro Val Phe Lys Glu Tyr Phe Tyr Glu
    210                 215                 220
Ser Leu Arg Glu Leu Tyr Glu Asp Asn Ile Gln Tyr Leu Glu Met Arg
225                 230                 235                 240
Ala Met Leu Pro Pro Val Tyr Glu Leu Asp Gly Thr Val His Asp Gln
                245                 250                 255
Phe Trp Ser Met Ala Ile Tyr Arg Asp Met Ala Asn Lys Phe Val Gly
            260                 265                 270
Ala His Pro Asp Phe Leu Gly Ala Lys Ile Ile Tyr Thr Val His Arg
        275                 280                 285
His Glu Asp Leu Ala Gln Val Thr Glu Ala Val His Leu Ala Met Lys
    290                 295                 300
Leu Met Glu Ala Phe Pro Glu Ile Met Ala Gly Phe Asp Leu Val Gly
305                 310                 315                 320
```

```
Gln Glu Asp Ala Gly His Ser Leu Tyr Gln Leu Ser Asp Ala Leu Asn
                325                 330                 335
Ile Pro Ser Lys Leu Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
            340                 345                 350
Glu Thr Asn Trp Gln Gly Lys Asp Val Asp Glu Asn Val Leu Asp Ala
        355                 360                 365
Leu Leu Leu Asn Thr Thr Arg Ile Gly His Gly Tyr Ala Leu Leu Lys
    370                 375                 380
His Pro Val Ala Arg Asn Leu Ser Leu Glu Leu Asn Val Pro Leu Glu
385                 390                 395                 400
Ile Cys Pro Ile Ser Asn Gln Val Leu Leu Leu Val Ser Asp Leu Arg
                405                 410                 415
Asn His Pro Ala Ala Val Leu Met Ala Glu Gly His Pro Leu Val Val
            420                 425                 430
Ser Ser Asp Asp Pro Ser Ile Phe Gly Ala Gln Gly Ile Ser Tyr Asp
        435                 440                 445
Phe Tyr Glu Met Phe Met Gly Ile Gly Gly Ala Lys Ala Asp Leu Arg
    450                 455                 460
Thr Leu Lys Lys Leu Ala Glu Asn Ser Ile Lys Tyr Ser Ala Leu Ser
465                 470                 475                 480
Lys Glu Gly Lys Glu Lys Leu Thr Glu Ile Trp Gln Lys Lys Trp Asp
                485                 490                 495
Lys Phe Ile Lys Asp Leu Ala Met Asn Trp Lys Lys Glu Leu
            500                 505                 510
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<210> 296
<211> 553
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform A)

<220>
<221> SIGNAL
<222> (1)...(30)

<300>
<308> GenBank: AAL40913.1
<309> 2001-12-13

<400> 296

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Met Ser Pro Val Ile Arg Arg Asn Leu Ile Ala Cys Leu Thr Leu Gly
 1               5                  10                  15
Leu Cys Val Cys Leu Ser Phe Gly Pro Gly Pro Val Glu Ser Arg Thr
            20                  25                  30
Arg Pro Lys Asn Gln Val Asp Arg Lys Leu Leu Thr Ile Tyr Gly Ser
        35                  40                  45
Thr Pro His Val Glu Ala Leu Leu Gly Pro Gly Arg Pro Thr Pro Asp
    50                  55                  60
Thr Tyr Lys Thr Leu Arg Ser Ala Phe Phe Arg Tyr Glu Glu Ser Arg
65                  70                  75                  80
Ser Leu Gly His Asp Leu Asp Leu Asn Ser Arg Glu Ile Lys Ala Asn
                85                  90                  95
Glu Thr Ile Met Lys Ala Lys Leu Lys Glu Phe Asp Glu Gly Leu Val
            100                 105                 110
Thr Pro His Leu Phe Lys Pro Ser Gln His Ile Phe Asp Val Leu Asp
        115                 120                 125
Gly Ile Arg Asn Thr Asp Leu Phe Lys Leu Leu Lys Lys Met Pro Lys
    130                 135                 140
Gly Ala Val Leu His Ala His Asp Thr Ala Leu Cys Ser Thr Ala Ala
145                 150                 155                 160
Ile Ile Asn Leu Thr Tyr Tyr Glu His Leu Trp Ser Cys Gln Gln Asp
                165                 170                 175
Gly Asp Leu Ser Ala Ser Ala Leu Arg Phe Ser Lys Asp Lys Pro Gln
            180                 185                 190
```

```
Ala Leu Ser Asp Cys Asp Trp Ser Leu Leu Ser Asp Val Arg Ala Lys
        195                 200                 205
Tyr Gly Ala Asp Lys Val Asp Asp Tyr Leu Ala Glu Arg Leu Thr Leu
    210                 215                 220
Tyr Pro Thr Lys Lys Phe Glu Asp Asn Asn Ala Ala Trp Ser Thr Phe
225                 230                 235                 240
Met Ser Ile Phe Asn Leu Leu Asp Gly Leu Val Met Tyr Ala Pro Val
                245                 250                 255
Trp Ala Asp Tyr Tyr Tyr Lys Ala Leu Glu Glu Phe Tyr Glu Asp Gly
            260                 265                 270
Val Leu Tyr Leu Glu Phe Arg Ser Val Val Pro Thr Leu Tyr Asp Met
        275                 280                 285
Asp Gly Thr Glu Phe Thr Pro Met Asp Thr Val Arg Ile Tyr Val Glu
    290                 295                 300
Thr Leu Glu Lys Phe Lys Glu Ala His Pro Asp Phe Ile Gly Ser Arg
305                 310                 315                 320
Met Ile Tyr Ala Pro Ile Arg Tyr Thr Asn Ala Glu Gly Val Thr Gly
                325                 330                 335
Tyr Ile Gln Thr Leu Lys Gln Ile Lys Glu Lys Tyr Pro Glu Phe Val
            340                 345                 350
Ala Gly Phe Asp Leu Val Gly Gln Glu Glu Met Gly Arg Pro Leu Arg
        355                 360                 365
Asp Phe Val Asp Glu Leu Leu Ser Ile Pro Asp Asp Ile Asp Phe Tyr
    370                 375                 380
Phe His Ala Gly Glu Thr Asn Trp Phe Gly Ser Thr Val Asp Glu Asn
385                 390                 395                 400
Leu Ile Asp Ala Ile Leu Leu Gly Thr Lys Arg Ile Gly His Gly Phe
                405                 410                 415
Gly Leu Val Lys His Pro Val Val Leu Asp Met Leu Lys Lys Leu Asn
            420                 425                 430
Val Ala Ile Glu Val Asn Pro Ile Ser Asn Gln Val Leu Gln Leu Val
        435                 440                 445
Ser Asp Phe Arg Asn His Pro Cys Ser His Phe Phe Ala Asp Gly Tyr
    450                 455                 460
Pro Val Val Ile Ser Ser Asp Asp Pro Ser Phe Trp Lys Ala Thr Pro
465                 470                 475                 480
Leu Thr His Asp Phe Tyr Ile Ala Phe Leu Gly Ile Ala Ser Gln His
                485                 490                 495
Ser Asp Leu Arg Leu Leu Lys Lys Leu Ala Leu Asn Ser Ile Gln Tyr
            500                 505                 510
Ser Ser Leu Thr Gly Asp Ala Gln Phe Glu Ala Leu Glu Lys Trp Gln
        515                 520                 525
Val Lys Trp Asp Gln Phe Ile Ala Asp Val Asn Asp Arg Ser Ser Asn
    530                 535                 540
Arg Gly Ser Pro Ser Gln Arg Ile Asp
545                 550


<210> 297
<211> 520
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform B)


<300>
<308> GenBank: AAL40920.1
<309> 2001-12-13

<400> 297
Met Thr Ala Ile Lys His Val Ala Ile Ser Cys Arg Arg Ala Leu Thr
 1                5                  10                  15
Lys Cys Ala Lys Ile Gly His Thr Thr Val Ser Val Ser Arg Ser Leu
            20                  25                  30
Arg Lys Leu Ser Pro Thr Ala Phe Lys Thr Leu Arg Gln Ala Ile Ala
        35                  40                  45
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```
Lys Val Gly His Leu Asn Ile Met Gly Gln Lys Ile Arg Leu Asn Asp
    50                  55                  60
Arg Glu Leu Ala Ala Asn Lys Val Ile Met Ala Val Lys Lys Glu Glu
65                  70                  75                  80
Ile Ser Lys Gly Ile Leu Asp Pro Ser Gln Phe Thr Pro Gly Gln His
                85                  90                  95
Ile Phe Lys Thr Leu Ala Glu Val Gln Lys Ser Pro Ile Phe Asn Leu
            100                 105                 110
Ile Lys Gly Met Pro Lys Gly Gly Ala Leu His Ala His Asp Thr Ala
        115                 120                 125
Leu Cys Ser Thr Asp Tyr Leu Ile Ser Leu Thr Tyr Arg Lys Asn Leu
    130                 135                 140
Trp Ile Cys Thr Ala Glu Glu Gly Cys Lys Ala Ile Ala Phe Arg Phe
145                 150                 155                 160
Ser Lys Glu Glu Pro Lys Glu Lys Pro Val Lys Glu Ser Ile Trp Glu
                165                 170                 175
Pro Met Glu Glu Phe Arg Glu Arg Arg Gly Glu Glu Asn Val Thr Lys
            180                 185                 190
Tyr Leu Thr Arg Arg Phe Ser Met Tyr Pro Phe Ser Lys Phe Ile Ser
        195                 200                 205
Asn Asn Gln Ala Trp Ala His Phe Met Gly Ile Phe Ile Leu Leu Asp
    210                 215                 220
Gly Leu Leu Cys His Ala Pro Ile Trp Ala Glu Tyr Tyr Tyr Asn Ala
225                 230                 235                 240
Leu Lys Glu Phe Ala Glu Asp Gly Val Gln Tyr Leu Glu Leu Arg Ser
                245                 250                 255
Leu Leu Pro Pro Leu Tyr Cys Ile Asp Gly Asp Met Leu Thr Ile Arg
            260                 265                 270
Asp Thr Val Ala Ile Tyr Asn Ser Glu Leu Glu Arg Phe Arg Ala Asp
        275                 280                 285
His Pro Asp Phe Ile Gly Ser Lys Leu Ile Tyr Ala Pro Leu Arg Gly
    290                 295                 300
Val Glu Pro Ser Val Val Glu Gln Tyr Val Lys Thr Ala Val Glu Leu
305                 310                 315                 320
Asn Lys Glu Phe Pro Asn Phe Met Val Gly Phe Asp Leu Val Gly Gln
                325                 330                 335
Glu Glu Leu Gly Arg Pro Leu Ile Asp Phe Val Glu Pro Leu Leu Lys
            340                 345                 350
Met Pro Glu His Ile Asn Phe Tyr Phe His Ala Gly Glu Thr Asn Trp
        355                 360                 365
Phe Gly Ser Pro Ile Asp Glu Asn Leu Val Asp Ala Ile Leu Leu Gly
    370                 375                 380
Thr Lys Arg Ile Gly His Gly Tyr Ala Leu Thr Lys His Pro Met Met
385                 390                 395                 400
Met Arg Leu Ala Lys Leu Leu Gly Ile Ala Ile Glu Val Cys Pro Val
                405                 410                 415
Ser Asn Gln Val Leu Gln Leu Gly Val Asp Tyr Arg Asn His Pro Ala
            420                 425                 430
Ala Leu Leu Leu Ala Ala Asn Val Pro Ile Val Ile Ser Ser Asp Asp
        435                 440                 445
Pro Ser Phe Trp His Cys Ala Pro Leu Ser His Asp Phe Tyr Phe Ala
    450                 455                 460
Phe Leu Gly Ile Ala Pro Met Lys Ala Asp Leu Arg Phe Leu Lys Ser
465                 470                 475                 480
Leu Ala Ile Asn Ser Ile Arg Tyr Ser Ala Leu Val Gly Glu Glu Lys
                485                 490                 495
Arg Val Gly Tyr Arg Lys Trp Gln Glu Lys Trp Asp Lys Trp Ile Asp
            500                 505                 510
Asp Val Val Glu His Lys Tyr Cys
        515                 520
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<210> 298
<211> 506
<212> PRT
<213> Drosophila melanogaster

<220>

<223> ADA2 (ADGF isoform C)

<220>
<221> SIGNAL
<222> (1)...(19)

<300>
<308> GenBank: AAL40911.1
<309> 2001-12-13

<400> 298
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Met Arg Arg Leu Leu Met Phe Val Val Leu Leu Thr Ala Gln Leu Gln
 1               5                  10                  15
Ile Gln Ala Gln Thr Ala Leu Ser Tyr Glu Gln Ala Arg Gln Ala Val
            20                  25                  30
Leu Thr Ala Glu Glu Glu Leu Met Thr Gly Gly His Thr His Leu Asn
        35                  40                  45
Thr Glu Glu Glu Lys Val Asp Asp Ile Phe Met Glu Tyr Lys Leu Gly
    50                  55                  60
Glu Leu Ala Gln Gly Phe Arg Asn Ala Glu Gln Asn Ala Ala Ala Leu
65                  70                  75                  80
His Phe Phe Lys Ala Lys Pro Leu Ile Asp Arg Ser Ala Ile Phe Arg
                85                  90                  95
Phe Leu Gln Lys Met Pro Lys Gly Ser Val Leu His Val His Asn Thr
            100                 105                 110
Ala Ser Val Ser Ser Lys Trp Val Val Asp Asp Leu Ser Tyr Met Pro
        115                 120                 125
Gly Leu Leu Arg Cys Thr Thr Ala Thr Gly Gln Ser Ile Leu Ser Phe
    130                 135                 140
Arg Arg Thr Pro Lys Glu His Lys Cys Gln Ser Gln Tyr Val Leu Val
145                 150                 155                 160
Ser Asp Glu Arg Arg Asn Ser Leu Asp Arg Gln Val Tyr Asp Arg Asn
                165                 170                 175
Phe Glu Arg Leu Ile Asn Leu Tyr Thr Pro Val Pro Glu Leu Glu Tyr
            180                 185                 190
Pro Thr Ile Thr Arg Val Trp Asp Arg Phe Gln Gly Met Phe Asp Gly
        195                 200                 205
Leu Ser Asp Ala Leu Ile Tyr Leu Pro Ala Phe Arg Ala Tyr His Trp
    210                 215                 220
Gln Met Leu Glu Glu Leu Tyr Asn Asp Asn Val Met Tyr Thr Glu Ile
225                 230                 235                 240
Arg Thr Ser Phe Lys Thr Leu Tyr Asp Ala Ser Gly Arg Thr Phe Pro
                245                 250                 255
Arg Glu Arg Thr Ile His Glu Leu Tyr Ala Leu Asn Gln Lys Phe Met
            260                 265                 270
Lys Leu His Pro Asp Phe Leu Gly Phe Lys Val Ile Met Ala Val Tyr
        275                 280                 285
Arg Gly Tyr Glu Leu Asp His Leu Lys Asp Ile Val Glu Val Phe Lys
    290                 295                 300
Lys Leu His Gln Ala Leu Pro His Phe Leu Val Gly Phe Asp Leu Val
305                 310                 315                 320
Gly Gln Glu Asp Lys Gly Lys Pro Leu Tyr Ser Leu Leu Pro Val Leu
                325                 330                 335
Arg Asp Leu Pro Pro Thr Ala Arg Leu Phe Leu His Gly Gly Glu Thr
            340                 345                 350
Asn Trp Phe Gly Ala Ser Thr Asp Ile Asn Leu Leu Asp Ala Leu Leu
        355                 360                 365
Met Asn Thr Thr Arg Ile Gly His Gly Tyr Ala Leu Ala Lys His Pro
    370                 375                 380
Ile Leu Leu Asn Ala Val Lys Ser Arg Arg Ile Ala Val Glu Leu Ser
385                 390                 395                 400
Pro Ile Ser Asn Gln Val Leu His Leu Val Trp Asp Leu Arg Asn His
                405                 410                 415
Pro Gly Ser Gln Phe Phe Ala Leu Asp Val Pro Val Val Ile Cys Asn
            420                 425                 430
Asp Asp Pro Gly Phe Trp Asn Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
        435                 440                 445
```

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Tyr Ala Ile Met Ser Leu Ala Pro Asn Asn Ala Gly Leu Arg Leu Leu
    450                 455                 460
Lys Thr Leu Val Trp Asn Ser Val Arg Tyr Ser Thr Leu Thr Glu Glu
465                 470                 475                 480
Glu Gln Thr Arg Ala Phe Lys Ile Leu Glu Leu Ser Trp Ser Arg Phe
                485                 490                 495
Ile Asp Asp Val Leu Glu Gly Ser Val Phe
            500                 505


<210> 299
<211> 502
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform D)


<220>
<221> SIGNAL
<222> (1)...(22)

<300>
<308> GenBank: AAL40912.1
<309> 2001-12-13

<400> 299
Met Ala Met Trp Phe Leu Gly Ala Leu Val Ala Thr Val Val Leu Leu
 1               5                  10                  15
Thr Gly Ser Val Gln Ala Thr Asp Leu Pro Tyr Glu Thr Leu Arg Glu
            20                  25                  30
Gln Ile Met Glu Ala Glu Arg Val Ala Ser Leu Gly Gly Asn Ile Trp
        35                  40                  45
Leu Ser Ser Asp Glu Glu Lys Ala Asn Ser Ile Leu Met Asn Ala Lys
    50                  55                  60
Arg Ala Glu Ile Ala Glu Gly Leu Lys Thr Pro Glu Lys Tyr Ala Pro
65                  70                  75                  80
Ala Met His Phe Phe Gln Gly Arg Gln Tyr Val Arg Gln Ser Glu Val
                85                  90                  95
Phe Arg Met Ile Gln Lys Ile Pro Lys Gly Ala Phe Leu His Gly His
            100                 105                 110
Asn Thr Gly Met Val Thr Ser Arg Trp Ile Ile Gln Asn Leu Thr Thr
        115                 120                 125
Thr Asn Asn Leu Tyr Thr Cys Arg Asn Val Asp Gly Leu Leu Val Phe
    130                 135                 140
Thr Tyr Asp Gln Ser Gly Cys His Ser Glu Val Gln Asn Val Cys Thr
145                 150                 155                 160
Glu Arg Ile Asn Ala Glu Asp Arg Gly Lys Tyr Glu Arg Gln Leu Glu
                165                 170                 175
Lys His Ile Asn Met His Gly Pro Arg Pro Glu Ala Leu Leu Pro Asn
            180                 185                 190
Arg Lys Lys Ile Trp Glu Arg Phe Glu Asn Ile Phe Thr Thr Val Asp
        195                 200                 205
Arg Leu Tyr Lys Tyr Arg Pro Thr Tyr Cys Ala Tyr His Lys Arg Met
    210                 215                 220
Leu Glu Glu Leu Cys Glu Asp Asn Ile Ile Tyr Ala Glu Ile Arg Ala
225                 230                 235                 240
Ser Leu Ser Pro Leu Tyr Asp Asp Asn Asn Arg Thr Leu Ser Thr Leu
                245                 250                 255
Glu Val Ala Asn Glu Leu Glu Arg Ile Val Glu Glu Phe Lys Ala Lys
            260                 265                 270
His His Asp Phe Ile Gly Val Lys Val Ile Tyr Ala Lys Arg Asn Arg
        275                 280                 285
Ala Ser Glu Glu Glu Met Leu Arg Arg Ile Thr Thr Phe Lys Gln Leu
    290                 295                 300
His His Ala Lys Pro Asn Phe Val Ile Gly Phe Asp Leu Ile Gly Gln
305                 310                 315                 320
```

Glu Asp Thr Gly Glu Pro Leu Asn Arg Tyr Ile Asn Gln Leu Ser Asp
325 330 335
Leu Pro Ser Thr Ala Asn Tyr Phe Phe His Ala Gly Glu Thr Asn Trp
340 345 350
Asn Gly Arg Thr Asp Trp Asn Met Met Asp Ala Ile Leu Leu Asn Thr
355 360 365
Lys Arg Ile Gly His Ala Phe Ala Leu Pro Lys His Pro Gln Leu Trp
370 375 380
Ser Thr Ile Lys Lys Arg Asn Ile Ala Ile Glu Val Asn Pro Ile Ser
385 390 395 400
Asn Gln Val Leu Gly Phe Val Trp Asp Leu Arg Asn His Pro Ala Ser
405 410 415
Phe Leu Ile Ala Glu Asn Phe Pro Ile Val Ile Ser Ser Asp Asp Pro
420 425 430
Gly Val Trp Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Tyr Ala Phe
435 440 445
Met Ala Leu Ala Pro Ala Asp Ala Asp Leu Arg Phe Leu Lys Gln Leu
450 455 460
Ala Leu Asn Ser Ile Lys Tyr Ala Val Leu Thr Ser Asp Glu Arg Arg
465 470 475 480
Lys Ile Asn Arg Val Phe Gln Arg Lys Trp Gln Glu Phe Ile Ala Asn
485 490 495
Val Leu Asn Pro Lys Phe
500

<210> 300
<211> 539
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform E)

<300>
<308> GenBank: AAL40910
<309> 2001-12-13

<400> 300
Met Thr Val Leu Leu Ser His Arg Met Leu Leu Ala Gly Trp Ala Arg
1 5 10 15
Arg Ala Thr Pro Thr Ala Ala Gln Trp Ile His His Asn Pro Glu Lys
20 25 30
Met Thr Leu Leu Glu Met Leu Gly Thr Thr Asn Leu Arg Lys Ser Thr
35 40 45
Pro Lys Asp Tyr Arg Ile Leu Arg Glu Ile Phe Asn Ser Phe Glu Arg
50 55 60
Tyr Ser Gly Val Gly Asn Asp Ile Gln Leu Thr Leu Pro Glu Arg Ala
65 70 75 80
Ala Asn Glu Leu Ile Met Cys Glu Lys Lys Arg Glu Tyr Glu Lys Gly
85 90 95
Ile Met Asp Pro Ser Lys Phe Ala Pro Gly His His Ile Phe Gln Val
100 105 110
Leu Thr Lys Val Lys Lys Ser Pro Leu Phe Gln Ile Leu Arg Arg Met
115 120 125
Pro Lys Gly Ala Ala Leu Lys Ala His Asp Thr Ser Met Cys Ser Ser
130 135 140
Arg Val Val Ile Glu Ile Thr Tyr Arg Asp Asn Leu Trp Val Cys Thr
145 150 155 160
Thr Gln Asn Gly Cys Arg Val Glu Glu Phe Arg Phe Ala Lys Asp Lys
165 170 175
Pro Lys Asp Val Ser Phe Glu Asn Gly Glu Trp Gln Pro Met Glu Lys
180 185 190
Leu Arg Glu Leu Arg Gly Glu Glu Asn Leu Arg Lys Tyr Leu Gln Met
195 200 205
Arg Phe Ser Met Tyr Pro Leu Ala Ser Phe Thr Thr Asn Ala His Ala
210 215 220

Trp Arg His Met Met Gly Ile Phe Gly Leu Leu Asp Gly Leu Leu Gln
225 230 235 240
Tyr Ala Pro Val Trp Gly Asp Tyr Tyr Tyr Asn Ala Leu Lys Glu Phe
245 250 255
Tyr Ala Asp Gly Val Gln Tyr Leu Glu Val Arg Ser Val Leu Pro Gln
260 265 270
Leu Tyr Ser Leu Asp Gly Ser Arg Met Pro Lys Arg Glu Thr Val Gln
275 280 285
Ile Tyr Lys Asp Thr Leu Glu Arg Phe Lys Lys Glu His Pro Gly Phe
290 295 300
Ile Asp Ser Lys Leu Ile Tyr Ala Pro Ile Arg His Val Gln Pro Glu
305 310 315 320
Leu Val Gly Glu Tyr Ile Lys Glu Cys Thr Glu Leu Asn Lys Glu Phe
325 330 335
Pro Ser Phe Val Val Gly Phe Asp Leu Val Gly Gln Glu Asp Val Gly
340 345 350
His Pro Leu Ser Asn Phe Ala Ala Glu Leu Leu Lys Leu Pro Asp His
355 360 365
Ile His Phe Tyr Phe His Ala Gly Gln Thr Asn Trp Tyr Gly Ser His
370 375 380
Val Asp Gln Asn Leu Leu Asp Ala Ile Val Leu Gly Thr Lys Arg Ile
385 390 395 400
Gly His Gly Tyr Thr Ile Thr Lys His Pro Val Leu Met Arg Leu Ala
405 410 415
Lys Tyr Leu Asn Ile Ala Leu Glu Val Cys Pro Val Ser Asn Gln Val
420 425 430
Leu Gln Leu Gly Ser Asp Tyr Arg Ser His Pro Ala Ala Thr Leu Ile
435 440 445
Ala Glu Asn Val Pro Met Val Ile Ala Ser Gly Ser Pro Gly Phe Trp
450 455 460
Arg Ala Ala Pro Leu Ser His Asp Phe Tyr Met Ala Phe Leu Gly Ile
465 470 475 480
Ala Pro Met Asn Ala Asp Leu Lys Phe Leu Lys Arg Thr Ala Lys Asn
485 490 495
Ser Ile Lys Tyr Ser Ser Leu Lys Asp Glu Ala Lys Ala Glu Ala Met
500 505 510
Glu Lys Trp Lys Lys Gln Trp Asp Lys Trp Val Glu Asn Ile Val Arg
515 520 525
Gln Arg Lys Lys Asp Ser Glu Thr Glu Lys Lys
530 535

<210> 301
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<212> PRT
<213> Bombyx mori

<220>
<223> ADA2 (ADGF)

<220>
<221> SIGNAL
<222> (1)...(16)

<300>
<308> NCBI: NP_001098698.1
<309> 2013-04-17

<400> 301
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1 5 10 15
Asp Pro Pro Asp Ile Asn Glu Tyr His Arg Arg Arg Asn Thr Leu Ser
20 25 30
Arg Asn Glu Leu Arg Leu Thr Val Gly Gly Asn Met Thr Leu Ser Asp
35 40 45
Lys Glu Ser Glu Val Asn Asn Cys Ile Met Gln Leu Lys Phe Gln Glu
50 55 60

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Ile Asp Tyr Ala Phe Asp His Pro Arg Tyr Tyr Asn Phe Ser Gln His
65                  70                  75                  80
Tyr Phe Lys Tyr Lys Asp Thr Met Arg Lys Arg Arg Leu Tyr Gln Ile
                85                  90                  95
Leu Lys Val Met Pro Lys Gly Ala Leu Leu His Val His Asp Met Ser
            100                 105                 110
Leu Leu Gly Pro Asp Tyr Leu Met Asn Ile Thr Tyr Met Gln Asp Leu
        115                 120                 125
Tyr Val Cys Leu Tyr Lys Glu Thr Val Gly Phe Arg Phe Ser Ser Lys
    130                 135                 140
Thr Pro Asn Ala Pro Cys Lys Gly Lys Trp Gln Asp Ile Ser Lys Val
145                 150                 155                 160
Arg Ser Ser Val Glu Asn Val Thr Lys Phe Asp Glu Glu Leu Arg Lys
                165                 170                 175
His Phe Thr Leu Val Val Asp Asp Pro Asp Thr Val Tyr Gly Cys Ile
            180                 185                 190
Thr Asp Thr Trp Thr Lys Phe Met Asp Tyr Phe Leu Thr Val Asp Pro
        195                 200                 205
Leu Leu Thr Tyr Arg Pro Val Trp Glu Lys Tyr Phe Tyr Asp Ala Leu
    210                 215                 220
Met Lys Phe Arg Glu Asp Asn Val Leu Tyr Val Glu Phe Arg Ser Val
225                 230                 235                 240
Leu Pro Ser Leu Tyr Glu Leu Asp Gly Thr Ala Phe Asp Pro Val Val
                245                 250                 255
Thr Ala Lys Ala Tyr Arg Lys Val Ile Arg Lys Phe Val Lys Asp Tyr
            260                 265                 270
Pro Asp Phe Ile Gly Ala Lys Leu Ile Tyr Ala Pro Ser Arg Arg Val
        275                 280                 285
Asn Arg Ser Val Leu Ser Thr Tyr Leu Gln Ile Ala Lys Asp Val Lys
    290                 295                 300
Asn Asp Met Pro Asp Ile Phe Ala Gly Phe Asp Leu Val Gly Gln Glu
305                 310                 315                 320
Asp Leu Gly Glu Pro Leu Ile Glu Phe Ala Pro Gln Leu Leu Glu Ala
                325                 330                 335
Ser Glu Ser Leu Asp Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Leu
            340                 345                 350
Gly Thr Leu Thr Asp Glu Asn Leu Met Asp Ala Ile Leu Leu Gly Ala
        355                 360                 365
Lys Arg Ile Gly His Ala Tyr Ala Leu Ala Lys His Pro Leu Leu Leu
    370                 375                 380
Glu Glu Val Ile Lys Asn Asp Ile Gly Leu Glu Ile Asn Ile Ile Ser
385                 390                 395                 400
Asn Ala Val Leu Ser Leu Val Arg Asp Val Arg Asn His Pro Leu Ser
                405                 410                 415
Thr Phe Leu Ser Lys Gly Leu Pro Val Val Ile Ser Ser Asp Asp Pro
            420                 425                 430
Gly Ala Trp Glu Ala Glu Pro Leu Thr Asp Asp Phe Tyr Val Ala Phe
        435                 440                 445
Val Gly Ala Ala Ser Arg Leu Ala Asp Leu Arg Leu Leu Lys Gln Leu
    450                 455                 460
Ala Leu Asn Ser Phe Thr Tyr Ser Ser Leu Glu Asp Arg Gln Lys Ile
465                 470                 475                 480
Glu Ala Leu Arg Arg Phe Lys Arg Asn Trp Asp Ser Phe Ile Asn Asn
                485                 490                 495
Phe Lys Cys Pro Leu
            500
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<210> 302
<211> 553
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<213> Sarcophaga perigrina

<220>
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<220>
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<222> (1)...(18)

<300>
<308> GenBank: BAA11812.1
<309> 2007-03-16

<400> 302
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Val Gln His Ala Pro His Ile Glu Pro Gln Ala Ser Val Ile Gly Gly
        35                  40                  45
Arg Pro Thr Pro Glu Ala Tyr Asn Ser Leu Arg Asp Ile Phe Phe Arg
    50                  55                  60
Tyr Glu Glu Ser Lys Thr Leu Gly Ala Asp Ile Thr Leu Thr Gln Lys
65                  70                  75                  80
Glu Leu Gln Ala Asn Gln Leu Ile Met Glu Ala Lys Thr Arg Glu Tyr
                85                  90                  95
Glu Glu Gly Leu Ala Thr Pro His Leu Phe Thr Pro Ser Gln His Leu
            100                 105                 110
Phe Glu Val Leu Asp Asp Ile Lys Gln Ser Pro Leu Phe Lys Tyr Ile
        115                 120                 125
Ser Ser Met Pro Lys Gly Ala Val Leu His Ala His Asp Thr Ala Leu
    130                 135                 140
Cys Ser Thr Asp Phe Leu Ile Arg Leu Thr Tyr Arg Asp Asn Leu Trp
145                 150                 155                 160
Val Cys Gln Gly Lys Gly Asp Lys Glu Val Ile Gly Met Arg Phe Ser
                165                 170                 175
Lys Thr Lys Pro Asp Val Ala Thr Gln Ala Asp Cys Thr Trp Glu Leu
            180                 185                 190
Leu Ser Lys Val Arg Glu Leu His Gly Ala Asp Lys Val Asp Thr Tyr
        195                 200                 205
Leu Arg Glu His Leu Thr Leu Tyr Pro Thr Val Lys Phe Leu Asp Asn
    210                 215                 220
Asn Glu Ala Trp Glu Gln Phe Gly Ser Ile Phe Ala Leu Leu Asp Gly
225                 230                 235                 240
Leu Leu Phe Tyr Ala Pro Ser Trp Ala Asp Tyr Tyr Tyr Asn Ala Leu
                245                 250                 255
Lys Glu Phe His Ala Asp Gly Val Gln Tyr Leu Glu Phe Arg Ser Thr
            260                 265                 270
Leu Pro Ile Leu Tyr Asp Leu Glu Gly Thr Ser Phe Thr Glu Leu Asp
        275                 280                 285
Thr Val Arg Ile Tyr Lys Glu Thr Leu Asp Lys Tyr Met Ala Glu His
    290                 295                 300
Ile Asp Phe Ile Gly Ser Lys Leu Ile Tyr Ala Pro Ile Arg Asn Thr
305                 310                 315                 320
Asp Lys Glu Gly Leu Asp Asn Tyr Ile Lys Val Cys Val Glu Ile Lys
                325                 330                 335
Glu Lys Tyr Pro Asp Phe Val Ala Gly Phe Asp Leu Val Gly Gln Glu
            340                 345                 350
Glu Lys Gly Arg Pro Leu Lys Asp Phe Ile Pro Gln Leu Leu Gly Met
        355                 360                 365
Pro Glu Asn Ile Asp Phe Tyr Phe His Ala Gly Glu Thr Asn Trp Phe
    370                 375                 380
Gly Ser Thr Val Asp Glu Asn Leu Ile Asp Ala Val Leu Leu Gly Thr
385                 390                 395                 400
Lys Arg Ile Gly His Gly Phe Ala Leu Val Lys His Pro Leu Val Leu
                405                 410                 415
Gln Met Leu Lys Glu Arg Asn Ile Ala Ile Glu Val Asn Pro Ile Ser
            420                 425                 430
Asn Gln Val Leu Gln Leu Val Ala Asp Tyr Arg Asn His Pro Cys Ala
        435                 440                 445
Tyr Phe Phe Ala Asp Asn Tyr Pro Val Val Ile Ser Ser Asp Asp Pro
    450                 455                 460
Ser Phe Trp Lys Ala Thr Pro Leu Ser His Asp Phe Tyr Ile Ala Phe
465                 470                 475                 480
Leu Gly Ile Ala Ser Ala His Ser Asp Met Arg Leu Leu Lys Lys Leu
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485 490 495
Ala Leu Asn Ser Ile Asn Tyr Ser Ser Leu Ser Pro Glu Gln Lys Arg
500 505 510
Val Ala Leu Ala Lys Trp Gln Ile Lys Trp Asp Asp Phe Ile Asp Glu
515 520 525
Val Leu Ser Gly Asn Tyr Asp Asn Asn Gly Ser Asn Asn Ala Ala Gln
530 535 540
His Arg Leu Asn Thr Asn Lys Ile Ile
545 550

<210> 303
<211> 32
<212> PRT
<213> Artificial Sequence

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<223> C-terminal peptide (CTP) of the beta Subunit of
Human Chorionic Gonadotropin

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Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser
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Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu
20 25 30

<210> 304
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal peptide (CTP) of the beta Subunit of
Human Chorionic Gonadotropin

<400> 304
Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
1 5 10 15
Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
20 25

<210> 305
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<212> PRT
<213> Homo sapiens

<220>
<223> human serum albumin

<220>
<221> SIGNAL
<222> (1)...(18)

<300>
<308> NCBI: NP_000468.1
<309> 2014-09-23

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Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
20 25 30
His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu

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        35                  40                  45
Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80
Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
            100                 105                 110
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125
His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
    130                 135                 140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145                 150                 155                 160
Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175
Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
            180                 185                 190
Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
        195                 200                 205
Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
    210                 215                 220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225                 230                 235                 240
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
                245                 250                 255
Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
            260                 265                 270
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
        275                 280                 285
Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
    290                 295                 300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305                 310                 315                 320
Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
                325                 330                 335
Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
            340                 345                 350
Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
        355                 360                 365
Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
    370                 375                 380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385                 390                 395                 400
Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
                405                 410                 415
Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
            420                 425                 430
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
        435                 440                 445
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
    450                 455                 460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465                 470                 475                 480
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
                485                 490                 495
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
            500                 505                 510
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
        515                 520                 525
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
    530                 535                 540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545                 550                 555                 560
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
                565                 570                 575
Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
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Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595 600 605
Leu

<210> 306
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Albumin Binding Consensus Sequence

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<222> (2)...(2)
<223> Xaa = Asp, Asn, Ser, Thr or Trp

<220>
<221> VARIANT
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<223> Xaa = Asn, Gln, His, Ile, Leu or Lys

<220>
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<222> (4)...(4)
<223> Xaa = Ala, Asp, Phe, Trp or Tyr

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Asp, Gly, Leu, Phe, Ser or Thr

<400> 306
Cys Xaa Xaa Xaa Xaa Cys
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<210> 307
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<212> PRT
<213> Artificial Sequence

<220>
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Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
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<210> 308
<211> 18
<212> PRT
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<220>
<223> albumin-binding peptide

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Arg Leu Ile Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu
1 5 10 15
Asp Asp

<210> 309
<211> 20
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<213> Artificial Sequence

<220>
<223> albumin-binding peptide

<400> 309
Gln Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
 1   5   10   15
Glu Asp Asp Phe
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<210> 310
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> albumin-binding peptide

<400> 310
Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
 1   5   10   15
Gly Asp Ser Val Lys
            20

<210> 311
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> albumin-binding peptide

<400> 311
Gly Glu Trp Trp Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
 1   5   10   15
Glu Glu Glu Asp
            20

<210> 312
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 312
Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
 1   5   10   15
Ser Ala Pro Ala
            20

<210> 313
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 313
Ala Ala Pro Ala Ser Pro Ala Pro Ala Ala Pro Ser Ala Pro Ala Pro
 1   5   10   15
Ala Ala Pro Ser
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<210> 314
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 314
Ala Pro Ser Ser Pro Ser Pro Ser Ala Pro Ser Ser Pro Ser Pro Ala
 1   5   10   15
Ser Pro Ser Ser
            20

<210> 315
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 315
Ala Pro Ser Ser Pro Ser Pro Ser Ala Pro Ser Ser Pro Ser Pro Ala
 1   5   10   15
Ser Pro Ser

<210> 316
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 316
Ser Ser Pro Ser Ala Pro Ser Pro Ser Ser Pro Ala Ser Pro Ser Pro
 1   5   10   15
Ser Ser Pro Ala
            20

<210> 317
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<212> PRT
<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 317
Ala Ala Ser Pro Ala Ala Pro Ser Ala Pro Pro Ala Ala Ala Ser Pro
 1   5   10   15
Ala Ala Pro Ser Ala Pro Pro Ala
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<210> 318
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PAS sequence

<400> 318
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Ser Ala Ala Ala
            20

<210> 319
<211> 2808
<212> DNA
<213> Homo sapiens

<220>
<223> transferrin (TF)

<300>
<308> NCBI: NM_001063
<309> 2014-05-25

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atcagtggga cgagtaagga agggggttg ggagaggggc gattgggcaa cccggctgca 180
caaacacggg aggtcaaaga ttgcgcccag cccgcccagg ccgggaatgg aataaaggga 240
cgcggggcgc cggaggctgc acagaagcga gtccgactgt gctcgctgct cagcgccgca 300
cccggaagat gaggctcgcc gtgggagccc tgctggtctg cgccgtcctg gggctgtgtc 360
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gccagagttt ccgcgaccat atgaaaagcg tcattccatc cgatggtccc agtgttgctt 480
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ctgtgacact ggatgcaggt ttggtgtatg atgcttacct ggctcccaat aacctgaagc 600
ctgtggtggc agagttctat gggtcaaaag aggatccaca gactttctat tatgctgttg 660
ctgtggtgaa gaaggatagt ggcttccaga tgaaccagct tcgaggcaag aagtcctgcc 720
acacgggtct aggcaggtcc gctgggtgga acatccccat aggcttactt tactgtgact 780
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gcgctttcag gtgtctggtt gagaagggag atgtggcctt tgtgaaacac cagactgtcc 1980
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gtgtgtgcca tggccacatc tcctgggtac agttcaagga gacatctttt ctaaaagggt 2760
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<210> 320
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<212> PRT
<213> Homo sapiens

<220>
<223> serotransferrin precursor

<220>
<221> SIGNAL
<222> (1)...(19)

<300>
<308> NCBI: NP_001054.1
<309> 2014-05-14

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His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
        35   40   45
Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
    50   55   60
Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
65   70   75   80
Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
                85   90   95
Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
            100   105   110
Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
        115   120   125
Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
    130   135   140
Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
145   150   155   160
Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
                165   170   175
Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
            180   185   190
Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
        195   200   205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
    210   215   220
Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
225   230   235   240
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
                245   250   255

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Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
            260                 265                 270
Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
        275                 280                 285
Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
    290                 295                 300
Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
305                 310                 315                 320
Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
                325                 330                 335
Glu Tyr Val Thr Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu
            340                 345                 350
Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
        355                 360                 365
His Glu Arg Leu Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys
    370                 375                 380
Ile Glu Cys Val Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile
385                 390                 395                 400
Met Asn Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr
                405                 410                 415
Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
            420                 425                 430
Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val
        435                 440                 445
Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
    450                 455                 460
Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn
465                 470                 475                 480
Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
                485                 490                 495
Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
            500                 505                 510
Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
        515                 520                 525
Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
    530                 535                 540
Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
545                 550                 555                 560
Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
                565                 570                 575
Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
            580                 585                 590
Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
        595                 600                 605
Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
    610                 615                 620
His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
625                 630                 635                 640
Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys
                645                 650                 655
Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu
            660                 665                 670
Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser
        675                 680                 685
Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
    690                 695


<210> 321
<211> 2298
<212> DNA
<213> Homo sapiens

<220>
<223> transferrin (TF)

<300>
<308> GenBank: M12530.1
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<309> 1995-01-14

<400> 321
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tcggagcatg aggccactaa gtgccagagt ttccgcgacc atatgaaaag cgtcattcca 180
tccgatggtc ccagtgttgc ttgtgtgaag aaagcctcct accttgattg catcagggcc 240
attgcggcaa acgaagcgga tgctgtgaca ctggatgcag gtttggtgta tgatgcttac 300
ttggctccca ataacctgaa gcctgtggtg gcagagttct atgggtcaaa agaggatcca 360
cagactttct attatgctgt tgctgtggtg aagaaggata gtggcttcca gatgaaccag 420
cttcgaggca agaagtcctg ccacacgggt ctaggcaggt ccgctgggtg gaacatcccc 480
ataggcttac tttactgtga cttacctgag ccacgtaaac ctcttgagaa agcagtggcc 540
aatttcttct cgggcagctg tgcccttgt gcggatggga cggacttccc ccagctgtgt 600
caactgtgtc cagggtgtgg ctgctccacc cttaaccaat acttcggcta ctcgggagcc 660
ttcaagtgtc tgaaggatgg tgctggggat gtggcctttg tcaagcactc gactatattt 720
gagaacttgg caaacaaggc tgacagggac cagtatgagc tgctttgcct agacaacacc 780
cggaagccgg tagatgaata caaggactgc cacttggccc aggtcccttc tcataccgtc 840
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gaacattttg gcaaagacaa atcaaaagaa ttccaactat tcagctctcc tcatgggaag 960
gacctgctgt ttaaggactc tgcccacggg tttttaaaag tccccccaag gatggatgcc 1020
aagatgtacc tgggctatga gtatgtcact gccatccgga atctacggga aggcacatgc 1080
ccagaagccc caacagatga atgcaagcct gtgaagtggt gtgcgctgag ccaccacgag 1140
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gagaccaccg aagactgcat cgccaagatc atgaatggag aagctgatgc catgagcttg 1260
gatggagggt ttgtctacat agcgggcaag tgtggtctgg tgcctgtctt ggcagaaaac 1320
tacaataaga gcgataattg tgaggataca ccagaggcag ggtattttgc tgtagcagtg 1380
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acggcagttg gcagaaccgc tggctggaac atccccatgg gcctgctcta caataagatc 1500
aaccactgca gatttgatga atttttcagt gaaggttgtg cccctgggtc taagaaagac 1560
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gagggatact acggctacac aggcgctttc aggtgtctgg ttgagaaggg agatgtggcc 1680
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gataaggaag cttgcgtcca caagatatta cgtcaacagc agcacctatt tggaagcaac 1920
gtaactgact gctcgggcaa cttttgtttg ttccggtcgg aaaccaagga ccttctgttc 1980
agagatgaca cagtatgttt ggccaaactt catgacagaa acacatatga aaaatactta 2040
ggagaagaat atgtcaaggc tgttggtaac ctgagaaaat gctccacctc atcactcctg 2100
gaagcctgca ctttccgtag accttaaaat ctcagaggta gggctgccac caaggtgaag 2160
atgggaacgc agatgatcca tgagtttgcc ctggtttcac tggcccaagt ggtttgtgct 2220
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ttattgattt tatatttc 2298

<210> 322
<211> 2299
<212> DNA
<213> Homo sapiens

<220>
<223> transferrin (TF)

<300>
<308> NCBI: XM_039845.1
<309> 2001-07-16

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gtcggagcat gaggccacta agtgccagag tttccgcgac catatgaaaa gcgtcattcc 180
atccgatggt cccagtgttg cttgtgtgaa gaaagcctcc taccttgatt gcatcagggc 240
cattgcggca aacgaagcgg atgctgtgac actggatgca ggtttggtgt atgatgctta 300
cctggctccc aataacctga agcctgtggt ggcagagttc tatgggtcaa aagaggatcc 360
acagactttc tattatgctg ttgctgtggt gaagaaggat agtggcttcc agatgaacca 420
gcttcgaggc aagaagtcct gccacacggg tctaggcagg tccgctgggt ggaacatccc 480
cataggctta ctttactgtg acttacctga gccacgtaaa cctcttgaga aagcagtggc 540
caatttcttc tcgggcagct gtgcccttg tgcggatggg acggacttcc cccagctgtg 600
tcaactgtgt ccagggtgtg gctgctccac ccttaaccaa tacttcggct actcgggagc 660
cttcaagtgt ctgaaggatg gtgctgggga tgtggccttt gtcaagcact cgactatatt 720

tgagaacttg gcaaacaagg ctgacaggga ccagtatgag ctgctttgcc tggacaacac 780
ccggaagccg gtagatgaat acaaggactg ccacttggcc caggtccctt ctcataccgt 840
cgtggcccga agtatgggcg gcaaggagga cttgatctgg gagcttctca accaggccca 900
ggaacatttt ggcaaagaca aatcaaaaga attccaacta ttcagctctc ctcatgggaa 960
ggacctgctg tttaaggact ctgcccacgg gtttttaaaa gtccccccca ggatggatgc 1020
caagatgtac ctgggctatg agtatgtcac tgccatccgg aatctacggg aaggcacatg 1080
cccagaagcc ccaacagatg aatgcaagcc tgtgaagtgg tgtgcgctga gccaccacga 1140
gaggctcaag tgtgatgagt ggagtgttaa cagtgtaggg aaaatagagt gtgtatcagc 1200
agagaccacc gaagactgca tcgccaagat catgaatgga gaagctgatg ccatgagctt 1260
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ggtgaagaaa tcagcttctg acctcacctg ggacaatctg aaaggcaaga agtcctgcca 1440
tacggcagtt ggcagaaccg ctggctggaa catccccatg ggcctgctct acaataagat 1500
caaccactgc agatttgatg aatttttcag tgaaggttgt gcccctgggt ctaagaaaga 1560
ctccagtctc tgtaagctgt gtatgggctc aggcctaaac ctctgtgaac ccaacaacaa 1620
agagggatac tacggctaca caggcgcttt caggtgtctg gttgagaagg gagatgtggc 1680
ctttgtgaaa caccagactg tcccacagaa cactggggga aaaaaccctg atccatgggc 1740
taagaatctg aatgaaaaag actatgagtt gctgtgcctt gatggtacca ggaaacctgt 1800
ggaggagtat gcgaactgcc acctggccag agccccgaat cacgctgtgg tcacacggaa 1860
agataaggaa gcttgcgtcc acaagatatt acgtcaacag cagcacctat ttggaagcaa 1920
cgtaactgac tgctcgggca acttttgttt gttccggtcg gaaaccaagg accttctgtt 1980
cagagatgac acagtatgtt tggccaaact tcatgacaga aacacatatg aaaaatactt 2040
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ggaagcctgc actttccgta gaccttaaaa tctcagaggt agggctgcca ccaaggtgaa 2160
gatgggaacg cagatgatcc atgagtttgc cctggtttca ctggcccaag tggtttgtgc 2220
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attattgatt ttatatttc 2299

<210> 323
<211> 2347
<212> DNA
<213> Homo sapiens

<220>
<223> transferrin (TF)

<220>
<221> unsure
<222> (44)...(44)
<223> n = unknown

<300>
<308> GenBank: S95936.1
<309> 2003-05-07

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ggggctgtgt ctggctgtcc ctgataaaac tgtgagatgg tgtgcagtgt cggagcatga 180
ggccactaag tgccagagtt tccgcgacca tatgaaaagc gtcattccat ccgatggtcc 240
cagtgttgct tgtgtgaaga aagcctccta ccttgattgc atcagggcca ttgcggcaaa 300
cgaagcggat gctgtgacac tggatgcagg tttggtgtat gatgcttacc tggctcccaa 360
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agggtgtggc tgctccaccc ttaaccaata cttcggctac tcaggagcct tcaagtgtct 720
gaaggatggt gctggggatg tggcctttgt caagcactcg actatatttg agaacttggc 780
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tatgggcggc aaggaggact tgatctggga gcttctcaac caggcccagg aacattttgg 960
caaagacaaa tcaaaagaat tccaactatt cagctctcct catgggaagg acctgctgtt 1020
taaggactct gcccacgggt ttttaaaagt ccccccccagg atggatgcca agatgtacct 1080
gggctatgag tatgtcactg ccatccggaa tctacgggaa ggcacatgcc cagaagcccc 1140
aacagatgaa tgcaagcctg tgaagtggtg tgcgctgagc caccacgaga ggctcaagtg 1200
tgatgagtgg agtgttaaca gtgtagggaa aatagagtgt gtatcagcag agaccaccga 1260
agactgcatc gccaagatca tgaatggaga agctgatgcc atgagcttgg atggagggtt 1320

tgtctacata gcgggcaagt gtggtctggt gcctgtcttg gcagaaaact acaataagag 1380
cgataattgt gaggatacac cagaggcagg gtattttgct gtagcagtgg tgaagaaatc 1440
agcttctgac ctcacctggg acaatctgaa aggcaagaag tcctgccata cggcagttgg 1500
cagaaccgct ggctggaaca tccccatggg cctgctctac aataagatca accactgcag 1560
atttgatgaa tttttcagtg aaggttgtgc ccctgggtct aagaaagact ccagtctctg 1620
taagctgtgt atgggctcag gcctaaacct gtgtgaaccc aacaacaaag agggatacta 1680
cggctacaca ggcgctttca ggtgtctggt tgagaaggga gatgtggcct ttgtgaaaca 1740
ccagactgtc ccacagaaca ctgggggaaa aaaccctgat ccatgggcta agaatctgaa 1800
tgaaaaagac tatgagttgc tgtgccttga tggtaccagg aaacctgtgg aggagtatgc 1860
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tttccgtaga ccttaaaatc tcagaggtag ggctgccacc aaggtgaaga tgggaacgca 2220
gatgatccat gagtttgccc tggtttcact ggcccaagtg gtttgtgcta accacgtctg 2280
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aaaaaaa 2347

<210> 324
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<223> transferrin (TF)

<300>
<308> GenBank: AAB22049.1
<309> 1993-05-07

<400> 324
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Cys Leu Ala Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu
            20   25   30
His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
        35   40   45
Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
    50   55   60
Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
65   70   75   80
Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
                85   90   95
Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
            100   105   110
Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
        115   120   125
Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
    130   135   140
Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
145   150   155   160
Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
                165   170   175
Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
            180   185   190
Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
        195   200   205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
    210   215   220
Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
225   230   235   240
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
                245   250   255
Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
            260   265   270
Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
        275   280   285

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Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
    290                 295                 300
Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
305                 310                 315                 320
Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
                325                 330                 335
Glu Tyr Val Thr Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu
            340                 345                 350
Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
        355                 360                 365
His Glu Arg Leu Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys
    370                 375                 380
Ile Glu Cys Val Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile
385                 390                 395                 400
Met Asn Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr
                405                 410                 415
Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
            420                 425                 430
Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val
        435                 440                 445
Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
    450                 455                 460
Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn
465                 470                 475                 480
Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
                485                 490                 495
Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
            500                 505                 510
Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
        515                 520                 525
Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
    530                 535                 540
Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
545                 550                 555                 560
Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
                565                 570                 575
Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
            580                 585                 590
Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
        595                 600                 605
Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
    610                 615                 620
His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
625                 630                 635                 640
Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys
                645                 650                 655
Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu
            660                 665                 670
Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser
        675                 680                 685
Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
    690                 695


<210> 325
<211> 698
<212> PRT
<213> Homo sapiens

<220>
<223> transferrin

<220>
<221> SIGNAL
<222> (1)...(19)

<300>
<308> GenBank: AAA61140.1
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<309> 1995-01-14

<400> 325
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            20                  25                  30
His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
        35                  40                  45
Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
    50                  55                  60
Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
65                  70                  75                  80
Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
                85                  90                  95
Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
            100                 105                 110
Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
        115                 120                 125
Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
    130                 135                 140
Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
145                 150                 155                 160
Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
                165                 170                 175
Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
            180                 185                 190
Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
        195                 200                 205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
    210                 215                 220
Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
225                 230                 235                 240
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
                245                 250                 255
Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
            260                 265                 270
Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
        275                 280                 285
Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
    290                 295                 300
Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
305                 310                 315                 320
Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
                325                 330                 335
Glu Tyr Val Thr Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu
            340                 345                 350
Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
        355                 360                 365
His Glu Arg Leu Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys
    370                 375                 380
Ile Glu Cys Val Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile
385                 390                 395                 400
Met Asn Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr
                405                 410                 415
Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
            420                 425                 430
Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val
        435                 440                 445
Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
    450                 455                 460
Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn
465                 470                 475                 480
Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
                485                 490                 495
Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
            500                 505                 510
Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
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        515                 520                 525
Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
    530                 535                 540
Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
545                 550                 555                 560
Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
                565                 570                 575
Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
            580                 585                 590
Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
        595                 600                 605
Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
    610                 615                 620
His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
625                 630                 635                 640
Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys
                645                 650                 655
Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu
            660                 665                 670
Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser
        675                 680                 685
Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
    690                 695


<210> 326
<211> 482
<212> PRT
<213> Pan troglodytes

<220>
<223> ADA2 (CECR1) mature form


<300>
<308> NCBI: XP_003317127.1
<309> 2012-10-05

<400> 326
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Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
```

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Val Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Ser Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 327
<211> 482
<212> PRT
<213> Gorilla gorilla

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI XP_004063024.1
<309> 2012-12-03

<400> 327
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Val Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Gln Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Asn Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 328
<211> 482
<212> PRT
<213> Pan paniscus

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI XP_003828345.1
<309> 2014-09-02

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<400> 328
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Val Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Ala Ser Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 329
<211> 482
<212> PRT
<213> Pongo abelii

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI NP_001125360.1
<309> 2014-09-28

<400> 329

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
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```
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Gln Ala Asn Glu
            20                  25                  30
Arg Leu Met Met Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Lys
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Gln Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly Arg Glu Asp Thr Gly His Ser
    290                 295                 300
Leu Gln Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Gly Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Ala Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Ile
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Ala Leu Leu Glu Ile Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 330
<211> 475
<212> PRT
<213> Nomascus leucogenys

<220>
<223> ADA2 (CECR1) mature form

<220>
<221> UNSURE
<222> (201)...(201)
<223> Xaa = unknown

<300>
<308> NCBI XP_004088517.1
<309> 2013-02-15

<400> 330
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Ser Thr Lys Glu Glu Gln Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Thr Glu Met Lys Glu Ala Met Lys Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Lys
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Xaa Asp Asn Val Leu Tyr Met Glu
        195   200   205
Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His
    210   215   220
Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe
225   230   235   240
Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp
                245   250   255
His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Thr Ala
            260   265   270
Met Gly Leu Arg Ala Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu
        275   280   285
Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala
    290   295   300
Leu Met Ile Pro Thr Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His
305   310   315   320
Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn Ile Leu
                325   330   335
Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu
            340   345   350
Ser Lys His Pro Ala Val Arg Ala Tyr Ser Trp Lys Lys Asp Ile Pro
        355   360   365
Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp
    370   375   380
Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met
385   390   395   400
Val Ile Ser Ser Asp Asp Pro Ala Ile Phe Gly Ala Lys Gly Leu Ser
                405   410   415
Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp
            420   425   430
Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr

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        435                 440                 445
Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg
    450                 455                 460
Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
465                 470                 475


<210> 331
<211> 480
<212> PRT
<213> Macaca fascicularis

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI XP_005568111.1
<309> 2013-09-19

<400> 331
Ile Asp Glu Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly
 1               5                  10                  15
Gly Pro Leu Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu
            20                  25                  30
Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile
        35                  40                  45
Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg
    50                  55                  60
Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu
65                  70                  75                  80
His Leu His Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn
                85                  90                  95
Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile
            100                 105                 110
Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys
        115                 120                 125
Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val
    130                 135                 140
Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln
145                 150                 155                 160
His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe
                165                 170                 175
Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val
            180                 185                 190
Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn
        195                 200                 205
Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu
    210                 215                 220
Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu
225                 230                 235                 240
Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys
                245                 250                 255
Ile Ile Tyr Ser Asp Asp Arg Ser Lys Asp Val Thr Val Ile Ala Glu
            260                 265                 270
Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val
        275                 280                 285
Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His
    290                 295                 300
Tyr Tyr Lys Glu Ala Leu Met Ile Pro Ala Arg Asp Gly Gly Lys Leu
305                 310                 315                 320
Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile
                325                 330                 335
Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly
            340                 345                 350
His Gly Phe Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp
        355                 360                 365
Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu
    370                 375                 380
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Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala
385                 390                 395                 400
Ile Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly
                405                 410                 415
Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly
            420                 425                 430
Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser
        435                 440                 445
Ile Arg Tyr Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu
    450                 455                 460
Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
465                 470                 475                 480


<210> 332
<211> 480
<212> PRT
<213> Chlorocebus sabaeus

<220>
<223> ADA2 (CECR1) mature form


<300>
<308> NCBI: XP_007972990.1
<309> 2014-05-14

<400> 332
Ile Asp Glu Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly
 1               5                  10                  15
Gly Pro Leu Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu
            20                  25                  30
Met Arg Leu Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile
        35                  40                  45
Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg
    50                  55                  60
Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu
65                  70                  75                  80
His Leu His Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn
                85                  90                  95
Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile
            100                 105                 110
Met Gln Phe Lys Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys
        115                 120                 125
Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val
    130                 135                 140
Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln
145                 150                 155                 160
His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Arg Phe
                165                 170                 175
Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val
            180                 185                 190
Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn
        195                 200                 205
Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu
    210                 215                 220
Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu
225                 230                 235                 240
Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys
                245                 250                 255
Ile Ile Tyr Ser Asp Asp Arg Phe Lys Asp Val Thr Val Ile Ala Glu
            260                 265                 270
Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val
        275                 280                 285
Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His
    290                 295                 300
Asp Tyr Lys Asp Ala Leu Met Ile Pro Ala Arg Asp Gly Val Lys Leu
305                 310                 315                 320
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Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile
325 330 335
Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Ser Arg Ile Gly
340 345 350
His Gly Phe Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp
355 360 365
Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu
370 375 380
Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala
385 390 395 400
Ile Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly
405 410 415
Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly
420 425 430
Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser
435 440 445
Ile Arg Tyr Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu
450 455 460
Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
465 470 475 480

<210> 333
<211> 480
<212> PRT
<213> Macaca mulatta

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> GenBank: AFH32795.1
<309> 2012-04-30

<400> 333
Ile Asp Glu Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly
1 5 10 15
Gly Pro Leu Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu
20 25 30
Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile
35 40 45
Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg
50 55 60
Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu
65 70 75 80
His Leu His Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn
85 90 95
Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile
100 105 110
Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys
115 120 125
Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val
130 135 140
Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln
145 150 155 160
His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe
165 170 175
Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val
180 185 190
Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn
195 200 205
Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu
210 215 220
Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu
225 230 235 240
Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys
245 250 255
Ile Ile Tyr Ser Asp Asp Arg Ser Lys Asp Val Thr Val Ile Ala Glu

```
            260                 265                 270
Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val
        275                 280                 285
Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His
    290                 295                 300
Tyr Tyr Lys Glu Ala Leu Met Ile Pro Ala Arg Asp Gly Gly Lys Leu
305                 310                 315                 320
Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile
                325                 330                 335
Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly
            340                 345                 350
His Gly Phe Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp
        355                 360                 365
Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu
    370                 375                 380
Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala
385                 390                 395                 400
Ile Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly
                405                 410                 415
Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly
            420                 425                 430
Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser
        435                 440                 445
Ile Arg Tyr Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu
    450                 455                 460
Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
465                 470                 475                 480


<210> 334
<211> 484
<212> PRT
<213> Callithrix jacchus

<220>
<223> ADA2 (CECR1) mature form


<300>
<308> NCBI: XP_009004591.1
<309> 2014-09-02

<400> 334
Leu Ser Met Asp Glu Thr Arg Glu His Leu Leu Thr Lys Glu Lys Met
 1               5                  10                  15
Met Gln Leu Gly Gly Gln Leu Val Leu Asn Ile Lys Glu Glu Arg Ala
            20                  25                  30
Asn Glu Lys Leu Met Thr Leu Lys Val Thr Glu Met Lys Glu Ala Met
        35                  40                  45
Lys Thr Leu Leu Phe Pro Pro Ser Met His Phe Phe Arg Ala Lys His
    50                  55                  60
Leu Ile Asp Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys
65                  70                  75                  80
Gly Ala Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp
                85                  90                  95
Leu Val Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr
            100                 105                 110
Thr Lys Gly Ile Val Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr
        115                 120                 125
Ser Glu Glu Cys Pro Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg
    130                 135                 140
Val Gln Asn Val Thr Asp Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
145                 150                 155                 160
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asp Gln Asn Ala Val
                165                 170                 175
Trp Ser Lys Phe Lys Thr Ile Phe Ser Thr Ile Ser Gly Leu Ile His
            180                 185                 190
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Gln Ser Met Gln Glu Phe
```

```
        195                 200                 205
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro
    210                 215                 220
Val Tyr Glu Leu Ser Gly Glu Gln His Asp Leu Gln Trp Ser Val Lys
225                 230                 235                 240
Gly Tyr Gln Glu Val Ala Glu Lys Phe Val Glu Thr His Pro Glu Phe
                245                 250                 255
Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Thr
            260                 265                 270
Val Ile Ala Gly Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe
        275                 280                 285
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly Arg Glu Asp Thr Gly
    290                 295                 300
His Ser Leu His Tyr His Asn Arg Ala Leu Met Ile Pro Ala Lys Asp
305                 310                 315                 320
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
                325                 330                 335
Gly Thr Ser Ile Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
            340                 345                 350
Thr Arg Ile Gly His Gly Phe Ala Leu Asn Lys His Pro Ala Leu Arg
        355                 360                 365
Ala Tyr Ser Arg Lys Lys Asp Val Pro Val Glu Val Cys Pro Ile Ser
    370                 375                 380
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Ala Ala
385                 390                 395                 400
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
                405                 410                 415
Ala Ile Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
            420                 425                 430
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
        435                 440                 445
Ala Ile Asn Ser Ile Lys Tyr Ser Ser Leu Leu Glu Thr Glu Lys Asn
    450                 455                 460
Thr Phe Met Ala Val Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala His
465                 470                 475                 480
Val Ala Thr Asp
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<210> 335
<211> 491
<212> PRT
<213> Xenopus laevis

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI: NP_001090531.1
<309> 2014-05-14

<400> 335

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Arg Pro Leu Trp Ser Glu Arg Asn Gly Leu Ile Glu Met Glu Asn Ser
 1               5                  10                  15
Ile Arg Leu Gly Gly Asn Ile Ile Leu Thr Pro Ser Glu Ala Thr Ala
            20                  25                  30
Asn Gln Lys Leu Met Thr Val Lys Gly Ala Glu Phe Lys Glu Ala Glu
        35                  40                  45
Ser Thr Gly Leu Phe Pro Pro Ser Met His Phe Phe Lys Ala Arg Pro
    50                  55                  60
Leu Ile Gln Gln Ser His Val Phe Ser Ile Leu Arg Gln Met Pro Lys
65                  70                  75                  80
Gly Gly Ala Leu His Leu His Asp Phe Ala Ile Leu Ser Val Asp Trp
                85                  90                  95
Leu Val Lys Asn Ala Ser Tyr Met Ala Asp Cys Tyr Met Cys Leu Thr
            100                 105                 110
Arg Asp Gly Gly Val Arg Phe Leu Phe Ala Lys Pro Ala Pro Val Gly
        115                 120                 125
```

```
Met Leu Pro Pro Gly Cys Ser Glu Trp Ile Leu Glu Thr Tyr Arg
    130                 135                 140
Lys Lys Leu Gly Asp Val Thr Glu Phe Asp Lys Gly Leu Ile Arg Asn
145                 150                 155                 160
Leu Thr Leu Leu Thr Asp Ser Pro Glu Pro His Ile Pro Ser Gln Asp
                165                 170                 175
Glu Ile Trp Arg Arg Phe Glu Gly Ala Phe Ile Thr Ala Ser Gly Leu
            180                 185                 190
Ile Cys Tyr Ala Pro Val Phe Lys Glu Tyr Phe Tyr Glu Ser Leu Arg
        195                 200                 205
Glu Leu Tyr Glu Asp Asn Ile Gln Tyr Leu Glu Met Arg Ala Met Leu
    210                 215                 220
Pro Pro Val Tyr Glu Leu Asp Gly Thr Val His Asp Gln Phe Trp Ser
225                 230                 235                 240
Met Ala Ile Tyr Arg Asp Met Ala Asn Lys Phe Val Gly Ala His Pro
                245                 250                 255
Asp Phe Leu Gly Ala Lys Ile Ile Tyr Thr Val His Arg His Glu Asp
            260                 265                 270
Leu Ala Gln Val Thr Glu Ala Val His Leu Ala Met Lys Leu Met Glu
        275                 280                 285
Ala Phe Pro Glu Ile Met Ala Gly Phe Asp Leu Val Gly Gln Glu Asp
    290                 295                 300
Ala Gly His Ser Leu Tyr Gln Leu Ser Asp Ala Leu Asn Ile Pro Ser
305                 310                 315                 320
Lys Leu Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asn
                325                 330                 335
Trp Gln Gly Lys Asp Val Asp Glu Asn Val Leu Asp Ala Leu Leu Leu
            340                 345                 350
Asn Thr Thr Arg Ile Gly His Gly Tyr Ala Leu Leu Lys His Pro Val
        355                 360                 365
Ala Arg Asn Leu Ser Leu Glu Leu Asn Val Pro Leu Glu Ile Cys Pro
    370                 375                 380
Ile Ser Asn Gln Val Leu Leu Leu Val Ser Asp Leu Arg Asn His Pro
385                 390                 395                 400
Ala Ala Val Leu Met Ala Glu Gly His Pro Leu Val Val Ser Ser Asp
                405                 410                 415
Asp Pro Ser Ile Phe Gly Ala Gln Gly Ile Ser Tyr Asp Phe Tyr Glu
            420                 425                 430
Met Phe Met Gly Ile Gly Gly Ala Lys Ala Asp Leu Arg Thr Leu Lys
        435                 440                 445
Lys Leu Ala Glu Asn Ser Ile Lys Tyr Ser Ala Leu Ser Lys Glu Gly
    450                 455                 460
Lys Glu Lys Leu Thr Glu Ile Trp Gln Lys Lys Trp Asp Lys Phe Ile
465                 470                 475                 480
Lys Asp Leu Ala Met Asn Trp Lys Lys Glu Leu
                485                 490


<210> 336
<211> 523
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform A) mature form


<300>
<308> GenBank: AAL40913.1
<309> 2001-12-13

<400> 336
Arg Thr Arg Pro Lys Asn Gln Val Asp Arg Lys Leu Leu Thr Ile Tyr
 1               5                  10                  15
Gly Ser Thr Pro His Val Glu Ala Leu Leu Gly Pro Gly Arg Pro Thr
            20                  25                  30
Pro Asp Thr Tyr Lys Thr Leu Arg Ser Ala Phe Phe Arg Tyr Glu Glu
        35                  40                  45
```

```
Ser Arg Ser Leu Gly His Asp Leu Asp Leu Asn Ser Arg Glu Ile Lys
    50                  55                  60
Ala Asn Glu Thr Ile Met Lys Ala Lys Leu Lys Glu Phe Asp Glu Gly
65                  70                  75                  80
Leu Val Thr Pro His Leu Phe Lys Pro Ser Gln His Ile Phe Asp Val
                85                  90                  95
Leu Asp Gly Ile Arg Asn Thr Asp Leu Phe Lys Leu Leu Lys Lys Met
            100                 105                 110
Pro Lys Gly Ala Val Leu His Ala His Asp Thr Ala Leu Cys Ser Thr
        115                 120                 125
Ala Ala Ile Ile Asn Leu Thr Tyr Tyr Glu His Leu Trp Ser Cys Gln
    130                 135                 140
Gln Asp Gly Asp Leu Ser Ala Ser Ala Leu Arg Phe Ser Lys Asp Lys
145                 150                 155                 160
Pro Gln Ala Leu Ser Asp Cys Asp Trp Ser Leu Leu Ser Asp Val Arg
                165                 170                 175
Ala Lys Tyr Gly Ala Asp Lys Val Asp Asp Tyr Leu Ala Glu Arg Leu
            180                 185                 190
Thr Leu Tyr Pro Thr Lys Lys Phe Glu Asp Asn Asn Ala Ala Trp Ser
        195                 200                 205
Thr Phe Met Ser Ile Phe Asn Leu Leu Asp Gly Leu Val Met Tyr Ala
    210                 215                 220
Pro Val Trp Ala Asp Tyr Tyr Tyr Lys Ala Leu Glu Glu Phe Tyr Glu
225                 230                 235                 240
Asp Gly Val Leu Tyr Leu Glu Phe Arg Ser Val Val Pro Thr Leu Tyr
                245                 250                 255
Asp Met Asp Gly Thr Glu Phe Thr Pro Met Asp Thr Val Arg Ile Tyr
            260                 265                 270
Val Glu Thr Leu Glu Lys Phe Lys Glu Ala His Pro Asp Phe Ile Gly
        275                 280                 285
Ser Arg Met Ile Tyr Ala Pro Ile Arg Tyr Thr Asn Ala Glu Gly Val
    290                 295                 300
Thr Gly Tyr Ile Gln Thr Leu Lys Gln Ile Lys Glu Lys Tyr Pro Glu
305                 310                 315                 320
Phe Val Ala Gly Phe Asp Leu Val Gly Gln Glu Glu Met Gly Arg Pro
                325                 330                 335
Leu Arg Asp Phe Val Asp Glu Leu Leu Ser Ile Pro Asp Asp Ile Asp
            340                 345                 350
Phe Tyr Phe His Ala Gly Glu Thr Asn Trp Phe Gly Ser Thr Val Asp
        355                 360                 365
Glu Asn Leu Ile Asp Ala Ile Leu Leu Gly Thr Lys Arg Ile Gly His
    370                 375                 380
Gly Phe Gly Leu Val Lys His Pro Val Val Leu Asp Met Leu Lys Lys
385                 390                 395                 400
Leu Asn Val Ala Ile Glu Val Asn Pro Ile Ser Asn Gln Val Leu Gln
                405                 410                 415
Leu Val Ser Asp Phe Arg Asn His Pro Cys Ser His Phe Phe Ala Asp
            420                 425                 430
Gly Tyr Pro Val Val Ile Ser Ser Asp Asp Pro Ser Phe Trp Lys Ala
        435                 440                 445
Thr Pro Leu Thr His Asp Phe Tyr Ile Ala Phe Leu Gly Ile Ala Ser
    450                 455                 460
Gln His Ser Asp Leu Arg Leu Leu Lys Lys Leu Ala Leu Asn Ser Ile
465                 470                 475                 480
Gln Tyr Ser Ser Leu Thr Gly Asp Ala Gln Phe Glu Ala Leu Glu Lys
                485                 490                 495
Trp Gln Val Lys Trp Asp Gln Phe Ile Ala Asp Val Asn Asp Arg Ser
            500                 505                 510
Ser Asn Arg Gly Ser Pro Ser Gln Arg Ile Asp
        515                 520
```

<210> 337
<211> 544
<212> PRT
<213> Macaca mulatta

<220>

<223> ADA2 (CECR1)

<300>
<308> GenBank: EHH20002.1
<309> 2011-11-04

<400> 337
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Met Leu Val Asp Gly Pro Ser Glu Trp Pro Ala Leu Arg Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Arg Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly Pro Leu
        35                  40                  45
Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu Met Thr Leu
    50                  55                  60
Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile Phe Pro Pro
65                  70                  75                  80
Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser Gln Val
                85                  90                  95
Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His Leu His
            100                 105                 110
Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val Thr Tyr
        115                 120                 125
Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile Met Gln Phe
    130                 135                 140
Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys Ser Lys Trp
145                 150                 155                 160
Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr Glu Phe
                165                 170                 175
Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu
            180                 185                 190
Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Gln Thr Ile
        195                 200                 205
Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val Phe Arg Asp
    210                 215                 220
Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr
225                 230                 235                 240
Met Glu Ile Arg Ala Arg Leu Leu Pro Leu Ser Pro Leu Cys Ser His
                245                 250                 255
Cys Val Pro Leu Leu Ser Leu Val Ala Leu Ala Ala Leu Gln Leu Leu
            260                 265                 270
His Leu Glu Leu Gly Lys Gln Cys Gly Gly Glu Gln Val Tyr Glu Leu
        275                 280                 285
Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu
    290                 295                 300
Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys
305                 310                 315                 320
Ile Ile Tyr Ser Asp Asp Arg Ser Lys Asp Val Thr Val Ile Ala Glu
                325                 330                 335
Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val
            340                 345                 350
Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His
        355                 360                 365
Tyr Tyr Lys Glu Ala Leu Met Ile Pro Ala Arg Asp Gly Gly Lys Leu
    370                 375                 380
Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile
385                 390                 395                 400
Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly
                405                 410                 415
His Gly Phe Ala Leu Ser Lys His Pro Ala Ala Arg Ala Tyr Ser Trp
            420                 425                 430
Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu
        435                 440                 445
Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Ala Leu Met Ala
    450                 455                 460
Ile Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly
465                 470                 475                 480
Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met Gly Ile Gly
```

485 490 495
Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser
500 505 510
Ile Arg Tyr Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Glu
515 520 525
Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
530 535 540

<210> 338
<211> 487
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform C) mature form

<300>
<308> GenBank: AAL40911.1
<309> 2001-12-13

<400> 338
Gln Thr Ala Leu Ser Tyr Glu Gln Ala Arg Gln Ala Val Leu Thr Ala
1 5 10 15
Glu Glu Glu Leu Met Thr Gly Gly His Thr His Leu Asn Thr Glu Glu
20 25 30
Glu Lys Val Asp Asp Ile Phe Met Glu Tyr Lys Leu Gly Glu Leu Ala
35 40 45
Gln Gly Phe Arg Asn Ala Glu Gln Asn Ala Ala Ala Leu His Phe Phe
50 55 60
Lys Ala Lys Pro Leu Ile Asp Arg Ser Ala Ile Phe Arg Phe Leu Gln
65 70 75 80
Lys Met Pro Lys Gly Ser Val Leu His Val His Asn Thr Ala Ser Val
85 90 95
Ser Ser Lys Trp Val Val Asp Asp Leu Ser Tyr Met Pro Gly Leu Leu
100 105 110
Arg Cys Thr Thr Ala Thr Gly Gln Ser Ile Leu Ser Phe Arg Arg Thr
115 120 125
Pro Lys Glu His Lys Cys Gln Ser Gln Tyr Val Leu Val Ser Asp Glu
130 135 140
Arg Arg Asn Ser Leu Asp Arg Gln Val Tyr Asp Arg Asn Phe Glu Arg
145 150 155 160
Leu Ile Asn Leu Tyr Thr Pro Val Pro Glu Leu Glu Tyr Pro Thr Ile
165 170 175
Thr Arg Val Trp Asp Arg Phe Gln Gly Met Phe Asp Gly Leu Ser Asp
180 185 190
Ala Leu Ile Tyr Leu Pro Ala Phe Arg Ala Tyr His Trp Gln Met Leu
195 200 205
Glu Glu Leu Tyr Asn Asp Asn Val Met Tyr Thr Glu Ile Arg Thr Ser
210 215 220
Phe Lys Thr Leu Tyr Asp Ala Ser Gly Arg Thr Phe Pro Arg Glu Arg
225 230 235 240
Thr Ile His Glu Leu Tyr Ala Leu Asn Gln Lys Phe Met Lys Leu His
245 250 255
Pro Asp Phe Leu Gly Phe Lys Val Ile Met Ala Val Tyr Arg Gly Tyr
260 265 270
Glu Leu Asp His Leu Lys Asp Ile Val Glu Val Phe Lys Lys Leu His
275 280 285
Gln Ala Leu Pro His Phe Leu Val Gly Phe Asp Leu Val Gly Gln Glu
290 295 300
Asp Lys Gly Lys Pro Leu Tyr Ser Leu Leu Pro Val Leu Arg Asp Leu
305 310 315 320
Pro Pro Thr Ala Arg Leu Phe Leu His Gly Gly Glu Thr Asn Trp Phe
325 330 335
Gly Ala Ser Thr Asp Ile Asn Leu Leu Asp Ala Leu Leu Met Asn Thr
340 345 350
Thr Arg Ile Gly His Gly Tyr Ala Leu Ala Lys His Pro Ile Leu Leu
355 360 365

```
Asn Ala Val Lys Ser Arg Arg Ile Ala Val Glu Leu Ser Pro Ile Ser
    370                 375                 380
Asn Gln Val Leu His Leu Val Trp Asp Leu Arg Asn His Pro Gly Ser
385                 390                 395                 400
Gln Phe Phe Ala Leu Asp Val Pro Val Val Ile Cys Asn Asp Asp Pro
                405                 410                 415
Gly Phe Trp Asn Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Tyr Ala Ile
            420                 425                 430
Met Ser Leu Ala Pro Asn Asn Ala Gly Leu Arg Leu Leu Lys Thr Leu
        435                 440                 445
Val Trp Asn Ser Val Arg Tyr Ser Thr Leu Thr Glu Glu Glu Gln Thr
    450                 455                 460
Arg Ala Phe Lys Ile Leu Glu Leu Ser Trp Ser Arg Phe Ile Asp Asp
465                 470                 475                 480
Val Leu Glu Gly Ser Val Phe
                485
```

<210> 339
<211> 480
<212> PRT
<213> Drosophila melanogaster

<220>
<223> ADA2 (ADGF isoform D) mature form

<300>
<308> GenBank: AAL40912.1
<309> 2001-12-13

<400> 339

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Thr Asp Leu Pro Tyr Glu Thr Leu Arg Glu Gln Ile Met Glu Ala Glu
 1               5                  10                  15
Arg Val Ala Ser Leu Gly Gly Asn Ile Trp Leu Ser Ser Asp Glu Glu
            20                  25                  30
Lys Ala Asn Ser Ile Leu Met Asn Ala Lys Arg Ala Glu Ile Ala Glu
        35                  40                  45
Gly Leu Lys Thr Pro Glu Lys Tyr Ala Pro Ala Met His Phe Phe Gln
    50                  55                  60
Gly Arg Gln Tyr Val Arg Gln Ser Glu Val Phe Arg Met Ile Gln Lys
65                  70                  75                  80
Ile Pro Lys Gly Ala Phe Leu His Gly His Asn Thr Gly Met Val Thr
                85                  90                  95
Ser Arg Trp Ile Ile Gln Asn Leu Thr Thr Thr Asn Asn Leu Tyr Thr
            100                 105                 110
Cys Arg Asn Val Asp Gly Leu Leu Val Phe Thr Tyr Asp Gln Ser Gly
        115                 120                 125
Cys His Ser Glu Val Gln Asn Val Cys Thr Glu Arg Ile Asn Ala Glu
    130                 135                 140
Asp Arg Gly Lys Tyr Glu Arg Gln Leu Glu Lys His Ile Asn Met His
145                 150                 155                 160
Gly Pro Arg Pro Glu Ala Leu Leu Pro Asn Arg Lys Lys Ile Trp Glu
                165                 170                 175
Arg Phe Glu Asn Ile Phe Thr Thr Val Asp Arg Leu Tyr Lys Tyr Arg
            180                 185                 190
Pro Thr Tyr Cys Ala Tyr His Lys Arg Met Leu Glu Glu Leu Cys Glu
        195                 200                 205
Asp Asn Ile Ile Tyr Ala Glu Ile Arg Ala Ser Leu Ser Pro Leu Tyr
    210                 215                 220
Asp Asp Asn Asn Arg Thr Leu Ser Thr Leu Glu Val Ala Asn Glu Leu
225                 230                 235                 240
Glu Arg Ile Val Glu Glu Phe Lys Ala Lys His His Asp Phe Ile Gly
                245                 250                 255
Val Lys Val Ile Tyr Ala Lys Arg Asn Arg Ala Ser Glu Glu Glu Met
            260                 265                 270
Leu Arg Arg Ile Thr Thr Phe Lys Gln Leu His His Ala Lys Pro Asn
        275                 280                 285
```

```
Phe Val Ile Gly Phe Asp Leu Ile Gly Gln Glu Asp Thr Gly Glu Pro
    290                 295                 300
Leu Asn Arg Tyr Ile Asn Gln Leu Ser Asp Leu Pro Ser Thr Ala Asn
305                 310                 315                 320
Tyr Phe Phe His Ala Gly Glu Thr Asn Trp Asn Gly Arg Thr Asp Trp
                325                 330                 335
Asn Met Met Asp Ala Ile Leu Leu Asn Thr Lys Arg Ile Gly His Ala
            340                 345                 350
Phe Ala Leu Pro Lys His Pro Gln Leu Trp Ser Thr Ile Lys Lys Arg
        355                 360                 365
Asn Ile Ala Ile Glu Val Asn Pro Ile Ser Asn Gln Val Leu Gly Phe
    370                 375                 380
Val Trp Asp Leu Arg Asn His Pro Ala Ser Phe Leu Ile Ala Glu Asn
385                 390                 395                 400
Phe Pro Ile Val Ile Ser Ser Asp Asp Pro Gly Val Trp Gly Ala Lys
                405                 410                 415
Gly Leu Ser Tyr Asp Phe Tyr Tyr Ala Phe Met Ala Leu Ala Pro Ala
            420                 425                 430
Asp Ala Asp Leu Arg Phe Leu Lys Gln Leu Ala Leu Asn Ser Ile Lys
        435                 440                 445
Tyr Ala Val Leu Thr Ser Asp Glu Arg Arg Lys Ile Asn Arg Val Phe
    450                 455                 460
Gln Arg Lys Trp Gln Glu Phe Ile Ala Asn Val Leu Asn Pro Lys Phe
465                 470                 475                 480


<210> 340
<211> 515
<212> PRT
<213> Macaca mulatta

<220>
<223> ADA2 (CECR1) mature form


<300>
<308> GenBank: EHH20002.1
<309> 2011-11-04

<400> 340
Ile Asp Glu Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly
 1               5                  10                  15
Gly Pro Leu Val Leu Thr Thr Lys Glu Glu Gln Ala Asn Glu Arg Leu
            20                  25                  30
Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Lys Thr Leu Ile
        35                  40                  45
Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg
    50                  55                  60
Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu
65                  70                  75                  80
His Leu His Asp Thr Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn
                85                  90                  95
Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Ser Lys Gly Ile
            100                 105                 110
Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Lys Cys
        115                 120                 125
Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val
    130                 135                 140
Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln
145                 150                 155                 160
His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe
                165                 170                 175
Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile Arg Tyr Ala Pro Val
            180                 185                 190
Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn
        195                 200                 205
Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Leu Ser Pro Leu
    210                 215                 220
```

Cys Ser His Cys Val Pro Leu Leu Ser Leu Val Ala Leu Ala Ala Leu
225 230 235 240
Gln Leu Leu His Leu Glu Leu Gly Lys Gln Cys Gly Gly Glu Gln Val
245 250 255
Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr
260 265 270
Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile
275 280 285
Gly Ile Lys Ile Ile Tyr Ser Asp Asp Arg Ser Lys Asp Val Thr Val
290 295 300
Ile Ala Glu Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro
305 310 315 320
Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His
325 330 335
Ser Leu His Tyr Tyr Lys Glu Ala Leu Met Ile Pro Ala Arg Asp Gly
340 345 350
Gly Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly
355 360 365
Thr Ser Ile Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr
370 375 380
Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Ala Arg Ala
385 390 395 400
Tyr Ser Trp Glu Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn
405 410 415
Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Ala
420 425 430
Leu Met Ala Ile Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala
435 440 445
Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Ala Phe Met
450 455 460
Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala
465 470 475 480
Met Asn Ser Ile Arg Tyr Ser Thr Leu Leu Glu Thr Glu Lys Asn Thr
485 490 495
Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val
500 505 510
Ala Thr Lys
515

<210> 341
<211> 485
<212> PRT
<213> Bombyx mori

<220>
<223> ADA2 (ADGF) mature form

<300>
<308> NCBI NP_001098698.1
<309> 2014-04-17

<400> 341
Asp Pro Pro Asp Ile Asn Glu Tyr His Arg Arg Arg Asn Thr Leu Ser
1 5 10 15
Arg Asn Glu Leu Arg Leu Thr Val Gly Gly Asn Met Thr Leu Ser Asp
20 25 30
Lys Glu Ser Glu Val Asn Asn Cys Ile Met Gln Leu Lys Phe Gln Glu
35 40 45
Ile Asp Tyr Ala Phe Asp His Pro Arg Tyr Tyr Asn Phe Ser Gln His
50 55 60
Tyr Phe Lys Tyr Lys Asp Thr Met Arg Lys Arg Arg Leu Tyr Gln Ile
65 70 75 80
Leu Lys Val Met Pro Lys Gly Ala Leu Leu His Val His Asp Met Ser
85 90 95
Leu Leu Gly Pro Asp Tyr Leu Met Asn Ile Thr Tyr Met Gln Asp Leu
100 105 110
Tyr Val Cys Leu Tyr Lys Glu Thr Val Gly Phe Arg Phe Ser Ser Lys

```
        115                 120                 125
Thr Pro Asn Ala Pro Cys Lys Gly Lys Trp Gln Asp Ile Ser Lys Val
    130                 135                 140
Arg Ser Ser Val Glu Asn Val Thr Lys Phe Asp Glu Glu Leu Arg Lys
145                 150                 155                 160
His Phe Thr Leu Val Val Asp Asp Pro Asp Thr Val Tyr Gly Cys Ile
                165                 170                 175
Thr Asp Thr Trp Thr Lys Phe Met Asp Tyr Phe Leu Thr Val Asp Pro
            180                 185                 190
Leu Leu Thr Tyr Arg Pro Val Trp Glu Lys Tyr Phe Tyr Asp Ala Leu
        195                 200                 205
Met Lys Phe Arg Glu Asp Asn Val Leu Tyr Val Glu Phe Arg Ser Val
    210                 215                 220
Leu Pro Ser Leu Tyr Glu Leu Asp Gly Thr Ala Phe Asp Pro Val Val
225                 230                 235                 240
Thr Ala Lys Ala Tyr Arg Lys Val Ile Arg Lys Phe Val Lys Asp Tyr
                245                 250                 255
Pro Asp Phe Ile Gly Ala Lys Leu Ile Tyr Ala Pro Ser Arg Arg Val
            260                 265                 270
Asn Arg Ser Val Leu Ser Thr Tyr Leu Gln Ile Ala Lys Asp Val Lys
        275                 280                 285
Asn Asp Met Pro Asp Ile Phe Ala Gly Phe Asp Leu Val Gly Gln Glu
    290                 295                 300
Asp Leu Gly Glu Pro Leu Ile Glu Phe Ala Pro Gln Leu Leu Glu Ala
305                 310                 315                 320
Ser Glu Ser Leu Asp Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Leu
                325                 330                 335
Gly Thr Leu Thr Asp Glu Asn Leu Met Asp Ala Ile Leu Leu Gly Ala
            340                 345                 350
Lys Arg Ile Gly His Ala Tyr Ala Leu Ala Lys His Pro Leu Leu Leu
        355                 360                 365
Glu Glu Val Ile Lys Asn Asp Ile Gly Leu Glu Ile Asn Ile Ile Ser
    370                 375                 380
Asn Ala Val Leu Ser Leu Val Arg Asp Val Arg Asn His Pro Leu Ser
385                 390                 395                 400
Thr Phe Leu Ser Lys Gly Leu Pro Val Val Ile Ser Ser Asp Asp Pro
                405                 410                 415
Gly Ala Trp Glu Ala Glu Pro Leu Thr Asp Asp Phe Tyr Val Ala Phe
            420                 425                 430
Val Gly Ala Ala Ser Arg Leu Ala Asp Leu Arg Leu Leu Lys Gln Leu
        435                 440                 445
Ala Leu Asn Ser Phe Thr Tyr Ser Ser Leu Glu Asp Arg Gln Lys Ile
    450                 455                 460
Glu Ala Leu Arg Arg Phe Lys Arg Asn Trp Asp Ser Phe Ile Asn Asn
465                 470                 475                 480
Phe Lys Cys Pro Leu
                485
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<210> 342
<211> 535
<212> PRT
<213> Sarcophaga perigrina

<220>
<223> ADA2 (IDGF) mature form

<300>
<308> GenBank: BAA11812.1
<309> 2007-03-16

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<400> 342
His Asn Glu Ala Arg Arg Ala Ser Leu Arg Ala Asn His Met Val Gln
 1               5                  10                  15
His Ala Pro His Ile Glu Pro Gln Ala Ser Val Ile Gly Gly Arg Pro
            20                  25                  30
Thr Pro Glu Ala Tyr Asn Ser Leu Arg Asp Ile Phe Phe Arg Tyr Glu
        35                  40                  45
```

```
Glu Ser Lys Thr Leu Gly Ala Asp Ile Thr Leu Thr Gln Lys Glu Leu
    50                  55                  60
Gln Ala Asn Gln Leu Ile Met Glu Ala Lys Thr Arg Glu Tyr Glu Glu
65                  70                  75                  80
Gly Leu Ala Thr Pro His Leu Phe Thr Pro Ser Gln His Leu Phe Glu
                85                  90                  95
Val Leu Asp Asp Ile Lys Gln Ser Pro Leu Phe Lys Tyr Ile Ser Ser
            100                 105                 110
Met Pro Lys Gly Ala Val Leu His Ala His Asp Thr Ala Leu Cys Ser
        115                 120                 125
Thr Asp Phe Leu Ile Arg Leu Thr Tyr Arg Asp Asn Leu Trp Val Cys
    130                 135                 140
Gln Gly Lys Gly Asp Lys Glu Val Ile Gly Met Arg Phe Ser Lys Thr
145                 150                 155                 160
Lys Pro Asp Val Ala Thr Gln Ala Asp Cys Thr Trp Glu Leu Leu Ser
                165                 170                 175
Lys Val Arg Glu Leu His Gly Ala Asp Lys Val Asp Thr Tyr Leu Arg
            180                 185                 190
Glu His Leu Thr Leu Tyr Pro Thr Val Lys Phe Leu Asp Asn Asn Glu
        195                 200                 205
Ala Trp Glu Gln Phe Gly Ser Ile Phe Ala Leu Leu Asp Gly Leu Leu
    210                 215                 220
Phe Tyr Ala Pro Ser Trp Ala Asp Tyr Tyr Tyr Asn Ala Leu Lys Glu
225                 230                 235                 240
Phe His Ala Asp Gly Val Gln Tyr Leu Glu Phe Arg Ser Thr Leu Pro
                245                 250                 255
Ile Leu Tyr Asp Leu Glu Gly Thr Ser Phe Thr Glu Leu Asp Thr Val
            260                 265                 270
Arg Ile Tyr Lys Glu Thr Leu Asp Lys Tyr Met Ala Glu His Ile Asp
        275                 280                 285
Phe Ile Gly Ser Lys Leu Ile Tyr Ala Pro Ile Arg Asn Thr Asp Lys
    290                 295                 300
Glu Gly Leu Asp Asn Tyr Ile Lys Val Cys Val Glu Ile Lys Glu Lys
305                 310                 315                 320
Tyr Pro Asp Phe Val Ala Gly Phe Asp Leu Val Gly Gln Glu Glu Lys
                325                 330                 335
Gly Arg Pro Leu Lys Asp Phe Ile Pro Gln Leu Leu Gly Met Pro Glu
            340                 345                 350
Asn Ile Asp Phe Tyr Phe His Ala Gly Glu Thr Asn Trp Phe Gly Ser
        355                 360                 365
Thr Val Asp Glu Asn Leu Ile Asp Ala Val Leu Leu Gly Thr Lys Arg
    370                 375                 380
Ile Gly His Gly Phe Ala Leu Val Lys His Pro Leu Val Leu Gln Met
385                 390                 395                 400
Leu Lys Glu Arg Asn Ile Ala Ile Glu Val Asn Pro Ile Ser Asn Gln
                405                 410                 415
Val Leu Gln Leu Val Ala Asp Tyr Arg Asn His Pro Cys Ala Tyr Phe
            420                 425                 430
Phe Ala Asp Asn Tyr Pro Val Val Ile Ser Ser Asp Asp Pro Ser Phe
        435                 440                 445
Trp Lys Ala Thr Pro Leu Ser His Asp Phe Tyr Ile Ala Phe Leu Gly
    450                 455                 460
Ile Ala Ser Ala His Ser Asp Met Arg Leu Leu Lys Lys Leu Ala Leu
465                 470                 475                 480
Asn Ser Ile Asn Tyr Ser Ser Leu Ser Pro Glu Gln Lys Arg Val Ala
                485                 490                 495
Leu Ala Lys Trp Gln Ile Lys Trp Asp Asp Phe Ile Asp Glu Val Leu
            500                 505                 510
Ser Gly Asn Tyr Asp Asn Asn Gly Ser Asn Asn Ala Ala Gln His Arg
        515                 520                 525
Leu Asn Thr Asn Lys Ile Ile
    530                 535
```

<210> 343
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 343
Gly Gly Gly Gly Ser
 1   5

<210> 344
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 344
Ser Ser Ser Ser Gly
 1   5

<210> 345
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 345
Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
 1   5   10

<210> 346
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 346
Gly Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
 1   5   10   15

<210> 347
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 347
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Ser Glu Gly Ser Gly Ser
 1   5   10   15
Thr Lys Gly

<210> 348
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 348
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 1   5   10   15
Lys Gly

<210> 349
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 349
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe
 1   5   10

<210> 350
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 350
Ala Ala Pro Ala
 1

<210> 351
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Gly4Ser with NcoI ends

<400> 351
ccatgggcgg cggcggctct gccatgg   27

<210> 352
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> (Gly4Ser)2 with NcoI ends

<400> 352
ccatgggcgg cggcggctct ggcggcggcg gctctgccat gg   42

<210> 353
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> (Ser4Gly)4 with NcoI ends

<400> 353
ccatggcctc gtcgtcgtcg ggctcgtcgt cgtcgggctc gtcgtcgtcg ggctcgtcgt 60
cgtcgggcgc catgg 75

<210> 354
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> (Ser4Gly)2 with NcoI ends

<400> 354
ccatggcctc gtcgtcgtcg ggctcgtcgt cgtcgggcgc catgg 45

<210> 355
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG1 heavy chain constant

<400> 355
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1   5   10   15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100   105   110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115   120   125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130   135   140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145   150   155   160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165   170   175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180   185   190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195   200   205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210   215   220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225   230   235   240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245   250   255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260   265   270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275   280   285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290   295   300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305   310   315   320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325   330

<210> 356
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG2 heavy chain constant

<400> 356
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1   5   10   15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65   70   75   80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100   105   110
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115   120   125
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130   135   140
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145   150   155   160
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165   170   175
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180   185   190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195   200   205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210   215   220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225   230   235   240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245   250   255
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260   265   270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275   280   285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290   295   300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305   310   315   320
Ser Leu Ser Pro Gly Lys
                325

<210> 357
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG3 heavy chain constant

<400> 357
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1   5   10   15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

```
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125
Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260                 265                 270
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300
Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340                 345                 350
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375


<210> 358
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG4 heavy chain constant

<400> 358
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110
```

```
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 359
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG1 Fc

<400> 359

```
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 1               5                  10                  15
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20                  25                  30
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35                  40                  45
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    50                  55                  60
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65                  70                  75                  80
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85                  90                  95
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            100                 105                 110
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    130                 135                 140
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        195                 200                 205
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
```

Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 360
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 360
Gly Gly Gly Gly Gly
1 5

<210> 361
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<223> fragment of IgG1 heavy chain

<400> 361
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1 5 10 15
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20 25 30
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
35 40 45
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85 90 95
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100 105 110
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115 120 125
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130 135 140
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145 150 155 160
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
165 170 175
Asp Gly Pro Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
180 185 190
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195 200 205
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 362
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 362
Gly Gly Gly Gly
1

<210> 363
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 363
Ser Gly Gly Ser Gly Gly Ser
 1   5

<210> 364
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 364
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly
 1   5   10   15

<210> 365
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 365
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 366
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 366
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 1   5   10   15
Gly Ser

<210> 367
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 367

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 368
<211> 1
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker (Gly)n, where n = 2 to 20

<220>
<221> REPEAT
<222> (1)...(1)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
      14, 15, 16, 17, 18, 19 or 20 times

<400> 368
Gly
 1

<210> 369
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 369
Gly Gly Gly
 1

<210> 370
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 370
Gly Gly Gly Gly Gly Gly Gly
 1   5

<210> 371
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 371
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1   5   10

<210> 372
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> linker

<400> 372
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1   5   10   15

<210> 373
<211> 864
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN

<400> 373
Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
 1   5   10   15
Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
            20   25   30
Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
        35   40   45
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
    50   55   60
Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65   70   75   80
Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
                85   90   95
Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly
            100   105   110
Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
        115   120   125
Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    130   135   140
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
145   150   155   160
Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
                165   170   175
Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            180   185   190
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
        195   200   205
Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
    210   215   220
Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
225   230   235   240
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
                245   250   255
Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            260   265   270
Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
        275   280   285
Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
    290   295   300
Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
305   310   315   320
Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
                325   330   335
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
            340   345   350
Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
        355   360   365
Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    370   375   380

```
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
385                 390                 395                 400
Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
                405                 410                 415
Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
            420                 425                 430
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
        435                 440                 445
Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
    450                 455                 460
Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
465                 470                 475                 480
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
                485                 490                 495
Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            500                 505                 510
Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
        515                 520                 525
Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
    530                 535                 540
Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
545                 550                 555                 560
Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
                565                 570                 575
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
            580                 585                 590
Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
        595                 600                 605
Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
    610                 615                 620
Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
625                 630                 635                 640
Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
                645                 650                 655
Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
            660                 665                 670
Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
        675                 680                 685
Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
    690                 695                 700
Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
705                 710                 715                 720
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
                725                 730                 735
Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
            740                 745                 750
Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
        755                 760                 765
Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
    770                 775                 780
Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
785                 790                 795                 800
Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
                805                 810                 815
Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
            820                 825                 830
Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
        835                 840                 845
Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
    850                 855                 860
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<210> 374
<211> 523
<212> PRT
<213> Callithrix jacchus

<220>

<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(27)

<300>
<308> NCBI XP_009004586.1
<309> 2014-09-02

<400> 374

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Met Leu Gly Asn Gly Pro Ser Gly Trp Ser Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Ala Ala Val Ser Phe Phe Gly Ser Ala Leu Ser Met Asp Glu
            20                  25                  30
Thr Arg Glu His Leu Leu Thr Lys Glu Lys Met Met Gln Leu Gly Gly
        35                  40                  45
Gln Leu Val Leu Asn Ile Lys Glu Glu Arg Ala Asn Glu Lys Leu Met
    50                  55                  60
Thr Leu Lys Val Thr Glu Met Lys Glu Ala Met Lys Thr Leu Leu Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Arg Ala Lys His Leu Ile Asp Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Thr Lys Gly Ile Val
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr Ser Glu Glu Cys Pro
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg Val Gln Asn Val Thr
                165                 170                 175
Asp Phe Asp Asp Arg Val His Pro Gly Val Leu Leu Leu Gly Asp Ala
            180                 185                 190
Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile
        195                 200                 205
Tyr Thr Asp Gln Asn Ala Val Trp Ser Lys Phe Lys Thr Ile Phe Ser
    210                 215                 220
Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val
225                 230                 235                 240
Phe Gln Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu
                245                 250                 255
Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu Gln His
            260                 265                 270
Asp Leu Gln Trp Ser Val Lys Gly Tyr Gln Glu Val Ala Glu Lys Phe
        275                 280                 285
Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp
    290                 295                 300
His Arg Ser Lys Asp Val Thr Val Ile Ala Gly Ser Ile Arg Thr Ala
305                 310                 315                 320
Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu
                325                 330                 335
Val Gly Arg Glu Asp Thr Gly His Ser Leu His Tyr His Asn Arg Ala
            340                 345                 350
Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His
        355                 360                 365
Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Lys Asn Ile Leu
    370                 375                 380
Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu
385                 390                 395                 400
Asn Lys His Pro Ala Leu Arg Ala Tyr Ser Arg Lys Lys Asp Val Pro
                405                 410                 415
Val Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp
            420                 425                 430
Leu Arg Asn His Pro Ala Ala Thr Leu Met Ala Thr Gly His Pro Met
        435                 440                 445
Val Ile Ser Ser Asp Asp Pro Ala Ile Phe Gly Ala Lys Gly Leu Ser
```

450 455 460
Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp
465 470 475 480
Leu Arg Thr Leu Lys Gln Leu Ala Ile Asn Ser Ile Lys Tyr Ser Ser
485 490 495
Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Ala Val Trp Lys Lys Arg
500 505 510
Trp Asp Lys Phe Ile Ala His Val Ala Thr Asp
515 520

<210> 375
<211> 496
<212> PRT
<213> Callithrix jacchus

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> NCBI XP_009004586.1
<309> 2014-09-02

<400> 375
Leu Ser Met Asp Glu Thr Arg Glu His Leu Leu Thr Lys Glu Lys Met
1 5 10 15
Met Gln Leu Gly Gly Gln Leu Val Leu Asn Ile Lys Glu Glu Arg Ala
20 25 30
Asn Glu Lys Leu Met Thr Leu Lys Val Thr Glu Met Lys Glu Ala Met
35 40 45
Lys Thr Leu Leu Phe Pro Pro Ser Met His Phe Phe Arg Ala Lys His
50 55 60
Leu Ile Asp Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys
65 70 75 80
Gly Ala Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp
85 90 95
Leu Val Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr
100 105 110
Thr Lys Gly Ile Val Gln Phe Arg Phe Ala His Pro Thr Pro Arg Thr
115 120 125
Ser Glu Glu Cys Pro Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg
130 135 140
Val Gln Asn Val Thr Asp Phe Asp Asp Arg Val His Pro Gly Val Leu
145 150 155 160
Leu Leu Gly Asp Ala Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln
165 170 175
His Pro Glu Val Ile Tyr Thr Asp Gln Asn Ala Val Trp Ser Lys Phe
180 185 190
Lys Thr Ile Phe Ser Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val
195 200 205
Phe Arg Asp Tyr Val Phe Gln Ser Met Gln Glu Phe Tyr Glu Asp Asn
210 215 220
Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu
225 230 235 240
Ser Gly Glu Gln His Asp Leu Gln Trp Ser Val Lys Gly Tyr Gln Glu
245 250 255
Val Ala Glu Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys
260 265 270
Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Thr Val Ile Ala Gly
275 280 285
Ser Ile Arg Thr Ala Met Gly Leu Arg Thr Lys Phe Pro Thr Val Val
290 295 300
Ala Gly Phe Asp Leu Val Gly Arg Glu Asp Thr Gly His Ser Leu His
305 310 315 320
Tyr His Asn Arg Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu
325 330 335
Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile
340 345 350

```
Asp Lys Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly
        355                 360                 365
His Gly Phe Ala Leu Asn Lys His Pro Ala Leu Arg Ala Tyr Ser Arg
    370                 375                 380
Lys Lys Asp Val Pro Val Glu Val Cys Pro Ile Ser Asn Gln Val Leu
385                 390                 395                 400
Lys Leu Val Ser Asp Leu Arg Asn His Pro Ala Ala Thr Leu Met Ala
                405                 410                 415
Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Ile Phe Gly
            420                 425                 430
Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly
        435                 440                 445
Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Ile Asn Ser
    450                 455                 460
Ile Lys Tyr Ser Ser Leu Leu Glu Thr Glu Lys Asn Thr Phe Met Ala
465                 470                 475                 480
Val Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala His Val Ala Thr Asp
                485                 490                 495


<210> 376
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<223> Dendritic cell derived growth factor (DCDGF)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<310> US 5968780
<311> 1998-02-05
<312> 1999-10-19

<400> 376
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1                5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
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```
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu Arg Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Ser Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510


<210> 377
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)


<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> GenBank: BAG36969.1
<309> 2008-05-24

<400> 377
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala Arg Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
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Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala Arg Pro Thr Pro Arg Pro Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu Arg Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385                 390                 395                 400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510
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<210> 378
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> GenBank: AAF65941.1
<309> 2000-04-27

<400> 378
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1   5   10   15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20   25   30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35   40   45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50   55   60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65   70   75   80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85   90   95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100   105   110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115   120   125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130   135   140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu Lys Cys Ser
145   150   155   160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165   170   175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180   185   190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195   200   205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210   215   220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225   230   235   240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245   250   255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260   265   270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275   280   285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290   295   300
Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala
305   310   315   320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu Arg Asp
                325   330   335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340   345   350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355   360   365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370   375   380
Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys
385   390   395   400
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405   410   415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420   425   430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435   440   445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450   455   460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465   470   475   480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
                485   490   495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500   505   510

<210> 379
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)

<220>
<221> SIGNAL
<222> (1)...(29)

<300>
<308> GenBank: AAH51755.1
<309> 2006-07-15

<400> 379

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Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 1               5                  10                  15
Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
            20                  25                  30
Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
        35                  40                  45
Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
    50                  55                  60
Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
65                  70                  75                  80
Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile Glu Arg Ser
                85                  90                  95
Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala Ala Leu His
            100                 105                 110
Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val Arg Asn Val
        115                 120                 125
Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg Gly Ile Met
    130                 135                 140
Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu Lys Cys Ser
145                 150                 155                 160
Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln Asn Val Thr
                165                 170                 175
Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His
            180                 185                 190
Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu
        195                 200                 205
Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe
    210                 215                 220
Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val
225                 230                 235                 240
Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser
                245                 250                 255
Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val
            260                 265                 270
Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile
        275                 280                 285
Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser
    290                 295                 300
Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala
305                 310                 315                 320
Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp
                325                 330                 335
Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro
            340                 345                 350
Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp
        355                 360                 365
Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His
    370                 375                 380
Gly Phe Ala Leu Ser Lys His Pro Ala Leu Arg Thr Tyr Ser Trp Lys
385                 390                 395                 400
```

```
Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys
                405                 410                 415
Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr
            420                 425                 430
Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala
        435                 440                 445
Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly
    450                 455                 460
Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile
465                 470                 475                 480
Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile
                485                 490                 495
Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
            500                 505                 510


<210> 380
<211> 482
<212> PRT
<213> Homo sapiens

<220>
<223> Dendritic cell derived growth factor (DCDGF)
      mature form

<300>
<310> US 5968780
<311> 1998-02-05
<312> 1999-10-19

<400> 380
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
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    290                 295                 300
Leu Arg Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Ser
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 381
<211> 482
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1) mature form

<300>
<308> GenBank: BAG36969.1
<309> 2008-05-24

<400> 381

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Ile Asp Glu Thr Arg Ala Arg Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala Arg Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Arg Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
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210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu Arg Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 382
<211> 482
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)
mature form

<300>
<308> GenBank: AAF65941.1
<309> 2000-04-27

<400> 382
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln

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    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu Arg Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 383
<211> 482
<212> PRT
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)
mature form

<300>
<308> GenBank: AAH51755.1
<309> 2006-07-15

<400> 383

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
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    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Leu Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 384
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-8

<400> 384
accacagcct ttatccaagc gggtgagccc cgtgaacaat 40

<210> 385
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-9

<400> 385
ccgacgtgcc gcaacttcaa ccctgcacaa ccaatccgcc 40

<210> 386
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-14

<400> 386
caacgaaagg tgctccacta agaatggaac ttctgcgatc 40

<210> 387
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-15

<400> 387
gtgctcaatc acgaacccgc tcgacttctt ctcccaagcc 40

<210> 388
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-18

<400> 388
tgctccaaca ctcacttcgg aaccacctgc attccgctct 40

<210> 389
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Ipilimumab heavy chain varible domain (VH)

<400> 389
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300
tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 390
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab heavy chain varible domain (VH)

<400> 390
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
                85   90   95
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 391
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Ipilimumab light chain varible domain (VH)

<400> 391
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttggc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
caagggacca aggtggaaat caaac   325

<210> 392
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab light chain varible domain (VH)

<400> 392
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 393
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VH CDR1

<400> 393
Ser Tyr Thr Met His
 1   5

<210> 394
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VH CDR2

<400> 394
Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 395
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VH CDR3

<400> 395
Thr Gly Trp Leu Gly Pro Phe Asp Tyr
 1   5

<210> 396
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VL CDR1

<400> 396
Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
 1   5   10

<210> 397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VL CDR2

<400> 397
Gly Ala Phe Ser Arg Ala Thr
 1   5

<210> 398
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab VL CDR3

<400> 398

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1   5

<210> 399
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Tremelimumab heavy chain varible domain (VH)

<400> 399
ggcgtggtcc agcctgggag gtccctgaga ctctcctgtg cagcgtctgg attcaccttc 60
agtagctatg gcatgcactg ggtccgccag gctccaggca aggggctgga gtgggtggca 120
gttatatggt atgatggaag taataaatac tatgcagact ccgtgaaggg ccgattcacc 180
atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagccgag 240
gacacggctg tgtattactg tgcgagagat ccgaggggag ctacccttta ctactactac 300
tacgggatgg acgtctgggg ccaagggacc acggtcaccg tctcctcagc ctccaccaag 360
ggcccatcgg tcttcccct ggcgccctgc tccaggagca cctccgagag cacagcggcc 420
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
gctctgacca gcggcgtgca   500

<210> 400
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab heavy chain varible domain (VH)

<400> 400
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 1   5   10   15
Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro
            20   25   30
Gly Lys Gly Leu Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn
        35   40   45
Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    50   55   60
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
65   70   75   80
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro Arg Gly Ala Thr Leu
                85   90   95
Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
            100   105   110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115   120   125
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
    130   135   140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145   150   155   160
Ala Leu Thr Ser Gly Val His
                165

<210> 401
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Tremelimumab light chain varible domain (VH)

<400> 401
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgccg ggcaagtcag 60
agcattaaca gctatttaga ttggtatcag cagaaaccag ggaaagcccc taaactcctg 120

atctatgctg catccagttt gcaaagtggg gtcccatcaa ggttcagtgg cagtggatct 180
gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 240
tgtcaacagt attacagtac tccattcact ttcggccctg ggaccaaagt ggaaatcaaa 300
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 360
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagta 417

<210> 402
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab light chain varible domain (VH)

<400> 402
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 1   5   10   15
Arg Ala Ser Gln Ser Ile Asn Ser Tyr Leu Asp Trp Tyr Gln Gln Lys
            20   25   30
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
        35   40   45
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
    50   55   60
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
65   70   75   80
Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys
                85   90   95
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
            100   105   110
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
        115   120   125
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130   135

<210> 403
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Nivolumab heavy chain variable region

<400> 403
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
gactgtaaag cgtctggaat caccttcagt aactctggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa aagatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gacaaacgac 300
gactactggg gccagggaac cctggtcacc gtctcctca 339

<210> 404
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab heavy chain variable region

<400> 404
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110
Ser

<210> 405
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Nivolumab light chain variable region

<400> 405
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagt agttacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcagcag agtagcaact ggcctcggac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 406
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab light chain variable region

<400> 406
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 407
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VH CDR1

<400> 407
Asn Ser Gly Met His
1 5

<210> 408
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VH CDR2

<400> 408
Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 409
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VH CDR3

<400> 409
Asn Asp Asp Tyr
 1

<210> 410
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VL CDR1

<400> 410
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1   5   10

<210> 411
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VL CDR2

<400> 411
Asp Ala Ser Asn Arg Ala Thr
 1   5

<210> 412
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab VL CDR3

<400> 412
Gln Gln Ser Ser Asn Trp Pro Arg Thr
 1   5

<210> 413
<211> 1340
<212> DNA
<213> Artificial Sequence

<220>
<223> MK-3475 full-length heavy chain

<400> 413
aggtgcagct ggtgcagtcc ggcgtggagg tgaagaagcc tggcgcctcc gtcaaggtgt 60
cctgtaaggc ctccggctac accttcacca actactacat gtactgggtg cggcaggccc 120
caggccaggg actggagtgg atgggcggca tcaacccttc caacggcggc accaacttca 180
acgagaagtt caagaaccgg gtgaccctga ccaccgactc ctccaccaca accgcctaca 240
tggaactgaa gtccctgcag ttcgacgaca ccgccgtgta ctactgcgcc aggcgggact 300
accggttcga catgggcttc gactactggg gccagggcac caccgtgacc gtgtcctccg 360
ctagcaccaa gggcccttcc gtgttccctc tggcccccttg ctcccggtcc acctccgagt 420
ccaccgccgc tctgggctgt ctggtgaagg actacttccc tgagcctgtg accgtgagct 480
ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg cagtcctccg 540
gcctgtactc cctgtcctcc gtggtgaccg tgccttcctc ctccctgggc accaagacct 600
acacctgcaa cgtggaccac aagccttcca acaccaaggt ggacaagcgg gtggagtcca 660
agtacggccc tccttgccct ccctgccctg cccctgagtt cctgggcgga ccctccgtgt 720
tcctgttccc tcctaagcct aaggacaccc tgatgatctc ccggacccct gaggtgacct 780
gcgtggtggt ggacgtgtcc caggaagatc ctgaggtcca gttcaattgg tacgtggatg 840
gcgtggaggt gcacaacgcc aagaccaagc ctcgggagga acagttcaac tccacctacc 900
gggtggtgtc tgtgctgacc gtgctgcacc aggactggct gaacggcaag gaatacaagt 960
gcaaggtcag caacaagggc ctgccctcct ccatcgagaa aaccatctcc aaggccaagg 1020
gccagcctcg cgagcctcag gtgtacaccc tgcctcctag ccaggaagag atgaccaaga 1080
atcaggtgtc cctgacatgc ctggtgaagg gcttctaccc ttccgatatc gccgtggagt 1140
gggagagcaa cggccagcca gagaacaact acaagaccac ccctcctgtg ctggactccg 1200
acggctcctt cttcctgtac tccaggctga ccgtggacaa gtcccggtgg caggaaggca 1260
acgtctttc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc cagaagtccc 1320
tgtccctgtc tctgggcaag 1340

<210> 414
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 full-length heavy chain

<400> 414
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20   25   30
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
    50   55   60
Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65   70   75   80
Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210   215   220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225   230   235   240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

```
                245                 250                 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210> 415
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> MK-3475 full-length light chain

<400> 415
cgagatcgtg ctgacccagt cccctgccac cctgtccctg agccctggcg agcgggctac 60
cctgagctgc agagcctcca agggcgtgtc cacctccggc tactcctacc tgcactggta 120
tcagcagaag ccaggccagg cccctcggct gctgatctac ctggcctcct acctggagtc 180
cggcgtgcct gcccggttct ccggctccgg aagcggcacc gacttcaccc tgaccatctc 240
ctccctggag cctgaggact tcgccgtgta ctactgccag cactcccggg acctgcctct 300
gacctttggc ggcggaacaa aggtggagat caag                             334

<210> 416
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 full-length light chain

<400> 416
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1                5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20                  25                  30
Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35                  40                  45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125
```

```
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Asn Asn Phe Tyr
    130                 135                 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> 417
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> MK-3475 heavy chain variable domain

<400> 417
ccaggtgcag ctggtgcagt ccggcgtgga ggtgaagaag cctggcgcct ccgtcaaggt 60
gtcctgcaag gcctccggct acaccttcac caactactac atgtactggg tgcggcaggc 120
tcccggccag ggactggagt ggatgggcgg catcaaccct tccaacggcg gcaccaactt 180
caacgagaag ttcaagaacc gggtgaccct gaccaccgac tcctccacca ccaccgccta 240
catggagctg aagtccctgc agttcgacga caccgccgtg tactactgcg ccaggcggga 300
ctaccggttc gacatgggct tcgactactg gggccagggc accaccgtga ccgtgtcctc 360
c                                                                   361

<210> 418
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 heavy chain variable domain

<400> 418
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60
Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 419
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> MK-3475 light chain variable domain

<400> 419
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
```

ctctcctgca gggccagcaa aggtgtcagt acatctggct atagttattt gcactggtat 120
caacagaaac ctggccaggc tcccaggctc ctcatctatc ttgcatccta cctagaatct 180
ggcgtcccag ccaggttcag tggtagtggg tctgggacag acttcactct caccatcagc 240
agcctagagc ctgaagattt tgcagtttat tactgtcagc acagcaggga ccttccgctc 300
acgttcggcg gagggaccaa agtggagatc aaa 333

<210> 420
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 light chain variable domain

<400> 420
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 421
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VH CDR1

<400> 421
Asn Tyr Tyr Met Tyr
 1   5

<210> 422
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VH CDR2

<400> 422
Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe Lys
 1   5   10   15
Asn

<210> 423
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VH CDR3

<400> 423

Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
 1   5   10

<210> 424
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VL CDR1

<400> 424
Arg Ala Ser Lys Gly Val Ser Thr Ser Gly Tyr Ser Tyr Leu His
 1   5   10   15

<210> 425
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VL CDR2

<400> 425
Leu Ala Ser Tyr Leu Glu Ser
 1   5

<210> 426
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MK-3475 VL CDR3

<400> 426
Gln His Ser Arg Asp Leu Pro Leu Thr
 1   5

<210> 427
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Pidilizumab full-length heavy chain

<400> 427
atggactgga cctggaggat cctcttcttg gtggcagcag caacaggtgc ccactcccag 60
gtgcagctgg tgcaatctgg gtctgagctt aagaagcctg gggcctcagt gaagatctcc 120
tgcaaggctt ctggatatac tttcacaaac tatggaatga actgggtgcg acaggcccct 180
ggacaagggc ttcagtggat gggatggata aacaccgaca gtggagagtc aacatatgct 240
gaagagttca agggacggtt tgtcttctcc ttggacacct ctgtcaacac ggcatatctg 300
cagatcacca gcctcacggc tgaggacact ggcatgtatt tctgtgtgag agtcggctac 360
gatgctttgg actactgggg ccagggaacc ctggtcaccg tctcgagcgc ctccaccaag 420
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 480
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080
cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
tccctgtctc cgggtaaatg a 1401

<210> 428
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab full-length heavy chain

<400> 428
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1   5   10   15
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
            20   25   30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45
Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50   55   60
Gln Trp Met Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala
65   70   75   80
Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Asn
                85   90   95
Thr Ala Tyr Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met
            100   105   110
Tyr Phe Cys Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln
        115   120   125
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130   135   140
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145   150   155   160
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165   170   175
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180   185   190
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195   200   205
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210   215   220
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
225   230   235   240
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245   250   255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260   265   270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275   280   285
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290   295   300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305   310   315   320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325   330   335
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340   345   350
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355   360   365
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370   375   380
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385   390   395   400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460
Gly Lys
465

<210> 429
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Pidilizumab full-length light chain

<400> 429
atggacatga gggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgcc 60
aaatgtgaaa ttgtgttgac gcagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgcagtgc caggtcaagt gtaagttaca tgcactggtt ccagcagaaa 180
ccagggaaag cccctaagct ctggatctat aggacatcca acctggcttc tggggtccca 240
tctagattca gcggcagtgg atctgggaca tcttactgtc tcaccatcaa cagcctgcag 300
cctgaagatt ttgcaactta ctattgccag caaaggagta gtttcccact cacgttcggc 360
ggagggacca agctggagat caaacgtact gtggctgcac catctgtctt catcttcccg 420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 708

<210> 430
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab full-length light chain

<400> 430
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Lys Cys Glu Ile Val Leu Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Arg
35 40 45
Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala
50 55 60
Pro Lys Leu Trp Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Cys Leu Thr Ile
85 90 95
Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110
Ser Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

```
        195                 200                 205
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 431
<211> 421
<212> DNA
<213> Artificial Sequence

<220>
<223> Pidilizumab heavy chain variable domain

<400> 431
atggactgga cctggaggat cctcttcttg gtggcagcag caacaggtgc ccactcccag 60
gtgcagctgg tgcaatctgg gtctgagctt aagaagcctg gggcctcagt gaagatctcc 120
tgcaaggctt ctggatatac tttcacaaac tatggaatga actgggtgcg acaggcccct 180
ggacaagggc ttcagtggat gggatggata aacaccgaca gtggagagtc aacatatgct 240
gaagagttca agggacggtt tgtcttctcc ttggacacct ctgtcaacac ggcatatctg 300
cagatcacca gcctcacggc tgaggacact ggcatgtatt tctgtgtgag agtcggctac 360
gatgctttgg actactgggg ccagggaacc ctggtcaccg tctcctcagg tgagtggatc 420
c                                                                   421

<210> 432
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab heavy chain variable domain

<400> 432
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
        35                  40                  45
Gly Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe
    50                  55                  60
Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Asn Thr Ala Tyr
65                  70                  75                  80
Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
                85                  90                  95
Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110
Val Thr Val Ser Ser
        115


<210> 433
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Pidilizumab light chain variable domain

<400> 433
atggacatga gggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgcc 60
aaatgtgaaa ttgtgttgac gcagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgcagtgc caggtcaagt gtaagttaca tgcactggtt ccagcagaaa 180
ccagggaaag cccctaagct ctggatctat aggacatcca acctggcttc tggggtccca 240
tctagattca gcggcagtgg atctgggaca tcttactgtc tcaccatcaa cagcctgcag 300
cctgaagatt ttgcaactta ctattgccag caaaggagta gtttcccact cacgttcggc 360
ggagggacca agctggagat caaa                                       384
```

<210> 434
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab light chain variable domain

<400> 434
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Arg Ser Ser Val Ser Tyr Met
            20   25   30
His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
        35   40   45
Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Tyr Cys Leu Thr Ile Asn Ser Leu Gln Pro Glu
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Phe Pro Leu Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 435
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VH CDR1

<400> 435
Asn Tyr Gly Met Asn
 1   5

<210> 436
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VH CDR2

<400> 436
Trp Ile Asn Thr Asp Ser Gly Glu Ser Thr Tyr Ala Glu Glu Phe Lys
 1   5   10   15
Gly

<210> 437
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VH CDR3

<400> 437
Val Gly Tyr Asp Ala Leu Asp Tyr
 1   5

<210> 438

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VL CDR1

<400> 438
Ser Ala Arg Ser Ser Val Ser Tyr Met His
 1   5   10

<210> 439
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VL CDR2

<400> 439
Arg Thr Ser Asn Leu Ala Ser
 1   5

<210> 440
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Pidilizumab VL CDR3

<400> 440
Gln Gln Arg Ser Ser Phe Pro Leu Thr
 1   5

<210> 441
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> BMS-936559 heavy chain variable region

<400> 441
caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaaga cttctggaga caccttcagc acctatgcta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tatttggtaa agcacactac 180
gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt atttttgtgc gagaaagttt 300
cactttgttt cggggagccc cttcggtatg gacgtctggg gccaagggac cacggtcacc 360
gtctcctca   369

<210> 442
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 heavy chain variable region

<400> 442
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Thr Ser Gly Asp Thr Phe Ser Thr Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Lys Ala His Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ala Arg Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val
100 105 110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 443
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> BMS-936559 light chain variable region

<400> 443
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggccgacgtt cggccaaggg 300
accaaggtgg aaatcaaa 318

<210> 444
<211> 106
<212> PRT
<213> Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Ly

<220>
<223> BMS-936559 light chain variable region

<400> 444
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 445
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VH CDR1

<400> 445
Thr Tyr Ala Ile Ser Trp
1 5

<210> 446
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VH CDR2

<400> 446
Gly Ile Ile Pro Ile Phe Gly Lys Ala His Tyr Ala Gln Lys Phe Gln
 1   5   10   15
Gly

<210> 447
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VH CDR3

<400> 447
Lys Phe His Phe Val Ser Gly Ser Pro Phe Gly Met Asp Val
 1   5   10

<210> 448
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VL CDR1

<400> 448
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1   5   10

<210> 449
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VL CDR2

<400> 449
Asp Ala Ser Asn Arg Ala Thr
 1   5

<210> 450
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> BMS-936559 VL CDR3

<400> 450
Gln Gln Arg Ser Asn Trp Pro Thr
 1   5

<210> 451
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MEDI4736 heavy chain variable region

<400> 451
gaggtgcagc tggtcgagtc tggcggcgga ctggtgaagc ctggcggctc cctgagactg 60
tcttgcgccg ccagtggctt tacattcagt acctactcca tgaactgggt ccgccaggca 120
ccaggcaagg gcctggaatg ggtgtcctcc atctcatcca gtggcgacta catctactac 180
gccgactccg tgaagggccg gttcaccatc tcccgggaca acgccaagaa ctccctgtat 240
ctgcagatga actccctgag agccgaggac accgccgtgt actactgcgc cagggacctg 300
gtgacatcca tggtggcctt cgactactgg ggtcagggca ctctcgtcac agtgtcctct 360

<210> 452
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 heavy chain variable region

<400> 452
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Ser Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Leu Val Thr Ser Met Val Ala Phe Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 453
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> MEDI4736 light chain variable region

<400> 453
tcttacgagc tgacccagcc tccttccgtg tccgtgtctc caggacagac ggccagaatc 60
acctgttccg gcgacgccct gcctcagaaa tacgtgttct ggtatcagca gaagtccggc 120
caggcccctg tgctggtgat ctacgaggac tccaagcggc cttccggcat ccctgagcgg 180
ttctccggct cctcttccgg caccatggcc accctgacca tctctggcgc ccaggtggag 240
gacgaggccg actactactg ctactccacc gacagatccg gcaaccacag agtgtttggt 300
gggggtacta agctgaccgt gctg   324

<210> 454
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 light chain variable region

<400> 454
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Gln Lys Tyr Val
            20   25   30
Phe Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Arg Ser Gly Asn His
                85   90   95
Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 455
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VH CDR1

<400> 455
Thr Tyr Ser Met Asn
 1   5

<210> 456
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VH CDR2

<400> 456
Ser Ile Ser Ser Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 457
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VH CDR3

<400> 457
Asp Leu Val Thr Ser Met Val Ala Phe Asp Tyr
 1   5   10

<210> 458
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VL CDR1

<400> 458
Ser Gly Asp Ala Leu Pro Gln Lys Tyr Val Phe

1 5 10

<210> 459
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VL CDR2

<400> 459
Glu Asp Ser Lys Arg Pro Ser
1 5

<210> 460
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MEDI4736 VL CDR3

<400> 460
Tyr Ser Thr Asp Arg Ser Gly Asn His Arg Val
1 5 10

<210> 461
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A heavy chain full length

<400> 461
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
20 25 30
Trp Ile His Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Tyr
35 40 45
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Gly Pro Ser Val Phe Pro Leu
115 120 125
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Pro Ser Asn Thr
195 200 205
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Thr His Thr Cys
210 215 220
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

```
Phe Pro Pro Pro Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255
Cys Trp Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270
Tyr Val Asp Gly Val Glu Val His Asn Ala Thr Lys Pro Arg Glu Glu
        275                 280                 285
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Val Ser Asn Ala Leu
305                 310                 315                 320
Pro Ala Pro Ile Glu Thr Ile Ser Lys Ala Gly Gln Pro Arg Glu Pro
                325                 330                 335
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Asn Gln Val
            340                 345                 350
Ser Leu Thr Cys Leu Val Gly Phe Tyr Pro Ser Asp Ala Val Glu Trp
        355                 360                 365
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro Pro Val Leu
    370                 375                 380
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
385                 390                 395                 400
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                405                 410                 415
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            420                 425                 430
Lys
```

<210> 462
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A light chain full length

<400> 462

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
            20                  25                  30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Trp Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130                 135                 140
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145                 150                 155                 160
Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                165                 170                 175
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            180                 185                 190
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        195                 200                 205
Arg Gly Glu Cys
    210
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<210> 463

<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A heavy chain variable region

<400> 463
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ala
        115

<210> 464
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A light chain variable region

<400> 464
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 465
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A VH CDR1

<400> 465
Gly Phe Thr Phe Ser Asp Ser Trp Ile His
 1   5   10

<210> 466
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A VH CDR2

<400> 466
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 1   5   10   15
Lys Gly

<210> 467
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A VH CDR3

<400> 467
Arg His Trp Pro Gly Gly Phe Asp Tyr
 1   5

<210> 468
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A LH CDR1

<400> 468
Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala
 1   5   10

<210> 469
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A LH CDR2

<400> 469
Ser Ala Ser Phe Leu Tyr Ser
 1   5

<210> 470
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MPDL3280A LH CDR3

<400> 470
Gln Gln Tyr Leu Tyr His Pro Ala Thr
 1   5

<210> 471
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VH CDR1

<400> 471
Gly Phe Thr Phe Ser Ser Tyr Gly Met His
 1   5   10

<210> 472
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VH CDR2

<400> 472
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 1   5   10   15

<210> 473
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VH CDR3

<400> 473
Asp Pro Arg Gly Ala Thr Leu Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
 1   5   10   15

<210> 474
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VL CDR1

<400> 474
Arg Ala Ser Gln Ser Ile Asn Ser Tyr Leu Asp
 1   5   10

<210> 475
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VL CDR2

<400> 475
Ala Ala Ser Ser Leu Gln Ser
 1   5

<210> 476
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Tremelimumab VL CDR3

<400> 476
Gln Gln Tyr Tyr Ser Thr Pro Phe Thr
 1   5

<210> 477
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-PD-L1 antibody heavy chain

<400> 477
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
            20   25   30
Trp Ile His Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115   120   125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130   135   140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145   150   155   160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165   170   175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180   185   190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Pro Ser Asn
        195   200   205
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Thr His Thr
    210   215   220
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225   230   235   240
Leu Phe Pro Pro Pro Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245   250   255
Thr Cys Trp Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260   265   270
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Thr Lys Pro Arg Glu
        275   280   285
Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290   295   300
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Val Ser Asn Ala
305   310   315   320
Leu Pro Ala Pro Ile Glu Thr Ile Ser Lys Ala Gly Gln Pro Arg Glu
                325   330   335
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Asn Gln
            340   345   350
Val Ser Leu Thr Cys Leu Val Gly Phe Tyr Pro Ser Asp Ala Val Glu
        355   360   365
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro Pro Val
    370   375   380
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385   390   395   400
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                405   410   415
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
            420   425   430

Gly Lys

<210> 478
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-PD-L1 antibody light chain

<400> 478
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Trp Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 479
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-PD-L1 antibody heavy chain

<400> 479
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115   120   125

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Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Pro Ser Asn
        195                 200                 205
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Thr His Thr
    210                 215                 220
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240
Leu Phe Pro Pro Pro Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255
Thr Cys Trp Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Thr Lys Pro Arg Glu
        275                 280                 285
Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Val Ser Asn Ala
305                 310                 315                 320
Leu Pro Ala Pro Ile Glu Thr Ile Ser Lys Ala Gly Gln Pro Arg Glu
                325                 330                 335
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Asn Gln
            340                 345                 350
Val Ser Leu Thr Cys Leu Val Gly Phe Tyr Pro Ser Asp Ala Val Glu
        355                 360                 365
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Thr Thr Pro Pro Val
    370                 375                 380
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385                 390                 395                 400
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                405                 410                 415
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
            420                 425                 430
Gly Lys
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<210> 480
<211> 474
<212> PRT
<213> Homo sapiens

<220>
<223> mature human PH20, amino acid residues 36-509

<400> 480

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
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130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
450 455 460
Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
465 470

<210> 481
<211> 447
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-482

<400> 481
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95

```
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr
        435                 440                 445


<210> 482
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-481


<400> 482
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
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85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
435 440 445

<210> 483
<211> 445
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-480

<400> 483
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80

```
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
        435                 440                 445


<210> 484
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-479

<400> 484
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
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Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln
        435                 440


<210> 485
<211> 443
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-478

<400> 485
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
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Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro
        435                 440


<210> 486
<211> 442
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-477

<400> 486
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
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```
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu
        435                 440


<210> 487
<211> 432
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-467

<400> 487
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
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```
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430


<210> 488
<211> 448
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-483

<400> 488
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
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```
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445


<210> 489
<211> 472
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-507

<400> 489
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
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Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu Ile Ile Ser Ser Val Ala
465                 470


<210> 490
<211> 470
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-505

<400> 490
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
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Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu Ile Ile Ser Ser
465                 470


<210> 491
<211> 468
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-503

<400> 491
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1                5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
```

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Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu Ile Ile
465
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<210> 492
<211> 466
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-501

<400> 492

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu
465
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<210> 493
<211> 464
<212> PRT
<213> Homo sapiens

<220>

<223> mature soluble human PH20, amino acid residues
36-499

<400> 493

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
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<210> 494
<211> 462
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-497

<400> 494
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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser
    450                 455                 460
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<210> 495
<211> 460

<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-495

<400> 495

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile
    450                 455                 460
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<210> 496
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-493

<400> 496

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met
    450                 455
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<210> 497
<211> 456
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-491

<400> 497
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445

Ala Ser Pro Ser Thr Leu Ser Ala
450 455

<210> 498
<211> 454
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues 36-489

<400> 498
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430

Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser Pro Ser Thr Leu
450

<210> 499
<211> 455
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues 36-490

<400> 499
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415

Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser Pro Ser Thr Leu Ser
450 455

<210> 500
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-487

<400> 500
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400

Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser Pro Ser
450

<210> 501
<211> 450
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-485

<400> 501
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380

Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser
450

<210> 502
<211> 449
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-484

<400> 502
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365

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Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala
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<210> 503
<211> 441
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-476

<400> 503

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu
        435                 440


<210> 504
<211> 440
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-475

<400> 504
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr
        435                 440


<210> 505
<211> 439
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-474

<400> 505
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu
        435


<210> 506
<211> 438
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-473

<400> 506
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met
        435


<210> 507
<211> 437
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-472

<400> 507
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1                5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro
        435


<210> 508
<211> 436
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-471

<400> 508
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
```

```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro
        435


<210> 509
<211> 435
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-470

<400> 509
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
```

```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys
        435


<210> 510
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-469

<400> 510
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
```

```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu
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<210> 511
<211> 433
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-468

<400> 511

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
```

```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe
```

<210> 512
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-466

<400> 512

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
```

```
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp
            420                 425                 430


<210> 513
<211> 430
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-465

<400> 513
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
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```
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile
            420                 425                 430


<210> 514
<211> 429
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-464

<400> 514
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
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```
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
            420                 425


<210> 515
<211> 427
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-462

<400> 515
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
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Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly
420 425

<210> 516
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues 36-460

<400> 516
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415

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Thr Asp Ala Val Asp Val Cys Ile Ala
            420                 425


<210> 517
<211> 423
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-458

<400> 517
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys
            420
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<210> 518
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-456

<400> 518
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp
420

<210> 519
<211> 419
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-454

<400> 519
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala

<210> 520
<211> 417

<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-452

<400> 520
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr

<210> 521
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-450

<400> 521
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1   5   10   15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20   25   30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35   40   45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50   55   60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65   70   75   80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85   90   95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100   105   110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115   120   125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130   135   140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145   150   155   160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165   170   175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180   185   190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195   200   205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210   215   220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225   230   235   240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245   250   255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260   265   270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275   280   285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290   295   300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305   310   315   320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325   330   335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340   345   350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355   360   365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370   375   380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385   390   395   400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys
                405   410   415

<210> 522
<211> 473
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-508

<400> 522
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1   5   10   15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20   25   30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35   40   45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50   55   60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65   70   75   80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85   90   95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100   105   110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115   120   125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130   135   140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145   150   155   160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165   170   175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180   185   190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195   200   205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210   215   220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225   230   235   240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245   250   255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260   265   270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275   280   285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290   295   300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305   310   315   320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325   330   335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340   345   350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355   360   365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370   375   380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385   390   395   400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405   410   415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420   425   430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435   440   445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450   455   460
Phe Leu Ile Ile Ser Ser Val Ala Ser
465   470

<210> 523
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-506

<400> 523
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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu Ile Ile Ser Ser Val
465                 470
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<210> 524
<211> 469
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-504

<400> 524

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
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Phe Leu Ile Ile Ser
465

<210> 525
<211> 467
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-502

<400> 525
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
370 375 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385 390 395 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430

```
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
    450                 455                 460
Phe Leu Ile
465
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<210> 526
<211> 465
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-500

<400> 526

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
```

Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
405 410 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
420 425 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
435 440 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
450 455 460
Phe
465

<210> 527
<211> 463
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
36-498

<400> 527
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1 5 10 15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20 25 30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35 40 45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50 55 60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65 70 75 80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85 90 95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100 105 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115 120 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130 135 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145 150 155 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165 170 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180 185 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
195 200 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
210 215 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225 230 235 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
245 250 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
260 265 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
275 280 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
290 295 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305 310 315 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
325 330 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
340 345 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
355 360 365

```
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile
    450                 455                 460


<210> 528
<211> 461
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-496

<400> 528
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1                5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
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Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
    450                 455                 460


<210> 529
<211> 459
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-494

<400> 529
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
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```
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe
    450                 455


<210> 530
<211> 457
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-492

<400> 530
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
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```
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr Leu Ser Ala Thr
    450                 455


<210> 531
<211> 453
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-488

<400> 531
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
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```
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro Ser Thr
    450


<210> 532
<211> 451
<212> PRT
<213> Homo sapiens

<220>
<223> mature soluble human PH20, amino acid residues
      36-486

<400> 532
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1               5                  10                  15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
            20                  25                  30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
        35                  40                  45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
    50                  55                  60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65                  70                  75                  80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
                85                  90                  95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
            100                 105                 110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
        115                 120                 125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
    130                 135                 140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145                 150                 155                 160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
                165                 170                 175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
            180                 185                 190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
        195                 200                 205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
    210                 215                 220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
225                 230                 235                 240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
                245                 250                 255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
            260                 265                 270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
        275                 280                 285
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Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
    290                 295                 300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
305                 310                 315                 320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
                325                 330                 335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
            340                 345                 350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
        355                 360                 365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
    370                 375                 380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
385                 390                 395                 400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
                405                 410                 415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
            420                 425                 430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
        435                 440                 445
Ala Ser Pro
    450


<210> 533
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A1

<300>
<308> NCBI: NP_000665.1
<309> 2014-04-06

<400> 533
Met Pro Pro Ser Ile Ser Ala Phe Gln Ala Ala Tyr Ile Gly Ile Glu
 1               5                  10                  15
Val Leu Ile Ala Leu Val Ser Val Pro Gly Asn Val Leu Val Ile Trp
            20                  25                  30
Ala Val Lys Val Asn Gln Ala Leu Arg Asp Ala Thr Phe Cys Phe Ile
        35                  40                  45
Val Ser Leu Ala Val Ala Asp Val Ala Val Gly Ala Leu Val Ile Pro
    50                  55                  60
Leu Ala Ile Leu Ile Asn Ile Gly Pro Gln Thr Tyr Phe His Thr Cys
65                  70                  75                  80
Leu Met Val Ala Cys Pro Val Leu Ile Leu Thr Gln Ser Ser Ile Leu
                85                  90                  95
Ala Leu Leu Ala Ile Ala Val Asp Arg Tyr Leu Arg Val Lys Ile Pro
            100                 105                 110
Leu Arg Tyr Lys Met Val Val Thr Pro Arg Arg Ala Ala Val Ala Ile
        115                 120                 125
Ala Gly Cys Trp Ile Leu Ser Phe Val Val Gly Leu Thr Pro Met Phe
    130                 135                 140
Gly Trp Asn Asn Leu Ser Ala Val Glu Arg Ala Trp Ala Ala Asn Gly
145                 150                 155                 160
Ser Met Gly Glu Pro Val Ile Lys Cys Glu Phe Glu Lys Val Ile Ser
                165                 170                 175
Met Glu Tyr Met Val Tyr Phe Asn Phe Phe Val Trp Val Leu Pro Pro
            180                 185                 190
Leu Leu Leu Met Val Leu Ile Tyr Leu Glu Val Phe Tyr Leu Ile Arg
        195                 200                 205
Lys Gln Leu Asn Lys Lys Val Ser Ala Ser Ser Gly Asp Pro Gln Lys
    210                 215                 220
Tyr Tyr Gly Lys Glu Leu Lys Ile Ala Lys Ser Leu Ala Leu Ile Leu
225                 230                 235                 240
Phe Leu Phe Ala Leu Ser Trp Leu Pro Leu His Ile Leu Asn Cys Ile
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                245                 250                 255
Thr Leu Phe Cys Pro Ser Cys His Lys Pro Ser Ile Leu Thr Tyr Ile
            260                 265                 270
Ala Ile Phe Leu Thr His Gly Asn Ser Ala Met Asn Pro Ile Val Tyr
        275                 280                 285
Ala Phe Arg Ile Gln Lys Phe Arg Val Thr Phe Leu Lys Ile Trp Asn
    290                 295                 300
Asp His Phe Arg Cys Gln Pro Ala Pro Pro Ile Asp Glu Asp Leu Pro
305                 310                 315                 320
Glu Glu Arg Pro Asp Asp
                325


<210> 534
<211> 412
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A2a

<300>
<308> NCBI: NP_000666.2
<309> 2014-05-26

<400> 534
Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
 1               5                  10                  15
Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
            20                  25                  30
Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
        35                  40                  45
Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
    50                  55                  60
Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65                  70                  75                  80
Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
                85                  90                  95
Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
            100                 105                 110
Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
        115                 120                 125
Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
    130                 135                 140
Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145                 150                 155                 160
Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
                165                 170                 175
Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
            180                 185                 190
Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
        195                 200                 205
Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
    210                 215                 220
Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225                 230                 235                 240
Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
                245                 250                 255
Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
            260                 265                 270
Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
        275                 280                 285
Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
    290                 295                 300
Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
305                 310                 315                 320
Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
                325                 330                 335
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Arg Leu Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro
            340                 345                 350
His Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly
        355                 360                 365
Gly Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu
    370                 375                 380
Leu Leu Ser His Glu Leu Lys Gly Val Cys Pro Glu Pro Pro Gly Leu
385                 390                 395                 400
Asp Asp Pro Leu Ala Gln Asp Gly Ala Gly Val Ser
                405                 410


<210> 535
<211> 332
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A2b

<300>
<308> NCBI: NP_000667.1
<309> 2014-05-30

<400> 535
Met Leu Leu Glu Thr Gln Asp Ala Leu Tyr Val Ala Leu Glu Leu Val
 1               5                  10                  15
Ile Ala Ala Leu Ser Val Ala Gly Asn Val Leu Val Cys Ala Ala Val
            20                  25                  30
Gly Thr Ala Asn Thr Leu Gln Thr Pro Thr Asn Tyr Phe Leu Val Ser
        35                  40                  45
Leu Ala Ala Ala Asp Val Ala Val Gly Leu Phe Ala Ile Pro Phe Ala
    50                  55                  60
Ile Thr Ile Ser Leu Gly Phe Cys Thr Asp Phe Tyr Gly Cys Leu Phe
65                  70                  75                  80
Leu Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu
                85                  90                  95
Leu Ala Val Ala Val Asp Arg Tyr Leu Ala Ile Cys Val Pro Leu Arg
            100                 105                 110
Tyr Lys Ser Leu Val Thr Gly Thr Arg Ala Arg Gly Val Ile Ala Val
        115                 120                 125
Leu Trp Val Leu Ala Phe Gly Ile Gly Leu Thr Pro Phe Leu Gly Trp
    130                 135                 140
Asn Ser Lys Asp Ser Ala Thr Asn Asn Cys Thr Glu Pro Trp Asp Gly
145                 150                 155                 160
Thr Thr Asn Glu Ser Cys Cys Leu Val Lys Cys Leu Phe Glu Asn Val
                165                 170                 175
Val Pro Met Ser Tyr Met Val Tyr Phe Asn Phe Phe Gly Cys Val Leu
            180                 185                 190
Pro Pro Leu Leu Ile Met Leu Val Ile Tyr Ile Lys Ile Phe Leu Val
        195                 200                 205
Ala Cys Arg Gln Leu Gln Arg Thr Glu Leu Met Asp His Ser Arg Thr
    210                 215                 220
Thr Leu Gln Arg Glu Ile His Ala Ala Lys Ser Leu Ala Met Ile Val
225                 230                 235                 240
Gly Ile Phe Ala Leu Cys Trp Leu Pro Val His Ala Val Asn Cys Val
                245                 250                 255
Thr Leu Phe Gln Pro Ala Gln Gly Lys Asn Lys Pro Lys Trp Ala Met
            260                 265                 270
Asn Met Ala Ile Leu Leu Ser His Ala Asn Ser Val Val Asn Pro Ile
        275                 280                 285
Val Tyr Ala Tyr Arg Asn Arg Asp Phe Arg Tyr Thr Phe His Lys Ile
    290                 295                 300
Ile Ser Arg Tyr Leu Leu Cys Gln Ala Asp Val Lys Ser Gly Asn Gly
305                 310                 315                 320
Gln Ala Gly Val Gln Pro Ala Leu Gly Val Gly Leu
                325                 330
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<210> 536
<211> 347
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A3 isoform 1

<300>
<308> NCBI: NP_065734.5
<309> 2014-04-20

<400> 536
Met Pro Asn Asn Ser Thr Ala Leu Ser Leu Ala Asn Val Thr Tyr Ile
 1   5   10   15
Thr Met Glu Ile Phe Ile Gly Leu Cys Ala Ile Val Gly Asn Val Leu
            20   25   30
Val Ile Cys Val Val Lys Leu Asn Pro Ser Leu Gln Thr Thr Thr Phe
        35   40   45
Tyr Phe Ile Val Ser Leu Ala Leu Ala Asp Ile Ala Val Gly Val Leu
    50   55   60
Val Met Pro Leu Ala Ile Val Val Ser Leu Gly Ile Thr Ile His Phe
65   70   75   80
Tyr Ser Cys Leu Phe Met Thr Cys Leu Leu Leu Ile Phe Thr His Ala
                85   90   95
Ser Ile Met Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Leu Arg Val
            100   105   110
Lys Leu Thr Val Arg Phe Arg Ile Pro Gly Leu Pro Gly Cys Ile Leu
        115   120   125
Ser Phe Gln Leu Lys Val Cys Phe Leu Pro Val Met Trp Leu Phe Ile
    130   135   140
Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met Val Met Asp Glu Lys
145   150   155   160
Val Lys Arg Ser Phe Val Leu Asp Thr Ala Ser Ala Ile Cys Asn Tyr
                165   170   175
Asn Ala His Tyr Lys Asn His Pro Lys Tyr Trp Cys Arg Gly Tyr Phe
            180   185   190
Arg Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro Asn Ser Thr Asn His
        195   200   205
Val Ala Leu Arg Asp Thr Gly Asn Gln Leu Ile Val Thr Met Ser Cys
    210   215   220
Leu Thr Lys Glu Asp Thr Gly Trp Tyr Trp Cys Gly Ile Gln Arg Asp
225   230   235   240
Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu Ile Val Thr Asp Asp
                245   250   255
Lys Gly Thr Leu Ala Asn Asp Phe Trp Ser Gly Lys Asp Leu Ser Gly
            260   265   270
Asn Lys Thr Arg Ser Cys Lys Ala Pro Lys Val Val Arg Lys Ala Asp
        275   280   285
Arg Ser Arg Thr Ser Ile Leu Ile Ile Cys Ile Leu Ile Thr Gly Leu
    290   295   300
Gly Ile Ile Ser Val Ile Ser His Leu Thr Lys Arg Arg Arg Ser Gln
305   310   315   320
Arg Asn Arg Arg Val Gly Asn Thr Leu Lys Pro Phe Ser Arg Val Leu
                325   330   335
Thr Pro Lys Glu Met Ala Pro Thr Glu Gln Met
            340   345

<210> 537
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A3 isoform 2

<300>
<308> NCBI: NP_000668.1
<309> 2014-05-03

<400> 537
Met Pro Asn Asn Ser Thr Ala Leu Ser Leu Ala Asn Val Thr Tyr Ile
 1   5   10   15
Thr Met Glu Ile Phe Ile Gly Leu Cys Ala Ile Val Gly Asn Val Leu
            20   25   30
Val Ile Cys Val Val Lys Leu Asn Pro Ser Leu Gln Thr Thr Thr Phe
        35   40   45
Tyr Phe Ile Val Ser Leu Ala Leu Ala Asp Ile Ala Val Gly Val Leu
    50   55   60
Val Met Pro Leu Ala Ile Val Val Ser Leu Gly Ile Thr Ile His Phe
65   70   75   80
Tyr Ser Cys Leu Phe Met Thr Cys Leu Leu Leu Ile Phe Thr His Ala
                85   90   95
Ser Ile Met Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Leu Arg Val
            100   105   110
Lys Leu Thr Val Arg Tyr Lys Arg Val Thr Thr His Arg Arg Ile Trp
        115   120   125
Leu Ala Leu Gly Leu Cys Trp Leu Val Ser Phe Leu Val Gly Leu Thr
    130   135   140
Pro Met Phe Gly Trp Asn Met Lys Leu Thr Ser Glu Tyr His Arg Asn
145   150   155   160
Val Thr Phe Leu Ser Cys Gln Phe Val Ser Val Met Arg Met Asp Tyr
                165   170   175
Met Val Tyr Phe Ser Phe Leu Thr Trp Ile Phe Ile Pro Leu Val Val
            180   185   190
Met Cys Ala Ile Tyr Leu Asp Ile Phe Tyr Ile Ile Arg Asn Lys Leu
        195   200   205
Ser Leu Asn Leu Ser Asn Ser Lys Glu Thr Gly Ala Phe Tyr Gly Arg
    210   215   220
Glu Phe Lys Thr Ala Lys Ser Leu Phe Leu Val Leu Phe Leu Phe Ala
225   230   235   240
Leu Ser Trp Leu Pro Leu Ser Ile Ile Asn Cys Ile Ile Tyr Phe Asn
                245   250   255
Gly Glu Val Pro Gln Leu Val Leu Tyr Met Gly Ile Leu Leu Ser His
            260   265   270
Ala Asn Ser Met Met Asn Pro Ile Val Tyr Ala Tyr Lys Ile Lys Lys
        275   280   285
Phe Lys Glu Thr Tyr Leu Leu Ile Leu Lys Ala Cys Val Val Cys His
    290   295   300
Pro Ser Asp Ser Leu Asp Thr Ser Ile Glu Lys Asn Ser Glu
305   310   315

<210> 538
<211> 266
<212> PRT
<213> Homo sapiens

<220>
<223> adenosine receptor A3 isoform 3

<300>
<308> NCBI: NP_001075445.1
<309> 2014-04-20

<400> 538
Met Glu Gly Ser Pro Ala Gly Pro Ile Glu Gln Lys Glu Ala Arg Trp
 1   5   10   15
Glu Ser Ser Trp Glu Glu Gln Pro Asp Trp Thr Leu Gly Cys Leu Ser
            20   25   30
Pro Glu Ser Gln Phe Arg Ile Pro Gly Leu Pro Gly Cys Ile Leu Ser
        35   40   45
Phe Gln Leu Lys Val Cys Phe Leu Pro Val Met Trp Leu Phe Ile Leu
    50   55   60

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Leu Ser Leu Ala Leu Ile Ser Asp Ala Met Val Met Asp Glu Lys Val
65                  70                  75                  80
Lys Arg Ser Phe Val Leu Asp Thr Ala Ser Ala Ile Cys Asn Tyr Asn
                85                  90                  95
Ala His Tyr Lys Asn His Pro Lys Tyr Trp Cys Arg Gly Tyr Phe Arg
            100                 105                 110
Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro Asn Ser Thr Asn His Val
        115                 120                 125
Ala Leu Arg Asp Thr Gly Asn Gln Leu Ile Val Thr Met Ser Cys Leu
    130                 135                 140
Thr Lys Glu Asp Thr Gly Trp Tyr Trp Cys Gly Ile Gln Arg Asp Phe
145                 150                 155                 160
Ala Arg Asp Asp Met Asp Phe Thr Glu Leu Ile Val Thr Asp Asp Lys
                165                 170                 175
Gly Thr Leu Ala Asn Asp Phe Trp Ser Gly Lys Asp Leu Ser Gly Asn
            180                 185                 190
Lys Thr Arg Ser Cys Lys Ala Pro Lys Val Val Arg Lys Ala Asp Arg
        195                 200                 205
Ser Arg Thr Ser Ile Leu Ile Ile Cys Ile Leu Ile Thr Gly Leu Gly
    210                 215                 220
Ile Ile Ser Val Ile Ser His Leu Thr Lys Arg Arg Arg Ser Gln Arg
225                 230                 235                 240
Asn Arg Arg Val Gly Asn Thr Leu Lys Pro Phe Ser Arg Val Leu Thr
                245                 250                 255
Pro Lys Glu Met Ala Pro Thr Glu Gln Met
            260                 265


<210> 539
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-1

<400> 539
ggggaattc taatacgact cactataggg agagaggaag agggataggc cgcccgagta 60
caaacgtact cgcctgtttg cccaaccgac ataacccaga ggtcgatagt acyggatccc 120
ccc                                                               123

<210> 540
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-4

<400> 540
cagccaaagg atatccaagc ggcacgccat aacacaacac                        40

<210> 541
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> CTLA-4 binding aptamer M9a-5

<400> 541
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<210> 542
<211> 510
<212> PRT
<213> Homo sapiens
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<220>
<223> ectonucleoside triphosphate diphosphohydrolase
(CD39) 1 isoform 1

<300>
<308> NCBI: NP_001767.3
<309> 2014-04-16

<400> 542

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Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
            20                  25                  30
Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
        35                  40                  45
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
    50                  55                  60
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65                  70                  75                  80
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
                85                  90                  95
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
            100                 105                 110
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
        115                 120                 125
Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
    130                 135                 140
Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145                 150                 155                 160
Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
                165                 170                 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
            180                 185                 190
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
        195                 200                 205
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
    210                 215                 220
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225                 230                 235                 240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
                245                 250                 255
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
            260                 265                 270
Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
        275                 280                 285
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
    290                 295                 300
Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305                 310                 315                 320
Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
                325                 330                 335
Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
            340                 345                 350
Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
        355                 360                 365
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
    370                 375                 380
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385                 390                 395                 400
Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
                405                 410                 415
Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
            420                 425                 430
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
        435                 440                 445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
    450                 455                 460
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
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465                 470                 475                 480
Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
                485                 490                 495
Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
            500                 505                 510


<210> 543
<211> 574
<212> PRT
<213> Homo sapiens

<220>
<223> 5'-ectonucleotidase (CD73) isoform 1 preproprotein

<220>
<221> SIGNAL
<222> (1)...(26)

<300>
<308> NCBI: NP_002517.1
<309> 2014-05-03

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Gly Ala Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu
            20                  25                  30
His Thr Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser
        35                  40                  45
Ser Lys Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu
    50                  55                  60
Phe Thr Lys Val Gln Gln Ile Arg Arg Ala Glu Pro Asn Val Leu Leu
65                  70                  75                  80
Leu Asp Ala Gly Asp Gln Tyr Gln Gly Thr Ile Trp Phe Thr Val Tyr
                85                  90                  95
Lys Gly Ala Glu Val Ala His Phe Met Asn Ala Leu Arg Tyr Asp Ala
            100                 105                 110
Met Ala Leu Gly Asn His Glu Phe Asp Asn Gly Val Glu Gly Leu Ile
        115                 120                 125
Glu Pro Leu Leu Lys Glu Ala Lys Phe Pro Ile Leu Ser Ala Asn Ile
    130                 135                 140
Lys Ala Lys Gly Pro Leu Ala Ser Gln Ile Ser Gly Leu Tyr Leu Pro
145                 150                 155                 160
Tyr Lys Val Leu Pro Val Gly Asp Glu Val Val Gly Ile Val Gly Tyr
                165                 170                 175
Thr Ser Lys Glu Thr Pro Phe Leu Ser Asn Pro Gly Thr Asn Leu Val
            180                 185                 190
Phe Glu Asp Glu Ile Thr Ala Leu Gln Pro Glu Val Asp Lys Leu Lys
        195                 200                 205
Thr Leu Asn Val Asn Lys Ile Ile Ala Leu Gly His Ser Gly Phe Glu
    210                 215                 220
Met Asp Lys Leu Ile Ala Gln Lys Val Arg Gly Val Asp Val Val Val
225                 230                 235                 240
Gly Gly His Ser Asn Thr Phe Leu Tyr Thr Gly Asn Pro Pro Ser Lys
                245                 250                 255
Glu Val Pro Ala Gly Lys Tyr Pro Phe Ile Val Thr Ser Asp Asp Gly
            260                 265                 270
Arg Lys Val Pro Val Val Gln Ala Tyr Ala Phe Gly Lys Tyr Leu Gly
        275                 280                 285
Tyr Leu Lys Ile Glu Phe Asp Glu Arg Gly Asn Val Ile Ser Ser His
    290                 295                 300
Gly Asn Pro Ile Leu Leu Asn Ser Ser Ile Pro Glu Asp Pro Ser Ile
305                 310                 315                 320
Lys Ala Asp Ile Asn Lys Trp Arg Ile Lys Leu Asp Asn Tyr Ser Thr
                325                 330                 335
Gln Glu Leu Gly Lys Thr Ile Val Tyr Leu Asp Gly Ser Ser Gln Ser
            340                 345                 350
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Cys Arg Phe Arg Glu Cys Asn Met Gly Asn Leu Ile Cys Asp Ala Met
        355                 360                 365
Ile Asn Asn Asn Leu Arg His Thr Asp Glu Met Phe Trp Asn His Val
    370                 375                 380
Ser Met Cys Ile Leu Asn Gly Gly Gly Ile Arg Ser Pro Ile Asp Glu
385                 390                 395                 400
Arg Asn Asn Gly Thr Ile Thr Trp Glu Asn Leu Ala Ala Val Leu Pro
                405                 410                 415
Phe Gly Gly Thr Phe Asp Leu Val Gln Leu Lys Gly Ser Thr Leu Lys
            420                 425                 430
Lys Ala Phe Glu His Ser Val His Arg Tyr Gly Gln Ser Thr Gly Glu
        435                 440                 445
Phe Leu Gln Val Gly Gly Ile His Val Val Tyr Asp Leu Ser Arg Lys
    450                 455                 460
Pro Gly Asp Arg Val Val Lys Leu Asp Val Leu Cys Thr Lys Cys Arg
465                 470                 475                 480
Val Pro Ser Tyr Asp Pro Leu Lys Met Asp Glu Val Tyr Lys Val Ile
                485                 490                 495
Leu Pro Asn Phe Leu Ala Asn Gly Gly Asp Gly Phe Gln Met Ile Lys
            500                 505                 510
Asp Glu Leu Leu Arg His Asp Ser Gly Asp Gln Asp Ile Asn Val Val
        515                 520                 525
Ser Thr Tyr Ile Ser Lys Met Lys Val Ile Tyr Pro Ala Val Glu Gly
    530                 535                 540
Arg Ile Lys Phe Ser Thr Gly Ser His Cys His Gly Ser Phe Ser Leu
545                 550                 555                 560
Ile Phe Leu Ser Leu Trp Ala Val Ile Phe Val Leu Tyr Gln
                565                 570
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<210> 544
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<223> CTLA4

<300>
<308> GenBank: AAL07473.1
<309> 2001-09-26

<400> 544

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 1               5                  10                  15
Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
            20                  25                  30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
        35                  40                  45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
    50                  55                  60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65                  70                  75                  80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
                85                  90                  95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
            100                 105                 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
        115                 120                 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
    130                 135                 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145                 150                 155                 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
                165                 170                 175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
            180                 185                 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
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195 200 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 545
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<223> Programmed cell death protein 1

<220>
<221> SIGNAL
<222> (1)...(20)

<300>
<308> Uniprot Q15116.3
<309> 2014-10-01

<400> 545
Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15
Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30
Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45
Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80
Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95
Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110
Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125
Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140
Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160
Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
165 170 175
Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
180 185 190
Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
195 200 205
Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
210 215 220
Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225 230 235 240
Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
245 250 255
Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
260 265 270
Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
275 280 285

<210> 546
<211> 290
<212> PRT
<213> Homo sapiens

<220>
<223> Programmed cell death 1 ligand 1

<220>
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<222> (1)...(18)

<300>
<308> Uniprot Q9NZQ7.1
<309> 2014-10-01

<400> 546
Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
 1   5   10   15
Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
            20   25   30
Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
        35   40   45
Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
    50   55   60
Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65   70   75   80
Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
                85   90   95
Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
            100   105   110
Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
        115   120   125
Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
    130   135   140
Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145   150   155   160
Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
                165   170   175
Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
            180   185   190
Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
        195   200   205
Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
    210   215   220
Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225   230   235   240
Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
                245   250   255
Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
            260   265   270
Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
        275   280   285
Glu Thr
    290

<210> 547
<211> 1536
<212> DNA
<213> Homo sapiens

<220>
<223> ADA2 (CECR1)

<300>
<308> ENA: CAG30303.1
<309> 2008-10-16

<400> 547
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gaaaagatga tgcggctggg ggggcggctg gtgctgaaca ccaaggagga gctggccaat 180
gagaggctca tgacgctcaa aatcgctgag atgaaggagg ccatgaggac cctgatattc 240
ccacccagca tgcacttttt ccaggccaag catctcattg agagaagtca agtgtttaat 300
attctaagga tgatgccaaa aggggctgcc ttgcacctcc atgacattgg catcgtgact 360

atggactggc tggtgaggaa tgtcacctac aggcctcact gccacatctg tttcacccca 420
aggggatca tgcagttcag atttgctcac ccaactcccc gtccatcaga aaaatgttcc 480
aagtggattc tgctggagga ttatcggaag cgggtgcaga acgtcactga gtttgatgac 540
agcttgctga ggaatttcac tctggtgacc cagcacccgg aggtgattta cacaaaccaa 600
aatgttgtct ggtcgaaatt tgaaaccatc ttcttcacca tctctggtct catccattac 660
gcaccagtgt tcagagacta tgtcttccgg agcatgcagg agttctacga ggacaacgtg 720
ctctacatgg agatcagagc caggctgctg ccggtgtatg agctcagtgg agagcaccat 780
gacgaagagt ggtcagtgaa gacttaccag gaagtagctc agaagtttgt ggaaactcac 840
cctgagttta ttggaatcaa aatcatttat tcggatcaca gatccaaaga tgtggctgtc 900
atcgcagaat ccatccgaat ggccatgggg ctccgaatca agttccccac ggtggtggca 960
gggtttgacc tggtggggca tgaggacact ggccactcct tgcatgacta caaggaagct 1020
ctgatgatcc ccgccaagga tggcgttaag ctgccttact tcttccacgc cggagaaaca 1080
gactggcagg gtacttccat agacaggaac attctggatg ctctgatgct gaacactacc 1140
agaatcggcc atggatttgc tttgagcaaa caccccgcag tcaggactta ctcctggaaa 1200
aaggacatcc ccatagaagt ctgtcccatc tctaaccagg tgctgaaact ggtgtctgac 1260
ttgaggaacc accctgtagc cactctgatg gccactgggc accccatggt gatcagctct 1320
gatgacccag ctatgtttgg tgccaaaggc ttgtcctatg atttctatga ggtcttcatg 1380
ggcattgggg ggatgaaggc tgacctgagg accctcaaac agctggccat gaactctatc 1440
aagtacagta ccctgttgga gagtgagaaa aatactttca tggaaatctg gaagaagaga 1500
tgggataagt tcatagcaga tgtggctaca aagtga 1536

<210> 548
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 N98-N156Del, mature numbering

<400> 548
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
            100   105   110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
        115   120   125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
    130   135   140
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
145   150   155   160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
                165   170   175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
            180   185   190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
        195   200   205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
    210   215   220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225   230   235   240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
                245   250   255
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
            260   265   270
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
        275   280   285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
    290   295   300

Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
305 310 315 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
325 330 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
340 345 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
355 360 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
370 375 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385 390 395 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
405 410 415
Ile Ala Asp Val Ala Thr Lys
420

<210> 549
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-E148Del, mature numbering

<400> 549
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
100 105 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
115 120 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
130 135 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145 150 155 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
165 170 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
180 185 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
195 200 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
210 215 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225 230 235 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
245 250 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
260 265 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
275 280 285
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
290 295 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305 310 315 320
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro

325 330 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
340 345 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
355 360 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
370 375 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385 390 395 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
405 410 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
420 425 430
Ala Asp Val Ala Thr Lys
435

<210> 550
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147Del, mature numbering

<400> 550
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
100 105 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
115 120 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
130 135 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145 150 155 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
165 170 175
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
180 185 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
195 200 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
210 215 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225 230 235 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
245 250 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
260 265 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
275 280 285
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
290 295 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305 310 315 320
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
325 330 335

```
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
            340                 345                 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
        355                 360                 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
    370                 375                 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385                 390                 395                 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
                405                 410                 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
            420                 425                 430
Ile Ala Asp Val Ala Thr Lys
        435
```

<210> 551
<211> 509
<212> PRT
<213> Homo sapiens

<220>
<223> human (PH20 precursor) (1-509)

<400> 551

```
Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1                5                  10                  15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
            20                  25                  30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
        35                  40                  45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
    50                  55                  60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65                  70                  75                  80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
                85                  90                  95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
            100                 105                 110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
        115                 120                 125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
    130                 135                 140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145                 150                 155                 160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
                165                 170                 175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
            180                 185                 190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
        195                 200                 205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
    210                 215                 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225                 230                 235                 240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
                245                 250                 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
            260                 265                 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
        275                 280                 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
    290                 295                 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305                 310                 315                 320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
                325                 330                 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
```

```
            340                 345                 350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
        355                 360                 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
    370                 375                 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385                 390                 395                 400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
                405                 410                 415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
            420                 425                 430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
        435                 440                 445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
    450                 455                 460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465                 470                 475                 480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
                485                 490                 495
Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
            500                 505


<210> 552
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R125N/P126A, mature numbering


<400> 552
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Asn Ala Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

```
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 553
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S127N/K129S, mature numbering

<400> 553

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Asn Glu
        115                 120                 125
Ser Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
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```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 554
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 P126N/E128T, mature numbering

<400> 554

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Asn Ser Thr
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
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```
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 555
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R112N/I114T, mature numbering

<400> 555

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Asn
            100                 105                 110
Gly Thr Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
```

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 556
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 I134N/L135C/L136T, mature numbering

<400> 556
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

```
        115                 120                 125
Lys Cys Ser Lys Trp Asn Cys Thr Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 557
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 I134N/L135S/L136T, mature numbering

<400> 557

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Asn Ser Thr Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 558
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R142N/Q144S, mature numbering

<400> 558

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
```

```
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Asn Val Ser
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 559
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 E137N/Y139T, mature numbering

<400> 559

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Asn Asp Thr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 560
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 P111N/G113S, mature numbering

<400> 560
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Asn Arg
            100                 105                 110
Ser Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 561
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 F119S, mature numbering

<400> 561
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Ser Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe

450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 562
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 F119K, mature numbering

<400> 562
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Lys Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 563
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y224R, mature numbering

<400> 563
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Arg
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 564
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y224N, mature numbering

<400> 564

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Asn
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
```

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 565
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y191S, mature numbering

<400> 565
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Ser Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 566
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y191D, mature numbering

<400> 566
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Asp Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 567
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 F183K, mature numbering

<400> 567
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser

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                165                 170                 175
Lys Phe Glu Thr Ile Phe Lys Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 568
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y191D/Y224R, mature numbering

<400> 568

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
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        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Asp Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Arg
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 569
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 F109S, mature numbering

<400> 569

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
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65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Ser Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 570
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 F109A, mature numbering

<400> 570
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Ala Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 571
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R118D, mature numbering

<400> 571
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Asp Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 572

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R118A, mature numbering

<400> 572

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Ala Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 573
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y139T, mature numbering

<400> 573
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Thr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly

```
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 574
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 Y139A, mature numbering

<400> 574

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Ala Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
```

370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 575
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 W133S, mature numbering

<400> 575
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Ser Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 576
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 W133T, mature numbering

<400> 576
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Thr Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr

275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 577
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 P124A, mature numbering

<400> 577
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Ala Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 578
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 P124S, mature numbering

<400> 578
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Ser Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

```
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 579
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V99-Q144del, mature numbering

<400> 579

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
            100                 105                 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
        115                 120                 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
    130                 135                 140
```

```
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145                 150                 155                 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro
                165                 170                 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys
            180                 185                 190
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
        195                 200                 205
Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala
    210                 215                 220
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225                 230                 235                 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
                245                 250                 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
            260                 265                 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
        275                 280                 285
Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
    290                 295                 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305                 310                 315                 320
Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
                325                 330                 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
            340                 345                 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
        355                 360                 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
    370                 375                 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385                 390                 395                 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
                405                 410                 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
            420                 425                 430
Val Ala Thr Lys
        435
```

<210> 580
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 580
```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                  10
```

<210> 581
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V99-Q144del->(GGGGS)n, mature numbering, where n = 1 to 5

<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 581

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 582
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(GGGGS)n, mature numbering, where n = 1 to 5

<220>

<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 582

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 583
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V99-Q144del->(GGGGS)1, mature numbering

<400> 583

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 584
<211> 446
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 V99-Q144del->(GGGGS)2, mature numbering

<400> 584
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Val Thr Glu
            100   105   110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115   120   125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130   135   140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145   150   155   160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165   170   175
Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180   185   190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195   200   205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210   215   220
Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225   230   235   240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245   250   255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260   265   270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275   280   285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290   295   300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305   310   315   320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys
                325   330   335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340   345   350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355   360   365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370   375   380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385   390   395   400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405   410   415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420   425   430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440   445

<210> 585
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 V99-Q144del->(GGGGS)3, mature numbering

<400> 585
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            100   105   110
Ser Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu
        115   120   125
Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp
    130   135   140
Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr
145   150   155   160
Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr
                165   170   175
Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val
            180   185   190
Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr
        195   200   205
Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile
    210   215   220
Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val
225   230   235   240
Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro
                245   250   255
Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His
            260   265   270
Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly
        275   280   285
Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly
    290   295   300
Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr
305   310   315   320
Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr
                325   330   335
Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn
            340   345   350
Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr
        355   360   365
Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala
    370   375   380
Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met
385   390   395   400
Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala
                405   410   415
Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr
            420   425   430
Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val
        435   440   445
Ala Thr Lys
    450

<210> 586
<211> 444
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 C105-T147del->(GGGGS)1, mature numbering

<400> 586

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 587
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 C105-T147del->(GGGGS)2, mature numbering

<400> 587

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195                 200                 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210                 215                 220
Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225                 230                 235                 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245                 250                 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260                 265                 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275                 280                 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290                 295                 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305                 310                 315                 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325                 330                 335
Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340                 345                 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355                 360                 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370                 375                 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385                 390                 395                 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405                 410                 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
            420                 425                 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
        435                 440                 445
Lys
```

<210> 588
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 C105-T147del->(GGGGS)3, mature numbering

<400> 588
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Gly Ser Gly Gly Gly Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn
        115                 120                 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
    130                 135                 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145                 150                 155                 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
                165                 170                 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
            180                 185                 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
        195                 200                 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210                 215                 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
225                 230                 235                 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245                 250                 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260                 265                 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445
Ala Asp Val Ala Thr Lys
    450
```

<210> 589
<211> 441

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/V99-Q144del->(GGGGS)1, mature numbering

<400> 589

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 590
<211> 446

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/V99-Q144del->(GGGGS)2, mature numbering

<400> 590

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Val Thr Glu
            100                 105                 110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115                 120                 125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130                 135                 140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145                 150                 155                 160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165                 170                 175
Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180                 185                 190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195                 200                 205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210                 215                 220
Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225                 230                 235                 240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245                 250                 255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260                 265                 270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275                 280                 285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290                 295                 300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305                 310                 315                 320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys
                325                 330                 335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340                 345                 350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355                 360                 365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370                 375                 380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385                 390                 395                 400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405                 410                 415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420                 425                 430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440                 445
```

<210> 591
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/V99-Q144del->(GGGGS)3, mature numbering

<400> 591

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            100                 105                 110
Ser Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu
        115                 120                 125
Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp
    130                 135                 140
Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr
145                 150                 155                 160
Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr
                165                 170                 175
Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val
            180                 185                 190
Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr
        195                 200                 205
Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile
    210                 215                 220
Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val
225                 230                 235                 240
Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro
                245                 250                 255
Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His
            260                 265                 270
Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly
        275                 280                 285
Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly
    290                 295                 300
Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr
305                 310                 315                 320
Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr
                325                 330                 335
Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn
            340                 345                 350
Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr
        355                 360                 365
Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala
    370                 375                 380
Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met
385                 390                 395                 400
Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala
                405                 410                 415
Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr
            420                 425                 430
Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val
        435                 440                 445
Ala Thr Lys
    450
```

<210> 592
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(GGGGS)1, mature numbering

<400> 592

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 593
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(GGGGS)2, mature numbering

<400> 593
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
            100   105   110
Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115   120   125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130   135   140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145   150   155   160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165   170   175
Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu
            180   185   190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195   200   205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210   215   220
Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225   230   235   240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245   250   255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260   265   270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275   280   285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290   295   300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305   310   315   320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325   330   335
Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340   345   350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355   360   365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370   375   380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385   390   395   400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405   410   415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
            420   425   430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
        435   440   445
Lys

<210> 594
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(GGGGS)3, mature numbering

<400> 594
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
            100   105   110
Gly Ser Gly Gly Gly Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn
        115   120   125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
    130   135   140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145   150   155   160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
                165   170   175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
            180   185   190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
        195   200   205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210   215   220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
225   230   235   240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245   250   255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260   265   270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275   280   285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290   295   300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305   310   315   320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325   330   335
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
            340   345   350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355   360   365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370   375   380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385   390   395   400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405   410   415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420   425   430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435   440   445

Ala Asp Val Ala Thr Lys
    450

<210> 595
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker Ser(Gly4Ser)n

<220>
<221> REPEAT
<222> (2)...(6)
<223> occurring 1, 2, 3, 4, 5 or more times

<400> 595
Ser Gly Gly Gly Gly Ser
 1   5

<210> 596
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/I1insNAS, mature numbering

<400> 596
Asn Ala Ser Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys
 1   5   10   15
Met Met Arg Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu
            20   25   30
Ala Asn Glu Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala
        35   40   45
Met Arg Thr Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys
    50   55   60
His Leu Ile Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro
65   70   75   80
Lys Gly Ala Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp
                85   90   95
Trp Leu Val Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe
            100   105   110
Thr Pro Arg Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg
        115   120   125
Pro Ser Glu Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys
    130   135   140
Arg Val Gln Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe
145   150   155   160
Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val
                165   170   175
Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile
            180   185   190
His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu
        195   200   205
Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu
    210   215   220
Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val
225   230   235   240
Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu
                245   250   255
Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val
            260   265   270
Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys
        275   280   285
Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr

290 295 300
Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys
305 310 315 320
Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp
325 330 335
Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn
340 345 350
Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val
355 360 365
Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile
370 375 380
Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val
385 390 395 400
Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp
405 410 415
Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val
420 425 430
Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln
435 440 445
Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys
450 455 460
Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala
465 470 475 480
Asp Val Ala Thr Lys
485

<210> 597
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R20N/V22S, mature numbering

<400> 597
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Asn Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 598
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371N/D373S, mature numbering

<400> 598

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
```

Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Asn Lys Ser Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 599
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K372N/I374S, mature numbering

<400> 599
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

```
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Asn Asp Ser Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 600
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/T403N/H405S, mature numbering

<400> 600

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Asn Gly Ser Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 601
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/G404N/P406S, mature numbering

<400> 601
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Asn His Ser Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 602
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)15,
mature numbering

<400> 602

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
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Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Gly Gly Gly Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn
        115                 120                 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
    130                 135                 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145                 150                 155                 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
                165                 170                 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
            180                 185                 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
        195                 200                 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210                 215                 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
225                 230                 235                 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245                 250                 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260                 265                 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445
Ala Asp Val Ala Thr Lys
    450
```

<210> 603
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)10,
mature numbering

<400> 603

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195                 200                 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210                 215                 220
Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225                 230                 235                 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245                 250                 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260                 265                 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275                 280                 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290                 295                 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305                 310                 315                 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325                 330                 335
Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340                 345                 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355                 360                 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370                 375                 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385                 390                 395                 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405                 410                 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
            420                 425                 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
        435                 440                 445
Lys
```

<210> 604
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)7,
mature numbering

<400> 604
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Glu
            100   105   110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115   120   125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130   135   140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145   150   155   160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165   170   175
Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180   185   190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195   200   205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210   215   220
Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225   230   235   240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245   250   255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260   265   270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275   280   285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290   295   300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305   310   315   320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys
                325   330   335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340   345   350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355   360   365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370   375   380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385   390   395   400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405   410   415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420   425   430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440   445

<210> 605
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)5,
      mature numbering

<400> 605
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Glu Phe Asp
            100   105   110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115   120   125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130   135   140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145   150   155   160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165   170   175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180   185   190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195   200   205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
    210   215   220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225   230   235   240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245   250   255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260   265   270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275   280   285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290   295   300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305   310   315   320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325   330   335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340   345   350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355   360   365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370   375   380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385   390   395   400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405   410   415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420   425   430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440

<210> 606
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)3,
      mature numbering

<400> 606
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Glu Phe Asp Asp Ser
            100   105   110
Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr
        115   120   125
Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr
    130   135   140
Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe
145   150   155   160
Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile
                165   170   175
Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp
            180   185   190
Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val
        195   200   205
Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His
    210   215   220
Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met
225   230   235   240
Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val
                245   250   255
Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu
            260   265   270
Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala
        275   280   285
Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp
    290   295   300
Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser
305   310   315   320
Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile
                325   330   335
Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu
            340   345   350
Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val
        355   360   365
Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr
    370   375   380
Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu
385   390   395   400
Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu
                405   410   415
Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp
            420   425   430
Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440

<210> 607
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R125N/P126A, mature
      numbering

<400> 607
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Asn Ala Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 608
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S127N/K129S, mature numbering

<400> 608

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Asn Glu
        115                 120                 125
Ser Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 609
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/P126N/E128T, mature numbering

<400> 609

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Asn Ser Thr
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
```

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 610
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R112N/I114T, mature numbering

<400> 610
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Asn
100 105 110
Gly Thr Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 611
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/I134N/L135C/L136T, mature numbering

<400> 611
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Asn Cys Thr Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 612
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/I134N/L135S/L136T, mature numbering

<400> 612
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Asn Ser Thr Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 613
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R142N/Q144S, mature numbering

<400> 613

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Asn Val Ser
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 614
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E137N/Y139T, mature numbering

<400> 614

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Asn Asp Thr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
```

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 615
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/P111N/G113S, mature numbering

<400> 615

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Asn Arg
            100                 105                 110
Ser Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 616
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/F119S, mature numbering

<400> 616
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg

```
            100                 105                 110
Gly Ile Met Gln Phe Arg Ser Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 617
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/F119K, mature numbering

<400> 617

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Lys Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 618
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y224R, mature numbering

<400> 618

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
```

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Arg
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 619
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y224N, mature numbering

<400> 619
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Asn
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 620
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y191S, mature numbering

<400> 620
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Ser Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 621
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y191D, mature numbering

<400> 621
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Asp Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
```

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 622
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/F183K, mature numbering

<400> 622
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Lys Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 623
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y191D/Y224R, mature numbering

<400> 623
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Asp Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Arg
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 624
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/F109S, mature numbering

<400> 624

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Ser Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
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```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 625
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/F109A, mature numbering

<400> 625

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Ala Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 626
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R118D, mature numbering

<400> 626
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Asp Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 627
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R118A, mature numbering

<400> 627

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Ala Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 628
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y139T, mature numbering

<400> 628
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Thr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 629
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/Y139A, mature numbering

<400> 629
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Ala Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 630
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/W133S, mature numbering

<400> 630
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Ser Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 631
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/W133T, mature numbering

<400> 631

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
```

```
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Thr Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 632
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/P124A, mature numbering

<400> 632

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Ala Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 633
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/P124S, mature numbering

<400> 633
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Ser Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 634
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V99-Q144del->(GGGGS)1,
mature numbering

<400> 634
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100   105   110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115   120   125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130   135   140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145   150   155   160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165   170   175
Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180   185   190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195   200   205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg
    210   215   220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225   230   235   240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245   250   255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260   265   270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275   280   285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290   295   300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305   310   315   320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu
                325   330   335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340   345   350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355   360   365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370   375   380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385   390   395   400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405   410   415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420   425   430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440

<210> 635
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V99-Q144del->(GGGGS)2,
mature numbering

<400> 635
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Val Thr Glu
            100   105   110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115   120   125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130   135   140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145   150   155   160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165   170   175
Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180   185   190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195   200   205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210   215   220
Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225   230   235   240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245   250   255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260   265   270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275   280   285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290   295   300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305   310   315   320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys
                325   330   335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340   345   350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355   360   365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370   375   380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385   390   395   400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405   410   415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420   425   430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435   440   445

<210> 636
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V99-Q144del->(GGGGS)3,
mature numbering

<400> 636
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            100   105   110
Ser Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu
        115   120   125
Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp
    130   135   140
Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr
145   150   155   160
Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr
                165   170   175
Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val
            180   185   190
Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr
        195   200   205
Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile
    210   215   220
Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val
225   230   235   240
Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro
                245   250   255
Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His
            260   265   270
Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly
        275   280   285
Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly
    290   295   300
Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr
305   310   315   320
Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr
                325   330   335
Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn
            340   345   350
Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr
        355   360   365
Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala
    370   375   380
Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met
385   390   395   400
Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala
                405   410   415
Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr
            420   425   430
Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val
        435   440   445
Ala Thr Lys

450

<210> 637
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(GGGGS)1,
mature numbering

<400> 637
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
100 105 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
115 120 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
130 135 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145 150 155 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
180 185 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
195 200 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
210 215 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225 230 235 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
245 250 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
260 265 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
275 280 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
290 295 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305 310 315 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430

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Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 638
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(GGGGS)2,
      mature numbering


<400> 638
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195                 200                 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210                 215                 220
Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225                 230                 235                 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245                 250                 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260                 265                 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275                 280                 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290                 295                 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305                 310                 315                 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325                 330                 335
Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340                 345                 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355                 360                 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370                 375                 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385                 390                 395                 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405                 410                 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
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420 425 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
435 440 445
Lys

<210> 639
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(GGGGS)3,
mature numbering

<400> 639
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110
Gly Ser Gly Gly Gly Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn
115 120 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
130 135 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145 150 155 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
165 170 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
180 185 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
195 200 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
210 215 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
225 230 235 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
245 250 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
260 265 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
275 280 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
290 295 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305 310 315 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
325 330 335
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
340 345 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
355 360 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
370 375 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385 390 395 400

Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
405 410 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
420 425 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
435 440 445
Ala Asp Val Ala Thr Lys
450

<210> 640
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/V99-Q144del->(GGGGS)1, mature
numbering

<400> 640
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
100 105 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
115 120 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
130 135 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145 150 155 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
165 170 175
Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
180 185 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
195 200 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg
210 215 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225 230 235 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
245 250 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
260 265 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
275 280 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
290 295 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305 310 315 320
His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu
325 330 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
340 345 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
355 360 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp

370 375 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385 390 395 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
405 410 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
420 425 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 641
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/V99-Q144del->(GGGGS)2, mature
numbering

<400> 641
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Val Thr Glu
100 105 110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
115 120 125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
130 135 140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145 150 155 160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
165 170 175
Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly
180 185 190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
195 200 205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
210 215 220
Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225 230 235 240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
245 250 255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
260 265 270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
275 280 285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
290 295 300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305 310 315 320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys
325 330 335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
340 345 350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
355 360 365

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His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370                 375                 380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385                 390                 395                 400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405                 410                 415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420                 425                 430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440                 445


<210> 642
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
      R219Q/S262N/K371D/V99-Q144del->(GGGGS)3, mature
      numbering

<400> 642
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            100                 105                 110
Ser Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu
        115                 120                 125
Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp
    130                 135                 140
Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr
145                 150                 155                 160
Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr
                165                 170                 175
Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val
            180                 185                 190
Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr
        195                 200                 205
Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile
    210                 215                 220
Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val
225                 230                 235                 240
Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro
                245                 250                 255
Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His
            260                 265                 270
Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly
        275                 280                 285
Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly
    290                 295                 300
Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr
305                 310                 315                 320
Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr
                325                 330                 335
Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn
            340                 345                 350
Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr
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        355                 360                 365
Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala
    370                 375                 380
Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met
385                 390                 395                 400
Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala
                405                 410                 415
Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr
            420                 425                 430
Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val
        435                 440                 445
Ala Thr Lys
    450
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<210> 643
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/C105-T147del->(GGGGS)1, mature
numbering

<400> 643

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
```

325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 644
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/C105-T147del->(GGGGS)2, mature
numbering

<400> 644
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110
Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
115 120 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
130 135 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145 150 155 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
165 170 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu
180 185 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
195 200 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
210 215 220
Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225 230 235 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
245 250 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
260 265 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
275 280 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
290 295 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile

305 310 315 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
325 330 335
Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
340 345 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
355 360 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
370 375 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385 390 395 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
405 410 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
420 425 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
435 440 445
Lys

<210> 645
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/C105-T147del->(GGGGS)3, mature
numbering

<400> 645
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Gly Gly Gly
100 105 110
Gly Ser Gly Gly Gly Gly Ser Glu Phe Asp Asp Ser Leu Leu Arg Asn
115 120 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
130 135 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145 150 155 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
165 170 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
180 185 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
195 200 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
210 215 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
225 230 235 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
245 250 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
260 265 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala

```
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445
Ala Asp Val Ala Thr Lys
    450


<210> 646
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)n, mature
      numbering,
      where n = 2 to 20


<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
      14, 15, 16, 17, 18, 19 or 20 times


<400> 646
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
            100                 105                 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
        115                 120                 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
    130                 135                 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145                 150                 155                 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
                165                 170                 175
Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
            180                 185                 190
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```
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
        195                 200                 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser
    210                 215                 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu
225                 230                 235                 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
                245                 250                 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
            260                 265                 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
        275                 280                 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
    290                 295                 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305                 310                 315                 320
Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val
                325                 330                 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
            340                 345                 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
        355                 360                 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
    370                 375                 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385                 390                 395                 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
                405                 410                 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
            420                 425                 430
Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 647
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)15, mature
      numbering

<400> 647
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Gly Gly Gly Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn
        115                 120                 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
    130                 135                 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145                 150                 155                 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
                165                 170                 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
            180                 185                 190
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```
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
        195                 200                 205
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210                 215                 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
225                 230                 235                 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245                 250                 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260                 265                 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445
Ala Asp Val Ala Thr Lys
    450
```

<210> 648
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)10, mature numbering

<400> 648

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
```

```
Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
        195                 200                 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
    210                 215                 220
Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225                 230                 235                 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
                245                 250                 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
            260                 265                 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
        275                 280                 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
    290                 295                 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305                 310                 315                 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
                325                 330                 335
Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
            340                 345                 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
        355                 360                 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
    370                 375                 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385                 390                 395                 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
                405                 410                 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
            420                 425                 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
        435                 440                 445
Lys
```

<210> 649
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)7, mature numbering

<400> 649

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Glu
            100                 105                 110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
        115                 120                 125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
    130                 135                 140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145                 150                 155                 160
```

```
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
                165                 170                 175
Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly
            180                 185                 190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
        195                 200                 205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
    210                 215                 220
Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225                 230                 235                 240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
                245                 250                 255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
            260                 265                 270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
        275                 280                 285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
    290                 295                 300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305                 310                 315                 320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys
                325                 330                 335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
            340                 345                 350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
        355                 360                 365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
    370                 375                 380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385                 390                 395                 400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
                405                 410                 415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
            420                 425                 430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440                 445


<210> 650
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)5, mature
      numbering

<400> 650
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
```

Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
180 185 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
195 200 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
210 215 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225 230 235 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
245 250 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
260 265 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
275 280 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
290 295 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305 310 315 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 651
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(Gly)3, mature numbering

<400> 651
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Glu Phe Asp Asp Ser
100 105 110
Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr
115 120 125
Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr
130 135 140
Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe
145 150 155 160

```
Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile
                165                 170                 175
Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp
            180                 185                 190
Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val
        195                 200                 205
Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His
    210                 215                 220
Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met
225                 230                 235                 240
Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val
                245                 250                 255
Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu
            260                 265                 270
Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala
        275                 280                 285
Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp
    290                 295                 300
Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser
305                 310                 315                 320
Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile
                325                 330                 335
Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu
            340                 345                 350
Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val
        355                 360                 365
Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr
    370                 375                 380
Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu
385                 390                 395                 400
Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu
                405                 410                 415
Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp
            420                 425                 430
Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 652
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/V99-Q144del->(GGGGS)n, mature
      numbering,
      where n = 1 to 5


<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 652
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
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            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 653
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147del->(GGGGS)n, mature
      numbering, where n = 1 to 5


<220>
<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 653
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
```

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
100 105 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
115 120 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
130 135 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145 150 155 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
180 185 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
195 200 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
210 215 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225 230 235 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
245 250 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
260 265 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
275 280 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
290 295 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305 310 315 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 654
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/N98-N156Del, mature numbering

<400> 654
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60

Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
100 105 110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
115 120 125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
130 135 140
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
145 150 155 160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
165 170 175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
180 185 190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
195 200 205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
210 215 220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225 230 235 240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
245 250 255
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
260 265 270
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
275 280 285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
290 295 300
Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys
305 310 315 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
325 330 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
340 345 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
355 360 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
370 375 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385 390 395 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
405 410 415
Ile Ala Asp Val Ala Thr Lys
420

<210> 655
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-E148Del, mature numbering

<400> 655
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

85 90 95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
100 105 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
115 120 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
130 135 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145 150 155 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu
165 170 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
180 185 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
195 200 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
210 215 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225 230 235 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
245 250 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
260 265 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
275 280 285
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
290 295 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305 310 315 320
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
325 330 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
340 345 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
355 360 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
370 375 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385 390 395 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
405 410 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
420 425 430
Ala Asp Val Ala Thr Lys
435

<210> 656
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/C105-T147Del, mature numbering

<400> 656
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95

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Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
            100                 105                 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
        115                 120                 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
    130                 135                 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145                 150                 155                 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
                165                 170                 175
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
            180                 185                 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
        195                 200                 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
    210                 215                 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225                 230                 235                 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
                245                 250                 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
            260                 265                 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
        275                 280                 285
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
    290                 295                 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305                 310                 315                 320
Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys
                325                 330                 335
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
            340                 345                 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
        355                 360                 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
    370                 375                 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385                 390                 395                 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
                405                 410                 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
            420                 425                 430
Ile Ala Asp Val Ala Thr Lys
        435


<210> 657
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 K371D/V99-Q144del, mature numbering

<400> 657
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
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            100                 105                 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
        115                 120                 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
    130                 135                 140
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145                 150                 155                 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro
                165                 170                 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys
            180                 185                 190
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
        195                 200                 205
Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala
    210                 215                 220
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225                 230                 235                 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
                245                 250                 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
            260                 265                 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
        275                 280                 285
Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
    290                 295                 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305                 310                 315                 320
Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
                325                 330                 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
            340                 345                 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
        355                 360                 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
    370                 375                 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385                 390                 395                 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
                405                 410                 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
            420                 425                 430
Val Ala Thr Lys
        435


<210> 658
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(Gly)n,
      mature numbering, where n = 2 to 20


<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
      14, 15, 16, 17, 18, 19 or 20 times


<400> 658
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
            100                 105                 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
        115                 120                 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
    130                 135                 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145                 150                 155                 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
                165                 170                 175
Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
            180                 185                 190
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
        195                 200                 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser
    210                 215                 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu
225                 230                 235                 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
                245                 250                 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
            260                 265                 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
        275                 280                 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
    290                 295                 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305                 310                 315                 320
Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val
                325                 330                 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
            340                 345                 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
        355                 360                 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
    370                 375                 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385                 390                 395                 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
                405                 410                 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Thr Lys Lys Arg Trp Asp Lys
            420                 425                 430
Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 659
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11A, mature numbering

<400> 659
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
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Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 660
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11D, mature numbering

<400> 660

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Asp Glu Lys Met Met Arg
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 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 661
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11E, mature numbering

<400> 661

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Glu Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 662
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K13A, mature numbering

<400> 662

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Ala Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 663
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K13D, mature numbering

<400> 663
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Asp Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 664
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V99-Q144del->(GGGGS)n,
mature numbering,
where n = 1 to 5

<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 664
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
100 105 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
115 120 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
130 135 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145 150 155 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
165 170 175
Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
180 185 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
195 200 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg
210 215 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225 230 235 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
245 250 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
260 265 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
275 280 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
290 295 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305 310 315 320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu

```
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 665
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147del->(GGGGS)n,
      mature
      numbering, where n = 1 to 5


<220>
<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 665
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
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```
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 666
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/N98-N156Del, mature
      numbering

<400> 666
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
            100                 105                 110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
        115                 120                 125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
    130                 135                 140
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
145                 150                 155                 160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
                165                 170                 175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
            180                 185                 190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
        195                 200                 205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
    210                 215                 220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225                 230                 235                 240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
                245                 250                 255
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
            260                 265                 270
```

Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
275 280 285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
290 295 300
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
305 310 315 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
325 330 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
340 345 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
355 360 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
370 375 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385 390 395 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
405 410 415
Ile Ala Asp Val Ala Thr Lys
420

<210> 667
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-E148Del, mature numbering

<400> 667
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
100 105 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
115 120 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
130 135 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145 150 155 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
165 170 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
180 185 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
195 200 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
210 215 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225 230 235 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
245 250 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
260 265 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
275 280 285

```
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
    290                 295                 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305                 310                 315                 320
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
                325                 330                 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
            340                 345                 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
        355                 360                 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
    370                 375                 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385                 390                 395                 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
                405                 410                 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
            420                 425                 430
Ala Asp Val Ala Thr Lys
        435


<210> 668
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/C105-T147Del, mature
      numbering

<400> 668
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
            100                 105                 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
        115                 120                 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
    130                 135                 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145                 150                 155                 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
                165                 170                 175
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
            180                 185                 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
        195                 200                 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
    210                 215                 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225                 230                 235                 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
                245                 250                 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
            260                 265                 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
        275                 280                 285
```

```
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
    290                 295                 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305                 310                 315                 320
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
                325                 330                 335
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
            340                 345                 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
        355                 360                 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
    370                 375                 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385                 390                 395                 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
                405                 410                 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
            420                 425                 430
Ile Ala Asp Val Ala Thr Lys
        435
```

<210> 669
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V99-Q144del, mature numbering

<400> 669

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
            100                 105                 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
        115                 120                 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
    130                 135                 140
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145                 150                 155                 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro
                165                 170                 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys
            180                 185                 190
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
        195                 200                 205
Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala
    210                 215                 220
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225                 230                 235                 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
                245                 250                 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
            260                 265                 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
        275                 280                 285
```

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Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
    290                 295                 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305                 310                 315                 320
Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
                325                 330                 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
            340                 345                 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
        355                 360                 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
    370                 375                 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385                 390                 395                 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
                405                 410                 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
            420                 425                 430
Val Ala Thr Lys
        435


<210> 670
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-T147del->(Gly)n,
      mature numbering,
      where n = 2 to 20


<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
      14, 15, 16, 17, 18, 19 or 20 times


<400> 670
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
            100                 105                 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
        115                 120                 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
    130                 135                 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145                 150                 155                 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
                165                 170                 175
Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
            180                 185                 190
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
        195                 200                 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser
```

210 215 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu
225 230 235 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
245 250 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
260 265 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
275 280 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
290 295 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305 310 315 320
Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val
325 330 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
340 345 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
355 360 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
370 375 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385 390 395 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
405 410 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
420 425 430
Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 671
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/C105-T147del->(Gly)15, mature
numbering

<400> 671
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110
Gly Gly Gly Gly Gly Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn
115 120 125
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
130 135 140
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
145 150 155 160
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
165 170 175
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
180 185 190
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
195 200 205

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Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
    210                 215                 220
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
225                 230                 235                 240
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
                245                 250                 255
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
            260                 265                 270
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
        275                 280                 285
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
    290                 295                 300
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
305                 310                 315                 320
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
                325                 330                 335
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
            340                 345                 350
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
        355                 360                 365
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
    370                 375                 380
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
385                 390                 395                 400
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
                405                 410                 415
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
            420                 425                 430
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
        435                 440                 445


<210> 672
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
      R219Q/S262N/K371D/C105-T147del->(Gly)10, mature
      numbering

<400> 672
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110
Gly Gly Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr
        115                 120                 125
Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys
    130                 135                 140
Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro
145                 150                 155                 160
Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp
                165                 170                 175
Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu
            180                 185                 190
Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln
```

195 200 205
Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile
210 215 220
Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala
225 230 235 240
Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val
245 250 255
Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu
260 265 270
His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys
275 280 285
Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser
290 295 300
Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile
305 310 315 320
Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser
325 330 335
Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val
340 345 350
Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met
355 360 365
Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe
370 375 380
Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile
385 390 395 400
Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn
405 410 415
Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met
420 425 430
Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr
435 440 445
Lys

<210> 673
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-T147del->(Gly)7,
mature numbering

<400> 673
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Gly Gly Glu
100 105 110
Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro
115 120 125
Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr
130 135 140
Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg
145 150 155 160
Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu
165 170 175
Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly

180 185 190
Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala
195 200 205
Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile
210 215 220
Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile
225 230 235 240
Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly
245 250 255
Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr
260 265 270
Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr
275 280 285
Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg
290 295 300
Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly
305 310 315 320
Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys
325 330 335
Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu
340 345 350
Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly
355 360 365
His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys
370 375 380
Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met
385 390 395 400
Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys
405 410 415
Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp
420 425 430
Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440 445

<210> 674
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-T147del->(Gly)5,
mature numbering

<400> 674
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Gly Glu Phe Asp
100 105 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
115 120 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
130 135 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145 150 155 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His

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            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 675
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-T147del->(Gly)3,
mature numbering

<400> 675

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Glu Phe Asp Asp Ser
            100                 105                 110
Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr
        115                 120                 125
Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr
    130                 135                 140
Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe
145                 150                 155                 160
Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile
                165                 170                 175
Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp
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            180                 185                 190
Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val
        195                 200                 205
Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His
    210                 215                 220
Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met
225                 230                 235                 240
Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val
                245                 250                 255
Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu
            260                 265                 270
Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala
        275                 280                 285
Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp
    290                 295                 300
Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser
305                 310                 315                 320
Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile
                325                 330                 335
Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu
            340                 345                 350
Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val
        355                 360                 365
Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr
    370                 375                 380
Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu
385                 390                 395                 400
Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu
                405                 410                 415
Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp
            420                 425                 430
Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440
```

<210> 676
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
R219Q/S262N/K371D/V99-Q144del->(GGGGS)n, mature
numbering, where n = 1 to 5

<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 676

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
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Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 677
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2
      R219Q/S262N/K371D/C105-T147del->(GGGGS)n, mature
      numbering, where n = 1 to 5


<220>
<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 677
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
100 105 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
115 120 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
130 135 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145 150 155 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
180 185 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
195 200 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
210 215 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225 230 235 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
245 250 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
260 265 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
275 280 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
290 295 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305 310 315 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile
325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 678
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/N98-N156Del, mature numbering

<400> 678
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
100 105 110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
115 120 125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
130 135 140
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
145 150 155 160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
165 170 175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
180 185 190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
195 200 205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
210 215 220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225 230 235 240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
245 250 255
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
260 265 270
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
275 280 285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
290 295 300
Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys
305 310 315 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
325 330 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
340 345 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
355 360 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
370 375 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385 390 395 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
405 410 415
Ile Ala Asp Val Ala Thr Lys
420

<210> 679
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-E148Del, mature numbering

<400> 679
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

85 90 95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
100 105 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
115 120 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
130 135 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145 150 155 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
165 170 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
180 185 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
195 200 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
210 215 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225 230 235 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
245 250 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
260 265 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
275 280 285
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
290 295 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305 310 315 320
Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro
325 330 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
340 345 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
355 360 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
370 375 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385 390 395 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
405 410 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
420 425 430
Ala Asp Val Ala Thr Lys
435

<210> 680
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/C105-T147Del, mature numbering

<400> 680
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

85 90 95
Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
100 105 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
115 120 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
130 135 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145 150 155 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
165 170 175
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
180 185 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
195 200 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
210 215 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225 230 235 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
245 250 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
260 265 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
275 280 285
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
290 295 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305 310 315 320
Ala Val Arg Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys
325 330 335
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
340 345 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
355 360 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
370 375 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385 390 395 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
405 410 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
420 425 430
Ile Ala Asp Val Ala Thr Lys
435

<210> 681
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371D/V99-Q144del, mature numbering

<400> 681
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

85 90 95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
100 105 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
115 120 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
130 135 140
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145 150 155 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro
165 170 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys
180 185 190
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
195 200 205
Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala
210 215 220
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225 230 235 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
245 250 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
260 265 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
275 280 285
Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
290 295 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305 310 315 320
Thr Tyr Ser Trp Asp Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
325 330 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
340 345 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
355 360 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
370 375 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385 390 395 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
405 410 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
420 425 430
Val Ala Thr Lys
435

<210> 682
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K13E, mature numbering

<400> 682
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Glu Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95

Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 683
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K371A, mature numbering

<400> 683
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 684
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K372A, mature numbering

<400> 684
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Ala Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 685
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 R219Q/S262N/K372D, mature numbering

<400> 685

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Asp Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 686

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K372E, mature numbering

<400> 686

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Glu Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 687
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K452A, mature numbering

<400> 687

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
```

435 440 445
Asn Ser Ile Ala Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 688
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K452D, mature numbering

<400> 688
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Asp Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 689
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K452E, mature numbering

<400> 689
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Glu Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 690
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R20A, mature numbering

<400> 690

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 691
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R20D, mature numbering

<400> 691

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Asp Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

```
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 692
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R366A, mature numbering

<400> 692

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Ala Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 693
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R366D, mature numbering

<400> 693

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

```
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Asp Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 694
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R366E, mature numbering

<400> 694

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
```

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Glu Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 695
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264A, mature numbering

<400> 695
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Ala Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 696
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264Q, mature numbering

<400> 696
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80

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Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Gln Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 697
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264N, mature numbering

<400> 697

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Asn Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 698
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264G, mature numbering

<400> 698

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Gly Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 699
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219K/S262N, mature numbering

<400> 699
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Lys Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 700
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219N/S262N, mature numbering

<400> 700
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Asn Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 701
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219A/S262N, mature numbering

<400> 701
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ala Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly

420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 702
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221A, mature numbering

<400> 702
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Ala Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 703
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221V, mature numbering

<400> 703
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Val Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg

340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 704
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221G, mature numbering

<400> 704
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Gly Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 705
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179D, mature numbering

<400> 705
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Asp Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 706
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179A, mature numbering

<400> 706
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Ala Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220

Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 707
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179S, mature numbering

<400> 707
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Ser Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

```
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 708
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179T, mature numbering

<400> 708

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
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Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Thr Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 709
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179V, mature numbering

<400> 709

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
```

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            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Val Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 710
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179G, mature numbering

<400> 710

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Gly Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 711
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262A, mature numbering

<400> 711

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
```

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ala Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 712
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262V, mature numbering

<400> 712
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Val Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 713
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262M, mature numbering

<400> 713
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Met Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 714
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11A/R20A, mature numbering

<400> 714
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
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Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 715
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11A/R20A/K371A, mature numbering

<400> 715
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 716
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R20A/K371A, mature numbering

<400> 716
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

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Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 717
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K11A/K371A, mature numbering

<400> 717

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
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Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 718
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K26A, mature numbering

<400> 718
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Ala Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 719
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K26D, mature numbering

<400> 719
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Asp Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220

Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 720
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K26E, mature numbering

<400> 720
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Glu Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

```
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 721
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R217A, mature numbering

<400> 721

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Ala Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 722
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R217D, mature numbering

<400> 722

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
```

```
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Asp Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 723
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R217E, mature numbering

<400> 723

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Glu Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 724
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K258A, mature numbering

<400> 724
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Ala Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 725
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K258D, mature numbering

<400> 725
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Asp Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 726
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K258E, mature numbering

<400> 726

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Glu Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 727
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R277A, mature numbering

<400> 727
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Ala Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 728
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R277D, mature numbering

<400> 728
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Asp Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 729
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R277E, mature numbering

<400> 729
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Glu Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 730
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R283A, mature numbering

<400> 730
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Ala Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 731
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R283D, mature numbering

<400> 731
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Asp Ile Lys Phe Pro Thr
275 280 285

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 732
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R283E, mature numbering

<400> 732

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
```

245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Glu Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 733
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K309A, mature numbering

<400> 733
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205

```
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Ala Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 734
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K309D, mature numbering

<400> 734

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
```

```
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Asp Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 735
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K309E, mature numbering

<400> 735

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Glu Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 736
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K317A, mature numbering

<400> 736
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

```
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Ala Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 737
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K317D, mature numbering

<400> 737

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Asp Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 738
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K317E, mature numbering

<400> 738

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
```

```
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Glu Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 739
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K321A, mature numbering

<400> 739

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Ala Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 740
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K321D, mature numbering

<400> 740

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Asp Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 741
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K321E, mature numbering

<400> 741
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Glu Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 742
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R352A, mature numbering

<400> 742
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Ala
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu

385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 743
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R352D, mature numbering

<400> 743
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Asp
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 744
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R352E, mature numbering

<400> 744

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
```

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Glu
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 745
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R441A, mature numbering

<400> 745
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Ala Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 746
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R441D, mature numbering

<400> 746

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
```

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Asp Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 747
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/R441E, mature numbering

<400> 747
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Glu Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 748
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K444A, mature numbering

<400> 748

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
```

```
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Ala Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 749
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K444D, mature numbering

<400> 749

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Asp Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 750
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K444E, mature numbering

<400> 750

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Glu Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 751
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K461A, mature numbering

<400> 751
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Ala Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 752
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K461D, mature numbering

<400> 752
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Asp Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 753
<211> 482
<212> PRT

<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K461E, mature numbering

<400> 753

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Glu Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 754
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K469A, mature numbering

<400> 754
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe

```
    450                 455                 460
Met Glu Ile Trp Ala Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 755
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K469D, mature numbering

<400> 755

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
```

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Asp Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 756
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K469E, mature numbering

<400> 756
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln

370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Glu Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 757
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K470A, mature numbering

<400> 757
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

```
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Ala Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 758
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K470D, mature numbering

<400> 758

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
```

290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Asp Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 759
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K470E, mature numbering

<400> 759
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Glu Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 760
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86A, mature numbering

<400> 760

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Ala Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
```

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 761
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86C, mature numbering

<400> 761
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Cys Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 762
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86E, mature numbering

<400> 762

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Glu Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
```

130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 763
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86F, mature numbering

<400> 763
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Phe Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95

Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 764
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86G, mature numbering

<400> 764
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Gly Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 765
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86H, mature numbering

<400> 765
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His His Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 766
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 R219Q/S262N/D86I, mature numbering

<400> 766

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Ile Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 767

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86K, mature numbering

<400> 767

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Lys Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 768
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86L, mature numbering

<400> 768

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Leu Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
```

435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 769
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86M, mature numbering

<400> 769
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Met Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 770
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86N, mature numbering

<400> 770
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asn Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 771
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86P, mature numbering

<400> 771

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Pro Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 772
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86Q, mature numbering

<400> 772

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Gln Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 773
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86R, mature numbering

<400> 773
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Arg Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 774
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86S, mature numbering

<400> 774

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Ser Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 775
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86T, mature numbering

<400> 775
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Thr Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 776
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86V, mature numbering

<400> 776
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Val Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

```
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 777
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86W, mature numbering

<400> 777

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Trp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 778
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/D86Y, mature numbering

<400> 778

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
```

```
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Tyr Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 779
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179C, mature numbering

<400> 779

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Cys Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 780
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179F, mature numbering

<400> 780
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Phe Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 781
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179H, mature numbering

<400> 781
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe His Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 782
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179I, mature numbering

<400> 782
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Ile Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly

420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 783
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179K, mature numbering

<400> 783
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Lys Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 784
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179L, mature numbering

<400> 784
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Leu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg

340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 785
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179M, mature numbering

<400> 785
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Met Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 786
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179N, mature numbering

<400> 786
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Asn Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 787
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179P, mature numbering

<400> 787
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Pro Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220

Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 788
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179Q, mature numbering

<400> 788
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Gln Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala

```
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 789
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179R, mature numbering

<400> 789

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
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Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Arg Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 790
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179W, mature numbering

<400> 790

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
```

100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Trp Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 791
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/E179Y, mature numbering

<400> 791
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60

```
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Tyr Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 792
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219C/S262N, mature numbering

<400> 792

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
```

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Cys Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 793
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219D/S262N, mature numbering

<400> 793
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Asp Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 794
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219E/S262N, mature numbering

<400> 794
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Glu Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 795
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219F/S262N, mature numbering

<400> 795
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Phe Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
```

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 796
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219G/S262N, mature numbering

<400> 796
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gly Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 797
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219H/S262N, mature numbering

<400> 797
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala His Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 798
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219I/S262N, mature numbering

<400> 798

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ile Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
```

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 799
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219L/S262N, mature numbering

<400> 799
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Leu Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 800
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219M/S262N, mature numbering

<400> 800

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Met Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
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245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 801
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219P/S262N, mature numbering

<400> 801
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205

Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Pro Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 802
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219S/S262N, mature numbering

<400> 802
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser

```
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Ser Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 803
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219T/S262N, mature numbering

<400> 803

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Thr Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 804
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219V/S262N, mature numbering

<400> 804
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

```
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Val Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 805
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219W/S262N, mature numbering

<400> 805

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Trp Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 806
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Y/S262N, mature numbering

<400> 806

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
```

```
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Tyr Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 807
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221C, mature numbering

<400> 807
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Cys Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 808
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221D, mature numbering

<400> 808

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Asp Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 809
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221E, mature numbering

<400> 809
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Glu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 810
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221F, mature numbering

<400> 810
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Phe Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu

385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 811
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221H, mature numbering

<400> 811
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu His Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 812
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221I, mature numbering

<400> 812

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Ile Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
```

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 813
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221K, mature numbering

<400> 813
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Lys Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 814
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221M, mature numbering

<400> 814

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Met Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
```

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 815
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221N, mature numbering

<400> 815
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Asn Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 816
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221P, mature numbering

<400> 816

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
```

```
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Pro Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 817
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221Q, mature numbering

<400> 817

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Gln Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 818
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221R, mature numbering

<400> 818

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Arg Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 819
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221S, mature numbering

<400> 819
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Ser Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 820
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221T, mature numbering

<400> 820
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Thr Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 821
<211> 482
<212> PRT

<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221W, mature numbering

<400> 821

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Trp Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 822
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/L221Y, mature numbering

<400> 822
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Tyr Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe

450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 823
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262C, mature numbering

<400> 823
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Cys Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 824
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262D, mature numbering

<400> 824
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asp Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln

370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 825
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262E, mature numbering

<400> 825
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Glu Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335

```
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 826
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262F, mature numbering

<400> 826

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Phe Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
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290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 827
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262G, mature numbering

<400> 827
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

```
Ile Lys Ile Ile Tyr Gly Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 828
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262H, mature numbering

<400> 828

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
```

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr His Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 829
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262I, mature numbering

<400> 829
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175

```
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ile Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
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<210> 830
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262K, mature numbering

<400> 830

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
```

130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Lys Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 831
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262L, mature numbering

<400> 831
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Leu Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 832
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262P, mature numbering

<400> 832

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
```

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Pro Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 833
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262Q, mature numbering

<400> 833
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Gln Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 834
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 R219Q/S262R, mature numbering

<400> 834
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Arg Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 835

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262T, mature numbering

<400> 835

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Thr Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 836
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262W, mature numbering

<400> 836
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Trp Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
```

435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 837
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262Y, mature numbering

<400> 837
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Tyr Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 838
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264C, mature numbering

<400> 838
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Cys Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

```
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 839
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264D, mature numbering

<400> 839

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Asp Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 840
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264E, mature numbering

<400> 840

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Glu Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

```
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 841
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264F, mature numbering

<400> 841

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
```

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Phe Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 842
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264I, mature numbering

<400> 842

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Ile Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 843
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264K, mature numbering

<400> 843
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Lys Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 844
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264L, mature numbering

<400> 844
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

```
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Leu Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 845
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264M, mature numbering

<400> 845

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
```

```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Met Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 846
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264P, mature numbering

<400> 846

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
```

```
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Pro Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 847
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264R, mature numbering

<400> 847

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Arg Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 848
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264S, mature numbering

<400> 848
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Ser Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 849
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264T, mature numbering

<400> 849
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp Thr Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 850
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264V, mature numbering

<400> 850
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Val Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly

420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 851
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264W, mature numbering

<400> 851
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp Trp Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380

```
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 852
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/H264Y, mature numbering

<400> 852

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp Tyr Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
```

340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 853
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266A, mature numbering

<400> 853
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ala Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300

Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 854
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266C, mature numbering

<400> 854
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Cys Lys Asp Val Ala Val Ile

260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 855
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266D, mature numbering

<400> 855
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220

```
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Asp Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 856
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266E, mature numbering

<400> 856

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
```

```
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Glu Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 857
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266F, mature numbering

<400> 857

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
```

```
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Phe Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 858
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266G, mature numbering

<400> 858

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
```

```
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Gly Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 859
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266H, mature numbering

<400> 859

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
```

Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg His Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 860
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266I, mature numbering

<400> 860
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu

```
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ile Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 861
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266K, mature numbering

<400> 861
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Lys Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 862
<211> 482

<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266L, mature numbering

<400> 862

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Leu Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 863
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266M, mature numbering

<400> 863
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Met Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445

Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 864
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266N, mature numbering

<400> 864
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Asn Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met

405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 865
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266P, mature numbering

<400> 865
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Pro Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365

```
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 866
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266Q, mature numbering

<400> 866

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Gln Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
```

325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 867
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266R, mature numbering

<400> 867
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Arg Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285

```
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 868
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266T, mature numbering

<400> 868

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
```

245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Thr Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 869
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266V, mature numbering

<400> 869
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205

```
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Val Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 870
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266W, mature numbering

<400> 870

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
```

```
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Trp Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 871
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/S266Y, mature numbering

<400> 871

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
```

Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Tyr Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 872
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267A, mature numbering

<400> 872
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val

```
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Ala Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 873
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267C, mature numbering

<400> 873

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
```

```
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Cys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 874
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267D, mature numbering

<400> 874

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
```

```
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Asp Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 875
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267E, mature numbering

<400> 875

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Glu Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 876
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267F, mature numbering

<400> 876

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Phe Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
```

465 470 475 480
Thr Lys

<210> 877
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267G, mature numbering

<400> 877
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Gly Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430

Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 878
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267H, mature numbering

<400> 878
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser His Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu

385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 879
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267I, mature numbering

<400> 879
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Ile Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350

```
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 880
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267L, mature numbering

<400> 880

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Leu Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
```

305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 881
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267M, mature numbering

<400> 881
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Met Asp Val Ala Val Ile
260 265 270

```
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 882
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267N, mature numbering

<400> 882

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
```

225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Asn Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 883
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267P, mature numbering

<400> 883
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190

```
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Pro Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 884
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267Q, mature numbering

<400> 884

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
```

```
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Gln Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 885
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267R, mature numbering

<400> 885

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
```

```
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Arg Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 886
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267S, mature numbering

<400> 886

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
```

65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Ser Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 887
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267T, mature numbering

<400> 887
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30

```
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Thr Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 888
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267V, mature numbering

<400> 888
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Val Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 889
<211> 482
<212> PRT

<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267W, mature numbering

<400> 889

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Trp Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 890
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/K267Y, mature numbering

<400> 890
```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Tyr Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
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    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 891
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296A, mature numbering

<400> 891

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Ala Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
```

Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 892
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296C, mature numbering

<400> 892
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Cys Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln

    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 893
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296D, mature numbering

<400> 893
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Asp Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335

Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 894
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296E, mature numbering

<400> 894
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Glu Gly His Glu Asp Thr Gly His Ser

290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 895
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296F, mature numbering

<400> 895
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255

Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Phe Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 896
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296G, mature numbering

<400> 896
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr

210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Gly Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 897
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296H, mature numbering

<400> 897
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175

Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu His Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 898
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296I, mature numbering

<400> 898
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln

130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Ile Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 899
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296K, mature numbering

<400> 899
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95

```
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Lys Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 900
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296L, mature numbering

<400> 900

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
```

50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Leu Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 901
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296M, mature numbering

<400> 901
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15

```
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Met Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 902
<211> 482
<212> PRT
<213> Artificial Sequence

<220>

<223> human ADA2 R219Q/S262N/V296N, mature numbering

<400> 902
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Asn Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 903

<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296P, mature numbering

<400> 903

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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Pro Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
```

Thr Lys

<210> 904
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296Q, mature numbering

<400> 904
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Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Gln Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
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435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 905
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296R, mature numbering

<400> 905
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Arg Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400

Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 906
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296S, mature numbering

<400> 906
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Ser Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr

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        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 907
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296T, mature numbering

<400> 907

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Thr Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
```

```
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 908
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296W, mature numbering

<400> 908

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
```

275 280 285
Val Val Ala Gly Phe Asp Leu Trp Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 909
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/S262N/V296Y, mature numbering

<400> 909
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240

```
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Tyr Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 910
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K11A/R20A, mature numbering

<400> 910

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
```

195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 911
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K11A/R20A/K371A, mature numbering

<400> 911
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
115 120 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
130 135 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145 150 155 160

Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
165 170 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
180 185 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
195 200 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
210 215 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225 230 235 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
245 250 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
260 265 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
275 280 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
290 295 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305 310 315 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
325 330 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
340 345 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
355 360 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
370 375 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385 390 395 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
405 410 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
420 425 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
435 440 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
450 455 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 912
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/R20A/K371A, mature numbering

<400> 912
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
100 105 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu

```
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 913
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/K11A/K371A, mature numbering

<400> 913

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
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```
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 914
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/K11A/R20A, mature numbering

<400> 914

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
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        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 915
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/K11A/R20A/K371A, mature numbering

<400> 915

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100                 105                 110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115                 120                 125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130                 135                 140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145                 150                 155                 160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165                 170                 175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180                 185                 190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195                 200                 205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210                 215                 220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225                 230                 235                 240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245                 250                 255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260                 265                 270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275                 280                 285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290                 295                 300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305                 310                 315                 320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325                 330                 335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340                 345                 350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355                 360                 365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370                 375                 380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385                 390                 395                 400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405                 410                 415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420                 425                 430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435                 440                 445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450                 455                 460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465                 470                 475                 480
Thr Lys
```

<210> 916
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/R20A/K371A, mature numbering

<400> 916
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Ala Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460
Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465   470   475   480
Thr Lys

<210> 917
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/K11A/K371A, mature numbering

<400> 917
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Ala Glu Lys Met Met Arg
 1   5   10   15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20   25   30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35   40   45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50   55   60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65   70   75   80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85   90   95
Arg Asn Val Thr Tyr Arg Pro His Cys His Ile Cys Phe Thr Pro Arg
            100   105   110
Gly Ile Met Gln Phe Arg Phe Ala His Pro Thr Pro Arg Pro Ser Glu
        115   120   125
Lys Cys Ser Lys Trp Ile Leu Leu Glu Asp Tyr Arg Lys Arg Val Gln
    130   135   140
Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr Leu Val
145   150   155   160
Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val Trp Ser
                165   170   175
Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His Tyr Ala
            180   185   190
Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe Tyr Glu
        195   200   205
Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr
    210   215   220
Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys Thr Tyr
225   230   235   240
Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe Ile Gly
                245   250   255
Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala Val Ile
            260   265   270
Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe Pro Thr
        275   280   285
Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly His Ser
    290   295   300
Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp Gly Val
305   310   315   320
Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln Gly Thr
                325   330   335
Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr Thr Arg
            340   345   350
Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg Thr Tyr
        355   360   365
Ser Trp Ala Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser Asn Gln
    370   375   380
Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala Thr Leu
385   390   395   400
Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro Ala Met
                405   410   415
Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly
            420   425   430
Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu Ala Met
        435   440   445
Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe
    450   455   460

Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp Val Ala
465 470 475 480
Thr Lys

<210> 918
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/C105-T147del->(Gly)n, mature numbering,
where n = 2 to 20

<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 times

<400> 918
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
100 105 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
115 120 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
130 135 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145 150 155 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
165 170 175
Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
180 185 190
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
195 200 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser
210 215 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu
225 230 235 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
245 250 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
260 265 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
275 280 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
290 295 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305 310 315 320
Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val
325 330 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn

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            340                 345                 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
        355                 360                 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
    370                 375                 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385                 390                 395                 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
                405                 410                 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
            420                 425                 430
Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 919
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/V99-Q144del->(GGGGS)n, mature
      numbering, where n = 1 to 5


<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 919
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
            100                 105                 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
        115                 120                 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
    130                 135                 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145                 150                 155                 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
                165                 170                 175
Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu
            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
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290 295 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305 310 315 320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu
325 330 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
340 345 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
355 360 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
370 375 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385 390 395 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
405 410 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
420 425 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 920
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/C105-T147del->(GGGGS)n, mature
numbering, where n = 1 to 5

<220>
<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 920
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
100 105 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
115 120 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
130 135 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145 150 155 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
165 170 175
Glu Ile Arg Ala Gln Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
180 185 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
195 200 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser
210 215 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225 230 235 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp

245 250 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
260 265 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
275 280 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
290 295 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305 310 315 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
325 330 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
340 345 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
355 360 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
370 375 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385 390 395 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
405 410 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
420 425 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 921
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/N98-N156Del, mature numbering

<400> 921
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
100 105 110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
115 120 125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
130 135 140
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
145 150 155 160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
165 170 175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
180 185 190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
195 200 205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
210 215 220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225 230 235 240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
245 250 255

```
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
            260                 265                 270
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
        275                 280                 285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
    290                 295                 300
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
305                 310                 315                 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
                325                 330                 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
            340                 345                 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
        355                 360                 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
    370                 375                 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385                 390                 395                 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
                405                 410                 415
Ile Ala Asp Val Ala Thr Lys
            420


<210> 922
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/C105-E148Del, mature numbering

<400> 922
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
            100                 105                 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
        115                 120                 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
    130                 135                 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145                 150                 155                 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu
                165                 170                 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
            180                 185                 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
        195                 200                 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp
    210                 215                 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225                 230                 235                 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
                245                 250                 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
            260                 265                 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
```

275 280 285
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
290 295 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305 310 315 320
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
325 330 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
340 345 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
355 360 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
370 375 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385 390 395 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
405 410 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
420 425 430
Ala Asp Val Ala Thr Lys
435

<210> 923
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/C105-T147Del, mature numbering

<400> 923
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
100 105 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
115 120 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
130 135 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145 150 155 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln
165 170 175
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
180 185 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
195 200 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys
210 215 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225 230 235 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
245 250 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
260 265 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
275 280 285

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Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
    290                 295                 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305                 310                 315                 320
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
                325                 330                 335
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
            340                 345                 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
        355                 360                 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
    370                 375                 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385                 390                 395                 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
                405                 410                 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
            420                 425                 430
Ile Ala Asp Val Ala Thr Lys
        435
```

<210> 924
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 R219Q/V99-Q144del, mature numbering

<400> 924

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
            100                 105                 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
        115                 120                 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
    130                 135                 140
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145                 150                 155                 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Gln Leu Leu Pro
                165                 170                 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys
            180                 185                 190
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
        195                 200                 205
Ile Gly Ile Lys Ile Ile Tyr Ser Asp His Arg Ser Lys Asp Val Ala
    210                 215                 220
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225                 230                 235                 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
                245                 250                 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
            260                 265                 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
        275                 280                 285
Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
```

290 295 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305 310 315 320
Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
325 330 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
340 345 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
355 360 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
370 375 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385 390 395 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
405 410 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
420 425 430
Val Ala Thr Lys
435

<210> 925
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/C105-T147del->(Gly)n, mature numbering, where n = 2 to 20

<220>
<221> REPEAT
<222> (105)...(105)
<223> occurring 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 times

<400> 925
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Gly Glu Phe Asp Asp Ser Leu Leu
100 105 110
Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn
115 120 125
Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser
130 135 140
Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser
145 150 155 160
Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala
165 170 175
Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu
180 185 190
Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr
195 200 205
His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser
210 215 220
Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu

225 230 235 240
Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His
245 250 255
Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile
260 265 270
Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu
275 280 285
Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu
290 295 300
Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His
305 310 315 320
Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val
325 330 335
Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn
340 345 350
His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser
355 360 365
Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe
370 375 380
Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr
385 390 395 400
Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu
405 410 415
Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys
420 425 430
Phe Ile Ala Asp Val Ala Thr Lys
435 440

<210> 926
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/V99-Q144del->(GGGGS)n, mature
numbering, where n = 1 to 5

<220>
<221> REPEAT
<222> (99)...(103)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 926
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Gly Gly Gly Gly Ser Asn Val Thr Glu Phe Asp Asp Ser Leu
100 105 110
Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr
115 120 125
Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile
130 135 140
Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg
145 150 155 160
Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg
165 170 175
Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu

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            180                 185                 190
Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu
        195                 200                 205
Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg
    210                 215                 220
Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly
225                 230                 235                 240
Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly
                245                 250                 255
His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met
            260                 265                 270
Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly
        275                 280                 285
Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala
    290                 295                 300
Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys
305                 310                 315                 320
His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu
                325                 330                 335
Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg
            340                 345                 350
Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile
        355                 360                 365
Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp
    370                 375                 380
Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg
385                 390                 395                 400
Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu
                405                 410                 415
Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp
            420                 425                 430
Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 927
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/C105-T147del->(GGGGS)n, mature
      numbering, where n = 1 to 5


<220>
<221> REPEAT
<222> (105)...(109)
<223> occurring 1, 2, 3, 4 or 5 times

<400> 927
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Gly Gly Gly Gly Ser Glu Phe Asp
            100                 105                 110
Asp Ser Leu Leu Arg Asn Phe Thr Leu Val Thr Gln His Pro Glu Val
        115                 120                 125
Ile Tyr Thr Asn Gln Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe
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    130                 135                 140
Phe Thr Ile Ser Gly Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr
145                 150                 155                 160
Val Phe Arg Ser Met Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met
                165                 170                 175
Glu Ile Arg Ala Arg Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His
            180                 185                 190
His Asp Glu Glu Trp Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys
        195                 200                 205
Phe Val Glu Thr His Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn
    210                 215                 220
Asp His Arg Ser Lys Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met
225                 230                 235                 240
Ala Met Gly Leu Arg Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp
                245                 250                 255
Leu Val Gly His Glu Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu
            260                 265                 270
Ala Leu Met Ile Pro Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe
        275                 280                 285
His Ala Gly Glu Thr Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile
    290                 295                 300
Leu Asp Ala Leu Met Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala
305                 310                 315                 320
Leu Ser Lys His Pro Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile
                325                 330                 335
Pro Ile Glu Val Cys Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser
            340                 345                 350
Asp Leu Arg Asn His Pro Val Ala Thr Leu Met Ala Thr Gly His Pro
        355                 360                 365
Met Val Ile Ser Ser Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu
    370                 375                 380
Ser Tyr Asp Phe Tyr Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala
385                 390                 395                 400
Asp Leu Arg Thr Leu Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser
                405                 410                 415
Thr Leu Leu Glu Ser Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys
            420                 425                 430
Arg Trp Asp Lys Phe Ile Ala Asp Val Ala Thr Lys
        435                 440


<210> 928
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/N98-N156Del, mature numbering

<400> 928
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1               5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
            100                 105                 110
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
        115                 120                 125
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
    130                 135                 140
```

Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
145 150 155 160
Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
165 170 175
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
180 185 190
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
195 200 205
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
210 215 220
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
225 230 235 240
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
245 250 255
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
260 265 270
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
275 280 285
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
290 295 300
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
305 310 315 320
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
325 330 335
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
340 345 350
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
355 360 365
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
370 375 380
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
385 390 395 400
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
405 410 415
Ile Ala Asp Val Ala Thr Lys
420

<210> 929
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/C105-E148Del, mature numbering

<400> 929
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Val Thr Tyr Arg Pro His Phe Asp Asp Ser Leu Leu Arg Asn
100 105 110
Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn
115 120 125
Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu
130 135 140
Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln
145 150 155 160
Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu

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                165                 170                 175
Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser
            180                 185                 190
Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro
        195                 200                 205
Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp
    210                 215                 220
Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile
225                 230                 235                 240
Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp
                245                 250                 255
Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala
            260                 265                 270
Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp
        275                 280                 285
Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu
    290                 295                 300
Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala
305                 310                 315                 320
Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro
                325                 330                 335
Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro
            340                 345                 350
Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp
        355                 360                 365
Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu
    370                 375                 380
Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys
385                 390                 395                 400
Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu
                405                 410                 415
Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile
            420                 425                 430
Ala Asp Val Ala Thr Lys
        435
```

<210> 930
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/C105-T147Del, mature numbering

<400> 930

```
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
 1                5                  10                  15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
            20                  25                  30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
        35                  40                  45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
    50                  55                  60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65                  70                  75                  80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
                85                  90                  95
Arg Asn Val Thr Tyr Arg Pro His Glu Phe Asp Asp Ser Leu Leu Arg
            100                 105                 110
Asn Phe Thr Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln
        115                 120                 125
Asn Val Val Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly
    130                 135                 140
Leu Ile His Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met
145                 150                 155                 160
Gln Glu Phe Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg
                165                 170                 175
```

Leu Leu Pro Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp
180 185 190
Ser Val Lys Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His
195 200 205
Pro Glu Phe Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys
210 215 220
Asp Val Ala Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg
225 230 235 240
Ile Lys Phe Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu
245 250 255
Asp Thr Gly His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro
260 265 270
Ala Lys Asp Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr
275 280 285
Asp Trp Gln Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met
290 295 300
Leu Asn Thr Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro
305 310 315 320
Ala Val Arg Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys
325 330 335
Pro Ile Ser Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His
340 345 350
Pro Val Ala Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser
355 360 365
Asp Asp Pro Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr
370 375 380
Glu Val Phe Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu
385 390 395 400
Lys Gln Leu Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser
405 410 415
Glu Lys Asn Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe
420 425 430
Ile Ala Asp Val Ala Thr Lys
435

<210> 931
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> human ADA2 S262N/V99-Q144del, mature numbering

<400> 931
Ile Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg
1 5 10 15
Leu Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu
20 25 30
Arg Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr
35 40 45
Leu Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys His Leu Ile
50 55 60
Glu Arg Ser Gln Val Phe Asn Ile Leu Arg Met Met Pro Lys Gly Ala
65 70 75 80
Ala Leu His Leu His Asp Ile Gly Ile Val Thr Met Asp Trp Leu Val
85 90 95
Arg Asn Asn Val Thr Glu Phe Asp Asp Ser Leu Leu Arg Asn Phe Thr
100 105 110
Leu Val Thr Gln His Pro Glu Val Ile Tyr Thr Asn Gln Asn Val Val
115 120 125
Trp Ser Lys Phe Glu Thr Ile Phe Phe Thr Ile Ser Gly Leu Ile His
130 135 140
Tyr Ala Pro Val Phe Arg Asp Tyr Val Phe Arg Ser Met Gln Glu Phe
145 150 155 160
Tyr Glu Asp Asn Val Leu Tyr Met Glu Ile Arg Ala Arg Leu Leu Pro
165 170 175
Val Tyr Glu Leu Ser Gly Glu His His Asp Glu Glu Trp Ser Val Lys

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            180                 185                 190                 
Thr Tyr Gln Glu Val Ala Gln Lys Phe Val Glu Thr His Pro Glu Phe
        195                 200                 205                 
Ile Gly Ile Lys Ile Ile Tyr Asn Asp His Arg Ser Lys Asp Val Ala
    210                 215                 220                 
Val Ile Ala Glu Ser Ile Arg Met Ala Met Gly Leu Arg Ile Lys Phe
225                 230                 235                 240
Pro Thr Val Val Ala Gly Phe Asp Leu Val Gly His Glu Asp Thr Gly
                245                 250                 255
His Ser Leu His Asp Tyr Lys Glu Ala Leu Met Ile Pro Ala Lys Asp
            260                 265                 270
Gly Val Lys Leu Pro Tyr Phe Phe His Ala Gly Glu Thr Asp Trp Gln
        275                 280                 285
Gly Thr Ser Ile Asp Arg Asn Ile Leu Asp Ala Leu Met Leu Asn Thr
    290                 295                 300
Thr Arg Ile Gly His Gly Phe Ala Leu Ser Lys His Pro Ala Val Arg
305                 310                 315                 320
Thr Tyr Ser Trp Lys Lys Asp Ile Pro Ile Glu Val Cys Pro Ile Ser
                325                 330                 335
Asn Gln Val Leu Lys Leu Val Ser Asp Leu Arg Asn His Pro Val Ala
            340                 345                 350
Thr Leu Met Ala Thr Gly His Pro Met Val Ile Ser Ser Asp Asp Pro
        355                 360                 365
Ala Met Phe Gly Ala Lys Gly Leu Ser Tyr Asp Phe Tyr Glu Val Phe
    370                 375                 380
Met Gly Ile Gly Gly Met Lys Ala Asp Leu Arg Thr Leu Lys Gln Leu
385                 390                 395                 400
Ala Met Asn Ser Ile Lys Tyr Ser Thr Leu Leu Glu Ser Glu Lys Asn
                405                 410                 415
Thr Phe Met Glu Ile Trp Lys Lys Arg Trp Asp Lys Phe Ile Ala Asp
            420                 425                 430
Val Ala Thr Lys
        435
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