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<120> ARTIFICIAL EUKARYOTIC EXPRESSION SYSTEM WITH ENHANCED PERFORMANCES

<130> B14313WO CS/PPT

<150> EP20305899.5

<151> 2020-08-04

<160> 42

<170> PatentIn version 3.5

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<212> DNA

<213> Artificial Sequence

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<223> Recombinant DNA: open-reading frame from pC3P3-G1 plasmid

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Ile Asn Phe Leu Leu Phe Lys Thr Val Tyr Glu Ala Leu Val Ala Gln
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Glu Ile Pro Ser Thr Ile Ser His Ser Ile Arg Cys Ile Lys Lys Val
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His His Glu Asn His Cys Arg Glu Lys Ile Leu Pro Ser Glu Asn Leu
65 70 75 80

Tyr Phe Lys Lys Gln Pro Leu Met Phe Phe Lys Phe Ser Glu Pro Ala
85 90 95

Ser Leu Gly Cys Lys Val Ser Leu Ala Ile Glu Gln Pro Ile Arg Lys
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Phe Ile Leu Asp Ser Ser Val Leu Val Arg Leu Lys Asn Arg Thr Thr
115 120 125

Phe Arg Val Ser Glu Leu Trp Lys Ile Glu Leu Thr Ile Val Lys Gln
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Leu Phe Asp Thr Pro Glu Gln Gln Thr Thr Lys Asn Met Met Thr Leu
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Gly Lys Pro Glu Ser Leu Thr Ala Ala Asp Val Ile Lys Ile Lys Asn
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Thr Val Leu Thr Leu Ile Ser Pro Asn His Leu Met Leu Thr Ala Tyr
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His Gln Ala Ile Glu Phe Ile Ala Ser His Ile Leu Ser Ser Glu Ile
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Leu Leu Ala Arg Ile Lys Ser Gly Lys Trp Gly Leu Lys Arg Leu Leu
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Pro Gln Val Lys Ser Met Thr Lys Ala Asp Tyr Met Lys Phe Tyr Pro
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Pro Val Gly Tyr Tyr Val Thr Asp Lys Ala Asp Gly Ile Arg Gly Ile
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Ala Val Ile Gln Asp Thr Gln Ile Tyr Val Val Ala Asp Gln Leu Tyr
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Ser Leu Gly Thr Thr Gly Ile Glu Pro Leu Lys Pro Thr Ile Leu Asp
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Gly Glu Phe Met Pro Glu Lys Lys Glu Phe Tyr Gly Phe Asp Val Ile
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Met Tyr Glu Gly Asn Leu Leu Thr Gln Gln Gly Phe Glu Thr Arg Ile
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Glu Ser Leu Ser Lys Gly Ile Lys Val Leu Gln Ala Phe Asn Ile Lys
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Ala Glu Met Lys Pro Phe Ile Ser Leu Thr Ser Ala Asp Pro Asn Val
370 375 380

Leu Leu Lys Asn Phe Glu Ser Ile Phe Lys Lys Lys Thr Arg Pro Tyr
385 390 395 400

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



530

535

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Glu Leu Ala Lys Gly Pro Ser Gly Met Tyr Phe Ala Gly Ala Lys Thr
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Arg Lys Phe Ser His Ala Thr Thr Arg Gln His Lys His Ala Thr Asn
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Glu Lys Val His Gln Ile Tyr Gly Phe Pro Lys Glu Gly Ala Ser Ser
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Ile Val Ser Asn Leu Phe Ile His Tyr Leu Met Lys Asn Thr Gln Gln
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Val Glu Asn Leu Ala Val Leu Cys His Lys Leu Leu Gln Pro Gly Gly
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Met Val Trp Phe Thr Thr Met Leu Gly Glu Gln Val Leu Glu Leu Leu
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His Glu Asn Arg Ile Glu Leu Asn Glu Val Trp Glu Ala Arg Glu Asn
755 760 765

Glu Val Val Lys Phe Ala Ile Lys Arg Leu Phe Lys Glu Asp Ile Leu
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Gln Glu Thr Gly Gln Glu Ile Gly Val Leu Leu Pro Phe Ser Asn Gly
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Asp Phe Tyr Asn Glu Tyr Leu Val Asn Thr Ala Phe Leu Ile Lys Ile
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Phe Lys His His Gly Phe Ser Leu Val Gln Lys Gln Ser Phe Lys Asp
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Thr Glu Ala Asp Lys Thr Trp Thr Ser Leu Phe Gly Phe Ile Cys Leu
850 855 860

Arg Lys Asn Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Asp Leu
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His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe Asn Gly Gly Ile
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Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala Ser Gly Asn Glu
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Val Ala Ala Tyr Ile Thr Met Lys Ile Val Met Asp Met Leu Asn Thr
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Asp Val Thr Leu Gln Ala Ile Ala Met Asn Val Ala Asp Arg Ile Glu
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Asp Gln Val Arg Phe Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe
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Glu Lys Val Lys Lys Ser Leu Lys Ala Ser Lys Thr Lys Ser Tyr
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<213> Artificial Sequence

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<400> 4

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20          25          30

```

```

Gln Thr Gln Pro Pro Gln Arg His Tyr Gly Ile Thr Ser Pro Ile Ser
35          40          45

```

```

Leu Ala Ala Pro Lys Glu Thr Asp Cys Leu Leu Thr Gln Lys Leu Ile
50          55          60

```

```

Glu Thr Leu Lys Pro Phe Gly Val Phe Glu Glu Glu Glu Leu Gln
65          70          75          80

```

```

Arg Arg Ile Leu Ile Leu Gly Lys Leu Asn Asn Leu Val Lys Glu Trp
85          90          95

```

```

Ile Arg Glu Ile Ser Glu Ser Lys Asn Leu Pro Gln Ser Val Ile Glu
100         105         110

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Asn Val Gly Gly Lys Ile Phe Thr Phe Gly Ser Tyr Arg Leu Gly Val
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His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys Val Ala Pro Arg His
130 135 140

Val Asp Arg Ser Asp Phe Phe Thr Ser Phe Tyr Asp Lys Leu Lys Leu
145 150 155 160

Gln Glu Glu Val Lys Asp Leu Arg Ala Val Glu Glu Ala Phe Val Pro
165 170 175

Val Ile Lys Leu Cys Phe Asp Gly Ile Glu Ile Asp Ile Leu Phe Ala
180 185 190

Arg Leu Ala Leu Gln Thr Ile Pro Glu Asp Leu Asp Leu Arg Asp Asp
195 200 205

Ser Leu Leu Lys Asn Leu Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly
210 215 220

Cys Arg Val Thr Asp Glu Ile Leu His Leu Val Pro Asn Ile Asp Asn
225 230 235 240

Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp Ala Lys Arg His Asn
245 250 255

Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly Val Ser Trp Ala Met
260 265 270

Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn Ala Ile Ala Ser Thr
275 280 285

Leu Val His Lys Phe Phe Leu Val Phe Ser Lys Trp Glu Trp Pro Asn
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Pro Val Leu Leu Lys Gln Pro Glu Glu Cys Asn Leu Asn Leu Pro Val
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Trp Asp Pro Arg Val Asn Pro Ser Asp Arg Tyr His Leu Met Pro Ile
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Ile Thr Pro Ala Tyr Pro Gln Gln Asn Ser Thr Tyr Asn Val Ser Val
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Ser Thr Arg Met Val Met Val Glu Glu Phe Lys Gln Gly Leu Ala Ile
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Thr Asp Glu Ile Leu Leu Ser Lys Ala Glu Trp Ser Lys Leu Phe Glu
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Ala Pro Asn Phe Phe Gln Lys Tyr Lys His Tyr Ile Val Leu Leu Ala
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Ser Ala Pro Thr Glu Lys Gln Arg Leu Glu Trp Val Gly Leu Val Glu
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Ser Lys Ile Arg Ile Leu Val Gly Ser Leu Glu Lys Asn Glu Phe Ile
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Thr Leu Ala His Val Asn Pro Gln Ser Phe Pro Ala Pro Lys Glu Ser
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Pro Asp Arg Glu Glu Phe Arg Thr Met Trp Val Ile Gly Leu Val Phe
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Lys Lys Thr Glu Asn Ser Glu Asn Leu Ser Val Asp Leu Thr Tyr Asp
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Ile Gln Ser Phe Thr Asp Thr Val Tyr Arg Gln Ala Ile Asn Ser Lys
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Met Phe Glu Leu Asp Met Lys Ile Ala Ala Met His Val Lys Arg Lys
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Gln Leu His Gln Leu Leu Pro Ser His Val Leu Gln Lys Arg Lys Lys
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His Ser Thr Glu Gly Val Lys Leu Thr Ala Leu Asn Asp Ser Ser Leu
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Asp Leu Ser Met Asp Ser Asp Asn Ser Met Ser Val Pro Ser Pro Thr
545 550 555 560

Ser Ala Met Lys Thr Ser Pro Leu Asn Ser Ser Gly Ser Ser Gln Gly
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Arg Asn Ser Pro Ala Pro Ala Val Thr Ala Ala Ser Val Thr Ser Ile
580 585 590

Gln Ala Ser Glu Val Ser Val Pro Gln Ala Asn Ser Ser Glu Ser Pro
595 600 605

Gly Gly Pro Ser Ser Glu Ser Ile Pro Gln Thr Ala Thr Gln Pro Ala
610 615 620

Ile Ala Pro Pro Pro Lys Pro Thr Val Ser Arg Val Val Ser Ser Thr
625 630 635 640

Arg Leu Val Asn Pro Ser Pro Arg Pro Ser Gly Asn Thr Ala Thr Lys
645 650 655



Val Pro Asn Pro Ile Val Gly Val Lys Arg Thr Ser Ala Pro Asn Lys
660 665 670

Glu Glu Ala Pro Arg Arg Thr Lys Thr Glu Glu Asp Glu Thr Ser Glu
675 680 685

Asp Ala Asn Cys Leu Ala Leu Ser Gly His Asp Lys Thr Glu Thr Lys
690 695 700

Glu Gln Val Asp Leu Glu Thr Ser Ala Val Gln Ser Glu Thr Val Pro
705 710 715 720

Ala Ser Ala Ser Leu Leu Ala Ser Gln Lys Thr Ser Ser Thr Asp Leu
725 730 735

Ser Asp Ile Pro Ala Leu Pro Ala Asn Pro Ile Pro Val Ile Lys Asn
740 745 750

Ser Ile Lys Leu Arg Leu Asn Arg Gly Ser Gly Pro Arg Pro Leu Leu
755 760 765

Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro
770 775 780

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
785 790 795 800

Glu Ser Asn Pro Gly Pro Ala Ser Leu Asp Asn Leu Val Ala Arg Tyr
805 810 815

Gln Arg Cys Phe Asn Asp Gln Ser Leu Lys Asn Ser Thr Ile Glu Leu
820 825 830

Glu Ile Arg Phe Gln Gln Ile Asn Phe Leu Leu Phe Lys Thr Val Tyr
835 840 845

Glu Ala Leu Val Ala Gln Glu Ile Pro Ser Thr Ile Ser His Ser Ile
850 855 860

Arg Cys Ile Lys Lys Val His His Glu Asn His Cys Arg Glu Lys Ile
865 870 875 880

Leu Pro Ser Glu Asn Leu Tyr Phe Lys Lys Gln Pro Leu Met Phe Phe
885 890 895

Lys Phe Ser Glu Pro Ala Ser Leu Gly Cys Lys Val Ser Leu Ala Ile
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Glu Gln Pro Ile Arg Lys Phe Ile Leu Asp Ser Ser Val Leu Val Arg
915 920 925

Leu Lys Asn Arg Thr Thr Phe Arg Val Ser Glu Leu Trp Lys Ile Glu



930

935

940

Leu Thr Ile Val Lys Gln Leu Met Gly Ser Glu Val Ser Ala Lys Leu
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Ala Ala Phe Lys Thr Leu Leu Phe Asp Thr Pro Glu Gln Gln Thr Thr
965 970 975

Lys Asn Met Met Thr Leu Ile Asn Pro Asp Asp Glu Tyr Leu Tyr Glu
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Ile Glu Ile Glu Tyr Thr Gly Lys Pro Glu Ser Leu Thr Ala Ala Asp
995 1000 1005

Val Ile Lys Ile Lys Asn Thr Val Leu Thr Leu Ile Ser Pro Asn
1010 1015 1020

His Leu Met Leu Thr Ala Tyr His Gln Ala Ile Glu Phe Ile Ala
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Ser His Ile Leu Ser Ser Glu Ile Leu Leu Ala Arg Ile Lys Ser
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Gly Lys Trp Gly Leu Lys Arg Leu Leu Pro Gln Val Lys Ser Met
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Thr Lys Ala Asp Tyr Met Lys Phe Tyr Pro Pro Val Gly Tyr Tyr
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Val Thr Asp Lys Ala Asp Gly Ile Arg Gly Ile Ala Val Ile Gln
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Asp Thr Gln Ile Tyr Val Val Ala Asp Gln Leu Tyr Ser Leu Gly
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Thr Thr Gly Ile Glu Pro Leu Lys Pro Thr Ile Leu Asp Gly Glu
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Phe Met Pro Glu Lys Lys Glu Phe Tyr Gly Phe Asp Val Ile Met
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Tyr Glu Gly Asn Leu Leu Thr Gln Gln Gly Phe Glu Thr Arg Ile
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Glu Ser Leu Ser Lys Gly Ile Lys Val Leu Gln Ala Phe Asn Ile
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Lys Ala Glu Met Lys Pro Phe Ile Ser Leu Thr Ser Ala Asp Pro
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Asn Val Leu Leu Lys Asn Phe Glu Ser Ile Phe Lys Lys Lys Thr
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Arg Pro Tyr Ser Ile Asp Gly Ile Ile Leu Val Glu Pro Gly Asn
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Ser Tyr Leu Asn Thr Asn Thr Phe Lys Trp Lys Pro Thr Trp Asp
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Asn Thr Leu Asp Phe Leu Val Arg Lys Cys Pro Glu Ser Leu Asn
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Val Pro Glu Tyr Ala Pro Lys Lys Gly Phe Ser Leu His Leu Leu
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Gln Asn Tyr Phe Pro Val Gln Phe Gln Pro Ser Asp Phe Pro Leu
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Ala Phe Leu Tyr Tyr His Pro Asp Thr Ser Ser Phe Ser Asn Ile
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Asp Gly Lys Val Leu Glu Met Arg Cys Leu Lys Arg Glu Ile Asn
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Tyr Val Arg Trp Glu Ile Val Lys Ile Arg Glu Asp Arg Gln Gln
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Asp Leu Lys Thr Gly Gly Tyr Phe Gly Asn Asp Phe Lys Thr Ala
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Glu Leu Thr Trp Leu Asn Tyr Met Asp Pro Phe Ser Phe Glu Glu
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Leu Ala Lys Gly Pro Ser Gly Met Tyr Phe Ala Gly Ala Lys Thr
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Gly Ile Tyr Arg Ala Gln Thr Ala Leu Ile Ser Phe Ile Lys Gln
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Glu Ile Ile Gln Lys Ile Ser His Gln Ser Trp Val Ile Asp Leu
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Gly Ile Gly Lys Gly Gln Asp Leu Gly Arg Tyr Leu Asp Ala Gly
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Val Arg His Leu Val Gly Ile Asp Lys Asp Gln Thr Ala Leu Ala
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Glu Leu Val Tyr Arg Lys Phe Ser His Ala Thr Thr Arg Gln His
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Lys His Ala Thr Asn Ile Tyr Val Leu His Gln Asp Leu Ala Glu
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Pro Ala Lys Glu Ile Ser Glu Lys Val His Gln Ile Tyr Gly Phe
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Pro Lys Glu Gly Ala Ser Ser Ile Val Ser Asn Leu Phe Ile His
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Tyr Leu Met Lys Asn Thr Gln Gln Val Glu Asn Leu Ala Val Leu
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Cys His Lys Leu Leu Gln Pro Gly Gly Met Val Trp Phe Thr Thr
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Met Leu Gly Glu Gln Val Leu Glu Leu Leu His Glu Asn Arg Ile
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Glu Leu Asn Glu Val Trp Glu Ala Arg Glu Asn Glu Val Val Lys
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Tyr Asn Glu Tyr Leu Val Asn Thr Ala Phe Leu Ile Lys Ile Phe
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Lys His His Gly Phe Ser Leu Val Gln Lys Gln Ser Phe Lys Asp
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Trp Ile Pro Glu Phe Gln Asn Phe Ser Lys Ser Leu Tyr Lys Ile
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Cys Leu Arg Lys Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile
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Ala Ser Gly Asn Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu
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Ser Glu Leu Ile Ala Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys
1730 1735 1740

Glu Glu Tyr Glu Gly Lys Arg Gly Arg Ala Pro Arg Ala Leu Ala
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Phe Ile Asn Cys Val Gly Asn Glu Val Ala Ala Tyr Ile Thr Met
1760 1765 1770

Lys Ile Val Met Asp Met Leu Asn Thr Asp Val Thr Leu Gln Ala
1775 1780 1785

Ile Ala Met Asn Val Ala Asp Arg Ile Glu Asp Gln Val Arg Phe
1790 1795 1800

Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe Glu Lys Val Lys
1805 1810 1815

Lys Ser Leu Lys Ala Ser Lys Thr Lys Ser Tyr Arg His Ala His
1820 1825 1830

Asn Val Ala Val Val Ala Glu Lys Ser Val Ala Asp Arg Asp Ala
1835 1840 1845

Asp Phe Ser Arg Trp Glu Ala Trp Pro Lys Asp Thr Leu Leu Gln
1850 1855 1860

Ile Gly Met Thr Leu Leu Glu Ile Leu Glu Asn Ser Val Phe Phe
1865 1870 1875

Asn Gly Gln Pro Val Phe Leu Arg Thr Leu Arg Thr Asn Gly Gly
1880 1885 1890

Lys His Gly Val Tyr Tyr Leu Gln Thr Ser Glu His Val Gly Glu
1895 1900 1905

Trp Ile Thr Ala Phe Lys Glu His Val Ala Gln Leu Ser Pro Ala
1910 1915 1920

Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro Trp Val Ser Pro Phe
1925 1930 1935

Asn Gly Gly Phe His Thr Glu Lys Val Ala Ser Arg Ile Arg Leu
1940 1945 1950

Val Lys Gly Asn Arg Glu His Val Arg Lys Leu Thr Lys Lys Gln
1955 1960 1965

Met Pro Ala Val Tyr Lys Ala Val Asn Ala Leu Gln Ala Thr Lys



1970

1975

1980

Trp	Gln	Val	Asn	Lys	Glu	Val	Leu	Gln	Val	Val	Glu	Asp	Val	Ile
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Arg	Leu	Asp	Leu	Gly	Tyr	Gly	Val	Pro	Ser	Phe	Lys	Pro	Leu	Ile
2000						2005					2010			
Asp	Arg	Glu	Asn	Lys	Pro	Ala	Asn	Pro	Val	Pro	Leu	Glu	Phe	Gln
2015						2020					2025			
His	Leu	Arg	Gly	Arg	Glu	Leu	Lys	Glu	Met	Leu	Thr	Pro	Glu	Gln
2030						2035					2040			
Trp	Gln	Ala	Phe	Ile	Asn	Trp	Lys	Gly	Glu	Cys	Thr	Lys	Leu	Tyr
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2060						2065					2070			
Met	Val	Gly	Gln	Ala	Arg	Lys	Tyr	Ser	Gln	Phe	Asp	Ala	Ile	Tyr
2075						2080					2085			
Phe	Val	Tyr	Ala	Leu	Asp	Ser	Arg	Ser	Arg	Val	Tyr	Ala	Gln	Ser
2090						2095					2100			
Ser	Thr	Leu	Ser	Pro	Gln	Ser	Asn	Asp	Leu	Gly	Lys	Ala	Leu	Leu
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Trp	Phe	Leu	Val	Asn	Gly	Ala	Asn	Asn	Trp	Gly	Trp	Asp	Lys	Lys
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Thr	Phe	Asp	Val	Arg	Thr	Ala	Asn	Val	Leu	Asp	Ser	Glu	Phe	Gln
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Asp	Met	Cys	Arg	Asp	Ile	Ala	Ala	Asp	Pro	Leu	Thr	Phe	Thr	Gln
2165						2170					2175			
Trp	Val	Asn	Ala	Asp	Ser	Pro	Tyr	Gly	Phe	Leu	Ala	Trp	Cys	Phe
2180						2185					2190			
Glu	Tyr	Ala	Arg	Tyr	Leu	Asp	Ala	Leu	Asp	Glu	Gly	Thr	Gln	Asp
2195						2200					2205			
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2210						2215					2220			
Gly	Ile	Gln	His	Tyr	Ser	Ala	Met	Leu	Ser	Asp	Ala	Val	Gly	Ala
2225						2230					2235			



Lys Ala Val Asn Leu Lys Pro Ser Asp Ser Pro Gln Asp Ile Tyr
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Gly Ala Val Ala Gln Val Val Ile Gln Lys Asn Tyr Ala Tyr Met
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Asn Ala Glu Asp Ala Glu Thr Phe Thr Ser Gly Ser Val Thr Leu
2270 2275 2280

Thr Gly Ala Glu Leu Arg Ser Met Ala Ser Ala Trp Asp Met Ile
2285 2290 2295

Gly Ile Thr Arg Gly Leu Thr Lys Lys Pro Val Met Thr Leu Pro
2300 2305 2310

Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr
2315 2320 2325

Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Arg Ala Ile Ala Glu
2330 2335 2340

Gly Arg Thr Ala Asn Pro Val His Pro Phe Asp Asn Asp Arg Lys
2345 2350 2355

Asp Ser Leu Thr Pro Ser Ala Ala Tyr Asn Tyr Met Thr Ala Leu
2360 2365 2370

Ile Trp Pro Ser Ile Ser Glu Val Val Lys Ala Pro Ile Val Ala
2375 2380 2385

Met Lys Met Ile Arg Gln Leu Ala Arg Phe Ala Ala Lys Arg Asn
2390 2395 2400

Glu Gly Leu Glu Tyr Pro Leu Pro Thr Gly Phe Ile Leu Gln Gln
2405 2410 2415

Lys Ile Met Ala Thr Asp Met Leu Arg Val Ser Thr Cys Leu Met
2420 2425 2430

Gly Glu Ile Lys Met Ser Leu Gln Ile Glu Thr Asp Val Val Asp
2435 2440 2445

Glu Thr Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly
2450 2455 2460

His Asp Ala Ser His Leu Ile Leu Thr Val Cys Asp Leu Val Asp
2465 2470 2475

Lys Gly Ile Thr Ser Val Ala Val Ile His Asp Ser Phe Gly Thr
2480 2485 2490



His Ala Gly Arg Thr Ala Asp Leu Arg Asp Ser Leu Arg Glu Glu
2495 2500 2505

Met Val Lys Met Tyr Gln Asn His Asn Ala Leu Gln Asn Leu Leu
2510 2515 2520

Asp Val His Glu Glu Arg Trp Leu Val Asp Thr Gly Ile Gln Val
2525 2530 2535

Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu Ile Leu Val Ser Asp
2540 2545 2550

Tyr Cys Phe Ala
2555

<210> 5
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant DNA: open-reading frame from
pADAR1-Zalpha/(G4S)2/E3L-dsDNA plasmid

<400> 5
atgctgtcca tctaccaaga ccaagaacag aggataactca aatttttggg ggaattgggt 60
gagggaaagg ccaccactgc acacgatttg tctgggaaac tcgggacccc aaaaaaggag 120
attaacaggg ttttgtactc cctggctaag aaaggcaaat tgcagaaaga agccggaact 180
ccccctctgt ggaagatcgc agtgagcaca caagcttgga atcaacatag cggagtcgtg 240
cgaccgatg gtcattcaca gggcgccccg aactccgacc cctccctaga accagaggac 300
aggaattcaa cgagcgtgag tgaagacctg cttgaaccgt tcatagctgt ctctgcacag 360
gcatggaatc agcactccgg tgtgttgaga cccgactctc atagccaggg aagccccaac 420
agcgaccggg gtctcgagcc tgaagactct aattcgacta gtgctcttga ggatccattg 480
gaatttctcg atatggcaga aatcaaggaa aaaatttgcg attacctttt taacgtctct 540
gatagcagcg ctctgaacct ggctaaaaat ataggtctta ccaaagctcg tgatatcaat 600
gccgtgtgta tcgatatgga gcggcagggg gacgtatatc gccagggcac tactccccca 660
atctggcacc tcacggatgg aggaggaggc tctggtggtg gcgggagcaa cccgtgacc 720
atcatcaacg agtactgcca gatcaccaag agagactgga gcttcagaat cgagagcgtg 780
ggccccagca acagccccac cttctacgcc tgcgtggaca tcgacggcag agtgttcgac 840
aaggccgacg gcaagagcaa gagagacgcc aagaacaacg ccgccaagct ggccgtggac 900
aagctgctgg gctacgtgat catcagattc tga 933

<210> 6
<211> 310
<212> PRT
<213> Artificial Sequence



<220>

<223> recombinant protein encoded by pADAR1-Zalpha/(G4S)2/E3L-dsDNA
plasmid

<400> 6

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

Ile Glu Ser Val Gly Pro Ser Asn Ser Pro Thr Phe Tyr Ala Cys Val
260 265 270

Asp Ile Asp Gly Arg Val Phe Asp Lys Ala Asp Gly Lys Ser Lys Arg
275 280 285

Asp Ala Lys Asn Asn Ala Ala Lys Leu Ala Val Asp Lys Leu Leu Gly
290 295 300

Tyr Val Ile Ile Arg Phe
305 310

<210> 7
<211> 567
<212> DNA
<213> Artificial Sequence

<220>
<223> recombinant DNA: open-reading frame from pE3L-Zalpha/NS1-dsDNA plasmid

<400> 7
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aacatcggca tcgagggcgc caccgccgcc cagctgacca gacagctgaa catggagaag 120
agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac 180
gacatcccc ccagatgggt catgaccacc gaggccgaca agcccgcgc cgacgccatg 240
gccgacgtga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc 300
ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgccga cccaataca 360
gtctcctctt ttcaagtgga ctgttttttg tggcatgttc gaaagcgggt tgctgaccaa 420
gagctggggg atgccccgtt tctagaccgg ctacggagag accaaaagag cttgcgtggg 480
agaggcagta ccctgggcct cgacatcgag accgctacac gcgccggcaa gcagatcgtg 540
gaacgcatct taaaagagga gtcctaa 567

<210> 8
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> recombinant protein encoded by pE3L-Zalpha/NS1-dsDNA plasmid

<400> 8

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
1 5 10 15

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
20 25 30

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
35 40 45



Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
100 105 110

Trp Lys Asp Ala Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys
115 120 125

Phe Leu Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp
130 135 140

Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
145 150 155 160

Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala Gly
165 170 175

Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser
180 185

<210> 9
<211> 567
<212> DNA
<213> Artificial Sequence

<220>
<223> recombinant DNA: open-reading frame from pE3L-Zalpha/B2-dsDNA
plasmid

<400> 9
atgagcaaga tctacatcga cgagagaagc gacgccgaga tcgtgtgcgc cgccatcaag 60
aacatcggca tcgagggcgc caccgccgcc cagctgacca gacagctgaa catggagaag 120
agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac 180
gacatccccc ccagatgggt catgaccacc gaggccgaca agcccgacgc cgacgccatg 240
gccgacgtga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc 300
ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgcccc ctctaaattg 360
gcattgatcc aggagctgcc cgataggatt caaacagccg tggaagcagc catgggaatg 420
tcataaccagg atgcacaaaa caatgttaga agagacctgg acaatttgca tgcctgcctt 480
aacaaagcaa agctcactgt gtccagaatg gtgactagcc tgttggaata accatccgtc 540
gtcgcgtacc tggagggaaa ggcataa 567

<210> 10



<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> recombinant protein encoded by pE3L-Zalpha/B2-dsDNA plasmid

<400> 10

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
 1 5 10 15

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
 20 25 30

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
 35 40 45

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
 50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
 65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
 85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
 100 105 110

Trp Lys Asp Ala Pro Ser Lys Leu Ala Leu Ile Gln Glu Leu Pro Asp
 115 120 125

Arg Ile Gln Thr Ala Val Glu Ala Ala Met Gly Met Ser Tyr Gln Asp
 130 135 140

Ala Pro Asn Asn Val Arg Arg Asp Leu Asp Asn Leu His Ala Cys Leu
 145 150 155 160

Asn Lys Ala Lys Leu Thr Val Ser Arg Met Val Thr Ser Leu Leu Glu
 165 170 175

Lys Pro Ser Val Val Ala Tyr Leu Glu Gly Lys Ala
 180 185

<210> 11

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> recombinant DNA: open-reading frame from
pE3L-Zalpha/hEIF2AK2-dsDNA plasmid

<400> 11

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60



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agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac 180
gacatcccc ccagatggtt catgaccacc gaggccgaca agcccgcgc cgacgccatg 240
gccgacgtga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc 300
ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgcctt cttcatggag 360
gaactgaaca cataccggca gaagcagggc gttgtgctga agtaccagga actgccgaat 420
tcaggctctc cccatgatcg ccggttcacg tttcaggtaa taatcgacgg cagggaattc 480
cccgaaaggcg agggcagatc taagaaggaa gcgaagaatg ccgcggccaa gttggctgtc 540
gaaatactta ataaagaaaa gaaggctgtc agtccactgc ttctgacaac aactaatagt 600
agcgaaggac taagcatggg aaattacatc ggtctaatac atcggattgc tcagaaaaaa 660
cgccttactg tgaattatga gcagtgcgcc tccggagtgc acggacctga gggattccac 720
tacaagtga agatggggcca aaaggagtat agcatcggca ctgggtctac taaacaagag 780
gctaagcagc tggccgcaaa gctggcgtat ctacagatcc tgagttaa 828

<210> 12

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> recombinant protein encoded by pE3L-Zalpha/hEIF2AK2-dsDNA plasmid

<400> 12

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
1 5 10 15

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
20 25 30

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
35 40 45

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
100 105 110

Trp Lys Asp Ala Phe Phe Met Glu Glu Leu Asn Thr Tyr Arg Gln Lys
115 120 125



Gln Gly Val Val Leu Lys Tyr Gln Glu Leu Pro Asn Ser Gly Pro Pro
 130 135 140

His Asp Arg Arg Phe Thr Phe Gln Val Ile Ile Asp Gly Arg Glu Phe
 145 150 155 160

Pro Glu Gly Glu Gly Arg Ser Lys Lys Glu Ala Lys Asn Ala Ala Ala
 165 170 175

Lys Leu Ala Val Glu Ile Leu Asn Lys Glu Lys Lys Ala Val Ser Pro
 180 185 190

Leu Leu Leu Thr Thr Thr Asn Ser Ser Glu Gly Leu Ser Met Gly Asn
 195 200 205

Tyr Ile Gly Leu Ile Asn Arg Ile Ala Gln Lys Lys Arg Leu Thr Val
 210 215 220

Asn Tyr Glu Gln Cys Ala Ser Gly Val His Gly Pro Glu Gly Phe His
 225 230 235 240

Tyr Lys Cys Lys Met Gly Gln Lys Glu Tyr Ser Ile Gly Thr Gly Ser
 245 250 255

Thr Lys Gln Glu Ala Lys Gln Leu Ala Ala Lys Leu Ala Tyr Leu Gln
 260 265 270

Ile Leu Ser
 275

<210> 13
 <211> 603
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> recombinant DNA: open-reading frame from pE3L-Zalpha/sigma3-dsDNA
 plasmid

<400> 13
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 aacatcgga tcgagggcgc caccgccgcc cagctgacca gacagctgaa catggagaag 120
 agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac 180
 gacatcccc ccagatgggt catgaccacc gaggccgaca agcccgacgc cgacgccatg 240
 gccgacgtga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc 300
 ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgccgt gtatgactat 360
 tctgagctag agcatgatcc tagtaagggg cgggcctatc ggaaggaatt agttaccctt 420
 gctagagact tcgggcattt tggccttagt cactactcta gagcgactac ccctatcctt 480
 gggaagatgc cggctgtctt tagtggaatg ttgaccggca actgtaagat gtatccgttt 540
 ataaaaggga cggccaaact gaagacagtg cgcaaactcg tagactccgt gaatcacgcc 600



tga

603

<210> 14

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> recombinant protein encoded by pE3L-Zalpha/sigma3-dsDNA plasmid

<400> 14

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
 1 5 10 15

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
 20 25 30

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
 35 40 45

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
 50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
 65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
 85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
 100 105 110

Trp Lys Asp Ala Val Tyr Asp Tyr Ser Glu Leu Glu His Asp Pro Ser
 115 120 125

Lys Gly Arg Ala Tyr Arg Lys Glu Leu Val Thr Pro Ala Arg Asp Phe
 130 135 140

Gly His Phe Gly Leu Ser His Tyr Ser Arg Ala Thr Thr Pro Ile Leu
 145 150 155 160

Gly Lys Met Pro Ala Val Phe Ser Gly Met Leu Thr Gly Asn Cys Lys
 165 170 175

Met Tyr Pro Phe Ile Lys Gly Thr Ala Lys Leu Lys Thr Val Arg Lys
 180 185 190

Leu Val Asp Ser Val Asn His Ala
 195 200

<210> 15

<211> 696

<212> DNA



<213> Artificial Sequence

<220>

<223> recombinant DNA: open-reading frame from
pE3L-Zalpha/NS1-dsDNA/(G4S)2/SZIP plasmid

<400> 15

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aacatcggca tcgagggcgc caccgccgcc cagctgacca gacagctgaa catggagaag      120
agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac      180
gacatcccc ccagatggtt catgaccacc gaggccgaca agcccgcgc cgacgccatg      240
gccgacgtga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc      300
ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgccga cccaataca      360
gtctcctctt ttcaagtgga ctgttttttg tggcatgttc gaaagcgggt tgctgaccaa      420
gagctggggg atgccccgtt tctagaccgg ctacggagag accaaaagag cttgcgtggg      480
agaggcagta ccctgggcct cgacatcgag accgctacac gcgccggcaa gcagatcgtg      540
gaacgcatct taaaagagga gtccggagga ggaggctctg gtggtggcgg gagcaggatg      600
gctcagttgg aggctaaggt agaggaacta ttgtccaaaa attggaatct cgagaacgaa      660
gtagctcgcc tcaagaaact ggtcggcgag cgctaa                                696

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<210> 16

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> recombinant protein encoded by pE3L-Zalpha/NS1-dsDNA/(G4S)2/SZIP
plasmid

<400> 16

```

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
1           5           10           15

```

```

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
20           25           30

```

```

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
35           40           45

```

```

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
50           55           60

```

```

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
65           70           75           80

```

```

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
85           90           95

```

```

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
100          105          110

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Trp Lys Asp Ala Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys
115 120 125

Phe Leu Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp
130 135 140

Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
145 150 155 160

Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala Gly
165 170 175

Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Gly Gly Gly Gly
180 185 190

Ser Gly Gly Gly Gly Ser Arg Met Ala Gln Leu Glu Ala Lys Val Glu
195 200 205

Glu Leu Leu Ser Lys Asn Trp Asn Leu Glu Asn Glu Val Ala Arg Leu
210 215 220

Lys Lys Leu Val Gly Glu Arg
225 230

<210> 17
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> recombinant DNA: open-reading frame from
pE3L-Zalpha/NS1-dsDNA/(G4S)2/GCN4 plasmid

<400> 17
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aacatcggca tcgagggcgc caccgccgcc cagctgacca gacagctgaa catggagaag 120
agagaggtga acaaggccct gtacgacctg cagagaagcg ccatggtgta cagcagcgac 180
gacatcccc ccagatgggt catgaccacc gaggccgaca agcccgcgc cgacgccatg 240
gccgactga tcatcgacga cgtgagcaga gagaagagca tgagagagga ccacaagagc 300
ttcgacgacg tgatccccgc caagaagatc atcgactgga aggacgccga cccaatata 360
gtctcctctt ttcaagtga ctgttttttg tggcatgttc gaaagcgggt tgctgaccaa 420
gagctggggg atgccccgtt tctagaccgg ctacggagag accaaaagag cttgcgtggg 480
agaggcagta ccctgggcct cgacatcgag accgctacac gcgccggcaa gcagatcgtg 540
gaacgcatct taaaagagga gtccggagga ggaggctctg gtggtggcgg gagcatgaag 600
gtcaagcaac tgggaagcgt tgtggaggag ttactctccg taaactatca cctggagaat 660
gtagttgcc gcctgaagaa actggtcggg gagagatga 699



<210> 18

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> recombinant protein encoded by pE3L-Zalpha/NS1-dsDNA/(G4S)2/GCN4 plasmid

<400> 18

Met Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp Ala Glu Ile Val Cys
1 5 10 15

Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala Thr Ala Ala Gln Leu
20 25 30

Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val Asn Lys Ala Leu Tyr
35 40 45

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
100 105 110

Trp Lys Asp Ala Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys
115 120 125

Phe Leu Trp His Val Arg Lys Arg Val Ala Asp Gln Glu Leu Gly Asp
130 135 140

Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly
145 150 155 160

Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala Gly
165 170 175

Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser Gly Gly Gly Gly
180 185 190

Ser Gly Gly Gly Gly Ser Met Lys Val Lys Gln Leu Glu Asp Val Val
195 200 205

Glu Glu Leu Leu Ser Val Asn Tyr His Leu Glu Asn Val Val Ala Arg
210 215 220

Leu Lys Lys Leu Val Gly Glu Arg
225 230



<210> 19
<211> 8502
<212> DNA
<213> Artificial Sequence

<220>

<223> recombinant DNA: open-reading frame from pC3P3-G3a plasmid

<400> 19

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gctaataccgt ttccagttac aacgcaggga tcacaacaaa cgcagccacc acagaggcac	120
tatggcatta cctctcttat cagcttagcg gcccccaagg agactgactg cctactcaca	180
cagaagctca tcgagacgct gaagcccttt ggggtttttg aagaagaaga ggaactgcag	240
cgcaggattt taattttggg aaaattaaat aacctggtga aagaatggat tcgagaaatc	300
agtgaagca agaactctcc acaatctgta attgaaaatg ttggaggga gatttttaca	360
tttggatctt acagactagg agtccacacg aaaggtgctg atattgatgc gttgtgtgtt	420
gcaccaagac atgttgatcg aagtgacttt ttcacctcat tctatgataa attgaaatta	480
caagaagaag tgaaagattt aagagctgtt gaagaggcat ttgtaccagt tatcaaactc	540
tgttttgatg gaatagagat tgatatattg tttgcaagat tagcactgca gactattcca	600
gaagatttgg acctacgaga tgacagtctg cttaaaaacc tagatataag atgcataaga	660
agccttaatg gttgcagggt aaccgatgaa attttacatc tagtaccaa cattgacaac	720
ttcagggtta ctctgagagc catcaaaactg tgggccaaac ggcacaacat ctattccaat	780
atattaggtt tcctcggtgg tgtttcctgg gctatgctag tagcaagaac ttgccagctt	840
tatccaaatg caatagcatc aactcttgta cataaatttt tcttggtatt ttctaaatgg	900
gaatggccaa atccagtgtc attgaaacag cctgaagaat gcaatcttaa tttgcctgtg	960
tgggacccaa gggtaaacc cagtgatagg taccatctta tgcctataat tacaccagca	1020
taccacagc agaactccac gtacaatgtg tccgtttcaa cacggatggt catggttgag	1080
gagtttaaac aaggtcttgc tatcacagat gaaattttgc tgagtaaggc agagtgttcc	1140
aaactttttg aagctccaaa cttctttcag aagtacaagc attatattgt acttctagca	1200
agtgcgccc cggaaaagca gcgtctggaa tgggtgggct tgggtggaatc aaaaatccgc	1260
atcctggttg gaagcttgga gaagaatgag tttattacac tggctcatgt gaatccccag	1320
tcattttcag ccccaaaga aagtcctgac agggagaagaat ttcgcacaat gtgggtgatt	1380
gggttagtgt ttaaaaaaac tgaaaactct gaaaatctca gtgtcgacct cacctatgat	1440
atccagtctt tcacagacac agtttatagg caagcaataa acagcaaaat gtttgagttg	1500
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```

```

Gln Thr Gln Pro Pro Gln Arg His Tyr Gly Ile Thr Ser Pro Ile Ser
35          40          45

```

```

Leu Ala Ala Pro Lys Glu Thr Asp Cys Leu Leu Thr Gln Lys Leu Ile
50          55          60

```

```

Glu Thr Leu Lys Pro Phe Gly Val Phe Glu Glu Glu Glu Leu Gln
65          70          75          80

```

```

Arg Arg Ile Leu Ile Leu Gly Lys Leu Asn Asn Leu Val Lys Glu Trp
85          90          95

```

```

Ile Arg Glu Ile Ser Glu Ser Lys Asn Leu Pro Gln Ser Val Ile Glu
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```

Asn Val Gly Gly Lys Ile Phe Thr Phe Gly Ser Tyr Arg Leu Gly Val
115         120         125

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His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys Val Ala Pro Arg His
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Val Asp Arg Ser Asp Phe Phe Thr Ser Phe Tyr Asp Lys Leu Lys Leu
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Val Ile Lys Leu Cys Phe Asp Gly Ile Glu Ile Asp Ile Leu Phe Ala
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Ser Leu Leu Lys Asn Leu Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly
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Cys Arg Val Thr Asp Glu Ile Leu His Leu Val Pro Asn Ile Asp Asn
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Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp Ala Lys Arg His Asn
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Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly Val Ser Trp Ala Met
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Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn Ala Ile Ala Ser Thr
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Pro Val Leu Leu Lys Gln Pro Glu Glu Cys Asn Leu Asn Leu Pro Val
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Ile Thr Pro Ala Tyr Pro Gln Gln Asn Ser Thr Tyr Asn Val Ser Val
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Ser Thr Arg Met Val Met Val Glu Glu Phe Lys Gln Gly Leu Ala Ile
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His Ser Thr Glu Gly Val Lys Leu Thr Ala Leu Asn Asp Ser Ser Leu
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Ser Ala Met Lys Thr Ser Pro Leu Asn Ser Ser Gly Ser Ser Gln Gly
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Arg Asn Ser Pro Ala Pro Ala Val Thr Ala Ala Ser Val Thr Ser Ile
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Gln Ala Ser Glu Val Ser Val Pro Gln Ala Asn Ser Ser Glu Ser Pro
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Gly Gly Pro Ser Ser Glu Ser Ile Pro Gln Thr Ala Thr Gln Pro Ala
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Ile Ala Pro Pro Pro Lys Pro Thr Val Ser Arg Val Val Ser Ser Thr
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Arg Leu Val Asn Pro Ser Pro Arg Pro Ser Gly Asn Thr Ala Thr Lys
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Val Pro Asn Pro Ile Val Gly Val Lys Arg Thr Ser Ala Pro Asn Lys
660 665 670

Glu Glu Ala Pro Arg Arg Thr Lys Thr Glu Glu Asp Glu Thr Ser Glu
675 680 685

Asp Ala Asn Cys Leu Ala Leu Ser Gly His Asp Lys Thr Glu Thr Lys
690 695 700

Glu Gln Val Asp Leu Glu Thr Ser Ala Val Gln Ser Glu Thr Val Pro



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Ser Asp Ile Pro Ala Leu Pro Ala Asn Pro Ile Pro Val Ile Lys Asn
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Ser Ile Lys Leu Arg Leu Asn Arg Gly Ser Gly Pro Arg Pro Leu Leu
755 760 765

Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro
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Glu Ser Asn Pro Gly Pro Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp
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850 855 860

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Asp Ala Asp Ala Met Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu
885 890 895

Lys Ser Met Arg Glu Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala
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Lys Lys Ile Ile Asp Trp Lys Asp Ala Asp Pro Asn Thr Val Ser Ser
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Gln Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln
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Lys Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr
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Ala Thr Arg Ala Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu
980 985 990



Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Met Ala Gln Leu
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His Gln Asp Leu Ala Glu Pro Ala Lys Glu Ile Ser Glu Lys Val



1760

1765

1770

His Gln Ile Tyr Gly Phe Pro Lys Glu Gly Ala Ser Ser Ile Val
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Leu His Glu Asn Arg Ile Glu Leu Asn Glu Val Trp Glu Ala Arg
1835 1840 1845

Glu Asn Glu Val Val Lys Phe Ala Ile Lys Arg Leu Phe Lys Glu
1850 1855 1860

Asp Ile Leu Gln Glu Thr Gly Gln Glu Ile Gly Val Leu Leu Pro
1865 1870 1875

Phe Ser Asn Gly Asp Phe Tyr Asn Glu Tyr Leu Val Asn Thr Ala
1880 1885 1890

Phe Leu Ile Lys Ile Phe Lys His His Gly Phe Ser Leu Val Gln
1895 1900 1905

Lys Gln Ser Phe Lys Asp Trp Ile Pro Glu Phe Gln Asn Phe Ser
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Lys Ser Leu Tyr Lys Ile Leu Thr Glu Ala Asp Lys Thr Trp Thr
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2000 2005 2010

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2015 2020 2025



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



965

970

975

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Leu Lys Lys Leu Val Gly Glu Arg Gly Ser Gly Pro Arg Pro Leu Leu
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Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
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Asp Val Glu Ser Asn Pro Gly Pro Ala Ser Leu Asp Asn Leu Val
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Ala Arg Tyr Gln Arg Cys Phe Asn Asp Gln Ser Leu Lys Asn Ser
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Phe Lys Thr Val Tyr Glu Ala Leu Val Ala Gln Glu Ile Pro Ser
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Thr Ile Ser His Ser Ile Arg Cys Ile Lys Lys Val His His Glu
1100 1105 1110

Asn His Cys Arg Glu Lys Ile Leu Pro Ser Glu Asn Leu Tyr Phe
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Thr Phe Arg Val Ser Glu Leu Trp Lys Ile Glu Leu Thr Ile Val
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Glu Ile Glu Tyr Thr Gly Lys Pro Glu Ser Leu Thr Ala Ala Asp
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Val Ile Lys Ile Lys Asn Thr Val Leu Thr Leu Ile Ser Pro Asn
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His Leu Met Leu Thr Ala Tyr His Gln Ala Ile Glu Phe Ile Ala
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Ser His Ile Leu Ser Ser Glu Ile Leu Leu Ala Arg Ile Lys Ser
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Gly Lys Trp Gly Leu Lys Arg Leu Leu Pro Gln Val Lys Ser Met
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Glu Leu Val Tyr Arg Lys Phe Ser His Ala Thr Thr Arg Gln His
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Glu Leu Asn Glu Val Trp Glu Ala Arg Glu Asn Glu Val Val Lys
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Phe Ala Ile Lys Arg Leu Phe Lys Glu Asp Ile Leu Gln Glu Thr
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Gly Gln Glu Ile Gly Val Leu Leu Pro Phe Ser Asn Gly Asp Phe
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Tyr Asn Glu Tyr Leu Val Asn Thr Ala Phe Leu Ile Lys Ile Phe
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Lys His His Gly Phe Ser Leu Val Gln Lys Gln Ser Phe Lys Asp
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Trp Ile Pro Glu Phe Gln Asn Phe Ser Lys Ser Leu Tyr Lys Ile
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Cys Leu Arg Lys Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Glu Glu Tyr Glu Gly Lys Arg Gly Arg Ala Pro Arg Ala Leu Ala
1985 1990 1995

Phe Ile Asn Cys Val Gly Asn Glu Val Ala Ala Tyr Ile Thr Met



2000

2005

2010

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



145 150 155 160

Gln Glu Glu Val Lys Asp Leu Arg Ala Val Glu Glu Ala Phe Val Pro
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Ser Leu Leu Lys Asn Leu Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly
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Cys Arg Val Thr Asp Glu Ile Leu His Leu Val Pro Asn Ile Asp Asn
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Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp Ala Lys Arg His Asn
245 250 255

Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly Val Ser Trp Ala Met
260 265 270

Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn Ala Ile Ala Ser Thr
275 280 285

Leu Val His Lys Phe Phe Leu Val Phe Ser Lys Trp Glu Trp Pro Asn
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Pro Val Leu Leu Lys Gln Pro Glu Glu Cys Asn Leu Asn Leu Pro Val
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Trp Asp Pro Arg Val Asn Pro Ser Asp Arg Tyr His Leu Met Pro Ile
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Ile Thr Pro Ala Tyr Pro Gln Gln Asn Ser Thr Tyr Asn Val Ser Val
340 345 350

Ser Thr Arg Met Val Met Val Glu Glu Phe Lys Gln Gly Leu Ala Ile
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Thr Asp Glu Ile Leu Leu Ser Lys Ala Glu Trp Ser Lys Leu Phe Glu
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Ala Pro Asn Phe Phe Gln Lys Tyr Lys His Tyr Ile Val Leu Leu Ala
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Ser Ala Pro Thr Glu Lys Gln Arg Leu Glu Trp Val Gly Leu Val Glu
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Ser Lys Ile Arg Ile Leu Val Gly Ser Leu Glu Lys Asn Glu Phe Ile
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Met Phe Glu Leu Asp Met Lys Ile Ala Ala Met His Val Lys Arg Lys
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His Ser Thr Glu Gly Val Lys Leu Thr Ala Leu Asn Asp Ser Ser Leu
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Asp Leu Ser Met Asp Ser Asp Asn Ser Met Ser Val Pro Ser Pro Thr
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Ser Ala Met Lys Thr Ser Pro Leu Asn Ser Ser Gly Ser Ser Gln Gly
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Arg Asn Ser Pro Ala Pro Ala Val Thr Ala Ala Ser Val Thr Ser Ile
580 585 590

Gln Ala Ser Glu Val Ser Val Pro Gln Ala Asn Ser Ser Glu Ser Pro
595 600 605

Gly Gly Pro Ser Ser Glu Ser Ile Pro Gln Thr Ala Thr Gln Pro Ala
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Ile Ala Pro Pro Pro Lys Pro Thr Val Ser Arg Val Val Ser Ser Thr
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Val Pro Asn Pro Ile Val Gly Val Lys Arg Thr Ser Ala Pro Asn Lys
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675 680 685

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690 695 700



Glu Gln Val Asp Leu Glu Thr Ser Ala Val Gln Ser Glu Thr Val Pro
705 710 715 720

Ala Ser Ala Ser Leu Leu Ala Ser Gln Lys Thr Ser Ser Thr Asp Leu
725 730 735

Ser Asp Ile Pro Ala Leu Pro Ala Asn Pro Ile Pro Val Ile Lys Asn
740 745 750

Ser Ile Lys Leu Arg Leu Asn Arg Gly Ser Gly Pro Arg Pro Leu Leu
755 760 765

Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro
770 775 780

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
785 790 795 800

Glu Ser Asn Pro Gly Pro Ser Lys Ile Tyr Ile Asp Glu Arg Ser Asp
805 810 815

Ala Glu Ile Val Cys Ala Ala Ile Lys Asn Ile Gly Ile Glu Gly Ala
820 825 830

Thr Ala Ala Gln Leu Thr Arg Gln Leu Asn Met Glu Lys Arg Glu Val
835 840 845

Asn Lys Ala Leu Tyr Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser
850 855 860

Asp Asp Ile Pro Pro Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro
865 870 875 880

Asp Ala Asp Ala Met Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu
885 890 895

Lys Ser Met Arg Glu Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala
900 905 910

Lys Lys Ile Ile Asp Trp Lys Asp Ala Asp Pro Asn Thr Val Ser Ser
915 920 925

Phe Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Arg Val Ala Asp
930 935 940

Gln Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln
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Lys Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asp Ile Glu Thr
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Ala Thr Arg Ala Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu
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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Met Ala Gln Leu
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Lys Lys Gln Pro Leu Met Phe Phe Lys Phe Ser Glu Pro Ala Ser
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Lys Thr Leu Leu Phe Asp Thr Pro Glu Gln Gln Thr Thr Lys Asn
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Glu Ile Glu Tyr Thr Gly Lys Pro Glu Ser Leu Thr Ala Ala Asp



1235

1240

1245

Val Ile Lys Ile Lys Asn Thr Val Leu Thr Leu Ile Ser Pro Asn
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His Leu Met Leu Thr Ala Tyr His Gln Ala Ile Glu Phe Ile Ala
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Ser His Ile Leu Ser Ser Glu Ile Leu Leu Ala Arg Ile Lys Ser
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Gly Lys Trp Gly Leu Lys Arg Leu Leu Pro Gln Val Lys Ser Met
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Thr Lys Ala Asp Tyr Met Lys Phe Tyr Pro Pro Val Gly Tyr Tyr
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Val Thr Asp Lys Ala Asp Gly Ile Arg Gly Ile Ala Val Ile Gln
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Asp Thr Gln Ile Tyr Val Val Ala Asp Gln Leu Tyr Ser Leu Gly
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Ala Phe Leu Tyr Tyr His Pro Asp Thr Ser Ser Phe Ser Asn Ile
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Tyr Val Arg Trp Glu Ile Val Lys Ile Arg Glu Asp Arg Gln Gln
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Gly Ile Tyr Arg Ala Gln Thr Ala Leu Ile Ser Phe Ile Lys Gln
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Glu Ile Ile Gln Lys Ile Ser His Gln Ser Trp Val Ile Asp Leu
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Gly Ile Gly Lys Gly Gln Asp Leu Gly Arg Tyr Leu Asp Ala Gly
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Val Arg His Leu Val Gly Ile Asp Lys Asp Gln Thr Ala Leu Ala
1685 1690 1695

Glu Leu Val Tyr Arg Lys Phe Ser His Ala Thr Thr Arg Gln His
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Lys His Ala Thr Asn Ile Tyr Val Leu His Gln Asp Leu Ala Glu
1715 1720 1725

Pro Ala Lys Glu Ile Ser Glu Lys Val His Gln Ile Tyr Gly Phe
1730 1735 1740

Pro Lys Glu Gly Ala Ser Ser Ile Val Ser Asn Leu Phe Ile His
1745 1750 1755



Tyr Leu Met Lys Asn Thr Gln Gln Val Glu Asn Leu Ala Val Leu
1760 1765 1770

Cys His Lys Leu Leu Gln Pro Gly Gly Met Val Trp Phe Thr Thr
1775 1780 1785

Met Leu Gly Glu Gln Val Leu Glu Leu Leu His Glu Asn Arg Ile
1790 1795 1800

Glu Leu Asn Glu Val Trp Glu Ala Arg Glu Asn Glu Val Val Lys
1805 1810 1815

Phe Ala Ile Lys Arg Leu Phe Lys Glu Asp Ile Leu Gln Glu Thr
1820 1825 1830

Gly Gln Glu Ile Gly Val Leu Leu Pro Phe Ser Asn Gly Asp Phe
1835 1840 1845

Tyr Asn Glu Tyr Leu Val Asn Thr Ala Phe Leu Ile Lys Ile Phe
1850 1855 1860

Lys His His Gly Phe Ser Leu Val Gln Lys Gln Ser Phe Lys Asp
1865 1870 1875

Trp Ile Pro Glu Phe Gln Asn Phe Ser Lys Ser Leu Tyr Lys Ile
1880 1885 1890

Leu Thr Glu Ala Asp Lys Thr Trp Thr Ser Leu Phe Gly Phe Ile
1895 1900 1905

Cys Leu Arg Lys Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe
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1955 1960 1965

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1970 1975 1980

Glu Glu Tyr Glu Gly Lys Arg Gly Arg Ala Pro Arg Ala Leu Ala
1985 1990 1995

Phe Ile Asn Cys Val Gly Asn Glu Val Ala Ala Tyr Ile Thr Met
2000 2005 2010



Lys Ile Val Met Asp Met Leu Asn Thr Asp Val Thr Leu Gln Ala
2015 2020 2025

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



2270

2275

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Met Lys Met Ile Arg Gln Leu Ala Arg Phe Ala Ala Lys Arg Asn
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Glu Gly Leu Glu Tyr Pro Leu Pro Thr Gly Phe Ile Leu Gln Gln
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Lys Ile Met Ala Thr Asp Met Leu Arg Val Ser Thr Cys Leu Met
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Glu Thr Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly
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Lys Gly Ile Thr Ser Val Ala Val Ile His Asp Ser Phe Gly Thr
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Met Val Lys Met Tyr Gln Asn His Asn Ala Leu Gln Asn Leu Leu
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Tyr Cys Phe Ala
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35 40 45

Asp Leu Gln Arg Ser Ala Met Val Tyr Ser Ser Asp Asp Ile Pro Pro
50 55 60

Arg Trp Phe Met Thr Thr Glu Ala Asp Lys Pro Asp Ala Asp Ala Met
65 70 75 80

Ala Asp Val Ile Ile Asp Asp Val Ser Arg Glu Lys Ser Met Arg Glu
85 90 95

Asp His Lys Ser Phe Asp Asp Val Ile Pro Ala Lys Lys Ile Ile Asp
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420

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Gly Leu Val Glu Ser Lys Ile Arg Ile Leu Val Gly Ser Leu Glu Lys
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915 920 925

Thr Ala Thr Lys Val Pro Asn Pro Ile Val Gly Val Lys Arg Thr Ser
930 935 940

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1490

1495

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His Gln Ile Tyr Gly Phe Pro Lys Glu Gly Ala Ser Ser Ile Val
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1850 1855 1860

Asp Ile Leu Gln Glu Thr Gly Gln Glu Ile Gly Val Leu Leu Pro
1865 1870 1875

Phe Ser Asn Gly Asp Phe Tyr Asn Glu Tyr Leu Val Asn Thr Ala
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Phe Leu Ile Lys Ile Phe Lys His His Gly Phe Ser Leu Val Gln
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675

680

685

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Cys His Lys Leu Leu Gln Pro Gly Gly Met Val Trp Phe Thr Thr
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1790 1795 1800

Glu Leu Asn Glu Val Trp Glu Ala Arg Glu Asn Glu Val Val Lys
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Gly Arg Glu Phe Pro Glu Gly Glu Gly Arg Ser Lys Lys Glu Ala Lys
50 55 60

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



580

585

590

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Arg Ser Leu Asn Gly Cys Arg Val Thr Asp Glu Ile Leu His Leu Val
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Pro Asn Ile Asp Asn Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp
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Ala Lys Arg His Asn Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly
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Val Ser Trp Ala Met Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn
675 680 685

Ala Ile Ala Ser Thr Leu Val His Lys Phe Phe Leu Val Phe Ser Lys
690 695 700

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



1640

1645

1650

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1895 1900 1905



Pro Lys Glu Gly Ala Ser Ser Ile Val Ser Asn Leu Phe Ile His
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2675

2680

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 35 40 45

Gly Arg Glu Phe Pro Glu Gly Glu Gly Arg Ser Lys Lys Glu Ala Lys
 50 55 60



Asn Ala Ala Ala Lys Leu Ala Val Glu Ile Leu Asn Lys Glu Lys Lys
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Ala Val Ser Pro Leu Leu Leu Thr Thr Thr Asn Ser Ser Glu Gly Leu
85 90 95

Ser Met Gly Asn Tyr Ile Gly Leu Ile Asn Arg Ile Ala Gln Lys Lys
100 105 110

Arg Leu Thr Val Asn Tyr Glu Gln Cys Ala Ser Gly Val His Gly Pro
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610

615

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885 890 895



Thr Met Trp Val Ile Gly Leu Val Phe Lys Lys Thr Glu Asn Ser Glu
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Asn Leu Ser Val Asp Leu Thr Tyr Asp Ile Gln Ser Phe Thr Asp Thr
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1670

1675

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His Gln Ile Tyr Gly Phe Pro Lys Glu Gly Ala Ser Ser Ile Val
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Ser Ile Lys Leu Arg Leu Asn Arg Gly Ser Gly Pro Arg Pro Leu Leu
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Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro
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Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
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Gln Glu Leu Pro Asn Ser Gly Pro Pro His Asp Arg Arg Phe Thr Phe
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Gln Val Ile Ile Asp Gly Arg Glu Phe Pro Glu Gly Glu Gly Arg Ser
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Lys Lys Glu Ala Lys Asn Ala Ala Ala Lys Leu Ala Val Glu Ile Leu
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Asn Lys Glu Lys Lys Ala Val Ser Pro Leu Leu Leu Thr Thr Thr Asn
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Ser Ser Glu Gly Leu Ser Met Gly Asn Tyr Ile Gly Leu Ile Asn Arg
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Gly Val His Gly Pro Glu Gly Phe His Tyr Lys Cys Lys Met Gly Gln
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His Leu Met Leu Thr Ala Tyr His Gln Ala Ile Glu Phe Ile Ala
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Ser His Ile Leu Ser Ser Glu Ile Leu Leu Ala Arg Ile Lys Ser
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Lys His Ala Thr Asn Ile Tyr Val Leu His Gln Asp Leu Ala Glu
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Pro Ala Lys Glu Ile Ser Glu Lys Val His Gln Ile Tyr Gly Phe
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Pro Lys Glu Gly Ala Ser Ser Ile Val Ser Asn Leu Phe Ile His
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Tyr Leu Met Lys Asn Thr Gln Gln Val Glu Asn Leu Ala Val Leu
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Cys His Lys Leu Leu Gln Pro Gly Gly Met Val Trp Phe Thr Thr
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Met Leu Gly Glu Gln Val Leu Glu Leu Leu His Glu Asn Arg Ile
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Phe Ala Ile Lys Arg Leu Phe Lys Glu Asp Ile Leu Gln Glu Thr
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Gly Gln Glu Ile Gly Val Leu Leu Pro Phe Ser Asn Gly Asp Phe
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Tyr Asn Glu Tyr Leu Val Asn Thr Ala Phe Leu Ile Lys Ile Phe
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Lys His Gly Val Tyr Tyr Leu Gln Thr Ser Glu His Val Gly Glu
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Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro Trp Val Ser Pro Phe
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Val Lys Gly Asn Arg Glu His Val Arg Lys Leu Thr Lys Lys Gln
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 35 40 45

Leu Ala Ala Pro Lys Glu Thr Asp Cys Leu Leu Thr Gln Lys Leu Ile
 50 55 60

Glu Thr Leu Lys Pro Phe Gly Val Phe Glu Glu Glu Glu Glu Leu Gln
 65 70 75 80

Arg Arg Ile Leu Ile Leu Gly Lys Leu Asn Asn Leu Val Lys Glu Trp
 85 90 95

Ile Arg Glu Ile Ser Glu Ser Lys Asn Leu Pro Gln Ser Val Ile Glu



100

105

110

Asn Val Gly Gly Lys Ile Phe Thr Phe Gly Ser Tyr Arg Leu Gly Val
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His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys Val Ala Pro Arg His
130 135 140

Val Asp Arg Ser Asp Phe Phe Thr Ser Phe Tyr Asp Lys Leu Lys Leu
145 150 155 160

Gln Glu Glu Val Lys Asp Leu Arg Ala Val Glu Glu Ala Phe Val Pro
165 170 175

Val Ile Lys Leu Cys Phe Asp Gly Ile Glu Ile Asp Ile Leu Phe Ala
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Arg Leu Ala Leu Gln Thr Ile Pro Glu Asp Leu Asp Leu Arg Asp Asp
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Ser Leu Leu Lys Asn Leu Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly
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Cys Arg Val Thr Asp Glu Ile Leu His Leu Val Pro Asn Ile Asp Asn
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Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp Ala Lys Arg His Asn
245 250 255

Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly Val Ser Trp Ala Met
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Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn Ala Ile Ala Ser Thr
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Leu Val His Lys Phe Phe Leu Val Phe Ser Lys Trp Glu Trp Pro Asn
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Pro Val Leu Leu Lys Gln Pro Glu Glu Cys Asn Leu Asn Leu Pro Val
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Trp Asp Pro Arg Val Asn Pro Ser Asp Arg Tyr His Leu Met Pro Ile
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Ser Thr Arg Met Val Met Val Glu Glu Phe Lys Gln Gly Leu Ala Ile
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Thr Asp Glu Ile Leu Leu Ser Lys Ala Glu Trp Ser Lys Leu Phe Glu
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Thr Leu Ala His Val Asn Pro Gln Ser Phe Pro Ala Pro Lys Glu Ser
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Pro Asp Arg Glu Glu Phe Arg Thr Met Trp Val Ile Gly Leu Val Phe
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Lys Lys Thr Glu Asn Ser Glu Asn Leu Ser Val Asp Leu Thr Tyr Asp
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485 490 495

Met Phe Glu Leu Asp Met Lys Ile Ala Ala Met His Val Lys Arg Lys
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Gln Leu His Gln Leu Leu Pro Ser His Val Leu Gln Lys Arg Lys Lys
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Asp Leu Ser Met Asp Ser Asp Asn Ser Met Ser Val Pro Ser Pro Thr
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Ser Ala Met Lys Thr Ser Pro Leu Asn Ser Ser Gly Ser Ser Gln Gly
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Arg Asn Ser Pro Ala Pro Ala Val Thr Ala Ala Ser Val Thr Ser Ile
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Gln Ala Ser Glu Val Ser Val Pro Gln Ala Asn Ser Ser Glu Ser Pro
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Gly Gly Pro Ser Ser Glu Ser Ile Pro Gln Thr Ala Thr Gln Pro Ala
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Ile Ala Pro Pro Pro Lys Pro Thr Val Ser Arg Val Val Ser Ser Thr
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Arg Leu Val Asn Pro Ser Pro Arg Pro Ser Gly Asn Thr Ala Thr Lys
645 650 655



Val Pro Asn Pro Ile Val Gly Val Lys Arg Thr Ser Ala Pro Asn Lys
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Glu Glu Ala Pro Arg Arg Thr Lys Thr Glu Glu Asp Glu Thr Ser Glu
675 680 685

Asp Ala Asn Cys Leu Ala Leu Ser Gly His Asp Lys Thr Glu Thr Lys
690 695 700

Glu Gln Val Asp Leu Glu Thr Ser Ala Val Gln Ser Glu Thr Val Pro
705 710 715 720

Ala Ser Ala Ser Leu Leu Ala Ser Gln Lys Thr Ser Ser Thr Asp Leu
725 730 735

Ser Asp Ile Pro Ala Leu Pro Ala Asn Pro Ile Pro Val Ile Lys Asn
740 745 750

Ser Ile Lys Leu Arg Leu Asn Arg Gly Ser Gly Pro Arg Pro Leu Leu
755 760 765

Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro
770 775 780

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
785 790 795 800

Glu Ser Asn Pro Gly Pro Ala Gly Asp Leu Ser Ala Gly Phe Phe Met
805 810 815

Glu Glu Leu Asn Thr Tyr Arg Gln Lys Gln Gly Val Val Leu Lys Tyr
820 825 830

Gln Glu Leu Pro Asn Ser Gly Pro Pro His Asp Arg Arg Phe Thr Phe
835 840 845

Gln Val Ile Ile Asp Gly Arg Glu Phe Pro Glu Gly Glu Gly Arg Ser
850 855 860

Lys Lys Glu Ala Lys Asn Ala Ala Ala Lys Leu Ala Val Glu Ile Leu
865 870 875 880

Asn Lys Glu Lys Lys Ala Val Ser Pro Leu Leu Leu Thr Thr Thr Asn
885 890 895

Ser Ser Glu Gly Leu Ser Met Gly Asn Tyr Ile Gly Leu Ile Asn Arg
900 905 910

Ile Ala Gln Lys Lys Arg Leu Thr Val Asn Tyr Glu Gln Cys Ala Ser
915 920 925



Gly Val His Gly Pro Glu Gly Phe His Tyr Lys Cys Lys Met Gly Gln
930 935 940

Lys Glu Tyr Ser Ile Gly Thr Gly Ser Thr Lys Gln Glu Ala Lys Gln
945 950 955 960

Leu Ala Ala Lys Leu Ala Tyr Leu Gln Ile Leu Ser Gly Ser Gly Pro
965 970 975

Arg Pro Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys
980 985 990

Ile Val Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu
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Glu Asp Phe Ser Leu Glu Asn Thr Leu Met Pro Leu Asn Glu Val
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Ser Leu Lys Gly Lys His Asp Ser Lys His Phe Asn Lys Gly Phe
1100 1105 1110

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Phe Tyr Ser Ser Val Lys Ile Arg Gln Arg Asp Val Lys Val Tyr
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1190

1195

1200

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Ala Gln Glu Ile Pro Ser Thr Ile Ser His Ser Ile Arg Cys Ile
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Lys Lys Val His His Glu Asn His Cys Arg Glu Lys Ile Leu Pro
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Glu Gln Pro Ile Arg Lys Phe Ile Leu Asp Ser Ser Val Leu Val
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Thr Leu Ile Ser Pro Asn His Leu Met Leu Thr Ala Tyr His Gln
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Pro Gln Val Lys Ser Met Thr Lys Ala Asp Tyr Met Lys Phe Tyr
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Leu Thr Ser Ala Asp Pro Asn Val Leu Leu Lys Asn Phe Glu Ser
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Trp Lys Pro Thr Trp Asp Asn Thr Leu Asp Phe Leu Val Arg Lys
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1745 1750 1755

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Leu Lys Arg Glu Ile Asn Tyr Val Arg Trp Glu Ile Val Lys Ile
1775 1780 1785

Arg Glu Asp Arg Gln Gln Asp Leu Lys Thr Gly Gly Tyr Phe Gly
1790 1795 1800

Asn Asp Phe Lys Thr Ala Glu Leu Thr Trp Leu Asn Tyr Met Asp
1805 1810 1815

Pro Phe Ser Phe Glu Glu Leu Ala Lys Gly Pro Ser Gly Met Tyr
1820 1825 1830

Phe Ala Gly Ala Lys Thr Gly Ile Tyr Arg Ala Gln Thr Ala Leu
1835 1840 1845

Ile Ser Phe Ile Lys Gln Glu Ile Ile Gln Lys Ile Ser His Gln
1850 1855 1860

Ser Trp Val Ile Asp Leu Gly Ile Gly Lys Gly Gln Asp Leu Gly
1865 1870 1875

Arg Tyr Leu Asp Ala Gly Val Arg His Leu Val Gly Ile Asp Lys
1880 1885 1890

Asp Gln Thr Ala Leu Ala Glu Leu Val Tyr Arg Lys Phe Ser His
1895 1900 1905

Ala Thr Thr Arg Gln His Lys His Ala Thr Asn Ile Tyr Val Leu
1910 1915 1920

His Gln Asp Leu Ala Glu Pro Ala Lys Glu Ile Ser Glu Lys Val
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His Gln Ile Tyr Gly Phe Pro Lys Glu Gly Ala Ser Ser Ile Val
1940 1945 1950

Ser Asn Leu Phe Ile His Tyr Leu Met Lys Asn Thr Gln Gln Val
1955 1960 1965



Glu Asn Leu Ala Val Leu Cys His Lys Leu Leu Gln Pro Gly Gly
1970 1975 1980

Met Val Trp Phe Thr Thr Met Leu Gly Glu Gln Val Leu Glu Leu
1985 1990 1995

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2225

2230

2235

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Lys Asp Thr Leu Leu Gln Ile Gly Met Thr Leu Leu Glu Ile Leu
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Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu
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Ser Asp Ala Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp
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Ser Pro Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Gln
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Ser Gly Ser Val Thr Leu Thr Gly Ala Glu Leu Arg Ser Met Ala
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Ser Ala Trp Asp Met Ile Gly Ile Thr Arg Gly Leu Thr Lys Lys
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Glu Ile Leu Val Ser Asp Tyr Cys Phe Ala
2990 2995

