

This file contains four parts:

- I. Aligned sequences, including secondary structures, of a partial 16S rRNA gene from the six species used in the paper, in interleaved format.
- II. Aligned sequences of the COI gene from the 8 OTUs used in the paper, in codon format (i.e., three nucleotide per group)
- III. Amino acid sequences translated from the COI gene, in interleaved format
- IV. Aligned amino acid sequences of coagulogen from the four horseshoe crabs.

I.
 Appendix 1. Aligned sequences, including secondary structures, of a partial 16S rRNA gene from *T. gigas*, *C. rotundicauda*, *T. tridentatus*, *L. polyphemus*, *I. hexagonus* and *A. franciscana*. Gaps are indicated by dashes. Numbers above the sequences correspond to those in Kambhampati et al. (1996). The underlined bases within squared brackets, designated by an unprimed number (e.g., 67) form pair-bonds with the complementary bases downstream, also enclosed by squared brackets but denoted by a primed number (e.g., 67'). Where no inference can be made about base pairing, e.g., when complementary sequence is unavailable (e.g., 61' and 64'), the nucleotides are not underlined even though some or all of them might be involved in base pairing. I have no confidence in aligning the two italicized segments, and consequently did not include them in the phylogenetic analysis.

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          66      67              68              69
TGU09394  AAAAAUCUG[GUC]U(GCCCAAUGAUAGGUAAUUAAAUGGC)(CGCGGUUAUUAUG
CRU09396  .....A[A..](.....UAAG....G.....)(.....
TTU09393  .....[A..](.....GAAA.....)(.....
LPU09397  .....GA[AC..](.....GGA.--...U.....)(.....
AF081828  ...UG.AAA[A..](..U.....UA---U.....U..)(U.U.....U...
MIASRR16  GG.GG..GA[.C..](.....C....GA---.....G....)(..U.....C...

          70              71
TGU09394  ACCGUG)CGAAGGUAGCAUAAUCAUUU(GCUUUUUAUUUGGAGGC)UAGAAUG
CRU09396  .....)(.....).G.....
TTU09393  .....)(.....A.....).G.....
LPU09397  .....)(.....AG.....)..U...
AF081828  ..UA.A).....UUGA...A.--G(.....A-...-.GU..)AG.-.
MIASRR16  ..A.).....A(.C...G...U.....).G.....

          67'      64'              61'
TGU09394  AAU[GAU]UGGA[CGGAAAAAG]-UC[UGUCUUAAUUUUAAAUUUUUA]AAUUUUAC
CRU09396  ...[...].U..[.....G.]-[.....G...U]..G.....
TTU09393  ...[.G.]...[.A.....]-[.....G....GU.....].G.....
LPU09397  ...[.G.]...[.U.....A]A..[.....GGAAA..G....G].....U
AF081828  ...[.G.]UA.[.AUU..UA]A-[.U...U.A..A.U.AAA.G]....A.U
MIASRR16  ...[.G.]U..[.AG.G.U.]G..[.....CUUCGA.U..A-.G]..G..A.U

          72              73              74
TGU09394  UU(UUUAGUGAAAAGGCUAAA)AUUUUAUCAAGGGACGAGAAGA[CCCUAUUA
CRU09396  ..(.....G.....).G.....[.....

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TTU09393 ..(.....).....CU.....[.....
LPU09397 ..(.....A...G...).....CU.....[.....
AF081828 ..(...U...G.A..A...)....A.AUU.....A.....[.....G.
MIASRR16 C.(.A.....A...U..)G.AC.UGGA..G...U.....[.....AG

TGU09394 AGCUU]U(AUUUUUGUUUGUUUUU-UAUUAUGUUUUUCGUUAUAAAAAUGG
 CRU09396](.....A..AU....GG.U.....AU...C.....A.
 TTU09393](.....A-.....-.....A.....A.....AA
 LPU09397](.C....U.GGU.....U.....AU...CGGU.GGG...GGC.AA
 AF081828 .UU...](...---AGAU.G.-----G...AGAA.UA..UG...-----
 MIASRR16 .U...](.CA...AA..C....GUCU.GCG..AGG.AA...G.C.G.G.AA

80

81

TGU09394 A-AGGAAU)UUU(ACUGGGGCGGU)A(GAGAAAGAA-GAGAAUCUU)UUUUUAG
 CRU09396 U-.AA...)(.....)(.....G-A.AG.....).....A
 TTU09393 G-.....)(.....)(.....-A.A.....).....
 LPU09397 --GA..G.).....)(.....-AUUU.....).....UU
 AF081828 --UCU...).G(GU.....U.A.)U(A.A.....UAUUA.....)....----
 MIASRR16 .ACAAUG.)CG(GU.....AC)G(UA.G.AC.GA.U..A.AC)..ACA.C

82

84

88

TGU09394 AAAUUAA(AACAUUUAUGUA)AAUUUUUGAUCCAUAUUAUGAUAGAAGA
 CRU09396(.....U).....A....
 TTU09393 ..G....(.....).....U.....U....
 LPU09397 .U.A...(U..U.A.U..G).....C...C.U...G..G..U.G..
 AF081828 GU.....(GA.A...AU.U)-----U...G.....C...U.A.U..
 MIASRR16 .U.AAC.(C.UCAA..AA.G).CC-A.....-...-G....AU.A.-..

74'

89

TGU09394 AG[GAGUUACUAUAGGG]AUAACAG(CGUAUUUUUUUCGGAGAGUUCAUAUCG
 CRU09396 ..[A.....].....(.....
 TTU09393 .A[.....].....(.....
 LPU09397 GA[A.....G.....].....U.....
 AF081828 GA[A.AA...C.....].....AA...U..U.....A.
 MIASRR16 CC[A.....CU.....].....C...UU.....A....

TGU09394 GCGAAGAAGUUUGCG)A-CCUCGAUGUUGAAUUAAGAAGUCAAUAGGGCGG
 CRU09396)(.....AG.....G..A.....
 TTU09393)(.....AG.....
 LPU09397)(.....AG.....G.....
 AF081828 AUA..AU.....)(.....G...G..UCCUUU.UUA.U.A
 MIASRR16 A.A..AG.....)(.....GU.C.G.G.CC.U.CUC..U.C

TGU09394 AGAAGUUCUAAAUGAGGGUCUGUUC
 CRU09396U..U.....
 TTU09393
 LPU09397UG..GA.....
 AF081828AA...AAGAA..U.....
 MIASRR16 ..C..CCUAG.GA.GCA.....

II. The COI gene in codon format:

8 582

LPU09391 GGG CAT CCT GAA GTC TAC ATT TTA ATT CTT CCT GGA TTT GGG ATA ATC TCT CAT ATT ATT
LPT09392 GGG CAC CCT GAA GTC TAC ATT TTA GTT CTT CCT GGG TTT GGA ATA ATC TCT CAT ATT ATT
CRU09389 GGA CAC CCT GAA GTC TAT ATT CTA ATC CTC CCA GGA TTT GGA ATA ATT TCT CAT ATC ATT
CRU09390 GGA CAC CCT GAA GTC TAT ATT CTA ATC CTC CCA GGA TTT GGA ATA ATT TCT CAT ATC ATT
TGU09388 GGT CAC CCT GAA GTT TAT ATT CTT ATC CTT CCA GGA TTT GGA ATA ATT TCT CAT ATT ATT
TTU09387 GGC CAC CCT GAA GTT TAT ATT TTA ATT CTC CCA GGA TTT GGA ATA ATT TCT CAT ATT ATT
AF081828 GGG CAC CCA GAA GTA TAT ATT CTC ATC CTA CCA GGA TTT GGG ATA GTA TCC CAT ATC ATC
MTAFDNA GGC CAT CCT GAA GTG TAT ATT TTA ATT TTA CCT GGA TTC GGG ATA GTG TCC CAC ATT ATT

LPU09391 AGC CAC CAA ACA GGA AAA AAG GAA CCT TTC GGG ACT CTT GGA ATA ATT TAC GCC ATA TTA
LPT09392 AGC CAC CAA ACA GGA AAA AAG GAA CCT TTC GGG ACT CTT GGA ATA ATT TAT GCC ATA TTA
CRU09389 AGC CAT CAA ACA GGA AAA AAA GAA CCC TTT GGA TCT ATA GGA ATA ATT TAT GCT ATA TTA
CRU09390 AGC CAT CAA ACA GGA AAA AAA GAA CCC TTT GGA ACT TTA GGA ATA ATT TAT GCT ATA TTA
TGU09388 AGC CAT CAA ACA GGA AAA AAA GAA CCC TTT GGA ACT TTA GGA ATA ATT TAT GCT ATA CTA
TTU09387 AGC CAT CAA ACA GGA AAA AAA GAA CCT TTG GGA ACT CTA GGA ACT ATA ATT TAC GCT ATA TTA
AF081828 TGT TTC CAT ACA GGA AAA AAA GAG CCT TTC GGC ACA TTA GGA ATA ATT TAT GCT ATA TTA
MTAFDNA AGC CAA GAA AGA GGT AAG AAG GAA GCA TTT GGT ACA TTA GGT ATG ATT TAT GCT ATA CTT

LPU09391 GCT ATT GGT ATT CTT GGT TTT ATA GTA TGA GCT CAC CAT ATA TTT ACA GTG GGA ATA GAC
LPT09392 GCT ATT GGC ATT CTT GGT TTT ATA GTA TGA GCT CAC CAT ATA TTT ACA GTG GGA ATA GAC
CRU09389 GCT ATT GGA ATT CTA GGA TTT GTA GTT TGA GCC CAC CAC ATA TTC ACA GTA GGC ATA GAT
CRU09390 GCA ATT GGA ATT CTA GGA TTT GTA GTT TGA GCC CAC CAC ATA TTC ACA GTA GGC ATA GAT
TGU09388 GCA ATT GGA ATT CTA GGA TTT GTA GTT TGA GCC CAC CAT ATA TTC ACA GTA GGC ATA GAT
TTU09387 GCT ATT GGA ATT TTA GGA TTT ATA GTT TGA GCT CAT CAT ATA TTT ACA GTA GGC ATA GAT
AF081828 GCA ATC GGT TTT CTA GGA TTC ATT GTC TGA GCA CAT CAT ATA TTT ACC GTG GGT ATA GAT
MTAFDNA GCA ATT GGT ATT CTT GGT TTT GTT GTC TGG GCT CAT CAT ATA TTT ACT GTG GGA ATG GAC

LPU09391 GTA GAC ACA CGA GCA TAC TTC ACA GCA GCT ACA ATA ATC ATT GCT GTT CCC ACA GGA ATT
LPT09392 GTA GAC ACA CGA GCA TAC TTC ACA GCA GCT ACA ATA ATC ATT GCT GTT CCC ACA GGA ATT
CRU09389 GTT GAT ACA CGA GCC TAT TTC ACA GCA GCT ACC ATA ATC ATT GCT GTC CCA ACC GGT ATT
CRU09390 GTT GAT ACA CGA GCC TAT TTC ACA GCA GCT ACC ATA ATC ATT GCT GTC CCA ACC GGT ATT
TGU09388 GTT GAT ACA CGA GCT TAT TTC ACA GCA GCT ACT ATA ATC ATT GCT GTA CCA ACT GGT ATT
TTU09387 GTT GAT ACA CGA GCT TAC TTT ACT GCA GCT ACT ATA ATT ATC GCT GTT CCA ACC GGT ATT
AF081828 ATT GAC ACA CGA GCC TAT TTT ACC GCA GCC ACC ATA ATT ATT GCC GTT CCT ACA GGA ATT
MTAFDNA GTG GAC ACT CGA GCT TAT TTT ACT GCT GCA ACT ATG ATT ATT GCA ATT CCT ACG GGG ATT

LPU09391 AAA ATC TTT AGA TGA CTA GCC ACC CTA CAT GGA TCA CAA CTC TCA TAC GAC CCA CCT CTT
LPT09392 AAA ATC TTT AGA TGA CTA GCT ACC CTA CAT GGA TCA CAA CTC TCA TAC GAC CCA CCT CTT
CRU09389 AAA ATC TTC AGA TGA CTA GCT ACT CTA CAT GGC TCT CAA ATC TCT TAT GAA CCT CCA CTT
CRU09390 AAA ATC TTC AGA TGA CTA GCT ACA CTA CAT GGA TCT CAA ATT TCT TAT GAA CCT CCA CTT
TGU09388 AAA ATC TTT AGA TGA CTA GCT ACT CTA CAT GGC TCT CAA ATT TCT TAT GAA CCT CCT CTT
TTU09387 AAA ATT TTT AGA TGA CTA GCT ACT TTA CAT GGC TCT CAA ATC TCT TAT GAA CCT CCT TTA
AF081828 AAA ATT TTT AGT TGA TTA GCT ACT CTT CAT GGA TCT AAC ATC AAT TTT AAC TCT TCT ATA
MTAFDNA AAG ATT TTT AGA TGA ATC GGA ACT TTA CAC GGG ACA CGA CTT ACT ATA ACT CCA TCT ATG

LPU09391 CTA TGA GCT CTA GGG TTT GTT TTC TTA TTT ACA ATT GGA GGA TTA ACC GGA GTA ATC CTA
LPT09392 CTA TGA GCC CTA GGG TTT GTT TTC TTA TTT ACA ATC GGA GGA TTA ACT GGA GTA ATC CTA
CRU09389 TTA TGA GCC TTA GGA TTT GTA TTC TTA TTC ACT ATT GGA GGA TTA ACA GGT GTT GTT TTA
CRU09390 TTA TGA GCT TTA GGA TTT GTA TTC TTA TTC ACT ATT GGA GGA TTA ACA GGT GTT GTT TTA
TGU09388 TTA TGA GCT TTA GGA TTT GGA TTC TTA TTT ACT ATT GGA GGA TTA ACA GGA GTT GTT TTA
TTU09387 TTA TGA GCC TTA GGA TTT GTA TTT CTA TTT ACT ATT GGA GGA TTA ACA GGT GTT GTC CTA
AF081828 TTA TGA GTA CTA GGA TTT GTC TTT TTA TTC ACC TTA GGG GGA CTA ACA GGA ATC ATT TTA
MTAFDNA TTT TGG GCC CTA GGA TTT GTA TTT TTG TTT ACT GTG GGA GGG CTT ACA GGA GTT GTC CTG

LPU09391 GCT AAC TCC TCC ATT GAT ATT ATC CTC CAT GAC ACA TAT TAC GTC GTA GCC CAT TTT CAC
LPT09392 GCT AAC TCC TCC ATT GAT ATT ATC CTC CAT GAC ACA TAC TAC GTC GTA GCC CAT TTT CAC
CRU09389 GCC AAC TCC TCT ATT GAC ATT ATT CTT CAT GAA ACA TAT TAC GTT GTG GCA CAT TTC CAC
CRU09390 GCC AAC TCC TCT ATT GAC ATT ATT CTT CAT GAA ACA TAT TAC GTT GTG GCC CAT TTC CAC
TGU09388 GCC AAC TCC TCT ATT GAC ATC ATT CTT CAT GAT ACA TAT TAC GTT GTA GCC CAT TTT CAC
TTU09387 GCA AAC TCT TCC ATT GAC ATT CTT CAT GAC ACA TAT TAC GTT GTA GCA CAT TTT CAT
AF081828 GCA AAT TCC TCA ATT GAC ATT ATT CTT CAC GAT ACT TAT TAT GTA GTA GCT CAC TTT CAC
MTAFDNA TCG AAC TCT AGA ATT GAT ATT GTT CTC CAT GAT ACT TAT TAT GTA GTT GCC CAT TTC CAC

LPU09391 TAT GTC CTC TCA ATA GGA GCA GTA TTT GCA ATC TTA GCA GGG GTC ACT CAT TGA TTT CCA
LPT09392 TAT GTC CTC TCA ATA GGA GCA GTA TTT GCA ATC TTA GCA GGG GTC ACT CAT TGA TTT CCA
CRU09389 TAT GTT CTA TCA ATA GGA GCA GTA TTT GCA ATT TTA GCA GGT GTT ACC CAC TGA TTT CCA
CRU09390 TAT GTC CTA TCA ATA GGA GCA GTA TTT GCA ATT TTA GCA GGT GTT ACC CAC TGA TTT CCA

TGU09388 TAT GTC CTA TCA ATA GGA GCA GTA TTT GCA ATT TTA GCA GGA GTA ACC CAC TGA TTT CCA
TTU09387 TAC GTT TTA TCA ATA GGA GCA GTA TTT GCA ATT TTA GCA GGA GTT ACC CAT TGA TTT CCA
AF081828 TAC GTT CTT TCA ATA GGA GCT GTA TTT GCT ATC ATA GGG TCA ATT ACC CAC TGA TTC CCT
MTAFDNA TAT GTT TTA TCA ATG GGT GCT GTC TTT GCT ATC ATA GCA GGA TTT GTA CAT TGA TTT CCT

LPU09391 TTA TTC TTT GGG ATA GCA ATA AAC CCC AAA TGA CTA AAA ATT CAC TTT TTA GTT ATA TTT
LPT09392 TTA TTC TTT GGA ATA GCA ATA AAC CCA AAA TGA CTA AAA ATT CAC TTT TTA GTT ATA TTT
CRU09389 CTA TTT TTT GGA ACA TCC ATA AAT CCC AAA TGA CCA AAA ATT CAC TTT GTA ATT ATA TTT
CRU09390 CTA TTT TTT GGA ACC TCC ATA AAT CCC AAA TGA CCA AAA ATT CAC TTT ACA ATT ATA TTT
TGU09388 CTT TTT TTT GGA ACC TCT ATA AAT CCC AAA TGA TTA AAA ATT CAT TTT ACA ATT ATA TTT
TTU09387 CTC TTT TTT GGA ACT TCT ATA AAT CCC AAA TGA CTA AAA ATT CAT TTT CTA ATT ATA TTT
AF081828 TTA TTT TTT GGA ATA AAT TTC AAT TCC TTA TGA CTT AAA ATT CAA TTC TAC TCC ATA TTC
MTAFDNA CTA ATG ACC GGA TTA AGA ATG AAT CAG TTT CTT CTT AAG GTA CAT TTC TTT ATT ATA TTT

LPU09391 ATT GGG GTA AAC GTC ACT TTC TTC CCT CAA CAT TTC CTA GGT
LPT09392 ATT GGA GTA AAC GTC ACT TTC TTC CCT CAA CAT TTC CTA GGT
CRU09389 ATT GGA GTT AAC ACC ACC TTT TTC CCT CAA CAT TTT TTA GGT
CRU09390 ATT GGT GTT AAC ACC ACC TTT TTC CCT CAA CAT TTT CTA GGT
TGU09388 ATT GGA GTT AAC ACC ACC TTT TTC CCT CAA CAT TTT CTA GGA
TTU09387 ATT GGA GTA AAT ACC ACT TTT TTC CCT CAA CAC TTT TTA GGT
AF081828 ATT GGA GTA AAT ATA ACT TTT TTT CCT CAA CAC TTT TTA GGG
MTAFDNA TTA GGA GTA AAC TTA ACT TTT TTC CCT CAA CAT TTC TTA GGT

III.

Amino acid sequences translated from the nucleotide sequences of the COI gene, in interleaved format

8 194

LPU09391	GHPEVYILIL	PGFGMISHII	SHQTGKKEPF	GTLGMIYAML	AIGILGFMVW
LPT09392	GHPEVYILVL	PGFGMISHII	SHQTGKKEPF	GTLGMIYAML	AIGILGFMVW
CRU09389	GHPEVYILIL	PGFGMISHII	SHQTGKKEPF	GSMGMIYAML	AIGILGFVVW
CRU09390	GHPEVYILIL	PGFGMISHII	SHQTGKKEPF	GTLGMIYAML	AIGILGFVVW
TGU09388	GHPEVYILIL	PGFGMISHII	SHQTGKKEPF	GTLGMIYAML	AIGILGFVVW
TTU09387	GHPEVYILIL	PGFGMISHII	SHQTGKKEPL	GTLGMIYAML	AIGILGFMVW
AF081828	GHPEVYILIL	PGFGMVSHII	CFHTGKKEPF	GTLGMIYAML	AIGFLGFIVW
MTAFDNA	GHPEVYILIL	PGFGMVSHII	SQESGKKEAF	GTLGMIYAML	AIGILGFVVW
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQLSYDPPL
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQLSYDPPL
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQISYEPPL
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQISYEPPL
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQISYEPPL
	AHHMFTVGMD	VDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSQISYEPPL
	AHHMFTVGMD	IDTRAYFTAA	TMI IAVPTGI	KIFSWLATLH	GSNINFNSSM
	AHHMFTVGMD	VDTRAYFTAA	TMI IAIPTGI	KIFSWIGTLH	GTRLTMTPSM
	LWALGFVFLF	TIGGLTGVIL	ANSSIDIILH	DTYYVVAHFH	YVLSMGAVFA
	LWALGFVFLF	TIGGLTGVIL	ANSSIDIILH	DTYYVVAHFH	YVLSMGAVFA
	LWALGFVFLF	TIGGLTGVVL	ANSSIDIILH	ETYYVVAHFH	YVLSMGAVFA
	LWALGFVFLF	TIGGLTGVVL	ANSSIDIILH	ETYYVVAHFH	YVLSMGAVFA
	LWALGFGFLF	TIGGLTGVVL	ANSSIDIILH	DTYYVVAHFH	YVLSMGAVFA
	LWALGFVFLF	TIGGLTGVVL	ANSSIDIILH	DTYYVVAHFH	YVLSMGAVFA
	LWVLGFVFLF	TLGGLTG IIL	ANSSIDIILH	DTYYVVAHFH	YVLSMGAVFA
	LWALGFVFLF	TVGGLTGVVL	SNSSIDIVLH	DTYYVVAHFH	YVLSMGAVFA
	ILAGVTHWFP	FFFGMAMNPK	WLKIHFLVMF	IGVNVTFPPQ	HFLG
	ILAGVTHWFP	FFFGMAMNPK	WLKIHFLVMF	IGVNVTFPPQ	HFLG
	ILAGVTHWFP	FFFGTSMNPK	WPKIHFMVIMF	IGVNTTFPPQ	HFLG
	ILAGVTHWFP	FFFGTSMNPK	WPKIHFTIMF	IGVNTTFPPQ	HFLG
	ILAGVTHWFP	FFFGTSMNPK	WLKIHFTIMF	IGVNTTFPPQ	HFLG
	ILAGVTHWFP	FFFGTSMNPK	WLKIHFLIMF	IGVNTTFPPQ	HFLG
	IMGSITHWFP	FFFGMNFNSL	WLKIQFYSMF	IGVNMTFPPQ	HFLG
	IMAGFVHWFP	LMTGLSMNQF	LLKVHFFIMF	LGVNLTFFPQ	HFLG

IV.

The amino acid sequences of the coagulogen gene (176 aa, with 174 aa remaining after deleting gaps) from four horseshoe crab species, in interleaved format:

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Lp  GDPNVPTCLC  EEPTLLGRKV  IVSQETKDKI  EEAVQAITDK  DEISGRGFSI  FGGHPAFKEC
Cr  A.T.A.L...  D..GI...NQ  L.TP.V.E...  .K..E.VAEE  SGV.....L  .SH..V.R..
Tg  D.T.A.L...  D..GI....E  F..DA..TI..  .K..EEVAKE  GGV.....L  .SH..V.R..
Tt  A.T.A.I...  D..GV...TQ  ..TT.I....  .K..E.VAQE  SGV.....  .SH..V.R..
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Lp  GKYE CRTVTS  EDSRCYNFFP  FHHFPSECPV  SVSACEPTFG  YTTSNELRII  VQAPKAGFRQ
Cr  .....RP  .HT.....P.  .V..T.....  .TRD...V..  ..VAG.F.V.  ....R.....
Tg  .....RP  .H.....P.  .I..K.....  .TRD...V..  ..AAG.F.V.  ....R.....
Tt  .....RP  .H.....P.  .I..K.....  .TRD...V..  ..VAG.F.V.  ....R.....
```

```
Lp  CVWQH KCRA Y  GSNFCQRTGR  CTQQRSVVRL  VTYDLEKGVF  FCENVRTCCG  CPCRS-
Cr  .....-  ...N.GFS..  .....  ...N...DG.  L..SF.....  .....NY
Tg  .....-  ...N.GFN..  .....  ..FN...NG.  L..TF.....  .....F
Tt  .....-F  ...S.GYN..  .....  ...N...DG.  L..SF.....  .....F
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