```
  1 ATG AGT CTG CTG CTT GTG TTT TCT CTG CTC TGG AGT CTC CAT TAC TGC CAT TCA GCA GCA GTG TTC GTG CAC AGA GAT GAA GCT CAC GAG GTG TTG ATC AGG AGC AAA AGA GCC AAC TCA 120
  1 met ser leu leu leu val phe ser leu leu trp ser leu his tyr cys his ser ala ala val phe val his arg asp glu ala his glu val leu ile arg ser lys arg ala asn ser 40
                                                                                                                                                        ◆
121 GGC TGG TTT GAG GAG CTG AAG ACG GGG AAT CTG GAG CGC GAG TGT CTG GAG GAG AAA TGC TCG TAT GAG GAG GCG CGC GAG GTG TTC GAG CAC ACA GAG GCC ACG AAT GAG TTC TGG AAG 240
 41 gly trp phe glu glu leu lys thr gly asn leu glu arg glu cys leu glu glu lys cys ser tyr glu glu ala arg glu val phe glu his thr glu ala thr asn glu phe trp lys 80
241 ATC TAC GAT GTT AAA GAT CAC TGC GCA TCC AGT CCA TGT GAG CAT GAC GGG CTC TGC ACC ACA CAG AAC GCG GAC TCC TAC ATG TGT TTG TGT GCG CCG GGC TTC AGC GGA CGC CAC TGT 360
 81 ile tyr asp val lys asp his cys ala ser ser pro cys glu his asp gly leu cys thr thr gln asn ala asp ser tyr met cys leu cys ala pro gly phe ser gly arg his cys 120
361 GAG CAA TCG ATT GGA GAC GTT CTC GAC TCC TGT CTG CAT GAT AAC GGC GGC TGC GAA CAC TTC TGC ACG GAG CAG GAC GGA CGG AGA AAC TGC TCC TGC GCA GAC GGG TAT TAC CTA GAT 480
121 glu gln ser ile gly asp val leu asp ser cys leu his asp asn gly gly cys glu his phe cys thr glu gln asp gly arg arg asn cys ser cys ala asp gly tyr tyr leu asp 160
481 AAC AGC GGG CAG AAG TGC CGG AGT CAC GAG GTG TTT CCA TGT GGG AAG GTT CCT CTC CTG CAG GCT GGA AAA GCT GCG GAT CAT CAG GTG GAT CTC AGA TCT CGT ATC GTT GGA GGA TCT 600
161 asn ser gly gln lys cys arg ser his glu val phe pro cys gly lys val pro leu leu gln ala gly lys ala ala asp his gln val asp leu arg ser arg ile val gly gly ser 200
                                                                                                      ↑
601 GAA TGT CCT AAA GGT CAC TGT CCG TGG CAG GTG CTG CTG AAG TAC GGT GAG AAG GGT TTC TGT GGA GGT GTG ATC TAC AAG CCC ACC TGG ATC CTC ACA GCT GCT CAC TGC TTG GAA AAG 720
201 glu cys pro lys gly his cys pro trp gln val leu leu lys tyr gly glu lys gly phe cys gly gly val ile tyr lys pro thr trp ile leu thr ala ala his cys leu glu lys 240
721 CTC AAG GTC AAG TTC CTC AGG ATA GTG GCA GGT GAG CAT GAT CTG GAG GTG GAC GAG GGC ACG GAG CAG CTC ATC CAG GTG GAT CAG ATG TTC ACA CCT GCG TAC GTG TCT GAG ACA 840
241 leu lys val lys phe leu arg ile val ala gly glu his asp leu glu val asp glu gly thr glu gln leu ile gln val asp gln met phe thr his pro ala tyr val ser glu thr 280
841 GCG GAC AGT GAC ATC GCC CTG CTG CGT CTG CGC ACC CCC ATC GTC TAC AGT GTG TAT GCG GTG CCG GTG TGT TTG CCG CTG CGG GAG ATG GCG GAG CGC GAG CTG TGG GCG GTC AGC AAA 960
281 ala asp ser asp ile ala leu leu arg leu arg thr pro ile val tyr ser val tyr ala val pro val cys leu pro leu arg glu met ala glu arg glu leu trp ala val ser lys 320
961 CAC ACG GTG AGC GGC TGG GGC AAA CGC AGC GAC GGG CCG ACC TCT CGC CTG CTC CGC CGG CTG CTG GTG CCG CGC ATC CAC ACG CAG GAG TGT GTG CAG GTC AGC AAC CTC ACG CTC 1080
321 his thr val ser gly trp gly lys arg ser asp gly pro thr ser arg leu leu arg arg leu leu val pro arg ile his thr gln glu cys val gln val ser asn leu thr leu 360
1081 ACC AGC AAC ATG TTC TGC GCC GGA TAC ATC GAG GGC CGG CAG GAC TCC TGT AAG GGT GAC AGC GGC GGC CCG CTG GTG ACC CGG TAC CGA GAC ACC GCC TTC CTA CTG GGC ATC GTG AGC 1200
361 thr ser asn met phe cys ala gly tyr ile glu gly arg gln asp ser cys lys gly asp ser gly gly pro leu val thr arg tyr arg asp thr ala phe leu leu gly ile val ser 400
1201 TGG GGG AAA GGC TGC GCT CGC CCG GGC TCC TAC GGC ATC TAC ACA CGC GTG TCC AAC TAC CTG CAG TGG ATC CGA CAA ACA ACC AAC ACC ACG ATA CAC TGATGAAGACATGACCCGGGTGCATTG 1326
401 trp gly lys gly cys ala arg pro gly ser tyr gly ile tyr thr arg val ser asn tyr leu gln trp ile arg gln thr thr asn thr thr ile his 433
1327 CTCATCAAGATTGCTACTCTTAGGTGAACAATTAACAAATATTAACTATTATAGTTAATGTTTGTAAAAAATAGCAAAATTATATTGAAAATAAAAAATATTTATATTAATTATGAAGTGACGGCGATTACTTTAATTATCCAAGACGGTGTTATAGCC 1485
1486 CAAAATACCCAATAGTTGAGCATCAGCTGCTTTCCTGACATCCTGTACATATTAGACTCGGATCTGATATTTTGCACAGGTTATATTGCATTTTTAGCAGGTATTTAATGATTTTGCTCTGATTAATCAGGAGATGTGCAGCTCATTATCTCCATATTA 1645
1646 TTAATGCTCAACTGTAGTAAACACTCG 1671
```