SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma GmbH & CO KG

<120> Improvement of protein production

<130> P01-2188

<160> 28

<170> PatentIn version 3.3

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<223> PCR primer for human DNA CERT-S272Arev

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<223> PCR primer for human DNA CERT-138truncation

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<210> 9
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<212> DNA
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<223> siRNA/DNA siLacZ

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<210> 10
<211> 1797
<212> DNA
<213> human: CERT cDNA

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acagagtatg gctgcagagg atccatctgt cttagcaagg ctgtcatcac acctcacgat 240

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aaatcccact ttggaggacc agattatgaa gaaggcccta acagtctgat taatgaagaa 960

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ggatgggcac cagcctcagt gttaagggca gtggcaaagc gagagtatcc taaatttcta 1740

aaacgtttta cttcttacgt ccaagaaaaa actgcaggaa agcctatttt gttctag 1797

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<211> 598
<212> PRT
<213> human: CERT protein

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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly

50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65 70 75 80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
85 90 95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115 120 125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165 170 175

Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
180 185 190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
195 200 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
210 215 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225 230 235 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
245 250 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
260 265 270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
275 280 285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
290 295 300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305 310 315 320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
325 330 335

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Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340                 345                 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
        355                 360                 365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
    370                 375                 380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
385                 390                 395                 400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
                405                 410                 415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
            420                 425                 430

Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
        435                 440                 445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
    450                 455                 460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465                 470                 475                 480

Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
                485                 490                 495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
            500                 505                 510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
        515                 520                 525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
    530                 535                 540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545                 550                 555                 560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
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Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
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Gly Lys Pro Ile Leu Phe
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<211> 2389
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cagagctgga actcgtcggg ctcggaggag gatccagaga cggagtctgg gccgcctgtg 480
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aaccaggaaa ttagcaggga caacattcta tgcaagatta catatgtagc taatgtgaac 2160

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<213> human: CERT L protein

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20 25 30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65 70 75 80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
85 90 95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115 120 125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165 170 175

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Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
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Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
        195                 200                 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
    210                 215                 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225                 230                 235                 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
                245                 250                 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
            260                 265                 270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
        275                 280                 285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
    290                 295                 300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305                 310                 315                 320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
                325                 330                 335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340                 345                 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
        355                 360                 365

Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
    370                 375                 380

Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met
385                 390                 395                 400

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
                405                 410                 415

Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
            420                 425                 430

Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
        435                 440                 445
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Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
    450                 455                 460

Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465                 470                 475                 480

Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
                485                 490                 495

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
            500                 505                 510

Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
        515                 520                 525

Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
    530                 535                 540

Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545                 550                 555                 560

Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
                565                 570                 575

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
            580                 585                 590

Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
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<211> 1797
<212> DNA
<213> human: CERT S132A cDNA

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acagagtatg gctgcagagg atccatctgt cttagcaagg ctgtcatcac acctcacgat    240

tttgatgaat gtcgatttga tattagtgta aatgatagtg tttggtatct tcgtgctcag    300

gatccagatc atagacagca atggatagat gccattgaac agcacaagac tgaatctgga    360

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tttaaagggg aagcgataac ttttaaagca actactgctg gaatccttgc aacactttct 780

cattgtattg aactaatggt taaacgtgag gacagctggc agaagagact ggataaggaa 840

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aaatcccact ttggaggacc agattatgaa gaaggcccta acagtctgat taatgaagaa 960

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acccatgcag ttaaaggcgt cacaggacat gaagtctgca attatttctg gaatgttgac 1320

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gccaaaataa atgttgctat gatttgtcaa accttggtaa gcccaccaga gggaaaccag 1620

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<211> 598
<212> PRT
<213> human: CERT S132A protein

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20 25 30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65 70 75 80

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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
                85                  90                  95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
            100                 105                 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
        115                 120                 125

Arg His Gly Ala Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
    130                 135                 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145                 150                 155                 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
                165                 170                 175

Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
            180                 185                 190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
        195                 200                 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
    210                 215                 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225                 230                 235                 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
                245                 250                 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
            260                 265                 270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
        275                 280                 285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
    290                 295                 300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305                 310                 315                 320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
                325                 330                 335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340                 345                 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
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        355                 360                 365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
    370                 375                 380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
385                 390                 395                 400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
                405                 410                 415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
            420                 425                 430

Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
        435                 440                 445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
    450                 455                 460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465                 470                 475                 480

Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
                485                 490                 495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
            500                 505                 510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
        515                 520                 525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
    530                 535                 540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545                 550                 555                 560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
                565                 570                 575

Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
            580                 585                 590

Gly Lys Pro Ile Leu Phe
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<212> DNA
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agagaagtag aagaaaatgg gattgttctg gatcctttaa aagctaccca tgcagttaaa 180

ggcgtcacag gacatgaagt ctgcaattat ttctggaatg ttgacgttcg caatgactgg 240

gaaacaacta tagaaaactt tcatgtggtg gaaacattag ctgataatgc aatcatcatt 300

tatcaaacac acaagagggt gtggcctgct tctcagcgag acgtattata tctttctgtc 360

attcgaaaga taccagcctt gactgaaaat gaccctgaaa cttggatagt ttgtaatttt 420

tctgtggatc atgacagtgc tcctctaaac aaccgatgtg tccgtgccaa aataaatgtt 480

gctatgattt gtcaaacctt ggtaagccca ccagagggaa accaggaaat tagcagggac 540

aacattctat gcaagattac atatgtagct aatgtgaacc ctggaggatg ggcaccagcc 600

tcagtgttaa gggcagtggc aaagcgagag tatcctaaat ttctaaaacg ttttacttct 660

tacgtccaa 669

<210> 17
<211> 223
<212> PRT
<213> human: START Domain CERT protein

<400> 17

Arg Phe Val Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr
1 5 10 15

Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu
20 25 30

Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile
35 40 45

Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly
50 55 60

His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp
65 70 75 80

Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn
85 90 95

Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln
100 105 110

Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr
115 120 125

Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His
130 135 140

Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val

145 150 155 160

Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu
165 170 175

Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val
180 185 190

Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys
195 200 205

Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln
210 215 220

<210> 18
<211> 658
<212> DNA
<213> human: START Domain CERT L cDNA

<400> 18
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gccaattggc agttggttgt agaagaagga gaaatgaagg tatacagaag agaagtagaa 120

gaaaatggga ttgttctgga tcctttaaaa gctacccatg cagttaaagg cgtcacagga 180

catgaagtct gcaattattt ctggaatgtt gacgttcgca atgactggga aacaactata 240

gaaaactttc atgtggtgga aacattagct gataatgcaa tcatcattta tcaaacacac 300

aagagggtgt ggcctgcttc tcagcgagac gtattatatc tttctgtcat tcgaaagata 360

ccagccttga ctgaaaatga ccctgaaact tggatagttt gtaatttttc tgtggatcat 420

gacagtgctc ctctaaacaa ccgatgtgtc cgtgccaaaa taaatgttgc tatgatttgt 480

caaaccttgg taagcccacc agagggaaac caggaaatta gcagggacaa cattctatgc 540

aagattacat atgtagctaa tgtgaaccct ggaggatggg caccagcctc agtgttaagg 600

gcagtggcaa agcgagagta tcctaaattt ctaaaacgtt ttacttctta cgtccaag 658

<210> 19
<211> 219
<212> PRT
<213> human: START Domain CERT L protein

<400> 19

Gln Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp
1 5 10 15

Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met
20 25 30

Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro
35 40 45

Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys
50 55 60

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Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile
65                  70                  75                  80

Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile
                85                  90                  95

Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu
            100                 105                 110

Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro
        115                 120                 125

Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro
    130                 135                 140

Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys
145                 150                 155                 160

Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp
                165                 170                 175

Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly
            180                 185                 190

Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro
        195                 200                 205

Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln
    210                 215
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<210> 20
<211> 2264
<212> DNA
<213> human: StarD4 cDNA

<400> 20

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aaacttaaaa acactctcat ccagtaccat agcattgaag aagataagtg gcgagttgct    180

aagaaaacga aagatgtaac tgtttggaga aaaccctcag aagaatttaa tggatatctc    240

tacaaagccc aaggtgttat agatgacctt gtctatagta taatagacca tatacgccca    300

gggccttgtc gtttggattg ggacagcttg atgacttctt tggatattct ggagaacttt    360

gaagagaatt gctgtgtgat gcgttacact actgctggtc agctttggaa tataatttcc    420

ccaagagaat ttgttgattt ctcctatact gtgggctata aagaagggct tttatcttgt    480

ggaataagtc ttgactggga tgaaaagaga ccagaatttg ttcgaggata taaccatccc    540

tgtggttggt tttgtgttcc acttaaagac aacccaaacc agagtctttt gacaggatat    600

attcagacag atctgcgtgg gatgattcct cagtctgcgg tagatacagc catggcaagc    660
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actttaacca acttctatgg tgatttacga aaagctttat gagaggcaaa atacattcaa 720

acttgtagta ctacagatca actctctcag ctacatggcc tgtaaaaatc attgattcca 780

cttttctgca tagccggtag aaaaatttga aatgtttttg gttcactagt acaatgtttg 840

gttttattcc taaagtaaat agctatctaa gagagggcat tttcactttt tttttttaa 900

attttgagac aggctctcac tctgttgccc atgctggagg gcagtggtat gatcacagct 960

cactgcagct ttgatctgac cgctcaaggg gttattctac ctcagcctcc tgaatagctg 1020

ggaatacagg tgcacgccac tatgcatggc taatttttgt ttaatttttt gtagagatgt 1080

ggtcacactg tgttgcccag gctggtcttg aactcctggc ctcaagtcat tccccacctt 1140

agcctcccaa agtgttggga ttataagcgt gagccaccat gcctggcccc aatttaaaat 1200

gtggaattca gttggtgtcc aagacttatc ttgagactct taaaagcatc agtctgtaac 1260

tagaacaaat acagtcttag atttacccaa gtgcctagat atcattttat aatgattaga 1320

attgagtatt gtgggtcccc taattctgtg ggtgccttaa gtgagaattt ctaaatgatt 1380

ttcacattct aaatgacttt gggttttgaa ctctccatct agtttacttc taaaatggga 1440

acttgaggca attcaggtat ccaggcaaat ctttgtatat attttttttgt gtacatgcac 1500

acatctcgaa atccatttcc gtgtttaatg ttagttgttt atgtgttagt attcctgtgt 1560

ctactgtttt gttgttgtta atatgggtaa agtgagccct gaaatacatg ctaaacaaga 1620

catgaaattc agaaaggtac atagtgtttc aagtgcatgg tagtttgatc tgtgttttac 1680

tttattgtgt tttcttgagt gtaaagaaag aataaatcaa agttcttcat acccattttg 1740

acaaagtgga acagtggagc tgtttttttgc ttttgttttt atttattttt tgccactggt 1800

gatgatagat ttcaaaaaac aaaaggtggc agcagcacaa tgttcatggt gaattatctc 1860

atagtatcta gattgatcaa gatctgacag aaggaatgca caaaggattc tatattctta 1920

atgatttatt aattaccagg atccttttct aaattgaatg tacttttgaa ttactaggtt 1980

tcttcttttt ttttgttctg caatagtgaa agaaaactca gtagtttagt ttcagtttct 2040

catggaaatt ggtaaatgtt agttttgact tcatctattt tttatttgtt tttattagcg 2100

tagagtagga agtctcatat tctactgttc tatctaggat ggtgaaattc caaaggtgcc 2160

taacttgagt aagggatttg tgacaagata gtacacatta ctataagggc tattatttcc 2220

tgaactggat gtccctaaaa gcaaataaac tgcccactat ctct 2264

<210> 21
<211> 205
<212> PRT
<213> human: StarD4 protein

<400> 21

Met Glu Gly Leu Ser Asp Val Ala Ser Phe Ala Thr Lys Leu Lys Asn
1 5 10 15

Thr Leu Ile Gln Tyr His Ser Ile Glu Glu Asp Lys Trp Arg Val Ala
20 25 30

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Lys Lys Thr Lys Asp Val Thr Val Trp Arg Lys Pro Ser Glu Glu Phe
        35                  40                  45

Asn Gly Tyr Leu Tyr Lys Ala Gln Gly Val Ile Asp Asp Leu Val Tyr
    50                  55                  60

Ser Ile Ile Asp His Ile Arg Pro Gly Pro Cys Arg Leu Asp Trp Asp
65                  70                  75                  80

Ser Leu Met Thr Ser Leu Asp Ile Leu Glu Asn Phe Glu Glu Asn Cys
                85                  90                  95

Cys Val Met Arg Tyr Thr Thr Ala Gly Gln Leu Trp Asn Ile Ile Ser
            100                 105                 110

Pro Arg Glu Phe Val Asp Phe Ser Tyr Thr Val Gly Tyr Lys Glu Gly
        115                 120                 125

Leu Leu Ser Cys Gly Ile Ser Leu Asp Trp Asp Glu Lys Arg Pro Glu
    130                 135                 140

Phe Val Arg Gly Tyr Asn His Pro Cys Gly Trp Phe Cys Val Pro Leu
145                 150                 155                 160

Lys Asp Asn Pro Asn Gln Ser Leu Leu Thr Gly Tyr Ile Gln Thr Asp
                165                 170                 175

Leu Arg Gly Met Ile Pro Gln Ser Ala Val Asp Thr Ala Met Ala Ser
            180                 185                 190

Thr Leu Thr Asn Phe Tyr Gly Asp Leu Arg Lys Ala Leu
        195                 200                 205
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<210> 22
<211> 1344
<212> DNA
<213> human: StarD5 cDNA

<400> 22

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gtggccgaga agatgctcca gtaccggcgg gacacagcag gctggaagat ttgccgggaa    180

ggcaatggag tttcagtttc ctggaggcca tctgtggagt ttccagggaa cctgtaccga    240

ggagaaggca ttgtatatgg gacactagag gaggtgtggg actgtgtgaa gccagctgtt    300

ggaggcctac gagtgaagtg ggatgagaat gtgaccggtt ttgaaattat ccaaagcatc    360

actgacaccc tgtgtgtaag cagaacctcc actccctccg ctgccatgaa gctcatttct    420

cccagagatt ttgtggactt ggtgctagtc aagagatatg aggatgggac catcagttcc    480

aacgccaccc atgtggagca tccgttatgt cccccgaagc caggttttgt gagaggattt    540
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aaccatcctt gtggttgctt ctgtgaacct cttccagggg aacccaccaa gaccaacctg 600

gtcacattct tccataccga cctcagcggt tacctcccac agaacgtggt ggactccttc 660

ttccccgca gcatgacccg gttttatgcc aaccttcaga aagcagtgaa gcaattccat 720

gagtaatgct atcgttactt cttggcaaag aactcccgtg actcatcgag gagctccagc 780

tgttgggaca ccaaggagcc tgggagcacg cagaggcctg tgttcactct ttggaacaag 840

ctgatggact gcgcatctct gagaatgcca accagaggcg gcagcccacc cttcctgcct 900

cctgccccac tcagggttgg cgtgtgatga gccattcatg tgttccaaac tccatctgcc 960

tgttacccaa acacgcctct cctggcaggg tagacccagg cctctaacca tctgacagag 1020

actcggcctg gacaccatgc gatgcactct ggcaccaagg ctttatgtgc ccatcactct 1080

cagagaccac gtttccctga ctgtcataga gaatcatcat cgccactgaa aaccaggccc 1140

tgttgccttt taagcatgta ccgctccctc agtcctgtgc tgcagccccc caaatatatt 1200

tttctgatat agaccttgta tatggcttta atgccgcaaa atatttattt ttccttaaaa 1260

aaggtgtcaa cttggaaata atggtttaaa aacaggataa gcattaagga aaaacaaaaa 1320

aaaaaaaaaa aaaaaaaaaa aaaa 1344

<210> 23
<211> 213
<212> PRT
<213> human: StarD5 protein

<400> 23

Met Asp Pro Ala Leu Ala Ala Gln Met Ser Glu Ala Val Ala Glu Lys
1 5 10 15

Met Leu Gln Tyr Arg Arg Asp Thr Ala Gly Trp Lys Ile Cys Arg Glu
20 25 30

Gly Asn Gly Val Ser Val Ser Trp Arg Pro Ser Val Glu Phe Pro Gly
35 40 45

Asn Leu Tyr Arg Gly Glu Gly Ile Val Tyr Gly Thr Leu Glu Glu Val
50 55 60

Trp Asp Cys Val Lys Pro Ala Val Gly Gly Leu Arg Val Lys Trp Asp
65 70 75 80

Glu Asn Val Thr Gly Phe Glu Ile Ile Gln Ser Ile Thr Asp Thr Leu
85 90 95

Cys Val Ser Arg Thr Ser Thr Pro Ser Ala Ala Met Lys Leu Ile Ser
100 105 110

Pro Arg Asp Phe Val Asp Leu Val Leu Val Lys Arg Tyr Glu Asp Gly
115 120 125

Thr Ile Ser Ser Asn Ala Thr His Val Glu His Pro Leu Cys Pro Pro
130 135 140

Lys Pro Gly Phe Val Arg Gly Phe Asn His Pro Cys Gly Cys Phe Cys
145 150 155 160

Glu Pro Leu Pro Gly Glu Pro Thr Lys Thr Asn Leu Val Thr Phe Phe
165 170 175

His Thr Asp Leu Ser Gly Tyr Leu Pro Gln Asn Val Val Asp Ser Phe
180 185 190

Phe Pro Arg Ser Met Thr Arg Phe Tyr Ala Asn Leu Gln Lys Ala Val
195 200 205

Lys Gln Phe His Glu
210

<210> 24
<211> 663
<212> DNA
<213> human: StarD6 cDNA

<400> 24
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acatcaggct ggaaagtggt taaaacttca aaaaagataa ctgtttccag taaggcttct 120

agaaaattcc atggaaatct atatcgtgtt gaagggataa ttccagaatc accagctaaa 180

ctatctgatt tcctctacca aactggagac agaattacat gggataaatc attgcaagtg 240

tataatatgg tacacaggat tgattcggac acattcatat gtcataccat tacacaaagt 300

tttgccgtgg gctccatttc ccctcgagac tttatcgact tagtgtacat caagcgctac 360

gaaggaaata tgaacattat cagttctaaa agtgtggatt ttccagaata tcctccatct 420

tcaaattata tccgcggtta taaccatcct tgtggctttg tatgttcacc aatggaagaa 480

aacccagcat attccaaact agtgatgttt gtccagacag aaatgagagg aaaattgtcc 540

ccatcaataa ttgaaaaaac catgccttcc aacttagtaa acttcatcct caatgcaaaa 600

gatggaataa aggcacacag aactccatca agacgtggat ttcatcataa tagtcattca 660

tga 663

<210> 25
<211> 220
<212> PRT
<213> human: StarD6 protein

<400> 25

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Tyr Asn Arg Asp Thr Ser Gly Trp Lys Val Val Lys Thr Ser Lys Lys
20 25 30

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Ile Thr Val Ser Ser Lys Ala Ser Arg Lys Phe His Gly Asn Leu Tyr
        35                  40                  45

Arg Val Glu Gly Ile Ile Pro Glu Ser Pro Ala Lys Leu Ser Asp Phe
    50                  55                  60

Leu Tyr Gln Thr Gly Asp Arg Ile Thr Trp Asp Lys Ser Leu Gln Val
65                  70                  75                  80

Tyr Asn Met Val His Arg Ile Asp Ser Asp Thr Phe Ile Cys His Thr
                85                  90                  95

Ile Thr Gln Ser Phe Ala Val Gly Ser Ile Ser Pro Arg Asp Phe Ile
            100                 105                 110

Asp Leu Val Tyr Ile Lys Arg Tyr Glu Gly Asn Met Asn Ile Ile Ser
        115                 120                 125

Ser Lys Ser Val Asp Phe Pro Glu Tyr Pro Pro Ser Ser Asn Tyr Ile
    130                 135                 140

Arg Gly Tyr Asn His Pro Cys Gly Phe Val Cys Ser Pro Met Glu Glu
145                 150                 155                 160

Asn Pro Ala Tyr Ser Lys Leu Val Met Phe Val Gln Thr Glu Met Arg
                165                 170                 175

Gly Lys Leu Ser Pro Ser Ile Ile Glu Lys Thr Met Pro Ser Asn Leu
            180                 185                 190

Val Asn Phe Ile Leu Asn Ala Lys Asp Gly Ile Lys Ala His Arg Thr
        195                 200                 205

Pro Ser Arg Arg Gly Phe His His Asn Ser His Ser
    210                 215                 220
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<210> 26
<211> 1932
<212> DNA
<213> human: PCTP cDNA

<400> 26

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gcctgcgccg agctccagca gcccgctctg gccggggccg actggcagct cctagtggag    120

acctcgggca tcagcatcta ccggctgctg gacaagaaga ctggacttca tgagtataaa    180

gtctttggtg ttctggagga ctgctcacca actctactgg cagacatcta tatggactca    240

gattacagaa aacaatggga ccagtatgtt aaagaactct atgaacaaga atgcaacgga    300

gagactgtgg tctactggga agtgaagtac ccttttccca tgtccaacag agactatgtc    360

taccttcggc agcggcgaga cctggacatg gaagggagga agatccatgt gatcctggcc    420
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cggagcacct ccatgcctca gcttggcgag aggtctgggg tgatccgggt gaagcaatac 480

aagcagagcc tggcgattga gagtgacggc aagaagggga gcaaagtttt catgtattac 540

ttcgataacc cgggtggcca aattccgtcc tggctcatta actgggccgc caagaatgga 600

gttcctaact tcttgaaaga catggcaaga gcctgtcaga actacctcaa gaaaacctaa 660

gaaagagaac tgggaacatt gcatccatgg gttgatgtct ctggaagtgc aaccacccaa 720

tgtctctgga agtgccacct ggaagtgcca cctggaagtg tctctggaag agcacccacc 780

actgttcagc cttcccctgc tgtttctgtc ttcagaggcc tacacactac cacatccttt 840

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ctgggctggg ctgccttctt ctacagttca atatggggca gactagggaa acctttgctt 960

gcttactatt aggaggggaa gtcttcagta gggaacacga tcattccatt gtgcaatttt 1020

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cctacttgtg gaggatcagt agctgttatg atgccagacc atttggagaa gtatcagagg 1320

cctgaccgga cacataatac gacaaccaca tttttcctca tcatccatga ggaaatggat 1380

gatttctctt ttccatatgt cactggggga aaggctgcct gtacctctca agctttgcat 1440

tttactggaa actgaggcgt caagatggct gtggcagcta gcaaaagcaa agatgctttg 1500

tgcatagcct tgtgaaaaag tatctttcta tgcaataaga tgaattttcc tcccagaata 1560

tttagaaatg tagaagggat aacagttcac agccaggtaa aatttaactg gtggcttaat 1620

gactctgcac ctttttctca ggaattctgc ctaagttgtc tgccttttct accaccaaaa 1680

agacttttag ttttctatgc tttctcctga attttggtag ggtaagtatt tctatgtcaa 1740

aggcacagcc ttgatgatct cagggaaaaa ttttaatcac tgtgtataat gatactgaac 1800

cttgattaat aacagaaatt caggatgtaa agccacagaa tgggatttat taatgtggga 1860

tacctcagac tgtttgtttt ctttctggga agaaaagtgt gttctataat gaataaatat 1920

agagtggttt tt 1932

<210> 27
<211> 214
<212> PRT
<213> human: PCTP protein

<400> 27

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Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu
20 25 30

Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys

35 40 45

Thr Gly Leu His Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
50 55 60

Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
65 70 75 80

Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
85 90 95

Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
100 105 110

Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg
115 120 125

Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
130 135 140

Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
145 150 155 160

Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
165 170 175

Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
180 185 190

Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln
195 200 205

Asn Tyr Leu Lys Lys Thr
210

<210> 28
<211> 271
<212> PRT
<213> Artificial

<220>
<223> START domain consensus sequence

<220>
<221> X
<222> (1)..(1)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (2)..(2)
<223> hydrophobic amino acids: Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp, Tyr or any modified hydrophobic amino acid

<220>
<221> X
<222> (3)..(4)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (5)..(5)
<223> turnlike amino acids: Ala, Cys, Asp, Glu, Gly, His, Lys, Asn, Gln, Arg, Ser, Thr or any modified turnlike amino acid

<220>
<221> X
<222> (6)..(8)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (9)..(9)
<223> turnlike amino acids: Ala, Cys, Asp, Glu, Gly, His, Lys, Asn, Gln, Arg, Ser, Thr or any modified turnlike amino acid

<220>
<221> X
<222> (10)..(10)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (11)..(11)
<223> hydrophobic amino acids: Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp, Tyr or any modified hydrophobic amino acid

<220>
<221> X
<222> (12)..(12)
<223> turnlike amino acids: Ala, Cys, Asp, Glu, Gly, His, Lys, Asn, Gln, Arg, Ser, Thr or any modified turnlike amino acid

<220>
<221> X
<222> (13)..(13)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (14)..(15)
<223> hydrophobic amino acids: Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp, Tyr or any modified hydrophobic amino acid

<220>
<221> X
<222> (16)..(16)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>

<221> X
<222> (17)..(17)
<223> turnlike amino acids: Ala, Cys, Asp, Glu, Gly, His, Lys, Asn, Gln, Arg, Ser, Thr or any modified turnlike amino acid

<220>
<221> X
<222> (18)..(20)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
<221> X
<222> (22)..(38)
<223> any amino acid: Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified amino acid

<220>
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<222> (39)..(40)
<223> hydrophobic amino acids: Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp, Tyr or any modified hydrophobic amino acid

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<223> positive amino acid: His, Lys, Arg or any modified positive amino acid

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240

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245 250 255

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260 265 270