

<110> CJ CheilJedang Corporation
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 <151> 2014-05-09
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Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
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Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
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Asp Ala Glu Ala Glu Ala Glu Val Val Arg Thr Val Val Glu Leu Ile
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Lys Gln Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
      275      280      285
Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
      290      295      300
Asn Val Val Glu Phe His Ser Asp Tyr Val Lys Val Lys Asn Ala Thr
      305      310      315      320
Phe Leu Gly Val Gln Met Lys Phe Ala Leu Gln Asn Leu Leu Lys Val
      325      330      335
Ile Pro Asp Val Val Lys Gly Tyr Lys Ser Val Pro Val Pro Thr Lys

```

[illegible]

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<210>      74
<211>      506
<212>      PRT
<213>      Saccharomyces cerevisiae ALD2
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<400>      74  
Met Pro Thr Leu Tyr Thr Asp Ile Glu Ile Pro Gln Leu Lys Ile Ser  
   1                               10                          15  
  
Leu Lys Gln Pro Leu Gly Leu Phe Ile Asn Asn Glu Phe Cys Pro Ser  
                                20                        25          30  
  
Ser Asp Gly Lys Thr Ile Glu Thr Val Asn Pro Ala Thr Gly Glu Pro  
    35                40              45  
  
Ile Thr Ser Phe Gln Ala Ala Asn Glu Lys Asp Val Asp Lys Ala Val  
   50                      55              60  
  
Lys Ala Ala Arg Ala Ala Phe Asp Asn Val Trp Ser Lys Thr Ser Ser  
   65                70              75              80  
  
Glu Gln Arg Gly Ile Tyr Leu Ser Asn Leu Leu Lys Leu Ile Glu Glu  
                    85              90              95
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OPA15034_Sequence_Listing.txt

Glu Gln Asp Thr Leu Ala Ala Leu Glu Thr Leu Asp Ala Gly Lys Pro
 100 105 110
 Tyr His Ser Asn Ala Lys Gly Asp Leu Ala Gln Ile Leu Gln Leu Thr
 115 120 125
 Arg Tyr Phe Ala Gly Ser Ala Asp Lys Phe Asp Lys Gly Ala Thr Ile
 130 135 140
 Pro Leu Thr Phe Asn Lys Phe Ala Tyr Thr Leu Lys Val Pro Phe Gly
 145 150 155 160
 Val Val Ala Gln Ile Val Pro Trp Asn Tyr Pro Leu Ala Met Ala Cys
 165 170 175
 Trp Lys Leu Gln Gly Ala Leu Ala Ala Gly Asn Thr Val Ile Ile Lys
 180 185 190
 Pro Ala Glu Asn Thr Ser Leu Ser Leu Leu Tyr Phe Ala Thr Leu Ile
 195 200 205
 Lys Lys Ala Gly Phe Pro Pro Gly Val Val Asn Ile Val Pro Gly Tyr
 210 215 220
 Gly Ser Leu Val Gly Gln Ala Leu Ala Ser His Met Asp Ile Asp Lys
 225 230 235 240
 Ile Ser Phe Thr Gly Ser Thr Lys Val Gly Gly Phe Val Leu Glu Ala
 245 250 255
 Ser Gly Gln Ser Asn Leu Lys Asp Val Thr Leu Glu Cys Gly Gly Lys
 260 265 270
 Ser Pro Ala Leu Val Phe Glu Asp Ala Asp Leu Asp Lys Ala Ile Asp
 275 280 285
 Trp Ile Ala Ala Gly Ile Phe Tyr Asn Ser Gly Gln Asn Cys Thr Ala
 290 295 300
 Asn Ser Arg Val Tyr Val Gln Ser Ser Ile Tyr Asp Lys Phe Val Glu
 305 310 315 320
 Lys Phe Lys Glu Thr Ala Lys Lys Glu Trp Asp Val Ala Gly Lys Phe
 325 330 335
 Asp Pro Phe Asp Glu Lys Cys Ile Val Gly Pro Val Ile Ser Ser Thr
 340 345 350
 Gln Tyr Asp Arg Ile Lys Ser Tyr Ile Glu Arg Gly Lys Arg Glu Glu
 355 360 365
 Lys Leu Asp Met Phe Gln Thr Ser Glu Phe Pro Ile Gly Gly Ala Lys
 370 375 380
 Gly Tyr Phe Ile Pro Pro Thr Ile Phe Thr Asp Val Pro Gln Thr Ser
 385 390 395 400
 Lys Leu Leu Gln Asp Glu Ile Phe Gly Pro Val Val Val Val Ser Lys
 405 410 415
 Phe Thr Asn Tyr Asp Asp Ala Leu Lys Leu Ala Asn Asp Thr Cys Tyr
 420 425 430
 Gly Leu Ala Ser Ala Val Phe Thr Lys Asp Val Lys Lys Ala His Met
 435 440 445
 Phe Ala Arg Asp Ile Lys Ala Gly Thr Val Trp Ile Asn Ser Ser Asn
 OPA15034_Sequence Listing.txt

450 455
Asp Glu Asp Val Thr Val Pro Phe Gly Gly Phe Lys Met Ser Gly Ile
465 470 475 480
Gly Arg Glu Leu Gly Gln Ser Gly Val Asp Thr Tyr Leu Gln Thr Lys
485 490 495
Ala Val His Ile Asn Leu Ser Leu Asp Asn
500 505

<210> 75
<211> 506
<212> PRT
<213> Saccharomyces cerevisiae ALD3

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

Ser Pro Ala Leu Val Phe Glu Asp Ala Asp Leu Asp Lys Ala Ile Glu
 275 280 285
 Trp Val Ala Asn Gly Ile Phe Phe Asn Ser Gly Gln Ile Cys Thr Ala
 290 300
 Asn Ser Arg Val Tyr Val Gln Ser Ser Ile Tyr Asp Lys Phe Val Glu
 305 310 315 320
 Lys Phe Lys Glu Thr Ala Lys Lys Glu Trp Asp Val Ala Gly Lys Phe
 325 330 335
 Asp Pro Phe Asp Glu Lys Cys Ile Val Gly Pro Val Ile Ser Ser Thr
 340 345 350
 Gln Tyr Asp Arg Ile Lys Ser Tyr Ile Glu Arg Gly Lys Lys Glu Glu
 355 360 365
 Lys Leu Asp Met Phe Gln Thr Ser Glu Phe Pro Ile Gly Gly Ala Lys
 370 375 380
 Gly Tyr Phe Ile Pro Pro Thr Ile Phe Thr Asp Val Pro Glu Thr Ser
 385 390 395 400
 Lys Leu Leu Arg Asp Glu Ile Phe Gly Pro Val Val Val Val Ser Lys
 405 410 415
 Phe Thr Asn Tyr Asp Asp Ala Leu Lys Leu Ala Asn Asp Thr Cys Tyr
 420 425 430
 Gly Leu Ala Ser Ala Val Phe Thr Lys Asp Val Lys Lys Ala His Met
 435 440 445
 Phe Ala Arg Asp Ile Lys Ala Gly Thr Val Trp Ile Asn Gln Thr Asn
 450 455 460
 Gln Glu Glu Ala Lys Val Pro Phe Gly Gly Phe Lys Met Ser Gly Ile
 465 470 475 480
 Gly Arg Glu Ser Gly Asp Thr Gly Val Asp Asn Tyr Leu Gln Ile Lys
 485 490 495
 Ser Val His Val Asp Leu Ser Leu Asp Lys
 500 505

<210> 76
 <211> 713
 <212> PRT
 <213> Saccharomyces cerevisiae ACS1

<400> 76
 Met Ser Pro Ser Ala Val Gln Ser Ser Lys Leu Glu Glu Gln Ser Ser
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 Glu Ile Asp Lys Leu Lys Ala Lys Met Ser Gln Ser Ala Ala Thr Ala
 20 25 30
 Gln Gln Lys Lys Glu His Glu Tyr Glu His Leu Thr Ser Val Lys Ile
 35 40 45
 Val Pro Gln Arg Pro Ile Ser Asp Arg Leu Gln Pro Ala Ile Ala Thr
 50 55 60
 His Tyr Ser Pro His Leu Asp Gly Leu Gln Asp Tyr Gln Arg Leu His
 65 70 75 80

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

Glu Val Trp Glu Trp Tyr Ser Glu Lys Ile Gly Lys Asn Glu Ile Pro
 450 455 460
 Ile Val Asp Thr Tyr Trp Gln Thr Glu Ser Gly Ser His Leu Val Thr
 465 470 475 480
 Pro Leu Ala Gly Gly Val Thr Pro Met Lys Pro Gly Ser Ala Ser Phe
 485 490 495
 Pro Phe Phe Gly Ile Asp Ala Val Val Leu Asp Pro Asn Thr Gly Glu
 500 505 510
 Glu Leu Asn Thr Ser His Ala Glu Gly Val Leu Ala Val Lys Ala Ala
 515 520 525
 Trp Pro Ser Phe Ala Arg Thr Ile Trp Lys Asn His Asp Arg Tyr Leu
 530 535 540
 Asp Thr Tyr Leu Asn Pro Tyr Pro Gly Tyr Tyr Phe Thr Gly Asp Gly
 545 550 555 560
 Ala Ala Lys Asp Lys Asp Gly Tyr Ile Trp Ile Leu Gly Arg Val Asp
 565 570 575
 Asp Val Val Asn Val Ser Gly His Arg Leu Ser Thr Ala Glu Ile Glu
 580 585 590
 Ala Ala Ile Ile Glu Asp Pro Ile Val Ala Glu Cys Ala Val Val Gly
 595 600 605
 Phe Asn Asp Asp Leu Thr Gly Gln Ala Val Ala Ala Phe Val Val Leu
 610 615 620
 Lys Asn Lys Ser Ser Trp Ser Thr Ala Thr Asp Asp Glu Leu Gln Asp
 625 630 635 640
 Ile Lys Lys His Leu Val Phe Thr Val Arg Lys Asp Ile Gly Pro Phe
 645 650 655
 Ala Ala Pro Lys Leu Ile Ile Leu Val Asp Asp Leu Pro Lys Thr Arg
 660 665 670
 Ser Gly Lys Ile Met Arg Arg Ile Leu Arg Lys Ile Leu Ala Gly Glu
 675 680 685
 Ser Asp Gln Leu Gly Asp Val Ser Thr Leu Ser Asn Pro Gly Ile Val
 690 695 700
 Arg His Leu Ile Asp Ser Val Lys Leu
 705 710

<210> 77
 <211> 348
 <212> PRT
 <213> Saccharomyces cerevisiae ADH1

<400> 77
 Met Ser Ile Pro Glu Thr Gln Lys Gly Val Ile Phe Tyr Glu Ser His
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 Gly Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Ala Asn
 20 25 30
 Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu
 35 40 45

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

<210> 78
 <211> 587
 <212> PRT
 <213> Saccharomyces cerevisiae DLD1

<400> 78
 Met Leu Trp Lys Arg Thr Cys Thr Arg Leu Ile Lys Pro Ile Ala Gln
 1 5 10 15

Pro Arg Gly Arg Leu Val Arg Arg Ser Cys Tyr Arg Tyr Ala Ser Thr
 OPA15034_Sequence Listing.txt

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

Glu Lys Pro Thr Met Phe Phe Lys Ile Gly Gly Arg Ser Pro Asn Ile
 385 390 400
 Val Asn Ala Leu Val Asp Glu Val Lys Ala Val Ala Gln Leu Asn His
 405 410 415
 Cys Asn Ser Phe Gln Phe Ala Lys Asp Asp Asp Glu Lys Leu Glu Leu
 420 425 430
 Trp Glu Ala Arg Lys Val Ala Leu Trp Ser Val Leu Asp Ala Asp Lys
 435 440 445
 Ser Lys Asp Lys Ser Ala Lys Ile Trp Thr Thr Asp Val Ala Val Pro
 450 455 460
 Val Ser Gln Phe Asp Lys Val Ile His Glu Thr Lys Lys Asp Met Gln
 465 470 475 480
 Ala Ser Lys Leu Ile Asn Ala Ile Val Gly His Ala Gly Asp Gly Asn
 485 490 495
 Phe His Ala Phe Ile Val Tyr Arg Thr Pro Glu Glu His Glu Thr Cys
 500 505 510
 Ser Gln Leu Val Asp Arg Met Val Lys Arg Ala Leu Asn Ala Glu Gly
 515 520 525
 Thr Cys Thr Gly Glu His Gly Val Gly Ile Gly Lys Arg Glu Tyr Leu
 530 535 540
 Leu Glu Glu Leu Gly Glu Ala Pro Val Asp Leu Met Arg Lys Ile Lys
 545 550 555 560
 Leu Ala Ile Asp Pro Lys Arg Ile Met Asn Pro Asp Lys Ile Phe Lys
 565 570 575
 Thr Asp Pro Asn Glu Pro Ala Asn Asp Tyr Arg
 580 585