

P01-2188_070322mitConsensus.ST25.txt
SEQUENCE LISTING

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<120> Improvement of protein production
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<170> PatentIn version 3.3
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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
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Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly
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55

60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
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Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
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Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
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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
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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
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 Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
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 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
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 Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
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 Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
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 Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
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 Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
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 Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
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 Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
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 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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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
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Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
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Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
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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
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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
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Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
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 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
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 Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
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 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
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 Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
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 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
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 Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
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 Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
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Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
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Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
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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
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Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
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Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
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Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
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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 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
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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
Seite 11

355

360

365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
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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
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Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
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Gly Lys Pro Ile Leu Phe
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<211> 669

<212> DNA

<213> human: START Domain CERT cDNA

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tatcaaacac acaagagggt gtggcctgct tctcagcgag acgtattata tctttctgtc    360
attcgaaaga taccagcctt gactgaaaat gaccctgaaa cttggatagt ttgtaatttt    420
tctgtggatc atgacagtgc tcctctaaac aaccgatgtg tccgtgccaa aataaatgtt    480
gctatgattt gtcaaactt ggtaagccca ccagagggaa accaggaaat tagcaggggac    540
aacattctat gcaagattac atatgtagct aatgtgaacc ctggaggatg ggcaccagcc    600
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<211> 223
<212> PRT
<213> human: START Domain CERT protein
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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
Seite 13

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

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<211> 658
<212> DNA
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gaaaatggga ttgttctgga tcctttaaaa gctacccatg cagttaaagg cgtcacagga 180
catgaagtct gcaattatct ctggaatggt gacgttcgca atgactggga aacaactata 240
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gacagtgtc ctctaaacaa ccgatgtgtc cgtgccaaaa taaatgttgc tatgatttgt 480
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<210> 19
<211> 219
<212> PRT
<213> human: START Domain CERT L protein

<400> 19
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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

<210> 20
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<212> DNA
<213> human: StarD4 cDNA

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 <212> PRT
 <213> human: StarD4 protein

<400> 21

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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

<210> 22
<211> 1344
<212> DNA
<213> human: StarD5 cDNA

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gtggccgaga agatgctcca gtaccggcgg gacacagcag gctggaagat ttgccgggaa 180
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cccagagatt ttgtggactt ggtgctagtc aagagatatg aggatgggac catcagttcc 480
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 <211> 213
 <212> PRT
 <213> human: StarD5 protein

<400> 23

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 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

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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
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<211> 663
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agaaaattcc atggaaatct atatcgtgtt gaagggataa ttccagaatc accagctaaa 180
ctatctgatt tcctctacca aactggagac agaattacat gggataaatc attgcaagtg 240
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tcaaattata tccgcgggta taaccatcct tgtggctttg tatgttcacc aatggaagaa 480
aaccagcat attccaaact agtgatgttt gtccagacag aaatgagagg aaaattgtcc 540
ccatcaataa ttgaaaaaac catgccttcc aacttagtaa acttcatcct caatgcaaaa 600
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<211> 220
<212> PRT
<213> human: StarD6 protein

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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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<211> 1932
<212> DNA
<213> human: PCTP cDNA

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<400> 27

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Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys
 Seite 21

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

<220>
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<220>
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 <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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amino acid

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Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified
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Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val or any modified
amino acid

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Met, Arg, Thr, Val, Trp, Tyr or any modified hydrophobic amino
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Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

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35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

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100 105 110

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115 120 125

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130 135 140

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145 150 155 160

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165 170 175

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180 185 190

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