Figure S1

Sequence and secondary structure predictions of avian BST-2 orthologs. Avian orders, and species names in English and Latin are indicated. Complete nucleotide coding sequences and predicted amino acid sequences are shown. The positions of predicted GPI anchor attachment are indicated by red letters, the predictions of transmembrane (TM) and coiled-coil (CC) regions are shown as graphical outputs of the prediction servers, described in the Materials and Methods section.

Galliformes

Gallus gallus (Red junglefowl)

nucleotide sequence

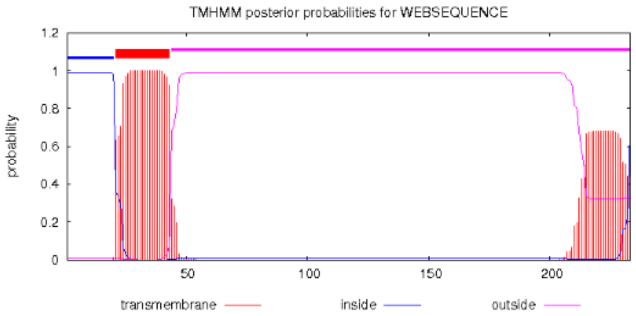
ATGGCTGCGCAGGGCAGCGTGTTGGACTGCAGCACGCACTGCCATTCCAAATACAAGCGAGCCTGCAGGGTCTATGG
GCTGATAGCTGGGCTGGTGGTTGGGCTGATGGCCGTGGTGCTGCTAGCTGCATCCCTGCCCTCCTCTCTGTGCCTGC
TGACCACCAAACCAGAGCCAGAGACGGGGCTGGGGACGGGGACAGGAAGAGTGCCCGGTTTGGAGAGGCTGGCACGG
CTGCGGGAGGTGCAAGAGCAGCTGCAGATGCAGGTGGCTGCGTTGGAGCAAGCATTGGCTGCCACCAACCGGACCCT
CACCACGGTGGTGGATGTCACCAACCGGTCCATCTCTGAGATGCACAAGCAATGGGATGACTGCAGGAGTCAATTGG
ACACAGTGAAGGGCTTCGTCGTGGAGTTGGAGCAGCAGATCTCCCAGCTGCAGCAGCACAGGGAGAAGCAGGAGGCT
GTGGTCAAGCAACTGCAAGAGAACAACAGGGCTCTCCAGGAGGAGGTGGCACAGCAGAAGGAGCAGTTGGAGGAGGT
GGAGAGGCTCAGGAGCAGCTTCCAGGAGCAGATCCAGGAGCTGTCAGCACGGATCTGGAACATACGGAGACACATTT
CCAGTGGGAGCACAGAGATGCCCTCCGGTGCAGCCATGTTCCTGACCCTCCTCATCGGAGTGATCGTTGCAAAGTGG
CTGTGCTGA

amino acid sequence

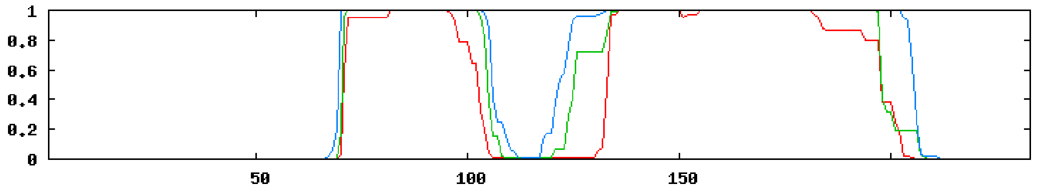
MAAQGSVLDCSTHCHSKYKRACRVYGLIAGLVVGLMAVVLLAASLPSSLCLLTTKPEPETGLGTGTGRVPGLERLAR
LREVQEQLQMQVAALEQALAATNRTLTTVVDVTNRSISEMHKQWDDCRSQLDTVKGFVVELEQQISQLQQHREKQEA
VVKQLQENNRALQEEVAQQKEQLEEVERLRSSFQEQIQELSARIWNIRRHISSGSTEMPSGAAMFLTLLIGVIVAKW
LC

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Bambusicola thoracicus (Chinese bamboo partridge)

nucleotide sequence

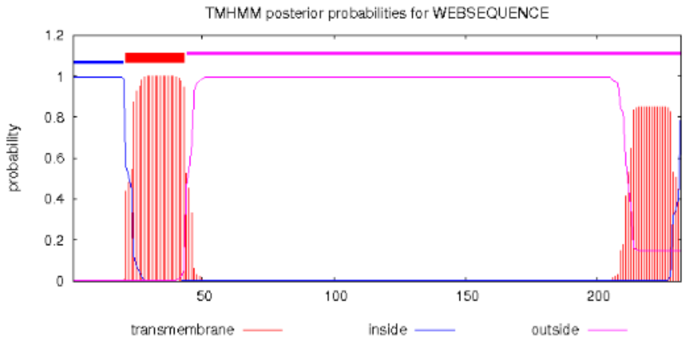
ATGGCTGCGCAGGGCGGCATGTTGGACTGCAGCACGCACTGCCATCCCAAATACAGGCGATCCTGCAGGGTCTACGG
GATGGTGGCTGGGCTGGTGGTCGGGCTGACGGCCGTGGTGCTGCTAGCTGCAACCCTGCCCTCCTCTCTGTGCCTGC
TGACCACCAAACCAGAGCCAGAGACAGGGCTGGGGACGGGGACAGGAAGACTGCCCGGTTTGGAGAGGCTGGCACGG
CTGCGGGAGGTGCAGCAGCAGCTGCAGGTGCAGGTGGCTGCGTTGGAGCAAGCATTGGCTGACACCAACCGGACCCT
CACCACGGCGGTGGGTGTCACCAACCGGTCCCTCGCTGAGATGCACAAGCAATGGGATGACTGCAGGAGTCAATTGG
AGACGGTGAAGGGCTCCGTCGTGAAGTTGGAGCAGCAGATCTCCCAGCTGCAGCAGCACAGGGAGAAGCAGGAGGCT
GTGGTCAGGCAACTGCAAGAGGACAACAGGGCTCTCCAGGAGGAGGTGGCGCAGCAGAAGGAGCAGTTGGAGGAGGT
GCAGAGGTTCAGGAGCAGCTTCCAGGAGCAGATCCAGCAGCAGATCCAGCAGCTGTCAGCACGGATCTGGAACATAC
AGAGCCACGTTTCCAGCGGGAGAACAGAGATGCCCTCCGGTGCAGCCATGGTCCTGAGCCTCCTCATTGTACTGATC
GTCATAAAGTGTCTGCGCTGA

amino acid sequence

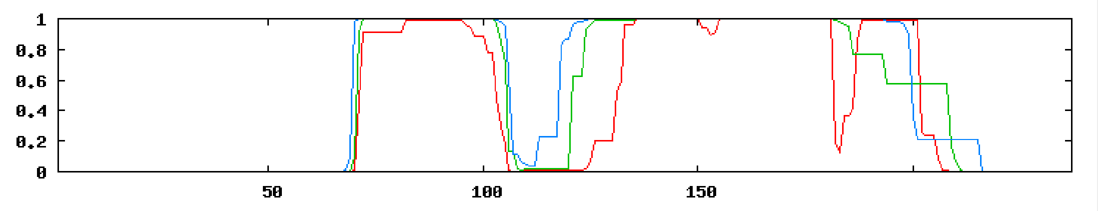
MAAQGGMLDCSTHCHPKYRRSCRVYGMVAGLVVGLTAVVLLAATLPSSLCLLTTKPEPETGLGTGTGRLPGLERLAR
LREVQQQLQVQVAALEQALADTNRTLTTAVGVTNRSLAEMHKQWDDCRSQLETVKGSVVKLEQQISQLQQHREKQEA
VVRQLQEDNRALQEEVAQQKEQLEEVQRFRSSFQEQIQQQIQQLSARIWNIQSHVSSGRTEMPSGAAMVLSLLIVLI
VIKCLR

potential GPI site at position 210 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Chrysolophus pictus (Golden pheasant)

nucleotide sequence

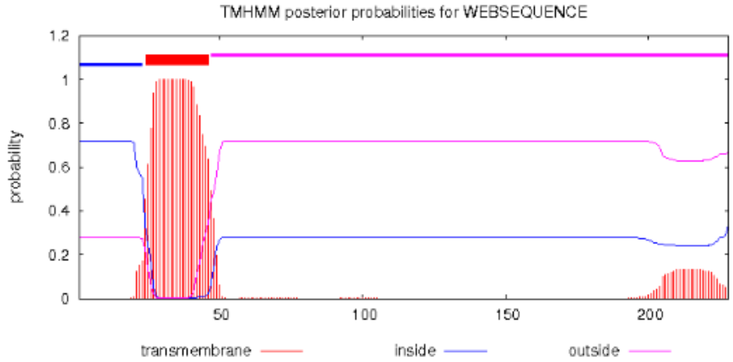
ATGGCTGTACAGGGCAGCATGTCGGACTACAGTGAGGACTGCCACCCTAAACCCAGGCGACACTGGAAGGTCTATGG
GCTAGTGGTCGTGCTGCTGGTTGTGGTGCTGCTGGCTGCAGCCCTGCCTTCCTATCTGTGCCTGGTGGCCACCAAAC
CAGAGCAAGAAACAGGGCTGGGGATGGGGGCAGGGAGAATGCCCAATTTGGAGGGGCTGGCACAGCTGCTGGGGGTG
CAGCAGCAGCTGAGGGTGCAGGTGGCTGCATTGGAGCAAGCATTGGTTGCCACCAACCAGACCCTCACCACCATGGT
GGATATCACCAACCCGTCCCTCGCTGAGATACTCAAGAAGTGGGATGACTGCAGGAGTCAATTGGATGCCATGCAGA
GCTTTGTTGCGGATTTGGGGCAGCAGATCTCCCAGCTGCAGCAGCAGAAGGAAAAGCAGGAGGCTGTGGTCAAGCAA
CTGCAAGAGGACAACAGGGCGCTCCAGGAGGAGGGGGCAAAGCAGAAGGAGCAGTTGGAGGAGGTGCAGAGGCACAG
GAGCAGCTTCCAGGAGCAGATCCAGGAGCAGATCCACAAGCTGTCAGCACAGATCTGGGACATATGGAGCAGCAGTT
CCAGTGGGAGCACAGCGATGCCCTCCAGYGCAGCCATGGCCCTGAGCCTCCTCGTGACGCTGCTCTCTGCAAAGTGG
CTGCACTGA

amino acid sequence

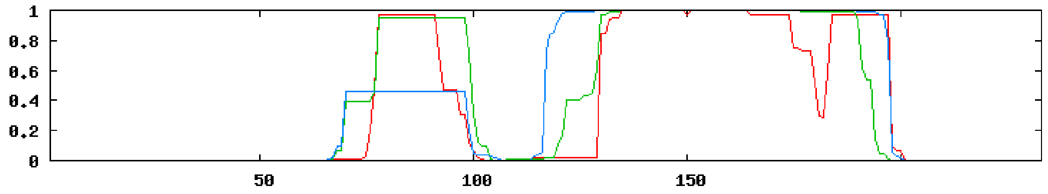
MAVQGSMSDYSEDCHPKPRRHWKVYGLVVVLLVVVLLAAALPSYLCLVATKPEQETGLGMGAGRMPNLEGLAQLLGV
QQQLRVQVAALEQALVATNQTLTTMVDITNPSLAEILKKWDDCRSQLDAMQSFVADLGQQISQLQQQKEKQEAVVKQ
LQEDNRALQEEGAKQKEQLEEVQRHRSSFQEQIQEQIHKLSAQIWDIWSSSSSGSTAMPSSAAMALSLLVTLLSAKW
LH

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Chrysolophus amherstiae (Lady Amherst´s pheasant)

nucleotide sequence

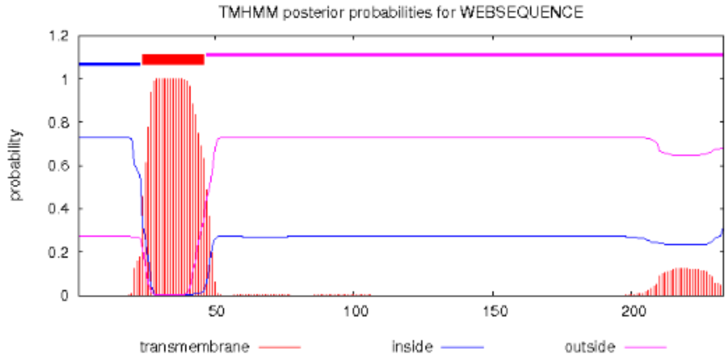
ATGGCTGTACAGGGCAGCATGTCGGACTACAGTGAGGACTGCCACCCTAAACCCAGGCGACACTGGAAGGTCTATGG
GCTAGTGGTCGTGCTGCTGGTTGTGGTGCTGCTGGCTGCAGCCCTGCCTTCCTATCTGTGCCTGGTGGCCACCAAAC
CAGAGCAAGAAACAGGGCTGGGGATGGGGGCAGGGAGAATGCCCAATTTGGAGGGGCTGGCACAGCTGCTGGGGGTG
CAGCAGCAGCTGAGGGTGCAGGTGGCTGCATTGGAGCAAGCATTGGTTGCCACCAACCAGACYCTCACCACCATGGT
GGATATCACCAACCCGTCCCTCGCTGAGATGCTCAAGAAGTGGGATGAGTGCAGGAGTCAATTGGATGCCATGCAGA
GCTTTGTTGCGGATTTGGGGCAGCAGATCTCCCAGCTGCAGCAGCAGAAGGAAAAGCAGGAGGCTGTGGTCAAGCAA
CTGCAAGAGGACAACAGGGCGCTCCAGGAGGAGGGGGCAAAGCAGAGGGAGCAGTTGGAGGAGGTGCAGAGGCACAG
GAGCAGCTTCCAGGAGCAGATCCAGGAGCAGATCCACAAGCTGTCAGCACAGATCTGGGACATATGGAGCAGCAGTT
CCAGTGGGAGCACAGCGATGCCCTCCAGTGCAGCCATGGCCCTGAGCCTCCTCGTGACGCTGCTCTCTGCAAAGTGG
CTGCACTGA

amino acid sequence

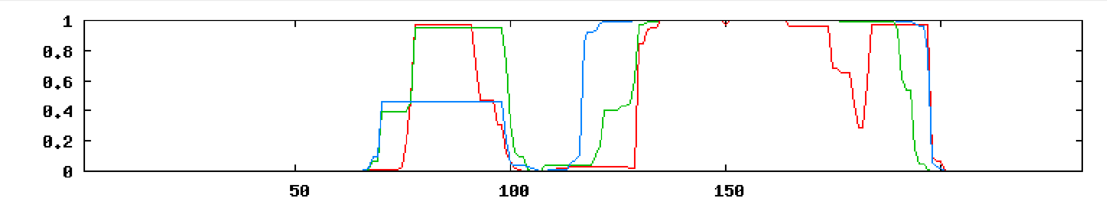
MAVQGSMSDYSEDCHPKPRRHWKVYGLVVVLLVVVLLAAALPSYLCLVATKPEQETGLGMGAGRMPNLEGLAQLLGV
QQQLRVQVAALEQALVATNQTLTTMVDITNPSLAEMLKKWDECRSQLDAMQSFVADLGQQISQLQQQKEKQEAVVKQ
LQEDNRALQEEGAKQREQLEEVQRHRSSFQEQIQEQIHKLSAQIWDIWSSSSSGSTAMPSSAAMALSLLVTLLSAKW
LH

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Tympanuchus cupido pinnatus (Greater Prairie chicken – Phasianidae)

nucleotide sequence

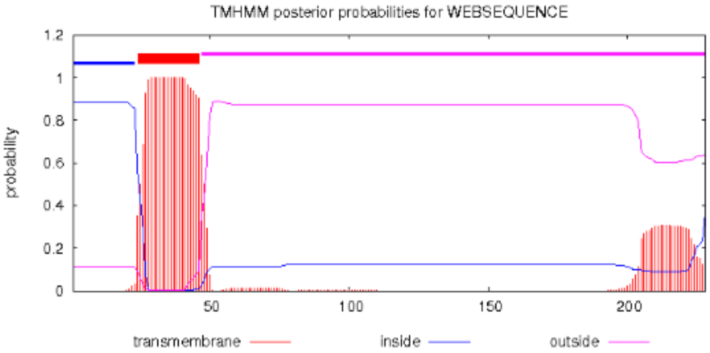
ATGGCTGTGCAGGGAAGTATGTTGGACTACAGTGAAAACTGCCACCCTAAACCCAGGCGAGACTGGAAGGTCTATGG
GCTGGTGGTCGCGCTGCTGGCTGTGGTGCTGCTGGCTGCAGCCCTGCCCTCCTATATGTGGCTGGTGGCCACCAAAC
CCGAGCAAGAAACGGGGCTGGGGATGGGAACAGGGAAGGTGGCCGGTTTGGAGGGGCTGACGCGGCTGCTGGGGATG
CAGCAGCAGCTGCGGGTGCAGGTGGCTGCATTGGAGCAAGCGTTGCTTGCCACCAACCAGACTCTCACCACCATGGT
GGATATCACCAACCCGTCCCTCGCTGAGATGCTCAAGAAGTGGGATGACTGCAGGAGTCAATTGGATAACATGCAGA
AGTTCGTCGTGGAGTTGGGGCAGCAGATCTCCCAGCTGCAGCAGCATAAGGAGAAGCAGGAGGCTGTGATCAAGCAA
CTGCAAGAGGACAGCAGGGCGCTCCAGGAGGAGGGGGCACAGCAGAAGGCGCAGTTGGAGGAGGTGCAGAAGCACAG
GAGCAGCTTGCAGGAGCAGATCCAGGAGCAGATCTACAGGCTGTCAGCACAGATCTGGGACTTATGGAGCAGCAGTT
CCAGTGGGAGCACAGtGATGCCCTCCGGTGCAGCCATGGCCCTGAGCCTCCTCGTGACGCTGCTCACTGCAAAGTGG
CTGCACTGA

amino acid sequence

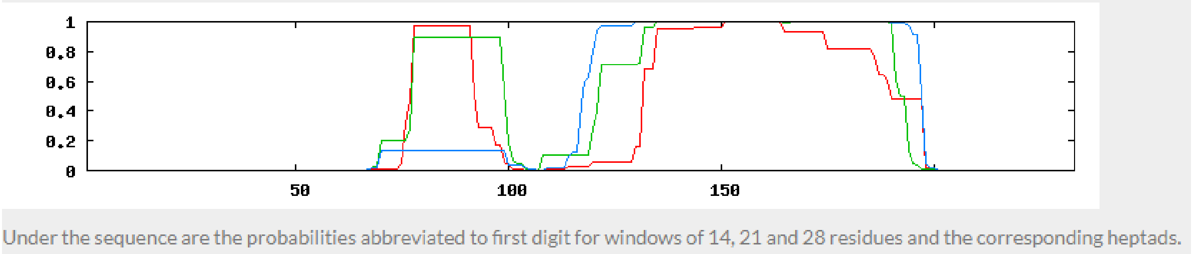
MAVQGSMLDYSENCHPKPRRDWKVYGLVVALLAVVLLAAALPSYMWLVATKPEQETGLGMGTGKVAGLEGLTRLLGM
QQQLRVQVAALEQALLATNQTLTTMVDITNPSLAEMLKKWDDCRSQLDNMQKFVVELGQQISQLQQHKEKQEAVIKQ
LQEDSRALQEEGAQQKAQLEEVQKHRSSLQEQIQEQIYRLSAQIWDLWSSSSSGSTVMPSGAAMALSLLVTLLTAKW
LH

potential GPI site at position 208 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Callipepla squamata (Scaled quail)

nucleotide sequence

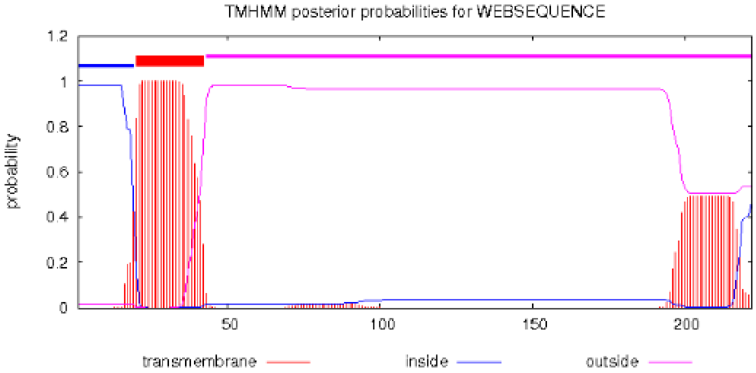
ATGCAGAGGGACTGCAGCGCGCTCTGCCACCCCAAATGCAGGAGAGCCTGGAGGCTCTACGGGCTGGTGCTCGTGGT
GGTGGTCGTGCTCATGCTGGCTACAGTGCTGCCATCTTCGCTGAGCCTGCAGACCACAGAGCCGGGGCCGAGGGCAG
AGCCGGGGCCGGGATCAGAGGAGCTGGCACGGCTGTACAGGGTGCAGCAGAGGCTGTGGGTGCAGGTGGGTGCGTTG
GGGCAGGAGTTGGCTGCCACCAACAAGTCCCTCGCTGCGCTGGTCGGGGCCACCAACAGGTCCCTCGCTGAGATGCA
CAAGCAGTGGGACAGCTGCAGGAGTCAACTGGATACGGTGCAAAGGTTCGCCCAGGAGCTGAGGCAGCAGCTCTCCC
AGCTGCAGCAGCACAGGGGGAAGCAGGAGGCCGTGGTCAATCAGCTGCAAGAGGAGAACAGGGCTCTCCAGGAGGAG
GTGGCAAAGCAGAAGGAGCAGTTGGAGGAGATACGGAGGGACAGGAGCAGCTTCCAGGAGGAGGTCAAGCAGCAGGT
CCGTAGGCTGTCGAACTGGATCTGGGAGATAAAGAGCAGCAGATCCAGCGGGAGCACAGTGCTGCTCACCAGCATGG
CAGTGCCCCTGAGCCTCCTCCTGGCACTGCTCACTGCCAAGTGTCTGCTCTGA

amino acid sequence

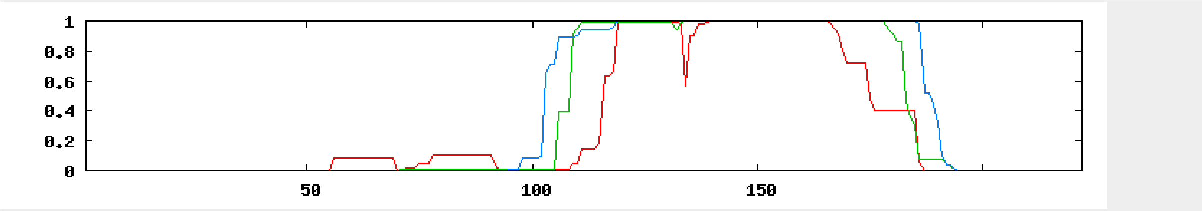
MQRDCSALCHPKCRRAWRLYGLVLVVVVVLMLATVLPSSLSLQTTEPGPRAEPGPGSEELARLYRVQQRLWVQVGAL
GQELAATNKSLAALVGATNRSLAEMHKQWDSCRSQLDTVQRFAQELRQQLSQLQQHRGKQEAVVNQLQEENRALQEE
VAKQKEQLEEIRRDRSSFQEEVKQQVRRLSNWIWEIKSSRSSGSTVLLTSMAVPLSLLLALLTAKCLL

potential GPI site at position 197 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Colinus virginianus (Northern bobwhite)

nucleotide sequence

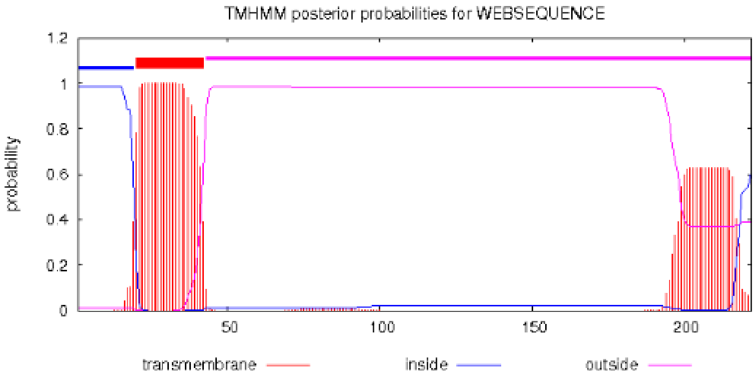
ATGCAGAGGGACTGCAGCGTGCTCTGCCACCCCAAATGCAGGAGAGCCTGGAGGGTCTACGGGCTGGTGCTCGTGGT
GGTGGTCGTGCTCATGCTGGCTACAGTGCTGCCATCCTTGCTGAGCCTGCAGACCACCGAGCCAGGGCCGAGGGCAG
AGCCGGGGCCGGGATCAGAGGAGCTGGCATGGCTGCAGGGGGTGCAGCAGAGGCTATGGGTGCAGGTGGGTGCGTTG
GGGCAGGAGTTGGCTGCCACCAATAAATCCCTCGCTGCGCTGGTCGGGGCCACCAACAGGTCCCTCGCTGAGATGCA
CAAGCAGTGGGACAGCTGCAGGAGTCAACTGGATACGGTGCAGAGGTTCGTCCAGGAGCTGAGGCAGCAGCTCTCCC
AGCTGCAGCAGCACAGGGAGAAGCAGGAGGCTGTGGTCAACCAGCTGCAAGAGGAGAACAGGGCACTCCAGGAGGAG
GTGGCACAGCAGAAGGAGCAGTTGGAGGAGATACGGAGGGACAGGAGCAGCTTCCAGGAGGAGGTCAAGCAGCAGGT
CCGTAGGCTGTCAAACTGGATCTGGGAAATAAAGAGCAGCAGCTCCAGCGGGAGCACAGTGCTGCTCACCGGCATGG
CAGTGCCTCTGAGCCTCCTCCTGGCACTGCTCACTGCCAAGTGTCTGCTCTGA

amino acid sequence

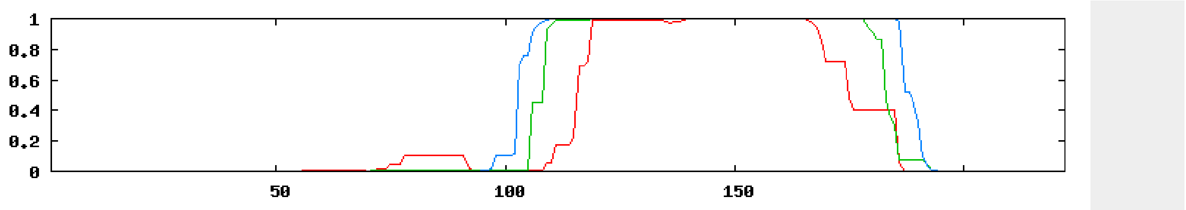
MQRDCSVLCHPKCRRAWRVYGLVLVVVVVLMLATVLPSLLSLQTTEPGPRAEPGPGSEELAWLQGVQQRLWVQVGAL
GQELAATNKSLAALVGATNRSLAEMHKQWDSCRSQLDTVQRFVQELRQQLSQLQQHREKQEAVVNQLQEENRALQEE
VAQQKEQLEEIRRDRSSFQEEVKQQVRRLSNWIWEIKSSSSSGSTVLLTGMAVPLSLLLALLTAKCLL

potential GPI site at position 197 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Numida meleagris (Helmeted guineafowl)

nucleotide sequence

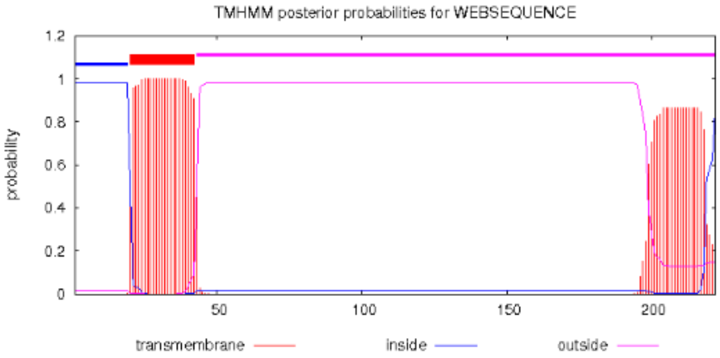
ATGGCTGCGCGGGGCAGCTTGCGGGACCGCGCTGTGCTCTGCTACTACAAATGCAAGTGGGCCTGGAGGCTCGTTGT
GGCGGTGGCCGTGGTGCTGCTGGCAGCAGTCCTGCTCTTTCTGTGCCTGCTATCCAGCAAGCCAGAGCCGGCGATGG
GGACAGAGCCCAGTTTGCAGGGGCTGGCACAGCTGCAGGAGGAGCAGCAGCAGCTGCAGGCACAGGTGACTGCGTTG
GAGCAAGAGCTGGCTGCCACCAACCGGTCCCTCGCCATGGGGGTGGATGTCACCAAGCGGTCCCTCGCTGAGATGCA
CAAGCAGTGGGACGGCTGCAGGAGTCAGCTGGACGCAGTGCAAGGCTTTGTCCCGGAGCTGAGGCAGCAGCTCACCC
AGCTGCAGCAGCACAGGGAGGAGCAGGAGGCCGTGATCAAGCAGCTGCAAGAGGAGAACAGGGCGCTCCGGGAGGAG
GTGGCACAGCAGAAGGAGCAGTTGGAGGAGATGCAGAGGGACGGGAAGAGCTTCCAGGAGCGGATCCGGCAGCAGAT
CGGTGGACTGTCGGAACGGATCTGGAACATACGGAGCCGCGATTCCGACGGGAGCACAACAGTGTCCTCCAGCGTGG
CCGTGCCCCTGGGCATCCTCCTGGTGCTGCTCGTTCTGAAGTGCCTGCGCTGA

amino acid sequence

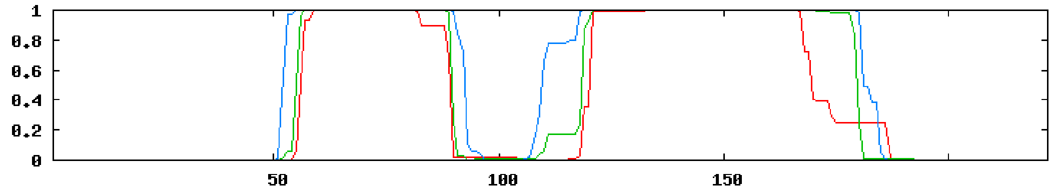
MAARGSLRDRAVLCYYKCKWAWRLVVAVAVVLLAAVLLFLCLLSSKPEPAMGTEPSLQGLAQLQEEQQQLQAQVTAL
EQELAATNRSLAMGVDVTKRSLAEMHKQWDGCRSQLDAVQGFVPELRQQLTQLQQHREEQEAVIKQLQEENRALREE
VAQQKEQLEEMQRDGKSFQERIRQQIGGLSERIWNIRSRDSDGSTTVSSSVAVPLGILLVLLVLKCLR

potential GPI site at position 197 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Coturnix japonica (Japanese quail)

nucleotide sequence

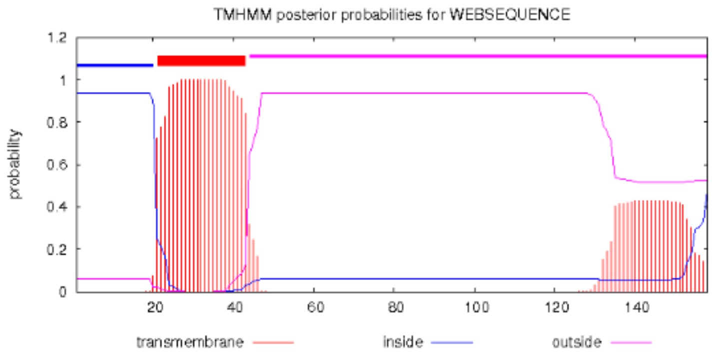
ATGATTGATCAGAGCAACATGTTGGACCGCCAGGAAAGCTTCCACCCCAAATACAGGCAAGCCTGGATGGTCTGTGG
GCTGGTGGTTGTGGTGATGCTAATTGCAGCCCTGACTTCTTCTATGTTCCTGCTGGCCACCAAACCAAAGAACACAG
TGCCGGGGTCCATGGAGGAGCTGGGGCAGCAGCTCTCCCAGCTGCAGCAGCAGAGGGAGCAGCAGGATGCCGCGATC
AAACAACTGCAAGAGGACAACAGGGCGCTCCAGGAGGAGATGGCACAGCAGAGGGAGCAGCTGGAGGAGGTGCAGAG
CCAAGGGAACAGCTTCCAGGAGCAGATCCAGCAGCAGATCCAGCTGTTGACATCGTGGATCTTGGACTTACAGAGCC
ACAGCTCCGGTGCAAGCACAGCAATGCCCTCCTGCCCAGCCATGGCCCTGAGCCTCCTCATGACTCTGCTGACTGCA
AAGTGGCTGCACTGA

amino acid sequence

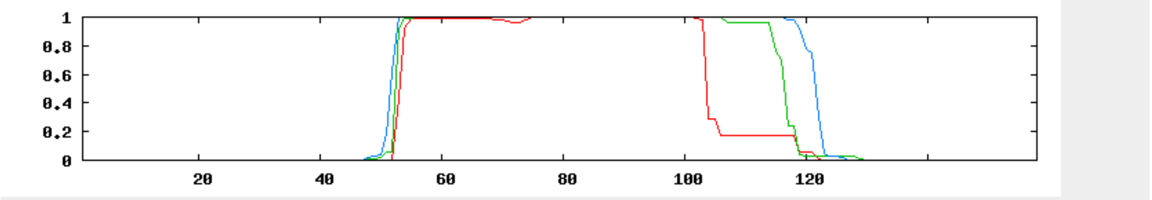
MIDQSNMLDRQESFHPKYRQAWMVCGLVVVVMLIAALTSSMFLLATKPKNTVPGSMEELGQQLSQLQQQREQQDAAI
KQLQEDNRALQEEMAQQREQLEEVQSQGNSFQEQIQQQIQLLTSWILDLQSHSSGASTAMPSCPAMALSLLMTLLTA
KWLH

potential GPI site at position 134 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Coturnix coturnix (The common quail)

nucleotide sequence

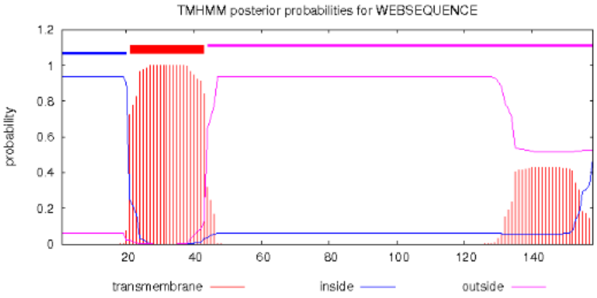
ATGATTGATCAGAGCAACATGTTGGACCGCCAGGAAAGCTTCCACCCCAAATACAGGCAAGCCTGGATGGTCTGTGG
GCTGGTGGTTGTGGTGATGCTAATTGCAGCCCTGACTTCTTCTATGTTCCTGCTGGCCACCAAACCAAAGAACACAG
TGCCGGGGTCCATGGAGGAGCTGGGGCAGCAGCTCTCCCAGCTGCAGCAGCAGAGGGAGCAGCAGGATGCCGCGATC
AAACAACTGCAAGAGGACAACAGGGCGCTCCAGGAGGAGATGGCACAGCAGAGGGAGCAGCTGGAGGAGGTGCAGAG
CCAAGGGAACAGCTTCCAGGAGCAGATCCAGCAGCAGATCCAGCTGTTGACATCGTGGATCTTGGACTTACAGAGCC
ACAGCTCCGGTGCRAGCACAGCAATGCCCTCCTGCCCAGCCATGGCCCTGAGCCTCCTCATGACTCTGCTGACTGCA
AAGTGGCTGCACTGA

amino acid sequence

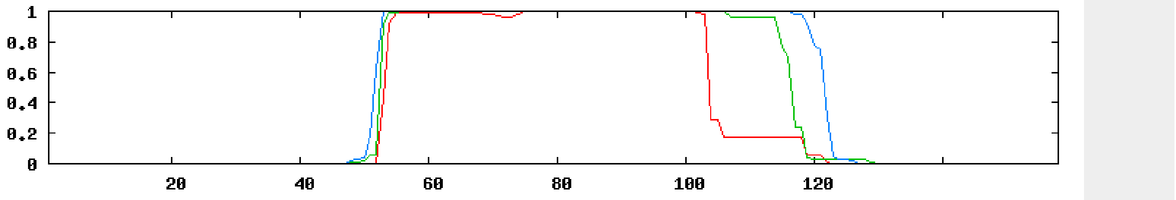
MIDQSNMLDRQESFHPKYRQAWMVCGLVVVVMLIAALTSSMFLLATKPKNTVPGSMEELGQQLSQLQQQREQQDAAI
KQLQEDNRALQEEMAQQREQLEEVQSQGNSFQEQIQQQIQLLTSWILDLQSHSSGASTAMPSCPAMALSLLMTLLTA
KWLH

potential GPI site at position 134 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Phasianus colchicus (common pheasant)

nucleotide sequence

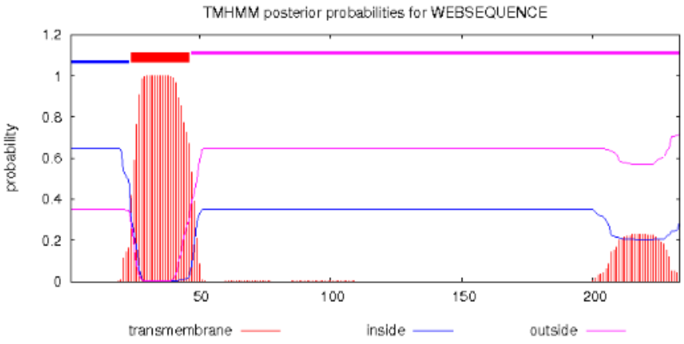
ATGGCTGTACAGGGCAGCATGTCAGACTACAGTGAGGACTGCCACCCTCAACCCAGGCGAAACTGGAAGGTCTATGG
GCTAGTGGTCGTGCTGGTGGTTGTGGTGCTGCTGGCTGCAGCCCTGCCTTCCTATCTGTGCCTGGTGGCCACCAAAC
CAGAGCAAGAAACAGGGCTGGGGATGGGGGCAGGGAGAATGCCCGATTTGGAGGGGCTGGCACGGCTGCTGGGGGTG
CAGCAGCAGCTGAGGGTGCAGGTGGCTGCATTGGAGCAAGCATTGGTTGCCACCAACCAGACCCTCACCACCATGGT
GGATATCACCAACCCGTCCCTCGCTGAGATGCTCAAGAAGTGGGATGACTGCAGGAGTCAATTGGATACCATGCAGA
GCTTTGTTGCGGATTTGGGGCAGCAGATCTCCCAGCTGCAGCAGCAGAAGGAAAAGCAGGAGGCTGTGGTCAAGCAA
CTGCAAGAGGACAACAGGGCTCTCCAGGAGGAGGGGGCAAAGCAGAGGGAGCAGCTGGAGGAGGTGCAGAGGCACAG
GAGCAGCTTCCAGGAGCAGATCCAGGAGCAGATCCACAGGCTGTCAGCACAGATCCGGGACATATGGAGCAGTAGTT
CTGGTGGGAGCACAGCGATGCCCTCCAGTGCAGCCATGGCCCTGAGCCTCCTCGTGACGCTGCTCACTGCAAAGTGG
CTGCACTGA

amino acid sequence

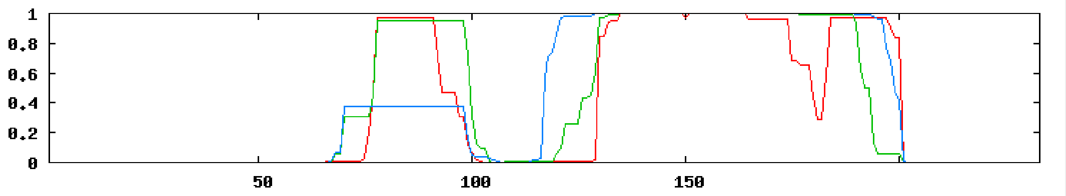
MAVQGSMSDYSEDCHPQPRRNWKVYGLVVVLVVVVLLAAALPSYLCLVATKPEQETGLGMGAGRMPDLEGLARLLGV
QQQLRVQVAALEQALVATNQTLTTMVDITNPSLAEMLKKWDDCRSQLDTMQSFVADLGQQISQLQQQKEKQEAVVKQ
LQEDNRALQEEGAKQREQLEEVQRHRSSFQEQIQEQIHRLSAQIRDIWSSSSGGSTAMPSSAAMALSLLVTLLTAKW
LH

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Pavo cristatus (Indian peafowl)

nucleotide sequence

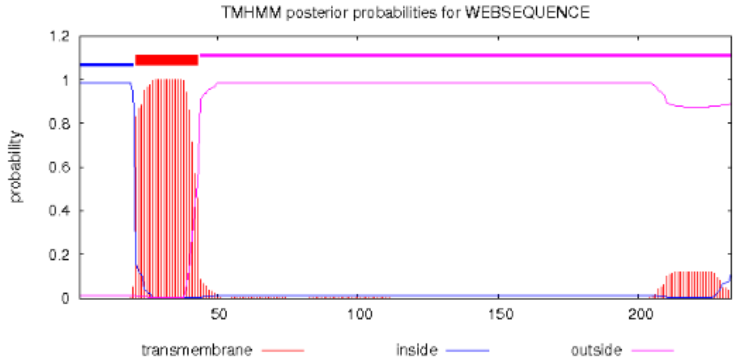
```
ATGGCTGCGAAGGGCAGCATGTCGGACTGCAGCGCGCACTGCCACCCCAAATGCAGGCGAGCCTGGAGGGTCTATGG
GCTGGTGGCCGTGCTGGTGGCTGTGGTGCTGCTAGCTGCATCCCTGCCCTCCTCTCTTTGCCTGCTGGCCACCAAAC
CAGAGCCAGAGACAGGGCTGGGGGTGGGGACAGGGAGAGTGCCTGGTTTGGAGGGGCTGGCACGGCTGCGGGAGGTG
CAGCAGCAGCTGCGGGTGCAGGTGGCTGCGTTGGAGCAAGCATTGGCTGCCACCAACCGGACCCTCACCACGGTGGT
GGGTGTCACCAACCGGTCCCTCGCTGAGATGCACGAGCAGTGGGATGGCTGCAGGAGTCAATTGGACACCGTGCAGG
GGGTCGTTGCGGAGCTGGGGCAGCAGCTCTCCCAGCTGCAGCAGCACAGGGAGAAGGAGGAGGCTGTGGTCAAACAA
CTGCAAGAGGACAACAGGGCGCTCCGGGAGGAGGTGGCACAGCAGAAGGAGCAGTTGGAGGAGGTGCAGAGGCTCAG
GAGCAGCTTCCAGGAGCAGATCCAGCGGCAGATCCACGGGCTGTCATCACAGATCTGGGACGTACAGAGACGCAGTT
CTGGTGGGAGCACAGCGTTGTCCTCTGGTGCAGCCACGGCCCTGAGCCTCCTCGTGACACTGCTGACTGCTAAGTGG
CTGCACTGA
```

amino acid sequence

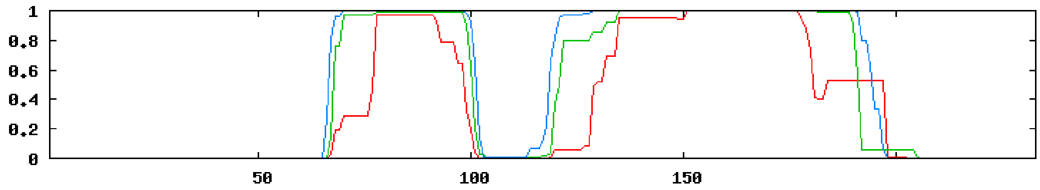
```
MAAKGSMSDCSAHCHPKCRRAWRVYGLVAVLVAVVLLAASLPSSLCLLATKPEPETGLGVGTGRVPGLEGLARLREV
QQQLRVQVAALEQALAATNRTLTTVVGVTNRSLAEMHEQWDGCRSQLDTVQGVVAELGQQLSQLQQHREKEEAVVKQ
LQEDNRALREEVAQQKEQLEEVQRLRSSFQEQIQRQIHGLSSQIWDVQRRSSGGSTALSSGAATALSLLVTLLTAKW
LH
```

potential GPI site at position 208 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Arborophila rufipectus (Sichuan partridge)

nucleotide sequence

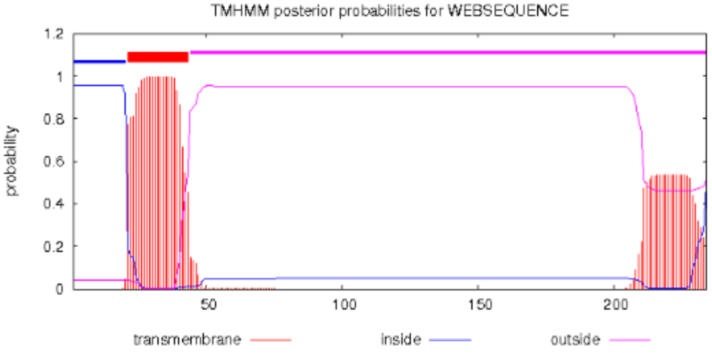
ATGGCCGCGCAGGRCAGCGTGCTGGACTGCAGCAAGCACTGCCACCCCAAATGCAGGCGAGCCTGGAAGGTCTATGG
GCTGCTGGCCCTGCTGCTGGCTGCGGTGCTGCTGGCTGCAACCCTGCCCTCCTCGGTCTGTCTGCTGGACACTGAAC
CAGAGCCAGGGCTGGGGACGGGGACAGGGAACGTGCCCGGTTTGGAGGGGCTGGCACGGCTGCAGGAGGTGCAGCAG
CGGCTGCAGGAGGTGCAGCAGCAGCTGCAGGCGCGGGTGGCTGCATTGGAGCAAGGGCTGGCTGCCGCCAACAGGAC
CCGCAGCACGGGGGGGGATGTCCCCAACCGGACCCTCGCTGAGATGCACAGACAGTGGGATGGCTGGAGGAGTCAGC
TGGACGCGGTGCAGGGGGTCATAGTGCAGTTGAGGCAGCAGCTCTCCCAGCTGCAGCAGCACAGGGAGACAAAGGAG
GCCGTGATCACGCAGCTGCAAGAGGACACCAGGGCGCTCCAGGAGGAGGTGGCACGGCAGAAGGAGCAGTTGCAGGA
GGCGTGGGTTCACAGGGGCAACTTCCAGGATCAGATCCAGAGGCTGTCATCAGAGGTCTGGTACCTACGGAGACACC
ACTCCAGTGCGAGCACAGCGATGCTCTCCGGTGCAGCCACGGCCCTGAGCCTCCTCGTGACGCTGCTCACGGCCCAG
TGGCTGCACTGA

amino acid sequence

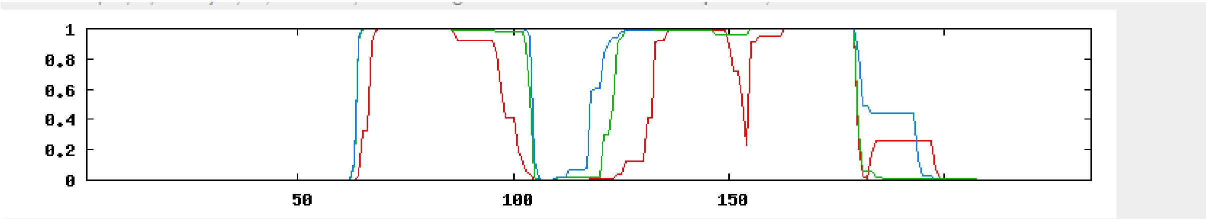
MAAQXSVLDCSKHCHPKCRRAWKVYGLLALLLAAVLLAATLPSSVCLLDTEPEPGLGTGTGNVPGLEGLARLQEVQQ
RLQEVQQQLQARVAALEQGLAAANRTRSTGGDVPNRTLAEMHRQWDGWRSQLDAVQGVIVQLRQQLSQLQQHRETKE
AVITQLQEDTRALQEEVARQKEQLQEAWVHRGNFQDQIQRLSSEVWYLRRHHSSASTAMLSGAATALSLLVTLLTAQ
WLH

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Arborophila ardens (Hainan partridge)

nucleotide sequence

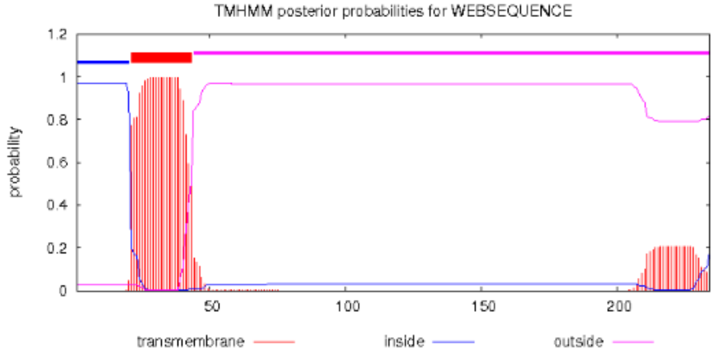
```
ATGGCTGCGCAGGGCAGCGTGCTGGACTGCAGCAAGCACTGCCACCCCAAATGCAGGCGAGCCTGGAAGGTCTATGG
GCTGCTGGCCCTGCTGCTGGCTGCGGTGCTGCTGGCTGCAACCCTGCCCTCCTCGGTCTGTCTGCTGGACACTGGAC
CAGAGCCAGGGCTGGGGACGGGGMCGGGGAACGTGCCCGGTTTGGAGGGGCTGGCACGGCTGCAGGAGGTGCAGCAG
CGGCTGCAGGAGGTGCAGCAGCAGCTGCAGGCGCGGGTGGCTGCGTTGGAGCAAGGGCTGGCTGCCRCCAACAGGAC
CCGCAGCACGGGGGGGRATGTCCCCAACCGGACCCTCGCTGAGATGCACAGACAGTGGGATGGCTGGAGGAGTCAGC
TGGACGCGGTGCAGGGGGTCATAGTGCAGTTGAGGCAGCAGCTCTCCCAGCTGCAGCAGCACAGGGAGAAGAAGGAG
GCCGTGATCGCGCAGCTGCAAGAGGACACCGGGGCGCTCCGGGAGGAGGTGGTACGGCAGAAGAAGCAGTTGGAGGA
GGTGTGGAGTGACAGGRGCAACTTCCAGGATCAGATCCAGAGGCTGTCATCAAAGGTCTGGTACCTACAGAGACAGC
ACTCCAGTGCGAGCACAGYGACGCTCTCCGGTGCAGCCACGGCCCTGAGCCTCCTCGTGACGCTGCTCACTGCCCAG
TGGCTGCACTGA
```

amino acid sequence

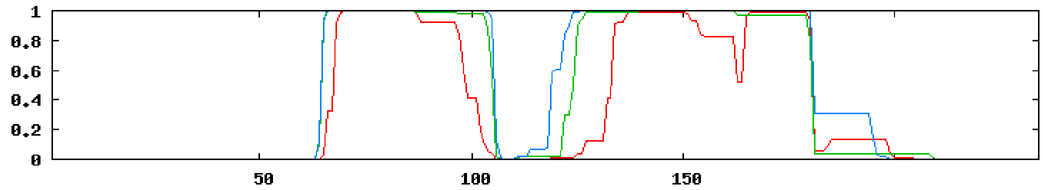
```
MAAQGSVLDCSKHCHPKCRRAWKVYGLLALLLAAVLLAATLPSSVCLLDTGPEPGLGTGtGNVPGLEGLARLQEVQQ
RLQEVQQQLQARVAALEQGLAAaNRTRSTGGdVPNRTLAEMHRQWDGWRSQLDAVQGVIVQLRQQLSQLQQHREKKE
AVIAQLQEDTGALREEVVRQKKQLEEVWSDRgNFQDQIQRLSSKVWYLQRQHSSASTaTLSGAATALSLLVTLLTAQ
WLH
```

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Gallus varius (green junglefowl)

nucleotide sequence

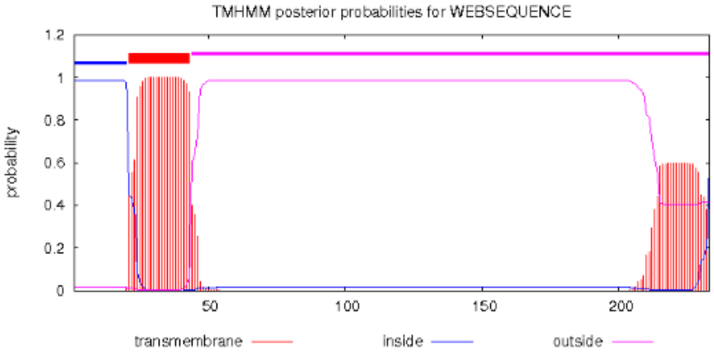
ATGGCTGCGCAGGGCAGCGTGTTGGACTGCAGCACACACTGCCATTCCAAATACAAGCGAGYCTGCAGGATCTATGG
GCTGGTGGCTGGGCTGGTGGTTGGGCTGACGGCCGTGGTGCTGCTAGCTGCATCCCTGCCCTCCTCTCTGTGCCTGC
TGACCACCAAACCAGAGCCAGAGACGGGGCTGGGGACGGGGACAGGAAGAGTGCCCGGTTTGGAGAGGCTGGCACGG
CTGCGGGAGGTGCAAGAGCAGCTGCAGATGCAGGTGGCTGCRTTGGAGCAAGCAYTGGCTGCCACCAACCGGACCCT
CACCACGGTGGTGGATGTCACCAACCGGTCCATCTCTGAGATGCACAAGCAATGGGATGACTGCAGGAGTCAGTTGG
ACACAGTGAAGGGCTTCGTCGTGGAGTTGGAGCAGCAGATCTCCCAGCTGCAGCAGCACAGGGAGAAGCAGGAGGCT
GTGGTCAAGCAACTGCAAGAGAACAACAGGGCTCTCCAGGAGGAGGTGGCACAGCAGAAGGAGCAGTTGGAGGAGGT
GGAGAGGCTCAGGAGCAGCTTCCAGGAGCAGATCCAGGAGCTGTCAGCACGGATCTGGAACATACGGAGACACATTT
CCAGTGGGAGCACAGAGATGCCCTCCGGTGCAGCCATGTTCCTGACCCTCCTCATCGCAGTGATCGCTGCAAAGTGG
CTGTGCTGA

amino acid sequence

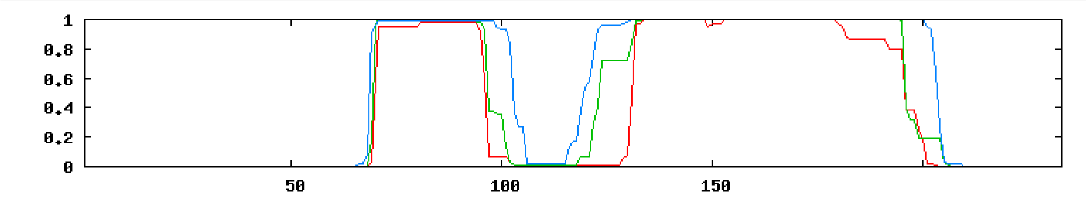
MAAQGSVLDCSTHCHSKYKRXCRIYGLVAGLVVGLTAVVLLAASLPSSLCLLTTKPEPETGLGTGTGRVPGLERLAR
LREVQEQLQMQVAALEQAXAATNRTLTTVVDVTNRSISEMHKQWDDCRSQLDTVKGFVVELEQQISQLQQHREKQEA
VVKQLQENNRALQEEVAQQKEQLEEVERLRSSFQEQIQELSARIWNIRRHISSGSTEMPSGAAMFLTLLIAVIAAKW
LC

potential GPI site at position 208 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Perdix perdix (Grey partridge)

nucleotide sequence

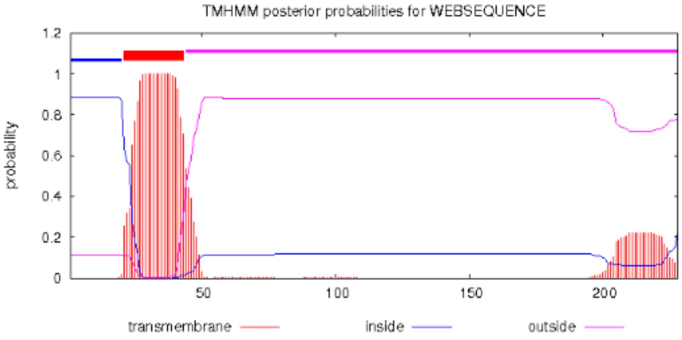
ATGGCTGCACAGGGCAGCATGTTGGACTACAGCGAGGACTGCCACCCTAAACCCAGGCGAAACTTGAAGGTCTATGG
GCTAGTGGTCGTGCTGGTGGCTGTGGTGCTGCTGGCTGCAGCCCTGCCCTCCTATATGTGCCTGCTGGCCACCAAAC
CAGAGCAAGAAGCAGGGCTGGGGATGGGGACAGGGCAAATGCATGGTTTGGAGGGGCTGGCACGGCTGCTGGGGGTG
CAGCAGCAGCTGCGGGTGCAGGTGGCTGCATTGGAGCAAGCATTGGTTGCCACCAACCAGACCCTCACCACCATGGT
GGATATCACCAACCCGTCCCTCGCTGAGATGCTCAAGAAGTGGGATGACTGCAGGAGTCAATTGGATACCATGCAGA
GGTTTGTGGCGGAGCTGGGGCAGCAGATCTCCCAGCTGCAGCAGCATAAGGAGAAGCAGGAGGCTGTGGTCAAGCAA
CTGCAAGAGGACAACAGGGCGCTCCAGGAGGAGGGGGCACAGCAGAAGGAGCAGTTGGCGGAGGTGCAGAGGCACAG
GAGCAGCTTTCAGGAGCAGATCCAGGAGCAGATCCACAGGCTGTCAGCACAGATCCGGGACATATGGAGCAGCAGTT
CCAGTGGGAGCACAGCGATGCCCTCCGGTGCAGCCATGGCTCTGAGCCTCCTCGTGACGCTGCTCACTGCAAAATGG
CTGCACTGA

amino acid sequence

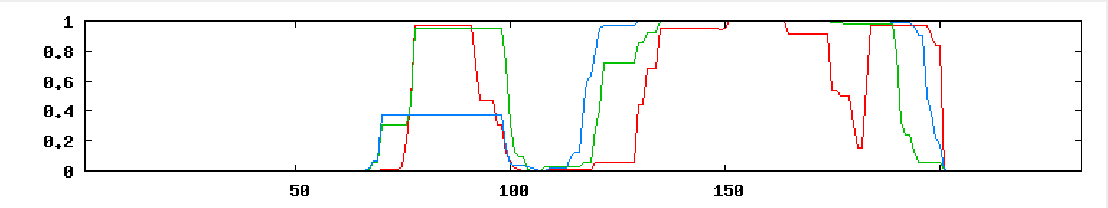
MAAQGSMLDYSEDCHPKPRRNLKVYGLVVVLVAVVLLAAALPSYMCLLATKPEQEAGLGMGTGQMHGLEGLARLLGV
QQQLRVQVAALEQALVATNQTLTTMVDITNPSLAEMLKKWDDCRSQLDTMQRFVAELGQQISQLQQHKEKQEAVVKQ
LQEDNRALQEEGAQQKEQLAEVQRHRSSFQEQIQEQIHRLSAQIRDIWSSSSSGSTAMPSGAAMALSLLVTLLTAKW
LH

potential GPI site at position 209 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Anseriformes

Anas platyrhynchos (the mallard)

nucleotide sequence

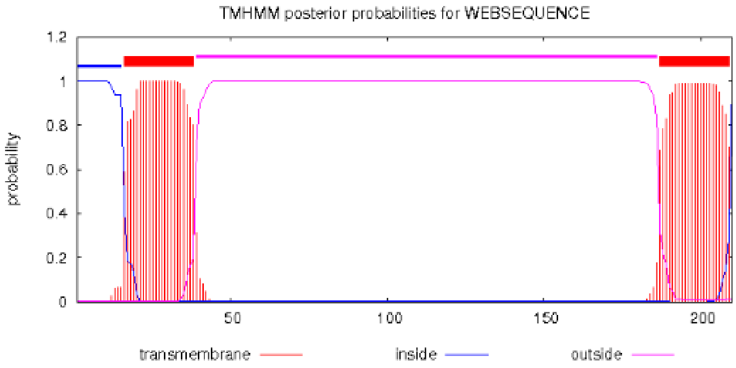
ATGGAGAACTGCTGCCTGCGCTGCCGCCTCCTCTACAAGCAGTGCTGGGGGGTGTGCGTGGGGCTGGCCATCGGGAT
GGTTTTGGTGGCCCTGGTCGCAGCCCTCGTCTCCGCGCRGGGGCCGCCGGGGGGCTCGGAGGGGCTGGAGGAGCTGC
AGGTGAAGGTGGCCAAGCTGGGGCAGGCGCTGGCCGCCACCGACAGGTCCCTCGCCGAGGTGCTGGCTGTCACCAAC
AGGTCCCTCGCCCAGGCGCTGGATGTCACCAACAGGTCCCTCGCCGAGACGCAGGGGCAGTGGGAGAGCTGCAGAAA
GGAGCTGGACGCGGTGAAGAGCAGCGTCTCGGAGCTGACACGGCGTTTAGCCCAGCTGCAGCACCACGGGGATGAGC
AGGAGGCCAACGTGGGGCGGCTGCAAGAGGACAACAGGGAGATCAAGGAGAAGCTGGAACAGCAGCGGCAGCAGCTG
GAGGAGGCGCAGAAGGACAGGAGAGATCTCCAGTCACAGATCTGGGACGCTTTGGCAAGGATCGGGTCCGGACAGAG
CTGGCATTCGAGTGGCACCAGCGCGACGTTCCCCGGCGTGGCCGTGCCCCTCGTCCTCCTGGCTCTGCTCTTGGTGG
GGACGCTGCTGCGTTGA

amino acid sequence

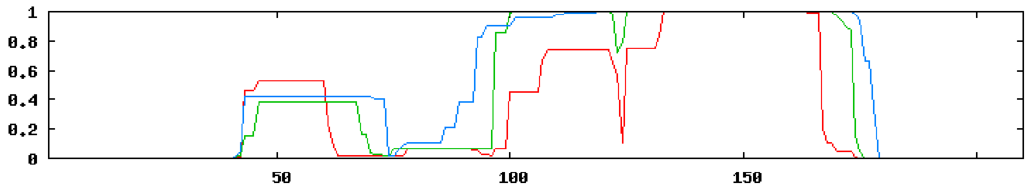
MENCCLRCRLLYKQCWGVCVGLAIGMVLVALVAALVSAXGPPGGSEGLEELQVKVAKLGQALAATDRSLAEVLAVTN
RSLAQALDVTNRSLAETQGQWESCRKELDAVKSSVSELTRRLAQLQHHGDEQEANVGRLQEDNREIKEKLEQQRQQL
EEAQKDRRDLQSQIWDALARIGSGQSWHSSGTSATFPGVAVPLVLLALLLVGTLLR

potential GPI site at position 183 (Red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Anser cygnoides (Swan goose)

nucleotide sequence

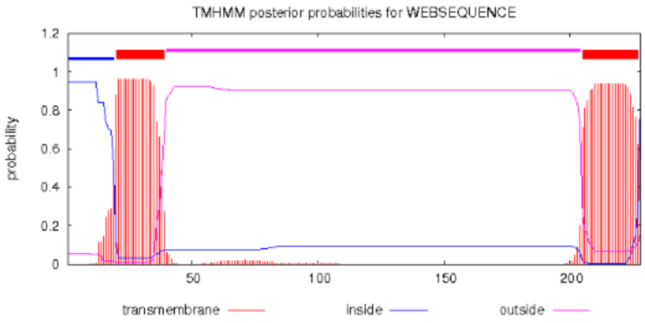
ATGGAGGGCTGCTGCCTGCGCTGCCGCCTCTGGCACAGGCAGTCCTGGAGGATGTGCGTGGCCCTGGCCATCGGGGT
GGCCGTGGTGGTCCTGGTGACAGCCCTCCCCTCCTCGGRGGAGCCACCGAGGGGCTTGGAGGGGCTGGAGCAGCTGG
GGACGGCGCAGCGGGAGCTGCAGGCGCAGGTGGCCGCGCTGGGGCAGGCGCTGGCCGTCACCAACCAGTCCCTCGCC
GAGGCGCTGGCCGTCACCAACCGGTCCCTCGCCGAGGCGCTGGCCGTCACCAACCGGTCCCTCGCTGAGGCGCTGGC
CGTCACCAGCAGGTCCCTCACCGAGGTGCGGGGGCAGTGGGAGAGCTGCAGAAACGAGCTGGACGCGCTGAAGAGCA
CTGTCTCGGAGCTGACACAGCGTTTAGCCCAGCTGCAGCACCACAGGGACGAGCAGGAGGCCAACGTGGTGCAGCTG
CAAGAGAACAACAGGGAGCTCCAGGAGAGGCTGGAACRGCAAGAGCATCAGCTGAAGGAGGCTCAGAGGAGCAGGAG
CAACCTCCAGTCGCAGATCTGGAACGCGTTGTCAGAGATCCAGTCCATACGGAGCTGGCGTTCGAGTGGGACCAGCG
TGACGTTCCCTGGCGTGGCCGTGCCCCTCGTCCTCCTGGCTCTGCTCTTCGCAGGGACGCTGCTGCTTTGA

amino acid sequence

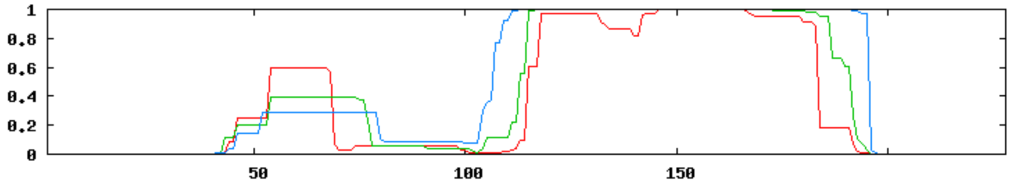
MEGCCLRCRLWHRQSWRMCVALAIGVAVVVLVTALPSSXEPPRGLEGLEQLGTAQRELQAQVAALGQALAVTNQSLA
EALAVTNRSLAEALAVTNRSLAEALAVTSRSLTEVRGQWESCRNELDALKSTVSELTQRLAQLQHHRDEQEANVVQL
QENNRELQERLEXQEHQLKEAQRSRSNLQSQIWNALSEIQSIRSWRSSGTSVTFPGVAVPLVLLALLFAGTLLL

potential GPI site at position 201 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Passeriformes

Sturnus vulgaris (Common starling)

nucleotide sequence

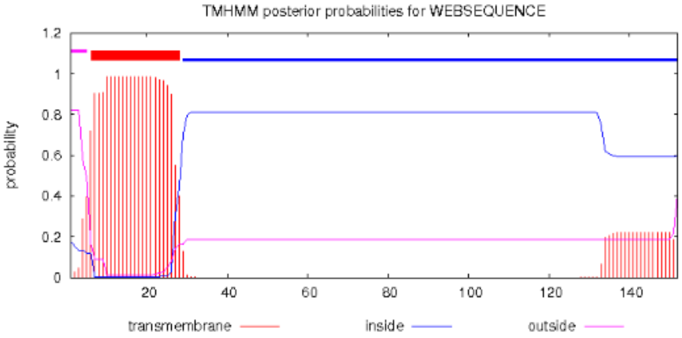
ATGGGGCTCTGGAAGGTGGTGGCAGCTGTGACCCTGGTGGCCGTGGTGGTGGTGGCAGTGACTGTCCCCACGCTGCT
GTGCCACTCCTGCCAGGAACAGGACAGGAATTCCACGGCGGAGCTGCAAAAAGCTCTGGATGTCACCAACAGGTCCC
TGGCTGTGTCGCGTGGGAGATGGCAGCGCTGCATGGAGGAGCTGGAAGAGCTGCGGGGACAAGGCTTGGAGCTGGAG
CGGGCGCTGGCCGATGTCACCCGGCTGGAGGAGCAGAACCGGGCGTTGGGGACAGAGGTGACACGGCAGCGGGAGCA
GCTGGAGGAGGAGCAGAGCCTCAGGGCGCAGCTCCAGATGCAGATCCGGCTCCTGCGGGAGCAGCTGCAGGACGTGA
GGAGCCAGCGCTCTACAGGGAACAGGCTCGGTGTCCCCACGCTCCTCCTCCTCCTCGGGATACTCCTCCTGTGA

amino acid sequence

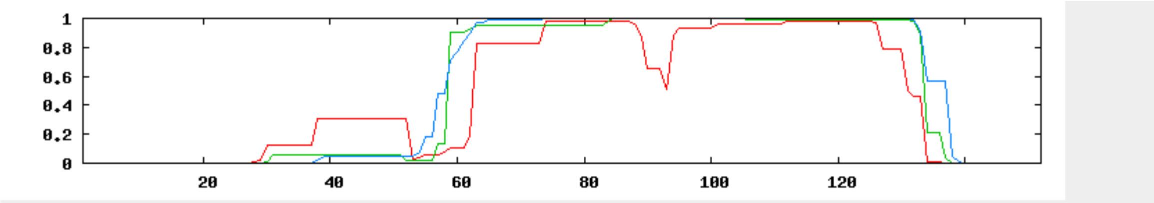
MGLWKVVAAVTLVAVVVVAVTVPTLLCHSCQEQDRNSTAELQKALDVTNRSLAVSRGRWQRCMEELEELRGQGLELE
RALADVTRLEEQNRALGTEVTRQREQLEEEQSLRAQLQMQIRLLREQLQDVRSQRSTGNRLGVPTLLLLLGILLL

potential GPI site at position 133 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Lamprotornis superbus (Superb starling)

nucleotide sequence

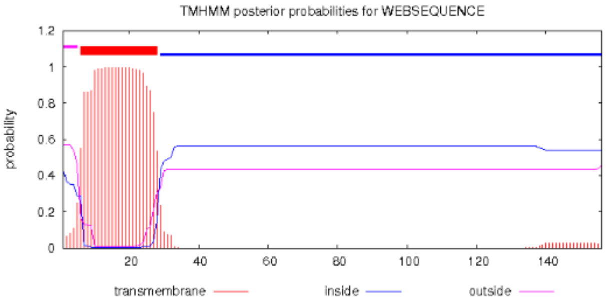
```
ATGGGGCTCTGGAAGGTGGTGGCAGCTGTGACCCTGGTGGTGGCCGTGGTGGTGGTGGCAGTGACTGTCCCCACGCT
GCTGTGTCACTCCTGCGGGGGACAGGACAGGAATTCCACGGCGGAGCTGCAAAAAGCTCTGGATGTCACCAACAGGT
CCCTGGCTGTGTCGCGTGGGAGGTGGCAGCGCTGCATGGAGGAGCTGGAAGAGCTGCGGGGACAAGGCTTGGAGCTG
GAGCGGGCCCTGGCCGATGTCACCCGGCTGGAGGAGCAGAACCGGGCGTTGGGGACAGAGATGACACGGCAGCGGGA
GCAGCTGGAGGAGGAGCAGAGCCTCAGGGCGCAGCTCCAGATGCAGATCCGGCTCCTGCGGGAGCAGCTGCAGGACG
TGAGGAGCCAGCGCTCCACAGGGGACAGGCCCGCGGTGTCCCCCggTGTCCCCatgcTCCTCCTCCTCGGGATGCTC
CTCCTGTGA
```

amino acid sequence

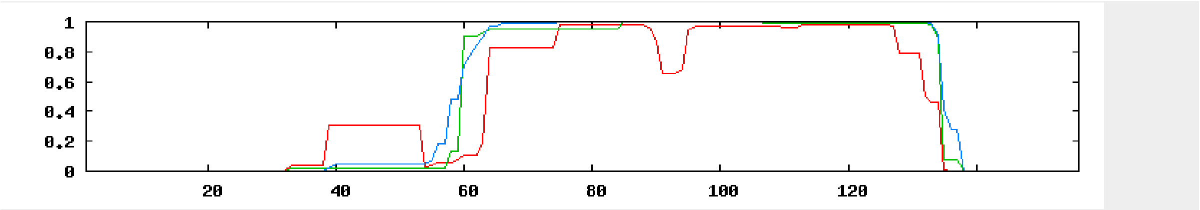
```
MGLWKVVAAVTLVVAVVVVAVTVPTLLCHSCGGQDRNSTAELQKALDVTNRSLAVSRGRWQRCMEELEELRGQGLEL
ERALADVTRLEEQNRALGTEMTRQREQLEEEQSLRAQLQMQIRLLREQLQDVRSQRSTGDRPAVSPGVPMLLLLGML
LL
```

potential GPI site at position 134 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Ficedula albicollis (Collared flycatcher)

nucleotide sequence

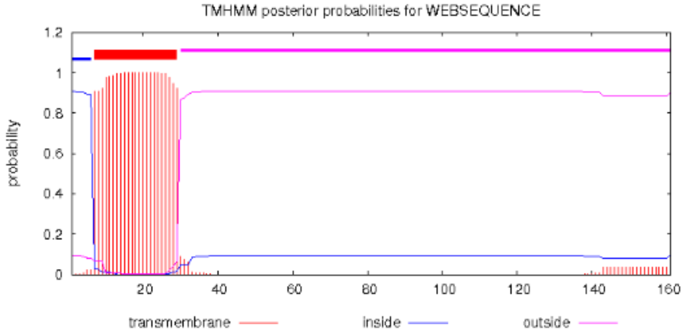
ATGACGGGGCTCTGGAAGGTGGCGGCGGCTGTGACCCTGGTGGCCACCGCGGCGCTGGTGGTGGCCGTGGTGGTGGC
GGTGGCCGTCCCCACGCTGTGCCACTGCGGGGGACAGGACGGGAATTCCACGGGGGAGCTGCGGAAAGCTCTGGATG
TCACCAACAGGTCCCTGGCCGTGTCGCGAGGGAGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGACAA
AGCTTGGAGCTGGAGAGGGCGCTGGCCAATGTCACCCGGCTGGAGGAGCAGAACCGGGCGTTGGGGACAGAGGTGAC
ACGGCAGCGAGAGCAGCTGGGGGAGGAGCAGAGCCTCAGGTCCCAGCTCCAGCGGCAGATCCGCCTCCTGCAGGAGC
AGCTGCGGGACGTGAGGAGCCAGCGCTCCGCAGGGGACAGGCCCGCGGTGTCCCCCGGTGTCCCCACCCTCCTCCTC
CTGCTCGGGATGCTGCTCCTGTGA

amino acid sequence

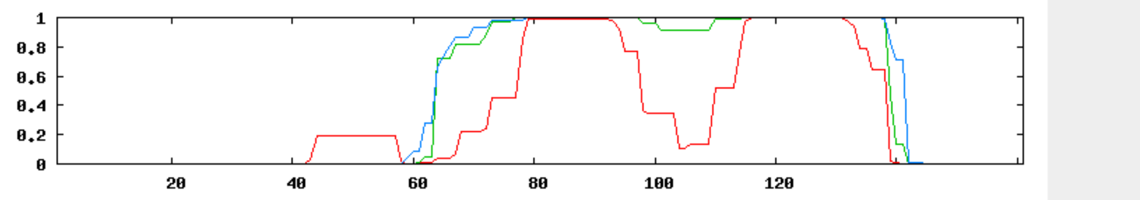
MTGLWKVAAAVTLVATAALVVAVVVAVAVPTLCHCGGQDGNSTGELRKALDVTNRSLAVSRGRWQRCREELGALQGQ
SLELERALANVTRLEEQNRALGTEVTRQREQLGEEQSLRSQLQRQIRLLQEQLRDVRSQRSAGDRPAVSPGVPTLLL
LLGMLLL

potential GPI site at position 138 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Corvus hawaiiensis (Hawaiian crow)

nucleotide sequence

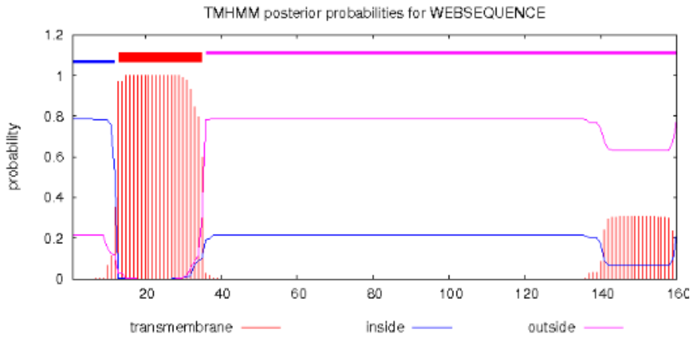
ATGGCGTTCTCCAGGTGCCCCTGGAAGGAGGTGGCCATCGTGACCCTGGTGGTGGCCACCGTGGTGGTGGTGGTGGT
GGTGGCGGTGGCGGTGCCCACCCTGCTGTGTCACCGCGGAGGGGACAGGAATTCCCTGGAGGCTCCGGATGTCACCA
ACAGGTCCCTGGCTGAGGCCCGCGGGCGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGAAAAATCCTG
GAGCTGGAGCAGGCGCTGGCCAATGTCACCTGGCTGGAGGAGCAGAACCGCGCGCTGGGCACGGAGCTGGAGTGGCA
GCGGGAGCAGCTGGGGCAGGAGCAGAGCCTCAGGGCCCAGCTCCAGCGGCAGAACCGGCTCCTGCAGGAGCAGCTGC
AGGACGCGCAGAGCCAGCGATCCGCAGGGGACAGGCTCCCGGTGTCCCCCGGTGTCCCCGTGCTCCTCCTCCTCCTC
CTCGGGATGCTCCTTCCGTGA

amino acid sequence

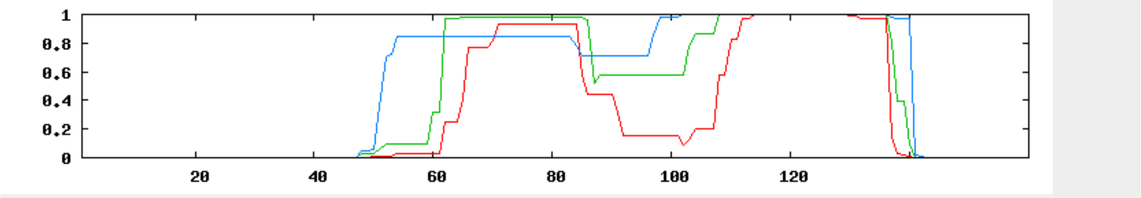
MAFSRCPWKEVAIVTLVVATVVVVVVVAVAVPTLLCHRGGDRNSLEAPDVTNRSLAEARGRWQRCREELGALQGKIL
ELEQALANVTWLEEQNRALGTELEWQREQLGQEQSLRAQLQRQNRLLQEQLQDAQSQRSAGDRLPVSPGVPVLLLLL
LGMLLP

potential GPI site at position 136 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Acridotheres javanicus (Javan myna)

nucleotide sequence

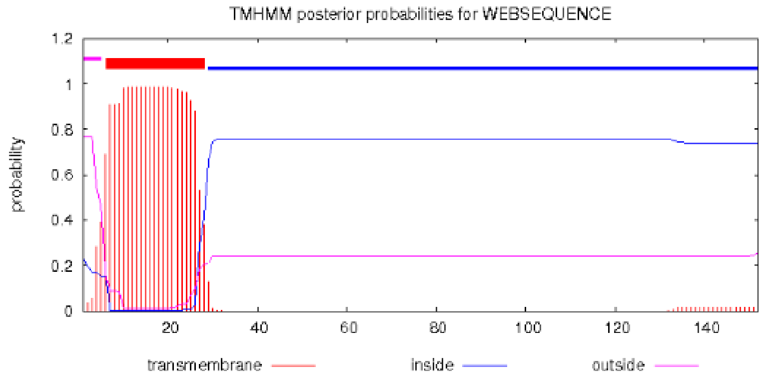
ATGGGGCTCTGGAAGGTGGTGGCAGCTGTGACCCTGGTGGCCGTGGTGGTGGTGGCAGTGACTGTCCCCACGCTGCT
GTGCCACTCCTGCCAGGAACAGGACAGGAATTCCACGGCGGAGCTGCAAAAAGCTCTGGATGTCACCAACAGGTCCC
TGGCTGTGTCGCGTGGGAGGTGGCAGCGCTGCATGGAGGAGCTGGAAGAGCTGCGGGGACAAGGCTTGGAGCTGGAG
CGGGCGCTGGCCGATGTCACCCGGCTGGAGGAGCAGAACCGGGCGTTGGGGACAGAGGTGACACGGCAGCGGGAGCA
GCTGGAGGAGGAGCAGAGCCTCAGGGCGCAGCTCCAGATGCAGATCCGGCTCCTGCGGGAGCAGCTGCAGGACGTGA
GGAGCCAGCGCTCCACAGGGAACAGGCCCGGTGTCCCCACGCTCCTCCTCCTCGGGATGCTCCTCCTGTGA

amino acid sequence

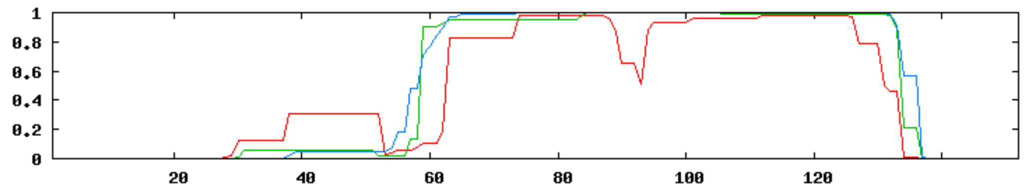
MGLWKVVAAVTLVAVVVVAVTVPTLLCHSCQEQDRNSTAELQKALDVTNRSLAVSRGRWQRCMEELEELRGQGLELE
RALADVTRLEEQNRALGTEVTRQREQLEEEQSLRAQLQMQIRLLREQLQDVRSQRSTGNRPGVPTLLLLLGMLLL

potential GPI site at position 133 (Red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Corvus cornix (Hooded crow)

nucleotide sequence

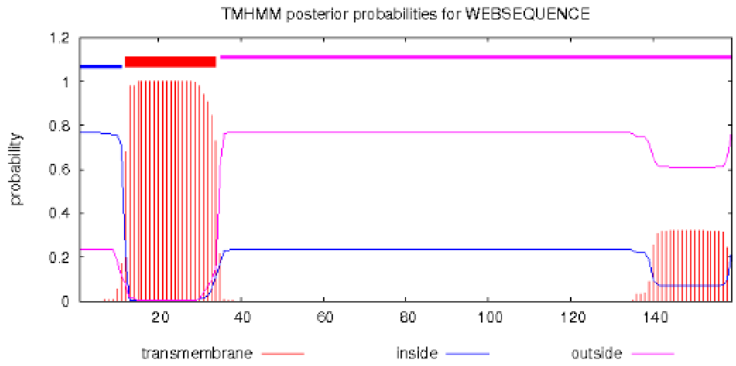
ATGGCGTTCTCCAGGTGCCCCTGGAAGGAGGTGGCCATCGTGACCCTGGTGGTGGCCACCGTGGTGGTGGTGGTGGT
GGCGGTGGCGGTGCCCACCCTGCTGTGTCACCGCGGAGGGGACAGGAATTCCCTGGAGGCTCCGGATGTCACCAACA
GGTCCCTGGCCGAGGCCCGCGGGCGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGAAAAATCCTGGAG
CTGGAGCAGGCGCTGGCCAATGTCACCTGGCTGGAGGAGCAGAACCGCGCGCTGGGCACGGAGCTGGAGTGGCAGCG
GGAGCAGCTGGGGCAGGAGCAGAGCCTCAGGGCCCAGCTCCAGCGGCAGAACCGGCTCCTGCAGGAGCAGCTGCAGG
ACGCGCAGAGCCAGCGATCCGCAGGGGACAGGCTCCCGGTGTCCCCCGGTGTCCCCGTGCTCCTCCTCCTCCTC
GGGATGCTCCTTCCGTGA

amino acid sequence

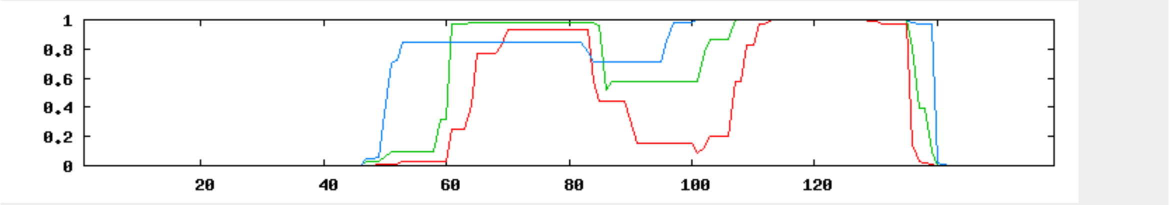
MAFSRCPWKEVAIVTLVVATVVVVVVAVAVPTLLCHRGGDRNSLEAPDVTNRSLAEARGRWQRCREELGALQGKILE
LEQALANVTWLEEQNRALGTELEWQREQLGQEQSLRAQLQRQNRLLQEQLQDAQSQRSAGDRLPVSPGVPVLLLLLL
GMLLP

potential GPI site at position 135 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Corvus corone (Carrion crow)

nucleotide sequence

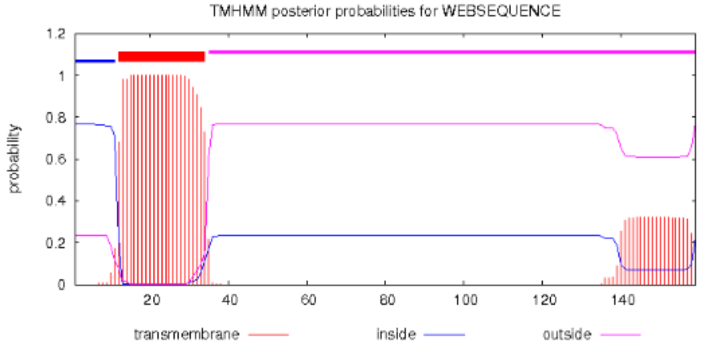
ATGGCGTTCTCCAGGTGCCCCTGGAAGGAGGTGGCCATCGTGACCCTGGTGGTGGCCACCGTGGTGGTGGTGGTGGT
GGCGGTGGCGGTGCCCACCCTGCTGTGTCACCGCGGAGGGGACAGGAATTCCCTGGAGGCTCCGGATGTCACCAACA
GGTCCCTGGCCGAGGCCCGCGGGCGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGAAAAATCCTGGAG
CTGGAGCAGGCGCTGGCCAATGTCACCTGGCTGGAGGAGCAGAACCGCGCGCTGGGCACGGAGCTGGAGTGGCAGCG
GGAGCAGCTGGGGCAGGAGCAGAGCCTCAGGGCCCAGCTCCAGCGGCAGAACCGGCTCCTGCAGGAGCAGCTGCAGG
ACGCGCAGAGCCAGCGATCCGCAGGGGACAGGCTCCCGGTGTCCCCCGGTGTCCCCGTGCTCCTCCTCCTCCTC
GGGATGCTCCTTCCGTGA

amino acid sequence

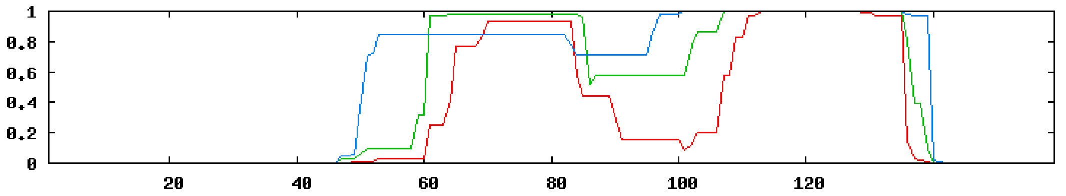
MAFSRCPWKEVAIVTLVVATVVVVVVAVAVPTLLCHRGGDRNSLEAPDVTNRSLAEARGRWQRCREELGALQGKILE
LEQALANVTWLEEQNRALGTELEWQREQLGQEQSLRAQLQRQNRLLQEQLQDAQSQRSAGDRLPVSPGVPVLLLLLL
GMLLP

potential GPI site at position 135 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Zosterops lateralis (Silvereye)

nucleotide sequence

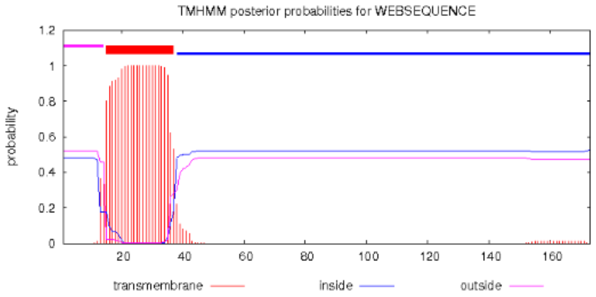
ATGGAGGAGAAGGGATTTCTCAGAGAGAAACCCAGGACGGGCGCCTGGAMAGCGGTGGCCGCTGTCACCCTGGTGGT
GGCCGCGGTGTTGGTGTTGGTGGTGGCCGTGACTGTCCCCACCGTGCTGTGCCACCGCGGGGGGGACGGCAATTCCA
CCGAGAGGCTGGAAAAGGCTCTGGATGTCACCAACAGGTCCCTGTCGCTGTCCCTCGGGAGGTGGCAGCGCTGCAAG
GAGGAGCTGGGAGAGGTGCAGGGGAAGGTGTCGGAGCTGGAGGAGGCGCTGGCCAATGTCACCCGGCTGGAGGAGGA
GAACCGGGCTCTGGTGACAGAGGTGACACGGCTGCGGGAGCGGCTGGGGGAGGAGCAGAACCTCAGGTGGCAGCTGG
AGCAGCAGAACCGGCTCATTCGGGAGGAGCTGCAGGACCTGAGGAGTGCCCGGAGCTCCCCAGGGGACAAGCCCGCG
CTGTCCCCCGAGGTCCAAAAATTCCTCCTCCTCCTCCTCCTTGTGTTCCTCACGATGTGA

amino acid sequence

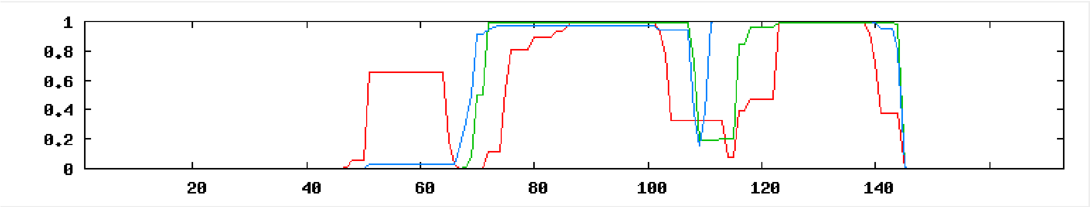
MEEKGFLREKPRTGAWXAVAAVTLVVAAVLVLVVAVTVPTVLCHRGGDGNSTERLEKALDVTNRSLSLSLGRWQRCK
EELGEVQGKVSELEEALANVTRLEEXNRALVTEVTRLREXLGEEQNLRWQLEQQNRLIREELQDLRSARSSPGDKPA
LSPEVQKFLLLLLLVFLTM

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Ficedula hypoleuca (European pied flycatcher)

nucleotide sequence

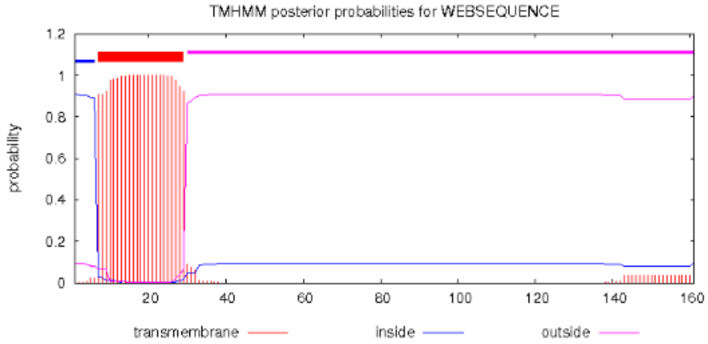
ATGACGGGGCTCTGGAAGGTGGCGGCGGCTGTGACCCTGGTGGCCACCGCGGCGCTGGTGGTGGCCGTGGTGGTGGC
GGTGGCYGTCCCCACGCTGTGCCACTGCGGGGGACAGGACGGGAATTCCACGGGGGAGCTGCGGAAAGCTCTGGATG
TCACCAACAGGTCCCTGGCCGTGTCGCGAGGGAGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGACAA
AGCTTGGAGCTGGAGAGGGCGCTGGCCAATGTCACCCGGCTGGAGGAGCAGAACCGGGCGTTGGGGACAGAGGTGAC
ACGGCAGCGAGAGCAGCTGGGGGAGGAGCAGAGCCTCAGGTCCCAGCTCCAGCGGCAGATCCGCCTCCTGCAGGAGC
AGCTGCGGGACGTGAGGAGCCAGCGCTCCGCAGGGGACAGGCCCGCGGTGTCCCCCGGTGTCCCCACCCTCCTCCTC
CTGCTCGGGATGCTGCTCCTGTGA

amino acid sequence

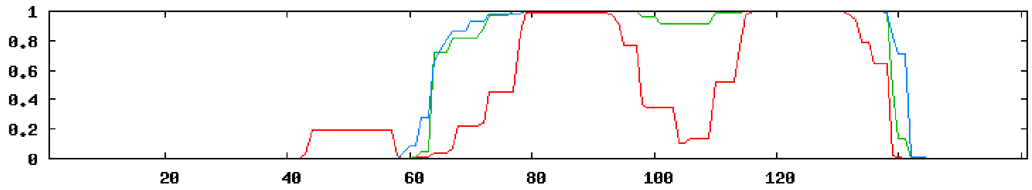
MTGLWKVAAAVTLVATAALVVAVVVAVAVPTLCHCGGQDGNSTGELRKALDVTNRSLAVSRGRWQRCREELGALQGQ
SLELERALANVTRLEEQNRALGTEVTRQREQLGEEQSLRSQLQRQIRLLQEQLRDVRSQRSAGDRPAVSPGVPTLLL
LLGMLLL

potential GPI site at position 138 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Corvus brachyrhynchos (American crow)

nucleotide sequence

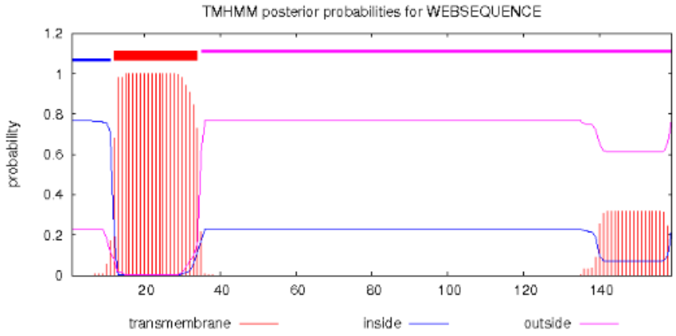
ATGGCGTTCTCCAGGTGCCCCTGGAAGGAGGTGGCCATCGTGACCCTGGTGGTGGCCACCGTGGTGGTGGTGGCGGT
GGCGGTGGCGGTGCCCACCCTGCTGTGTCACCGCGGAGGGGACAGGAATTCCCTGGAGGCTCCGGATGTCACCAACA
GGTCCCTGGCCGAGGCCCGCGGGCGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGAAAAATCCTGGAG
CTGGAGCAGGCGCTGGCCAATGTCACCTGGCTGGAGGAGCAGAACCGCGCGCTGGGCACGGAGCTGGAGTGGCAGCG
GGAGCAGCTGGGGCAGGAGCAGAGCCTCAGGGCCCAGCTCCAGCGGCAGAACCGGCTCCTGCAGGAGCAGCTGCAGG
ACGCGCAGAGCCAGCGATCCGCAGGGGACAGGCTCCCGGTGTCCCCCGGTGTCCCCGTGCTCCTCCTCCTCCTC
GGGATGCTCCTTCCGTGA

amino acid sequence

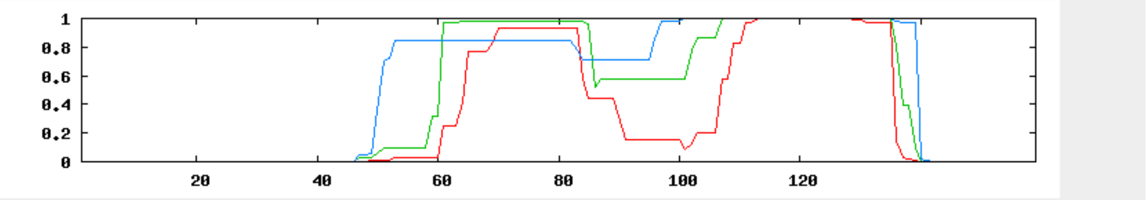
MAFSRCPWKEVAIVTLVVATVVVVAVAVAVPTLLCHRGGDRNSLEAPDVTNRSLAEARGRWQRCREELGALQGKILE
LEQALANVTWLEEQNRALGTELEWQREQLGQEQSLRAQLQRQNRLLQEQLQDAQSQRSAGDRLPVSPGVPVLLLLLL
GMLLP

potential GPI site at position 135 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Phylloscopus trochiloides (Greenish warbler)

nucleotide sequence

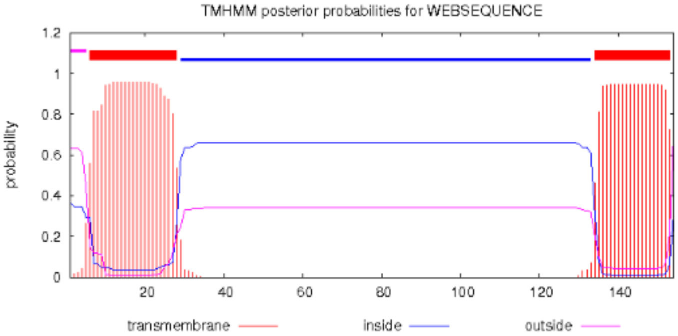
ATGGGGCTCTGCAGGGCGGCCGYCGCTGTCACCCTGCTGGTGGCCGCGGTGCTGGCGGCCGCCACTGTCCCCACGCT
GCTGTGCCACCGCGGGAGTTCCGCGGAGGGGCTGCGGGAGGCTCTGGATGTCACCAACAGGTCCCTGGCCCTGGCCC
GCGGGCGGTGGCAGCGCTGCCGGGAGGAGCTGGGAGCGCTGCAGGGAAAAGCTTCGGAGCTGGAGCGGGCGCTGGCC
AATGTCACCCGGCTGGAGGAGCAGAACCGGGCCCTGGGGACAGAGGTGAGGCGGCAGCGGGAGCAGCTGAGGGAGGA
GCAGAGCCTCAGGGCCCGGCTGCAGCAGCAGAACCGGCTCCTGCAGGAGCAGCTGCGGGACGCCAGGAGCCAGCGCG
ACACGGGGGACAGGCCCGCGGCGTCCCCTGCTGTCCTCACCCTCCTCCTCCTCctcctcGGGATGTTCCTCCTG
TGA

amino acid sequence

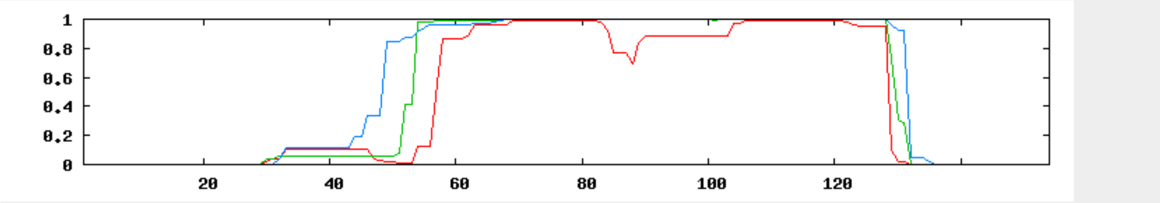
MGLCRAAXAVTLLVAAVLAAATVPTLLCHRGSSAEGLREALDVTNRSLALARGRWQRCREELGALQGKASELERALA
NVTRLEEQNRALGTEVRRQREQLREEQSLRARLQQQNRLLQEQLRDARSQRDTGDRPAASPAVLTLLLLLLLGMFLL

potential GPI site at position 129 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Eopsaltria australis (Eastern yellow robin)

nucleotide sequence

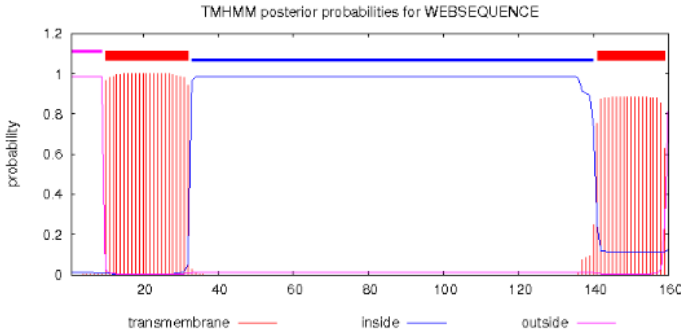
ATGGAGCCCCCCAGGTGGCCCTGGAAGGTGGTGGCCGCTGTGACCCTCGCGGTGGCAGCCGCGGTGGTGGCGGTGAC
TGTCCCCACSCTGCTGTGGCACCGCGGGGGTGACAGGAATTCCACCGAGGGGCTGGCGAGGGCTCTGGATGTCACCA
ACAGGTCCCTGGCCGAGACCCRCGGGAGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGAAGGGGAAGGTGYTG
GATCTGGAGAGGGCGCTGGCCAATGTCACCCTGCTGGATGAGCAGAACCAAGYGCTGGTGACAGAGGTGACRCGGCA
GCGGGAGCAGCTGCGGGAGGAGCAGCGCCTCAGGGCYCAGCTCCAGCAGCAGAACCGGCTCCTGCAGGAGCAGCTGC
GGGACGTGAGGAGCCAGCGTTCCACAGGGGACAGGCTGGCGATGTCCCCCGCTGTCCCCACCCTCCTCCTCCTCCTC
CTCGRGGTGCTCCTCCTGTGA

amino acid sequence

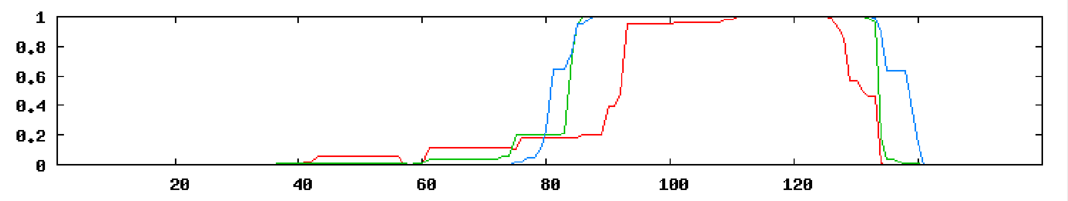
MEPPRWPWKVVAAVTLAVAAAVVAVTVPTLLWHRGGDRNSTEGLARALDVTNRSLAETXGRWQRCREELGALKGKVX
DLERALANVTLLDEQNQXLVTEVTRQREQLREEQRLRAQLQQQNRLLQEQLRDVRSQRSTGDRLAMSPAVPTLLLLL
LXVLLL

potential GPI site at position 136 (Red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Saxicola maurus (Siberian stonechat)

nucleotide sequence

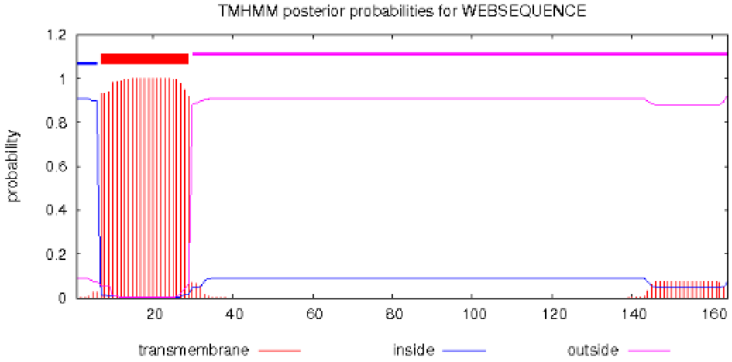
ATGGCGGGGCTGTGGAAGGTGGTGGCAGCTGTGACCCTGGTGGCCACCGTGGCGCTGGTGGTGGCCGTGGYGGTGGC
CGTGGCTGTCCCCACGCTGCTGTGTCGCTGCGGGGGACAGGACGGGAATTCCACGGGGGAGCTGCGCAAAGCTCTGG
ATGTCACCAACAAGTCCCTGGCCGTGTCGCGAGGGAGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGA
CAAAGCGTGGAGCTGGAGCGGGCGCTGGCCAATGTCACCTGGCTGGAGGAGCAGAACCGGGTGTTGGTGACAGAGGT
GACACGGCAGCGGGAGCAGCTGGGGGAGGAGCAGAGCCTCAGGTCCCAGCTCCAGCGGCAGGTCCGGCTCCTGCAGG
AGCAGCTGCGGGACGAGAGGATCCAGCGCTCGGCAGGGGACAGGCCCGCGCTGTCCCCCGCTGTCCCCTCCCTCCTC
CTCCTCCTCCCCCTCGGGATGCTGCTCCTGTGA

amino acid sequence

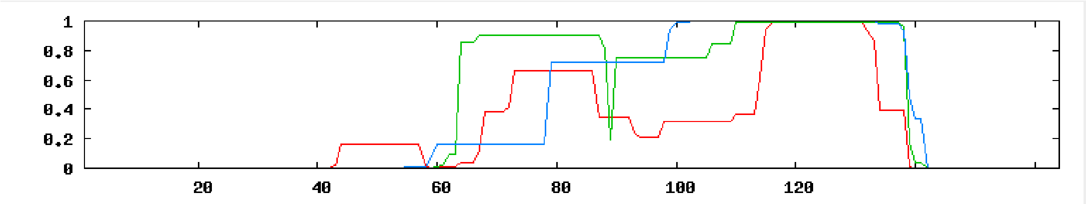
MAGLWKVVAAVTLVATVALVVAVXVAVAVPTLLCRCGGQDGNSTGELRKALDVTNKSLAVSRGRWQRCREELGALQG
QSVELERALANVTWLEEQNRVLVTEVTRQREQLGEEQSLRSQLQRQVRLLQEQLRDERIQRSAGDRPALSPAVPSLL
LLLPLGMLLL

potential GPI site at position 139 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Turdus merula (Common blackbird)

nucleotide sequence

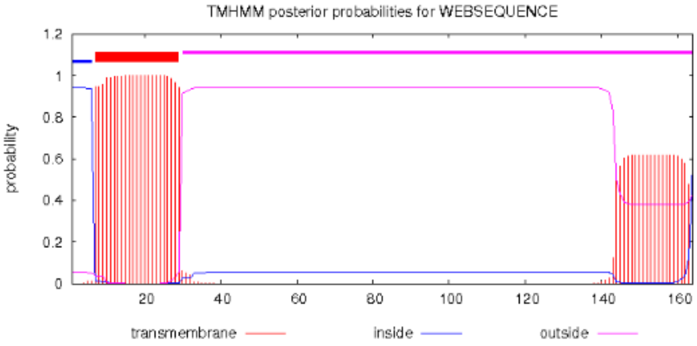
```
ATGAGGGGACACTGGAAGGTGGTGGCAGCTGTCGCCCTGGTGGCCACCGTGACCCTGGTGGTGGCCGCGGTGGTGGC
GGTGGCTGTCCCCACGCTGTGTCACCTCGGGGGACGCGACAGCAATGTCACGGAGGAGCTGCAAAAAGCTCTGGATG
TCACCAACATGTCGCTGGCCGTGTCGCGAGAGAGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCGGGGACAG
AGTTCGGAGCTGGAGCGGGCGCTGGCCGATGTCACCCGGCTGGAGGAGCAGAACCGCGCCTTGGGGACAGAGGTGAC
AGAGCAGCGAGAGCAGCTGGAGGAGGAGCAGAGGCTCAGGTCCCAGCTCCAGCAGCGGATCCGGTTCCTGCAGGAGC
AGCTGCAGGACGCGAGGAGCCAGCGCTCGGCAGGGGACAGGCCCGCGGTGTCCCCCGCTGTCCCCACCCTCCTCCTC
CTCCTCCTCCTTCTCGGGACGCTCCTGCTGTGA
```

amino acid sequence

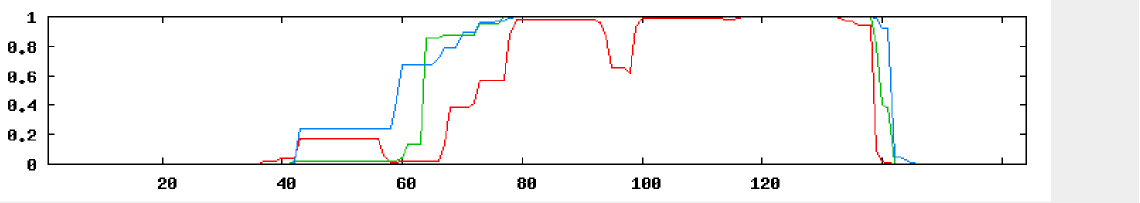
```
MRGHWKVVAAVALVATVTLVVAAVVAVAVPTLCHLGGRDSNVTEELQKALDVTNMSLAVSRERWQRCREELGALRGQ
SSELERALADVTRLEEQNRALGTEVTEQREQLEEEQRLRSQLQQRIRFLQEQLQDARSQRSAGDRPAVSPAVPTLLL
LLLLLGTLLL
```

potential GPI site at position 138 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Catharus ustulatus (Swainson´s trush)

nucleotide sequence

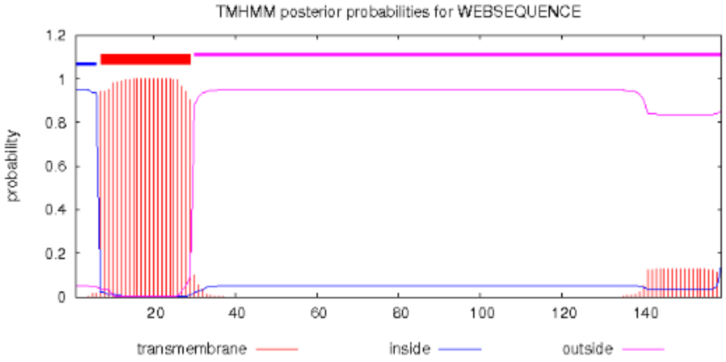
```
ATGACGCGACCCTGGAAGGTGGTGGCAGCTGTCACCACCCTGGTGGCCACCGTGACCCTGGTGGTGGCCGCGGTGGT
GGCGGTGGCTGTCCCCACCCTGCGGTGTCACAGCAATTCCACGGCGGAGCTGCAGAAAGCTCTGGATGTCACCAACA
GGTCCCTGGCCGTGTCGCGAGAGGGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCGGGGACAAAGCTCGGAG
CTGGAGCGGGCGCTGGCCGATGTCACCCGGCTGGAGGAGCAGAACCGCGCCTTGGGGACAGAGGTGACGCAGCAGCG
AGAGCAGCTGGAGGAGGAGCAGAGGCTCAGGTcGcAGCTCCAGCAGCGGCTCCGGTTCCTGCAGGAGCAGCTGCAGG
ACGCGAGGAGCCCGCGCTCCGCAGGGGACAGGCCCGCGGTGTCCCCCGCTGTCCCCACCCTGCTCCTGCTCCTCCTC
GGGACGCTCCTGCTGTGA
```

amino acid sequence

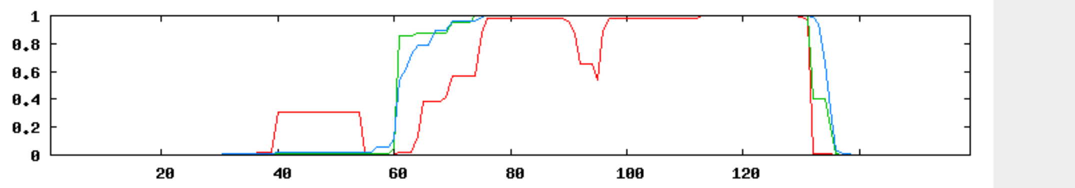
```
MTRPWKVVAAVTTLVATVTLVVAAVVAVAVPTLRCHSNSTAELQKALDVTNRSLAVSREGWQRCREELGALRGQSSE
LERALADVTRLEEQNRALGTEVTQQREQLEEEQRLRSQLQQRLRFLQEQLQDARSPRSAGDRPAVSPAVPTLLLLLL
GTLLL
```

potential GPI site at position 135 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Eurillas virens (Little greenbul)

nucleotide sequence

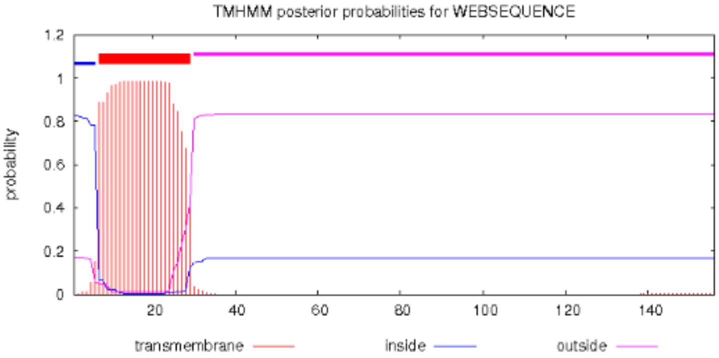
ATGAGGGGCTGGAAAGCGGCGGCCGCTGTCACgCTggTGGTGGCCGCGGTGGCcGcGgTGGCCGTGACTGTCCCCAC
GCTGCTGTGTCACCGCGGAGGGGACAGCAATTCCACGGAGAGGCTGGAAAAGGCTCTGGATGTCACCAACAGGTCCC
TGGCCGTGTCCCTCGGGCGGTGGCAGCGCTGCAAGGAGGAGCTGGGAGCGCTGCAGGAGAAAGTTCTGGAGCTGGAG
CAGGCGCTGGCCAATGTCACCCGGCTGGAGGAGCAGAACCGGGCTCTgGGGACAGAGCTGAGGCGGCAGCGGGAGCA
GCTGGAGGAGGAGCAGAGCCTCAGGGCGGAGCTGCAGCGGCAGAACGCGCTCCTGCAGGAGCAGCTGTGGGACGCGG
GGAGCCAGCGCTCCAGCGGGGACAGCCCCGAGAGCGCCATCGACACCAAACTGCTCCTCCTCTTCCTCTGGAGCCTC
CTCCTGTGA

amino acid sequence

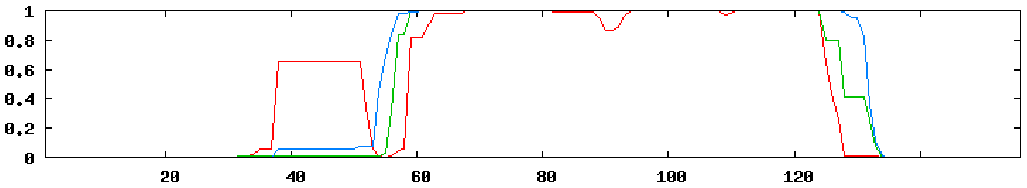
MRGWKAAAAVTLVVAAVAAVAVTVPTLLCHRGGDSNSTERLEKALDVTNRSLAVSLGRWQRCKEELGALQEKVLELE
QALANVTRLEEQNRALGTELRRQREQLEEEQSLRAELQRQNALLQEQLWDAGSQRSSGDSPESAIDTKLLLLFLWSL
LL

potential GPI site at position 134 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Hirundo rustica (Barn swallow)

nucleotide sequence

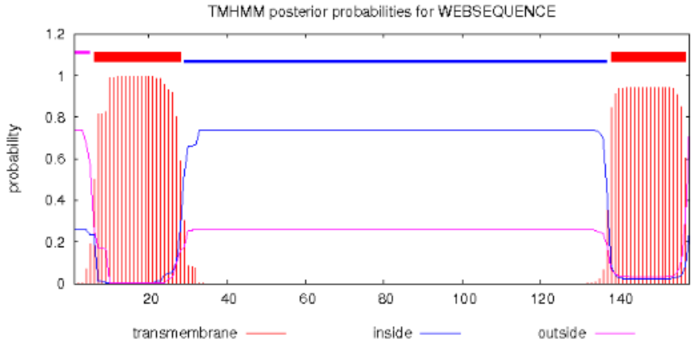
ATGGGGCCCTGGAAGGCGGTGGCCGCTGTCACCCTGGTGGTGGCCGCGGTGCTGGTGGCCGTGACTGTCCCCACCCT
GCTGTGCCACCGCGCCGGGGACGGGAATTCCAGCGAGAGGCTGGAGAAGGCTCTGGATGTCACCAACAGGTCCCTGG
CCGTGTCCCTGGGGCGGTGGCAGCGCTGCAGGGAGGAGCTGGGAGCGCTGCAGGGAAAACTCCTGGAGCTGGAGCGG
GCGCTGGACAACGTCACCCGGCTGGAGGAGCAGAACCGGGCGYTGGGGACAGAGGTGACGCGGCAGCGGGAGCAGCT
GGAGGAGGAGCAGAGCCTCAGGGCCCAGCTCCAGCGGCAGAACCGCCTCCTGCAGGAGCAGCTGTGGGACATGAGGA
GCCAGCGTTCCCCTGGGGACAGGCCCGCGGTGTCCCCTGCTGTCCTCACGCCACTCCTCCTCCTCCTCctcGGG
ATGCTCCTCCTGTGA

amino acid sequence

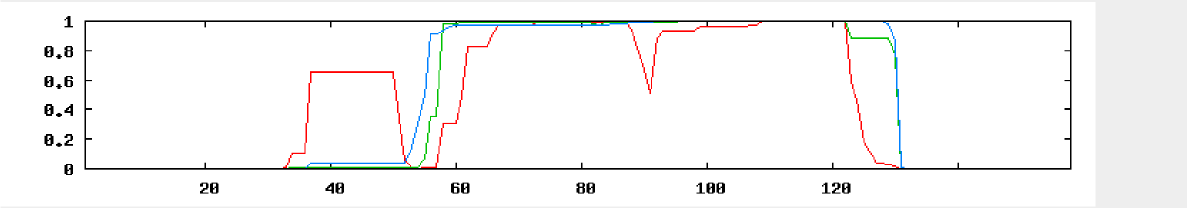
MGPWKAVAAVTLVVAAVLVAVTVPTLLCHRAGDGNSSERLEKALDVTNRSLAVSLGRWQRCREELGALQGKLLELER
ALDNVTRLEEQNRAXGTEVTRQREQLEEEQSLRAQLQRQNRLLQEQLWDMRSQRSPGDRPAVSPAVLTPLLLLLLLG
MLLL

potential GPI site at position 132 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Lepidothrix coronata (Blue-crowned manakin)

nucleotide sequence

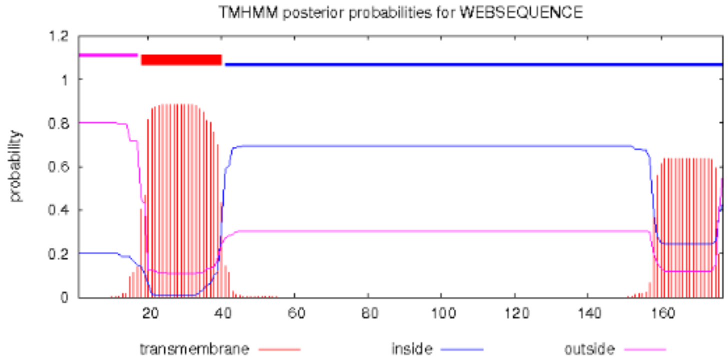
```
ATGGAGATCTCCCGGCCGCACCCCCCGCCCCCGGCCCGGCACCCCTGGAAGGCGGTGGCGGCCGCGACCCTGGGGGT
GGCCGCGGTGGTGGTGGCGGTGACCGTGCCCACCGTGCTGTGCCGCTCGGCCGGGGGCTGCGCCGGGGCCGGGGGTG
CCTCGGAGGGGCTGGCACGGCTGGAGGAGGAGCTGGATGTCACCAACCGGTCCCTCGCCGAAGCCCGCGAGCAGCGG
GACGGCTGCAGGAAGGAGCTGGGAGTGCTGGAGGGGAAAGCCTCGGAGCTGAAGCAGGCGCTGGCTGAAGTGATCCG
GCTGGAGGAGGAGAACAAGGAGCTCAGGACAGAGGTTTCCCGGCAGCAGGAGCAGCTGGAGCAGGAGCAGAGCCGCA
GGGAGGAGCTCCAGCAGCAGAACCAGGCCCTGCAGGAGCAGCTCCAGGACACGAGGAGCCAGCAGACCTCTGGGAAC
GGGGACAAGCCCTCTGGCCTCCTGCCTTTCACCTTTTTCCTCCTCCTCCTTGGGTTGCTCCTCCGACAGTGA
```

amino acid sequence

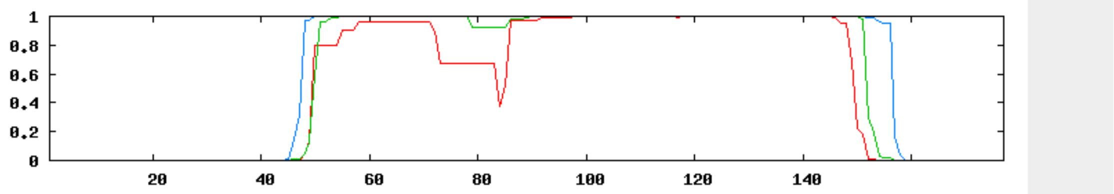
```
MEISRPHPPPPARHPWKAVAAATLGVAAVVVAVTVPTVLCRSAGGCAGAGGASEGLARLEEELDVTNRSLAEAREQR
DGCRKELGVLEGKASELKQALAEVIRLEEENKELRTEVSRQQEQLEQEQSRREELQQQNQALQEQLQDTRSQQTSGN
GDKPSGLLPFTFFLLLLGLLLRQ
```

potential GPI site at position 154 (Red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Manacus vitellinus (Golden-collared manakin)

nucleotide sequence

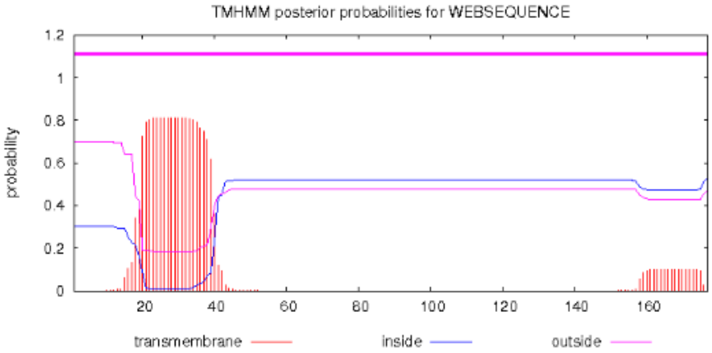
ATGGAGATCTCCCGGCCGCACCCCCCGCCCCCGGCCCGGCGCCCCTGGAAGGCGGTGGCGGCCGCGACCCTGGGGGT
GGCCGTGGTGGTGGCGGCGGTGACCGTGCCCACCGTGCTGTGCCGCTCGGCCGGGGGCTGCGCCGGGGCCGGGGGTG
CCTCGGAGGGGCTGGCACGGCTGGAGGAGGAGCTGGATGTCACCAACCGGTCCCTCGCCGAGGCCCGCGAGCAGCGG
GACGGCTGCAGGAAGGAGCTGGGAGTGCTGGAGGGGGAAGCCTCGGAGCTGAAGCAGGCGCTGGCTGAAATGACCTG
GCTGGAGGAGGAGAACAAGGAGCTCAGGACAGAGGTTTCCCGGCAGCAGGAGCAGCTGGAGCAGGAGCAGAGCCGCA
GGGAGGAGCTCCAGCAGCAGAACCAGGCCCTGCAGGAGCAGCTCCAGGACGCGAGGAGCCAGCAGACCTCTGGGAAC
GGGGACAAGCCCTCTGGCCTCCTGCCTTCCCCCTTTTTCCTCCTCCTCCTTGGGTTGCTCCTCCGACAGTGA

amino acid sequence

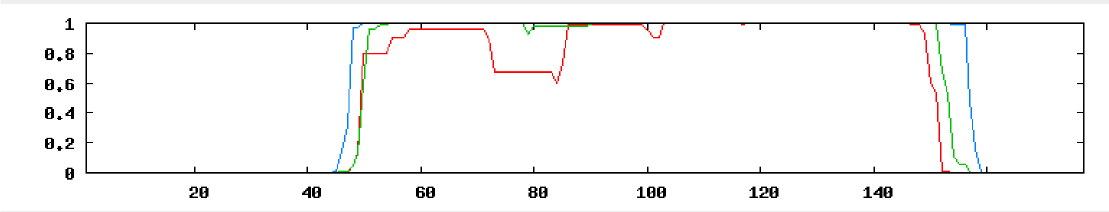
MEISRPHPPPPARRPWKAVAAATLGVAVVVAAVTVPTVLCRSAGGCAGAGGASEGLARLEEELDVTNRSLAEAREQR
DGCRKELGVLEGEASELKQALAEMTWLEEENKELRTEVSRQQEQLEQEQSRREELQQQNQALQEQLQDARSQQTSGN
GDKPSGLLPSPFFLLLLGLLLRQ

potential GPI site at position 154 (Red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Pipra filicauda (Wire-tailed manakin)

nucleotide sequence

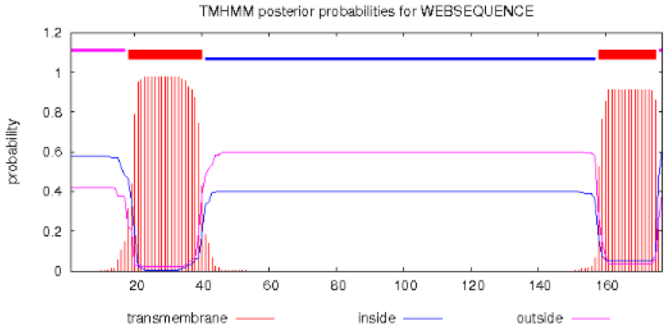
ATGGAGATCTCCCGGCCGCACCCCCCGCCCCCGGCCCGGCGCCCCTGGAAGGCGGTGGCGGCCGCGGCCCTGGGGGT
GGCCGTGGTGGTGGTGGCGGTGACGGTGCCCACCGTGCTGTGCCGCTCGGCCGGGGGCTGCGCGGGGGCCGGGGGTG
CCTCGGAGGGGCTGGCACGGCTGGAGGAGGAGYTGGATGTCACCAATCGGTCCCTCGTGGAGGCCCGCGAGCAGCGG
GACGGCTGCAGGGAGGAGCTGGGAGTGCTGGAGGGGAAAGCCTCGGAGCTGAAGCAGGCGCTGGCTGAAGTGACCCG
GCTGGAGGAGGAGAACAAGGAGCTCAGGACGGAGGTTTCCCGGCAGCAGGAGCAGCTGGAGCAGGAGCAGAGSCGCA
GGGAGRARCTCCAGCAGCAGAACCAGGCCCTGCAGGAGCAGCTCCAGGACGCGAGGAGCCAGCAGACCTCTGGGAAC
GGGGACAAGCCCTCTGGCCTCCTGCCTTTCCTCTTTTTCCTCCTCCTCCTTGGSTTRCTCCTCCGAAAGTGA

amino acid sequence

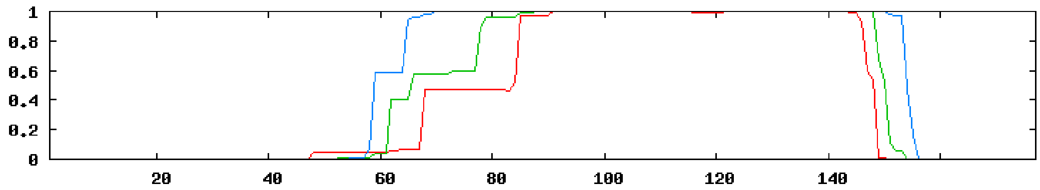
MEISRPHPPPPARRPWKAVAAAALGVAVVVVAVTVPTVLCRSAGGCAGAGGASEGLARLEEEXDVTNRSLVEAREQR
DGCREELGVLEGKASELKQALAEVTRLEEENKELRTEVSRQQEQLEQEQXRREXLQQQNQALQEQLQDARSQQTSGN
GDKPSGLLPFLFFLLLLGLLLRK

potential GPI site at position 154 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Erythrura gouldiae (Gouldian finch)

nucleotide sequence

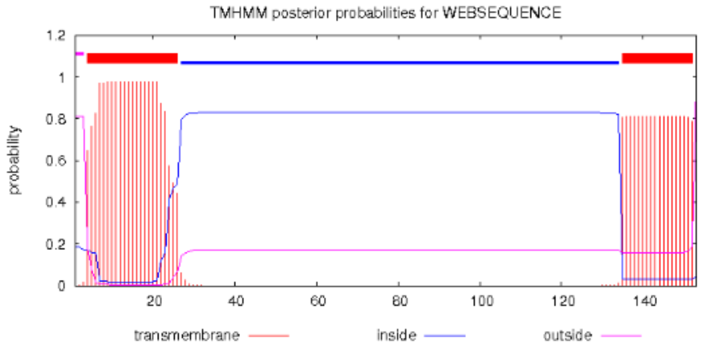
ATGAAGCTCTGGCGGGCGGTGGCCGCCGTGGCCCTGGCGGTGGCCGCCGTGGCCCTGGCGGTGACTGTCCCCACGCT
GCAGTGCCGGCGCGGGGGCGGCTCCGGGGAGGGGCTGCAGGAGGCTCTGGATGCCACCAACAGGTCCCTGGCCGAGT
CCCGCGGGAGGTGGCAGCGCTGCAGGGAGGAGCTGGCAGCGCTGCAGGGAAAGGTCCTGGAGCTGGAGCAGGCGCTG
GCCGATGTCACCCGGCTGGAGGAGCAGAACCGGGAGCTGGGGACAGAGGTGACGCGGCAGCGGGAGCAGCTGGAGGA
GGAGCAGAGCCTCAGGGCCAAGCTCCAGCGGCAGAACCGGTTCCTGCAGGAGGAGCTGTGGGACATGAGGAGACAGC
GCTCGGCAGGGGACAGGCTGGCCCTGTCCCGCACTGTCCCTGCGCTCCTCCTCCTCCTCGGGATGCTGCTCCTGTGA

amino acid sequence

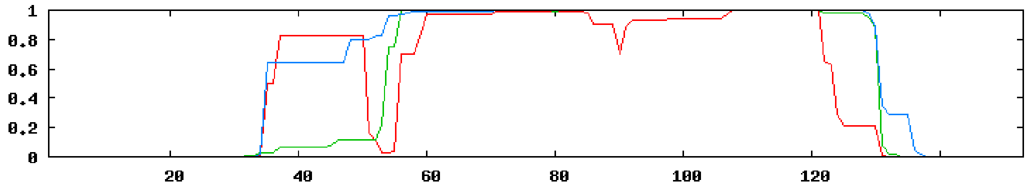
MKLWRAVAAVALAVAAVALAVTVPTLQCRRGGGSGEGLQEALDATNRSLAESRGRWQRCREELAALQGKVLELEQAL
ADVTRLEEQNRELGTEVTRQREQLEEEQSLRAKLQRQNRFLQEELWDMRRQRSAGDRLALSRTVPALLLLLGMLLL

potential GPI site at position 130 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Psittaciformes

Melopsittacus undulatus (Budgerigar)

nucleotide sequence

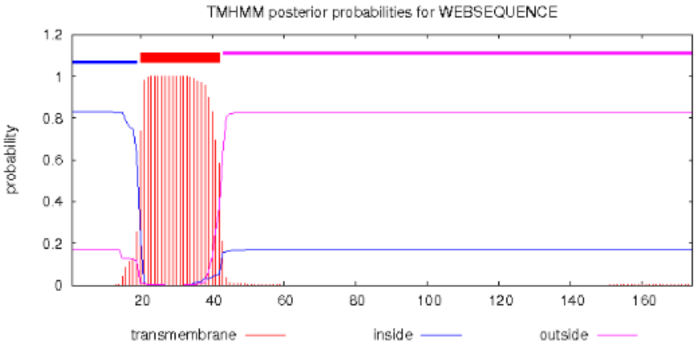
ATGAAGGGGGGGATGAAGGACCCACTGCCACCGAGGAAGCGACCTTGGATGATGTACGTGGCCTTGGCCTTCGGGAT
GGCcATCGTGGTGCTGGTGGCCGCGCTCCCCACTGCACTCTGGCCACTGGCCACGGGCTCTGCCATGGTCGGGAACT
GCTCTGCCAGGATAGGGGGCCTGGAGAAAGCTYTGGCCACCACCAACCAGTCTCTTGCCGAAGCCTATGGGCAGAGA
GATGACTGCAAGAGGCAGCTGAGTCTGCTGCAGGGGAAAGCTTTGGAGCTGGAGGAGGCACTTCGYGATGTGAACCG
GCTGCAAGGGGAGAACAAGGCACTGCAGGCAGCGGTGGCAGAGCAGCAGCAGCAGCTCGAGGACCTGCAGAGCAGCA
GGGACCAGCTCCAGCAGCAGAACCAGYTCCTGCAGCAGCAGCTCCAGGCCATGAGGAGCCTGTACTCAGATGGGACC
AGGCCTTCGGATGCATCCCTTGGCCTCCTGGTTCTCCTCCTCACCAAGATGCTCCTCCTGTGA

amino acid sequence

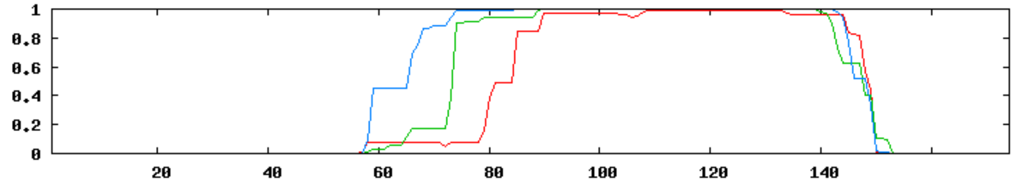
MKGGMKDPLPPRKRPWMMYVALAFGMAIVVLVAALPTALWPLATGSAMVGNCSARIGGLEKAXATTNQSLAEAYGQR
DDCKRQLSLLQGKALELEEALRDVNRLQGENKALQAAVAEQQQQLEDLQSSRDQLQQQNQXLQQQLQAMRSLYSDGT
RPSDASLGLLVLLLTKMLLL

potential GPI site at position 152 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Strigiformes

Asio otus (Long-eared owl)

nucleotide sequence

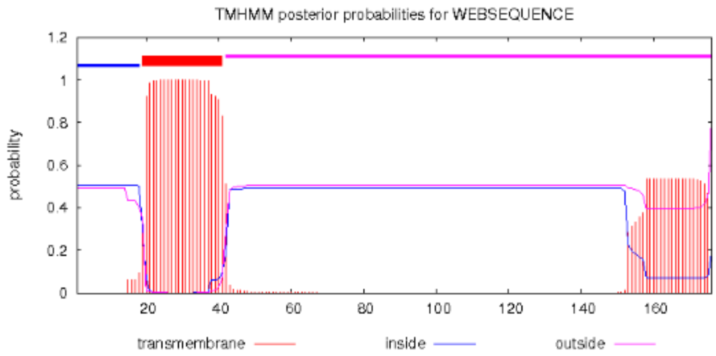
ATGGAGGGCTGCAAGCCACGTCGGCCTCCCCTGGGCAAGGAAGCTTGGAAGATGTACGTGGCCGTGGCCGTGGTCAT
CGGGGTGGTCATGGTGGTGCTGGTAGCAGCCCTCCCCGCCGTGCTCTGCCAGGGGGCTGTGGGCTCTGCGATGGCGG
GGAATGGCTCGGCGGAGCTGGCACAGCTGGAGGAGGTGCTGGCCATCACCAACCAGTCCCTCGCCGAAGCCCGCGGG
CAGTGGGaaGGCTGCAGGAAGCAGCTGGGAGCGCTGGAGGGGAAAGTCTCAGAGATGGAGCTGGTGCTTGCCAGGGT
GACGCAGCTGCAAGAGCAGAACAGGATGCTCCAGGCAGAGGTGGCCCAGCAGCAGCAGGAGCTGGAGGACCTGCAGA
GCAGCAGGGACAAGCTCCAGCAGGASAACCAGATCCTGGAGAAGCAGCTCCAGGACATGAGGAGCCAGTACTCAGGT
GGGAACAGGTTCCCGGCCACGTCCTTCAGCCTCCTGGCTCTCCTCCTCCCCGGGGTGCTCCTCCTGTGA

amino acid sequence

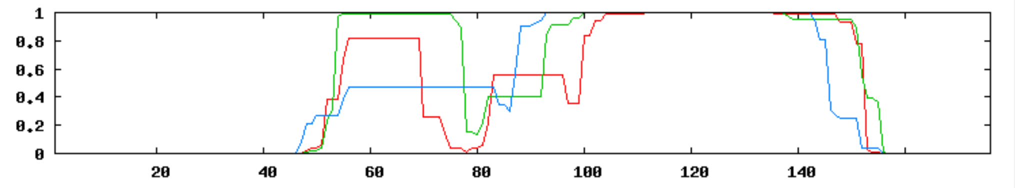
MEGCKPRRPPLGKEAWKMYVAVAVVIGVVMVVLVAALPAVLCQGAVGSAMAGNGSAELAQLEEVLAITNQSLAEARG
QWEGCRKQLGALEGKVSEMELVLARVTQLQEQNRMLQAEVAQQQQELEDLQSSRDKLQQXNQILEKQLQDMRSQYSG
GNRFPATSFSLLALLLPGVLLL

potential GPI site at position 153 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Stix occidentalis caurina (Spotted owl)

nucleotide sequence

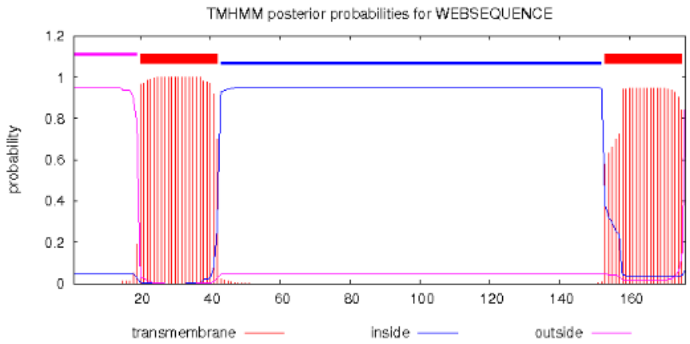
ATGGAGGGCTGCAAGCCACATCAGCCACCCCTGGGCAAGCGACCTTGGAAGACGTACGTGGCCATGGCCGTGGCCTT
CGGGGTGGTCATGGTGGTGCTGGCAGCAGCCCTCCCCGCCGTGCTCTGCCGGGGGGCTGTGGGCTCTGCGATGGCGG
GGAATGGCTCGGCGGAGCTGGCACAGCTGGAGGAGGTGCTGGCCATCACCAACCAGTCCCTCGCCGAAGCCCGCGGG
CAGTGGGAAGGCTGCAGGAAGCAGCTGGGAGCGCTGGAGGAGAAAGTCTCGGAGCTGGAGCCGGCGCTCGCCAGGGT
GACGCAGCTGCAAGAGGAGAACATGGTGCTCCGGGCAGAGGTGGCCCAGCAGCAGCAGGAGCTGGAGGACCTGCAGA
GCAGCAGGGACAAGCTCCAGCAGGAGAACCAGATCCTGGAGAAGCAGCTCCAGGACATGAGGAGCCAGCACTCAGGT
GGGAACAGGCTCCCGGCCATGTCCTTCAGCCTCCTGGCTCTCCTCCTCGCTGGGGTGCTCCTCCTGTGA

amino acid sequence

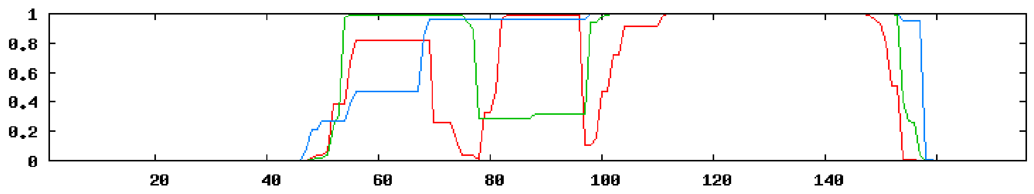
MEGCKPHQPPLGKRPWKTYVAMAVAFGVVMVVLAAALPAVLCRGAVGSAMAGNGSAELAQLEEVLAITNQSLAEARG
QWEGCRKQLGALEEKVSELEPALARVTQLQEENMVLRAEVAQQQQELEDLQSSRDKLQQENQILEKQLQDMRSQHSG
GNRLPAMSFSLLALLLAGVLLL

potential GPI site at position 153 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Bubo bubo (Eurasian eagle-owl)

nucleotide sequence

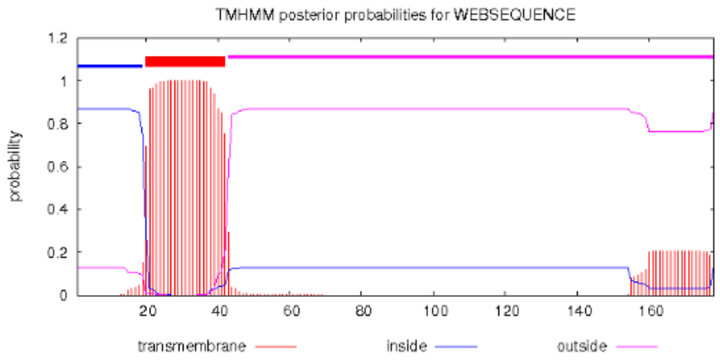
ATGGAGGGCTGCAAGCCACGTCGGCCGCCCCTGGGCAAGCGAGCTTGGAAGATGTACGTGGCCATGGCCGTGGCCGT
GGCCTTCGGGGTGGTCATGGTGGTGCTGGCAGCAGCCCTCCCCGCCGYGCTCAGATGGGGGGCTGTGGGCTCTGCGA
TGGCGGGGAATGGCTCGGCAGAGCTGGCACAGCTGGAGGAGGTGCTGGCCATCACCAACCAGTCCCTCGCCGAAGCC
CGCGGGCAGTGGGAAGGCTGCAGGAAGCAGCTGGGAGCTCTGGAGGAGAAAGTCTCGGCGCTGGAGCCGGCGCTCGC
CAGGGTGACGCAGCTGCAAGAGGAGAACAGGGTGCTCCGGGCAGAGGTGGCCCAGCAGCAGCAGGAGCTGGAGGACC
TGCAGAGCAGCAGGGACAAGCTCCAGCAGGAGAACCAGATCCTGGAGAAGCAGCTCCAGGACATGAGGAGCCAGCAC
TCAGGTGGGAACAGGCTCCCGGCCACGTCCTTCAGCCTCCTGGCTCTCCTCCTCCCCGGGGTGCTCCTCCTGTGA

amino acid sequence

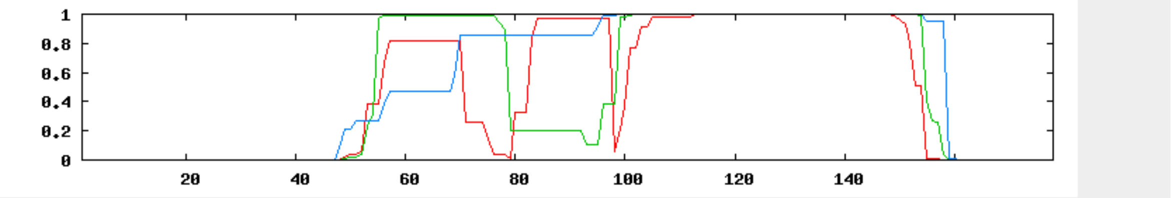
MEGCKPRRPPLGKRAWKMYVAMAVAVAFGVVMVVLAAALPAXLRWGAVGSAMAGNGSAELAQLEEVLAITNQSLAEA
RGQWEGCRKQLGALEEKVSALEPALARVTQLQEENRVLRAEVAQQQQELEDLQSSRDKLQQENQILEKQLQDMRSQH
SGGNRLPATSFSLLALLLPGVLLL

potential GPI site at position 155 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Tyto longimembris (Eastern grass owl)

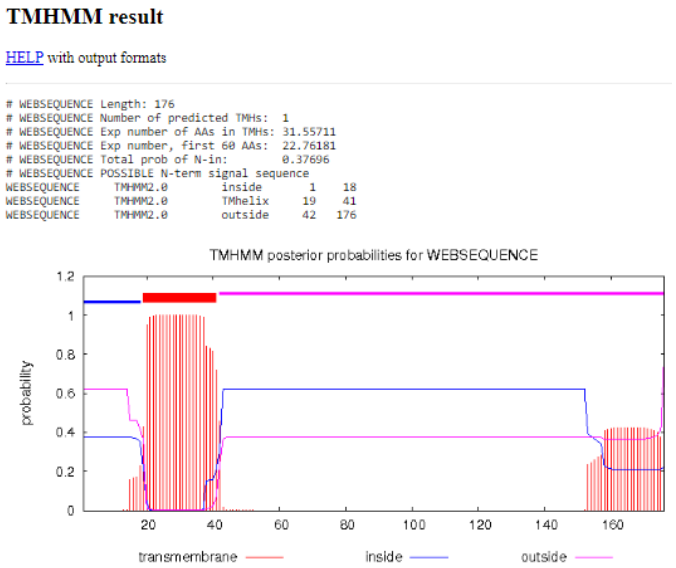
nucleotide sequence

ATGGAAGTCTGCAGCCCGCGCCAGCTGCCTACGGGCAAAAAAATTTGGAAGGTGTACGTAGCCGCGGCCTTGGCCTT
TGGGGTGGCCACAGTGGTGCTGGCAGTAGCCCTCCCCTCCATCCTCTGCCAGCAGGCCATGGGCTCCATGATGGCTG
GGAACGGCTCGGCAAGGCTGGCGTGGCTGGAGAAGGAGCTGGATGTCACCAACCTGTCCCTGGCCGAAGCCCGGGGG
CAGTGGGAAGGTTGCAGGAAGCAGTTGAGAGTGCTGGAGGGGAAAGTCTTGGAGCTGGAGCCGGCACTCGTCAGGGT
AACCCAGCTGCAAGAGgAGAACGGGGTGCTCCGGGCACAGGTGGCCCAGCAGGAGAAGCAGCTGGAGGACCTGCAGA
GCGGCAGGGACAAGCTCCAGCTGAAGAACCAGGCCCTGGAGAAGCAGCTCCAGGATATGAGGAGCCAGCATTCGAGT
GGGAACAGGACCCCGGCTGTGTCACTCAGCCTCCTGGCTCTCCTCCTCCCCGGGATGCTCCTCTTGTGA

amino acid sequence

MEVCSPRQLPTGKKIWKVYVAAALAFGVATVVLAVALPSILCQQAMGSMMAGNGSARLAWLEKELDVTNLSLAEARG
QWEGCRKQLRVLEGKVLELEPALVRVTQLQEENGVLRAQVAQQEKQLEDLQSGRDKLQLKNQALEKQLQDMRSQHSS
GNRTPAVSLSLLALLLPGMLLL

potential GPI site at position 153 (red)



TMHMM result

HELP with output formats

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# WEBSEQUENCE Length: 176
# WEBSEQUENCE Number of predicted TMHs:  1
# WEBSEQUENCE Exp number of AAs in TMHs: 31.55711
# WEBSEQUENCE Exp number, first 60 AAs:  22.76181
# WEBSEQUENCE Total prob of N-in:        0.37696
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE	TMHMM2.0	inside	     1    18
WEBSEQUENCE	TMHMM2.0	TMhelix	    19    41
WEBSEQUENCE	TMHMM2.0	outside	    42   176
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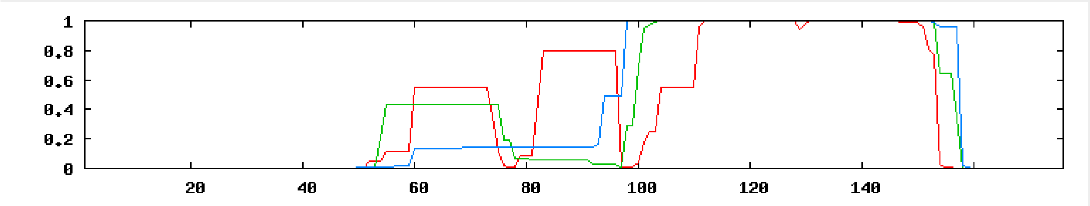


Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Athene noctua (Little owl)

nucleotide sequence

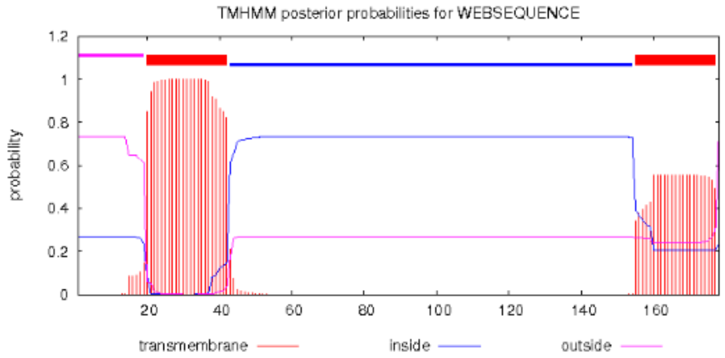
```
ATGGAGGGCTGCAAGCCACACCAGCCACCCCTGGGCAAGCCAGCTTGGAAGACATTAGTGGCCGTGGCCGTGGCCTT
GGCCGTCGGAGTGGTCATGGTGGTGCTGGCAGGAGCCCTCCCCGCCGTGCTCTGCCGGGGGGCTGTGGGCTCCGGGA
TGGCGGGGAAAGGCTCGGCAGAGCTGGCCCAGCTGGAGGACGTGCTGGCCATCACCAACCAGTCCCTCGCCGAAGCC
CGCGGGCAATGGGAAGGCTGCAGGAAGCAGCTGGGAGCGCTGGAGGGGAAAGTCTCGGAGCTGGAGCCGGCGCTCGC
CAGGGTGACGCAGCTGCAAGAGGAGAACAGGGTGCTCCAGGCAGAGGTGGCCCAGCAGCAAAGGGAGCTGGAGGACC
TGCAGAGCAGCAGGGAcAaGCTCCAgCAGGASAACCAGATCCTGGAGAAGCAGCTCCAGGACATGAGGAGCCACCAC
TCAGGTGGGAACAGGCTCCCGGCCACATCCTTCAGCCTCCTGGCTCTCCTCCTCCCCGGGGTGCTCCTCCTGTGA
```

amino acid sequence

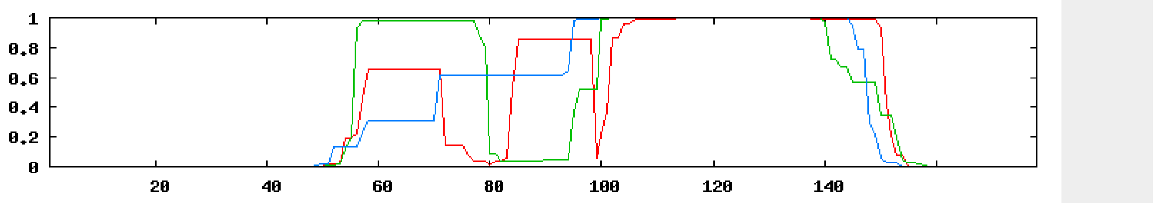
```
MEGCKPHQPPLGKPAWKTLVAVAVALAVGVVMVVLAGALPAVLCRGAVGSGMAGKGSAELAQLEDVLAITNQSLAEA
RGQWEGCRKQLGALEGKVSELEPALARVTQLQEENRVLQAEVAQQQRELEDLQSSRDKLQQXNQILEKQLQDMRSHH
SGGNRLPATSFSLLALLLPGVLLL
```

potential GPI site at position 155 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Otus bakkamoena (Indian scops owl)

nucleotide sequence

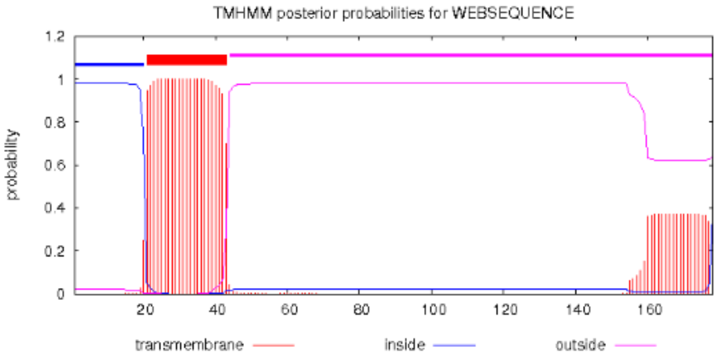
```
ATGGAGGKCTGCAAGCCACGTCGGCCGCTYCTGRGCAAGCGAGCTTGGAAGATGTACATGGCCATGGCCGTGGCCGT
GGCCTTCGGGGTGGTCACGGTGGTGCTGGCCGCAGCCCTCCCCGCYGTGCTCTGCCAGGGGCCTGTGGGCTCTGCGA
TGGCGGGGAATGGCTCGGCGGAGCTGGCACAGCTGGAGGAGGTGCTGGCCGTCACCAACCAGTCCCTCGCCGAAGCC
CGCGGGCAGTGGGAAGGCTGCAGGAAGCAGCTGGGMGYGCTGGAGGAGAAAGTCTCGGAGCTGGAGCCGGCGCTCGC
CAGGGTGACGCAGCTGCAAGAGGAGAACAGGGTGCTCCGGGCAGAGGTGGCCCAGCAGCAGCAGGAGCTGGAGGACC
TGCAGAGCAGCAGGGACAAGCTCCAGCAGGAGAACCAGAWCCTGGAGAAGCAGCTCCAGGACATGAGGAGCCAGCAC
TCAGGTGGGAACAGGCTCCCGGCCACGTCCTTCAGCCTCCTGGCTCTCCTCCTCCTCAGGGTGCTCCTCCTGTGA
```

amino acid sequence

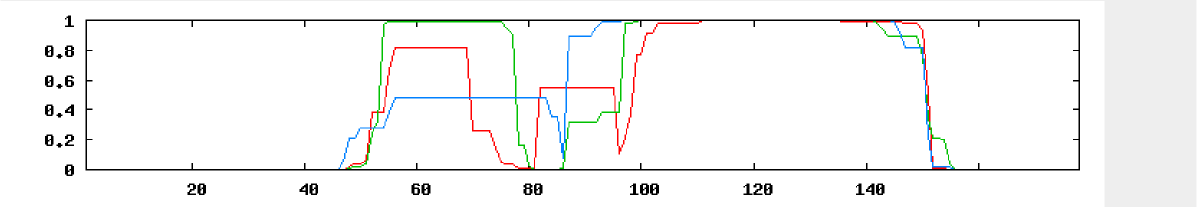
```
MEXCKPRRPLLXKRAWKMYMAMAVAVAFGVVTVVLAAALPAVLCQGPVGSAMAGNGSAELAQLEEVLAVTNQSLAEA
RGQWEGCRKQLGXLEEKVSELEPALARVTQLQEENRVLRAEVAQQQQELEDLQSSRDKLQQENQXLEKQLQDMRSQH
SGGNRLPATSFSLLALLLLRVLLL
```

potential GPI site at position 155 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Upupiformes

Upupa epops (Common Hoopoe)

nucleotide sequence

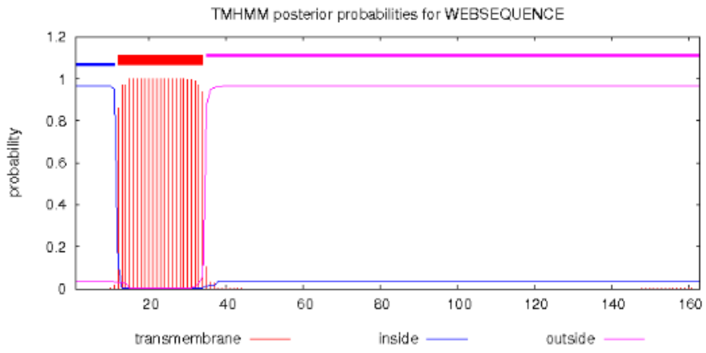
```
ATGCCCCTGGGCAAAGGAGATGGGAAGAAGTCGGTGGCCCTGGCTGTGGCTTTCGGGGTGGYCGTGGTGACGCTGGT
GGTAGCCACCCCCATCGCCCTGTGGCAGCTGGCACCGGGCTCTGCTATGGTGGGGAATTCCTCGTGGGAGCTGGGGA
GGCTGGAGAAGGCTCTGGCCGTCACCAATTTGTCCCTCGTGGAAGCCCGGGAGCACTGGGATGACTGCAAGAGGCAA
CTGGGGGTGCTGGAGGGCAAAGCTGAGGAGCTGGAGGAGGCGCTGGCCAGGATCACCCAGCTGCAAGAGGAGAACAG
GGTGCTCCACGAGGAGSTGTCTGAGCAGCAGAAGCAGCTGAAGGCCCTGCAGAGCAGCAGGGATGAGGTCCAGCAGG
AGAAGCAGCTCCTGGAGAGGCAGCTCCAGGACATCACCAGCCAGTCCTCACGTGGGGACCAGCTCCAGGTGACCCTC
AGCCTCCTGGCTCTCCTGCTGCTCCTGTGA
```

amino acid sequence

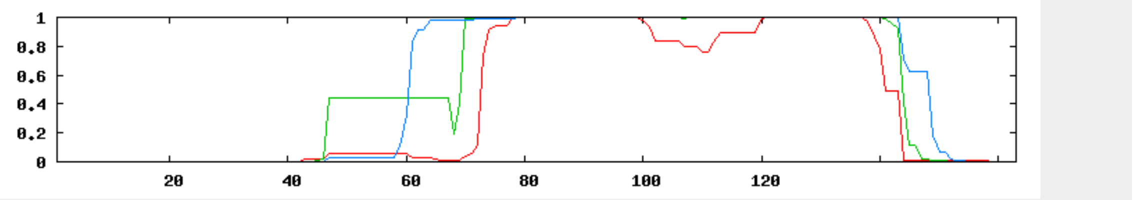
```
MPLGKGDGKKSVALAVAFGVXVVTLVVATPIALWQLAPGSAMVGNSSWELGRLEKALAVTNLSLVEAREHWDDCKRQ
LGVLEGKAEELEEALARITQLQEENRVLHEEXSEQQKQLKALQSSRDEVQQEKQLLERQLQDITSQSSRGDQLQVTL
SLLALLLL
```

potential GPI site at position 145 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Apodiformes

Aerodramus fuciphagus (Edible-nest swiftlet)

nucleotide sequence

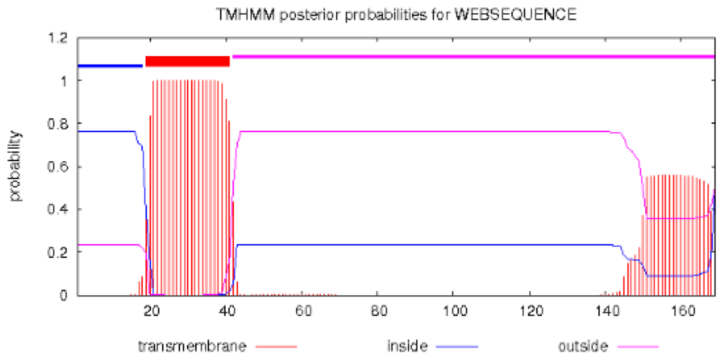
ATGGAGGACTACAAACCCTACAATGCCCTGGACAAGCAACCTAGGAAGACATACGTGGCTGTGGCCCTTGTGCTGGT
CATCGTGGCCACCATGGTGGTGGCAGTGACCATCCCCGCTGTGCTCTGCCAGGATGTGGACTCCATGATGGCAGGGA
ACAGCTCGGTGGGGCTGGAGAAAGCTCTGGCTGTCACCAACCGGTCCCTCGCTGAAGCCCGCTGGCAGCGGGACAGC
TACAGGAAGAAGCTGGAGGTGAAAGAGTCCGAGCTGGAGCAGGCACGAGCCAATGTCACCCAGCTGCAGGAGGAGAA
CCGAGTGCTCCAGGCAACAGTGGCCCAGCAGCAGGAGCAGCTGGAGGAGCTGCAGAACATCAGGGACAAGCTCCAGC
TGCAGAACCAGCTCCTGCAGGAGCAGCTCTGGAACATGGGAAGTCGGCTTTCGGGTGGGGACACACTCCCAGTCATG
TCCCTCAGCCTCCTGGCTCTCCTTCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

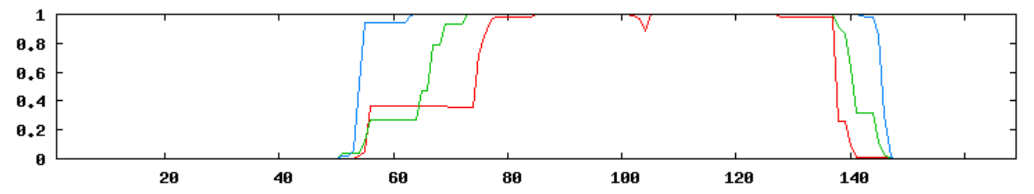
MEDYKPYNALDKQPRKTYVAVALVLVIVATMVVAVTIPAVLCQDVDSMMAGNSSVGLEKALAVTNRSLAEARWQRDS
YRKKLEVKESELEQARANVTQLQEENRVLQATVAQQQEQLEELQNIRDKLQLQNQLLQEQLWNMGSRLSGGDTLPVM
SLSLLALLLPGMLLL

potential GPI site at position 146 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Aerodramus maximus (Black-nest swiftlet)

nucleotide sequence

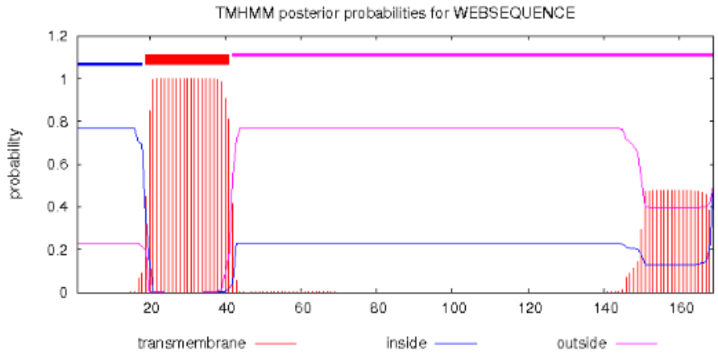
ATGGAGGACTACAAACCCTACAATGCCCTGGACAAGCAACCTAGGAAGACATACGTGGCTGTGGCCCTTGCGCTGGT
CATCGTGGCCACCATGGTGGTGGCAGTGACCATCCCYGCTGTGCTCTGCCAGGATGTGGACTCCATGATGGCAGGGA
ACAGCTCGGTGGGGCTGGAGAAAGCTCTGGCTGTCACCAACCGGTCCCTCGCTGAAGCCCGCTGGCAGCGGGACAGC
TACAGGAAGAAGCTGGAGGTGAAAGAGTCTGAGCTGGAGCAGGCACGAGCCAATGTCACCCAGCTGCAGGAGGAGAA
CCGAGTGCTCCAGGCAACAGTGGCCCAGCAGCAGGAGCAGCTGGAGGAGCTGCAGAACATCAGGGACAAGCTCCAGC
TGCAGAACCAGCTCCTGCAGGAGCAGCTCTGGAACATGGGAAGTCGGCCTTCAGGTGGGGACACACTCCCAGTCATG
TCCCTCAGCCTCCTGGCTCTCCTTCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

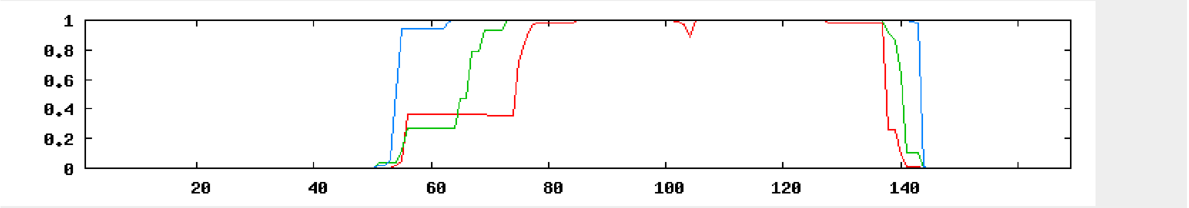
MEDYKPYNALDKQPRKTYVAVALALVIVATMVVAVTIPAVLCQDVDSMMAGNSSVGLEKALAVTNRSLAEARWQRDS
YRKKLEVKESELEQARANVTQLQEENRVLQATVAQQQEQLEELQNIRDKLQLQNQLLQEQLWNMGSRPSGGDTLPVM
SLSLLALLLPGMLLL

potential GPI site at position 146 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Apus afinis (Little swift)

nucleotide sequence

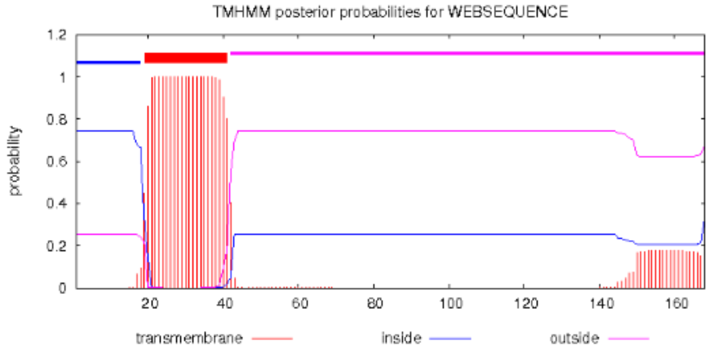
ATGGAGGACTACAAACCCTACAATGCCCTGGACAAGCAACCTAGGAAGACATACGTGGCTGTGGCCCTTGCGCTGGT
CATCGTGGCCACCATGGTGGTGGCAGTGACCATCCCCGCTGTGCTCTGCCAGGATGTGGACTCCATGATGGCAGGGA
ACAGCTCGGTGGGGCTGGAGAAAGCTCTGGCTCTCACCAACCGGTCCCTCGCTGAAGCCCGCTGGCAGCGGGACAGC
TACAGGAAGAAGCTGGAGGTGAAAGAGTCTGAGCTGGAGCAGGCACGAGCCAATGTCACCCAGCTGCAGGAGGAGAA
CCGAGTGCTCCGGGCAACAGTGGTCCAGCAGCAGGAGCAGCTGGAGGACCTGCAGTACACCAGGGACAAGCTCCAGC
TGCAGAACCAGCTCCTGCAGGAGCAGCTCCGGAACATGGGAAGTCGGCCCTCGGGTGGGGACACACTTCCAGTCATG
TCCCTCAGCCTCCTGGCTCTCCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

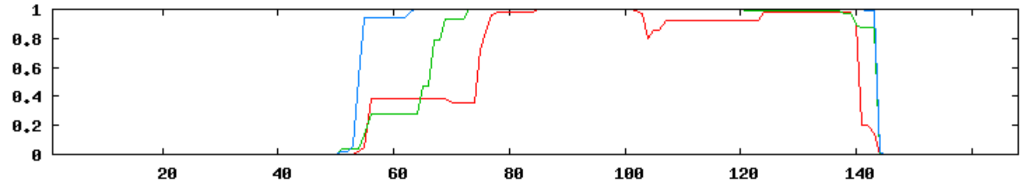
MEDYKPYNALDKQPRKTYVAVALALVIVATMVVAVTIPAVLCQDVDSMMAGNSSVGLEKALALTNRSLAEARWQRDS
YRKKLEVKESELEQARANVTQLQEENRVLRATVVQQQEQLEDLQYTRDKLQLQNQLLQEQLRNMGSRPSGGDTLPVM
SLSLLALLPGMLLL

potential GPI site at position 146 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Chaetura pelagica (Chimney swift)

nucleotide sequence

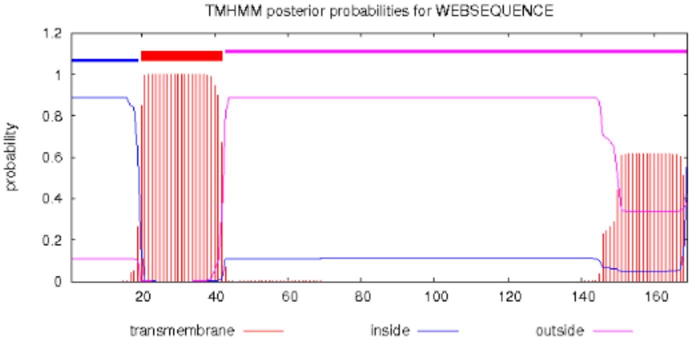
ATGGAGGACTGCAAACCCTACAGTGCCCTGAACAAGCAACCTAGGAAGACATACGTGGCTGTGGCCCTTGCTGTGGT
CATCGTGGCCACCATAGGGGTGGCAGTGACCATCCCCGCTGTGCTCTACCGGGATGTGGACTCCCTGATGGCAGGGA
ACAGCTCGGTGGGGCTGGAGAAAGCTCTGGCTGTCACCAACCGGTCCCTCGCGGAAGCCCGCTGGCAGCGGGACAGC
TACAGGAAGAAGCTGGAGGTGAGAGAGTCTGAGCTGGAGCAGGCACGAGCCAATGTCACCCAGCTGCAGGAGGAGAA
CCGAGTGCTCCAGGCAAAAGTGGCCCAGCAGCAGGAGCAGCTGGAGGACCTGCAGAACACCAGGGACAAGCTCCAGC
GGCTGAACGAGCTCCTGCAGGAGCAGCTCCGGAACACGGGAAGTCGGCCCTTGGGTGGGGACACACTCCCAGTCATG
TCCCTCAGCCTCCTGGCTCTCCTTCTCCCCGGGCTGCTCCTCCTGTGA

amino acid sequence

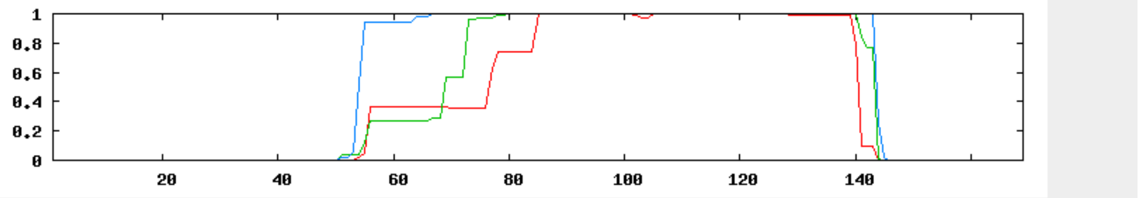
MEDCKPYSALNKQPRKTYVAVALAVVIVATIGVAVTIPAVLYRDVDSLMAGNSSVGLEKALAVTNRSLAEARWQRDS
YRKKLEVRESELEQARANVTQLQEENRVLQAKVAQQQEQLEDLQNTRDKLQRLNELLQEQLRNTGSRPLGGDTLPVM
SLSLLALLLPGLLLL

potential GPI site at position 149 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Charadriiformes

Calidris pugnax (Ruff)

nucleotide sequence

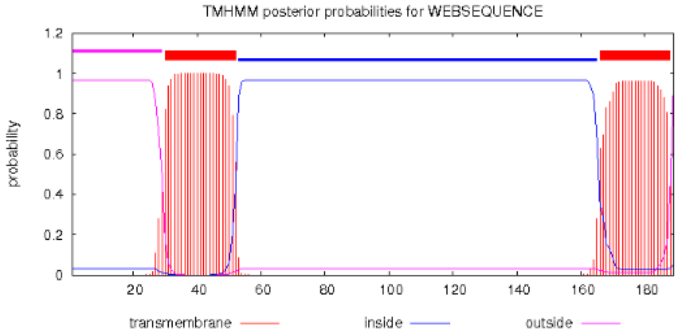
ATGGGGATTCTCCTCAGGCAGGACAGCGGAGAAGGGATGGAGGGCTACCACCCCCAGTGCCCCCACCCCGCCAAGAG
AGCCTGGGTGACGTACGTGGCCGTGGCTCTTGGGGTGGCCGTGGTGGCACTGGTGGCAGCCCTTGTCACCGTCCTCT
ACCAGAGAGCCGAGGGCTCCGCCATGGCGAGGAACAGCTCGGAAGTGCTGGTGCAGCTGGAGAAGGCACTGGATGTC
ACCAACCAGTCCCTCGTCGATGCCCGCGGGCGGTGGGAAGGGTGCAGGAAGCAGCTGGGTGCGCTGGAGGGAAAGGC
CTTGGAACTGGAGTGGGCACTGGCCAATGTCACCGAGCTGCAAGAGGAGAACAGGGCGCTCAAGGCGGAGGTGGCCC
AGCAGCAGGAGCAACTGAGAGACCTGCAGAGCAAATGGGAGAAGCTCCAGCTGCAGAACCAGATCCTGGAGAACCAG
CTCTGGGACATGAGGAGCCAGCACTCGAATGGGAACAGTCTCCAGGCCACGTCCCTCAGCCTCCTGGCTCTCCTCCT
CCTCCTCCTCCCTGGGATGCTCCTCCTGTGA

amino acid sequence

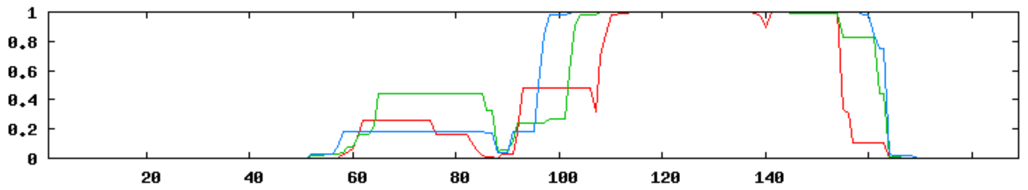
MGILLRQDSGEGMEGYHPQCPHPAKRAWVTYVAVALGVAVVALVAALVTVLYQRAEGSAMARNSSEVLVQLEKALDV
TNQSLVDARGRWEGCRKQLGALEGKALELEWALANVTELQEENRALKAEVAQQQEQLRDLQSKWEKLQLQNQILENQ
LWDMRSQHSNGNSLQATSLSLLALLLLLLPGMLLL

potential GPI site at position 166 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Cuculiformes

Cuculus canorus (Common cuckoo)

nucleotide sequence

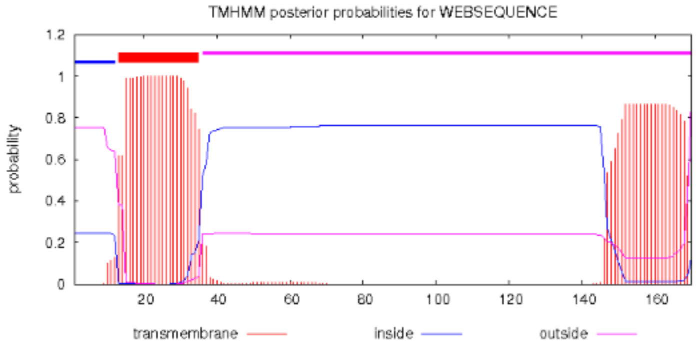
ATGAAGGGTGGCACCTCAGGAAAGCGACCTTGGAGGACATACCTGGCTGTAGCCTTCGGAGCGTTGCTGGTGGTGGT
GCTGGCGGTAATCCTCCCCACCGTGCTCTGTCGGTTGACCGTGGGCTGTGCGGTGGCAGGGAATGGCTCGGCGGAGC
TGGCACAGCTGGAGAAGGCACTGGTCATCACCAACCTGTCCCTCGCCGAAGCCCGCGGGCAGTGGGACAGCTGCAGG
AAGCAGCTGGGTGAGCTGGAGGGGAAAGCCTCGGAGCTGGAGCAGGCACTGGCCAGGATGAGCGAGCTGCAAGAAGA
GAACGGGGCGCTCAAGGCGGAGGTGGCCCAGCAGCAGGAGCAGCTGGCGGACCTGCAGAGCAGCAGGGCCAGGCTCC
AGCTGCAGAACCAGCAGCTGGAGCAGGAGCTCCAGGACATGAGGAGACAGTACTCAGGTGGGAACGGGCTCCCAGCC
GTGTCCCTCAGCCTCTTGGCTCTCCTGCTCTCCGGGATGCTCCTCCTGTGA

amino acid sequence

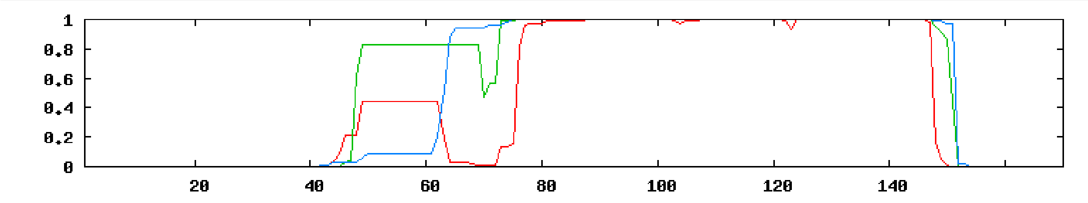
MKGGTSGKRPWRTYLAVAFGALLVVVLAVILPTVLCRLTVGCAVAGNGSAELAQLEKALVITNLSLAEARGQWDSCR
KQLGELEGKASELEQALARMSELQEENGALKAEVAQQQEQLADLQSSRARLQLQNQQLEQELQDMRRQYSGGNGLPA
VSLSLLALLLSGMLLL

potential GPI site at position 147 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Pelecaniformes

Nipponia nippon (Crested ibis)

nucleotide sequence

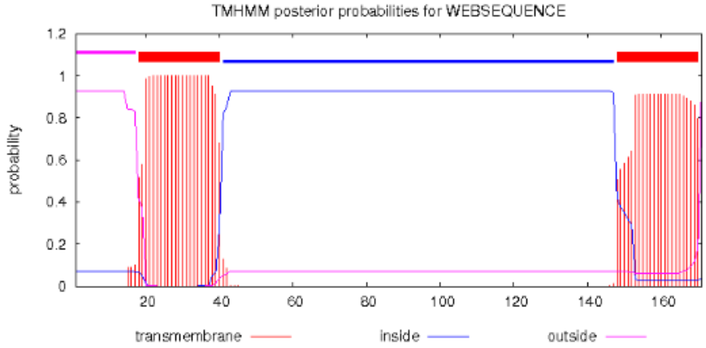
ATGGAGGTCTCCAGCTGGCACAAGCAGCCCACAGGCAAGCGAGCTTGGAAGATGTACGTGATCGTGGCCCTCGGAGT
GGCTGTCATCACGCTGATGGCAGCCCTCCTCGCCGTGCTCTGCCAGCCGGATGTGGGCTCCATGATGGCGAGGAATG
GCTCGGTGGAGCTGGAGAAGGCGCTGGCCGTCACCAACCAGTCCCTGGCCGAAGCCCGCGGGCAGTGGGATAGCTGC
AGAAAGCAGCTGGGTGCGCTGGAGGGGAAAGTCTCGGAGCTGGACCAGGCGCTCGCCAACATAGCCCAGCTGCAAGA
GGAGAACAGGGCGCTGAAGAAGGAGGTGGCCCAGCAGCAGGAGCAGCTGGGGAACCTGAAGAGCAGCCAGGACAACC
TCCAGCTGCAGAACCAGGACCTGCAGAAGCAGCTCCAGGACATGAGGAGGCAGAACTCGGGTGGGAACAGGCTCCCC
GCCGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCCCTGGGATGCTCCTCCTGTGA

amino acid sequence

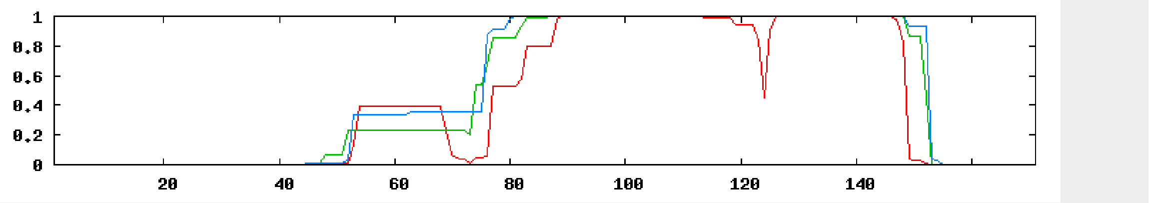
MEVSSWHKQPTGKRAWKMYVIVALGVAVITLMAALLAVLCQPDVGSMMARNGSVELEKALAVTNQSLAEARGQWDSC
RKQLGALEGKVSELDQALANIAQLQEENRALKKEVAQQQEQLGNLKSSQDNLQLQNQDLQKQLQDMRRQNSGGNRLP
AVSLSLLALLLPGMLLL

potential GPI site at position 148 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Falconiformes

Falco cherrug (Saker falcon)

nucleotide sequence

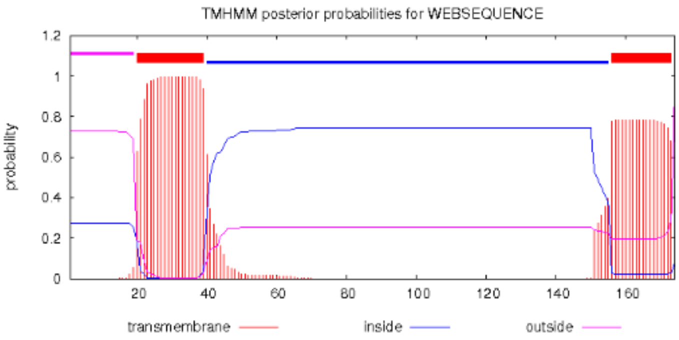
ATGGTGGGCTGCAGTCCGTGCCGGCTGCTCCCAGAAAAGATGTCTTGGAAGAGGTGTAGCGCCCTGGCCTTTGGGGT
AGCTGTCTTGGTGCTGTCGGCGGTCCTCACCTTCTTGTTCTGCCARCAAGTCGTGGGTTCCGTGGTGGCAATGAACT
GCTCGGTGGGGCTGGCACAGCTGGAGGAGGCACTGGCCAACACCAACCAGTCCCTCACCGAAGCCCGCGGGCAGAGG
GATGCCTGCAGGAAGAGGCTGGGTATGCTGGAGGGGAAATCCTTGGAGCTGGAGCAGGCACTCGCCAATATAACCCA
GCTGCAAGAGGAGAACAAGGCGCTCAAGACAGAGGTGGCCCAGCAGCAGAGGCAGCTGCAGGACCTGCAGAGCAGCA
GGGACAAGCTCCAGCTGCAGAACCAGCTCCTGCAGAACCACCTGCAGGACATGAAGAGACAGCACTCAGGTGGGAAC
AGGCTCTCGGCAGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

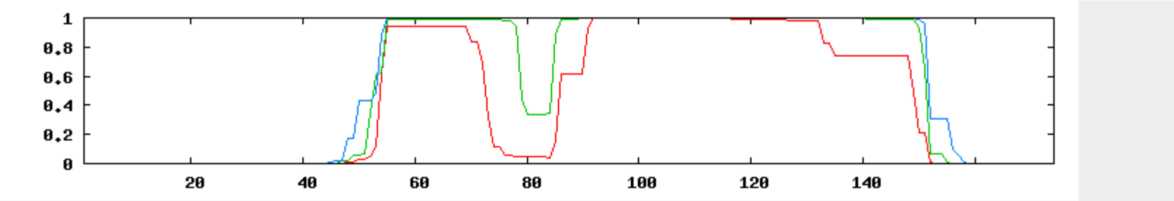
MVGCSPCRLLPEKMSWKRCSALAFGVAVLVLSAVLTFLFCQQVVGSVVAMNCSVGLAQLEEALANTNQSLTEARGQR
DACRKRLGMLEGKSLELEQALANITQLQEENKALKTEVAQQQRQLQDLQSSRDKLQLQNQLLQNHLQDMKRQHSGGN
RLSAVSLSLLALLLPGMLLL

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Falco sparverius (American kestrel)

nucleotide sequence

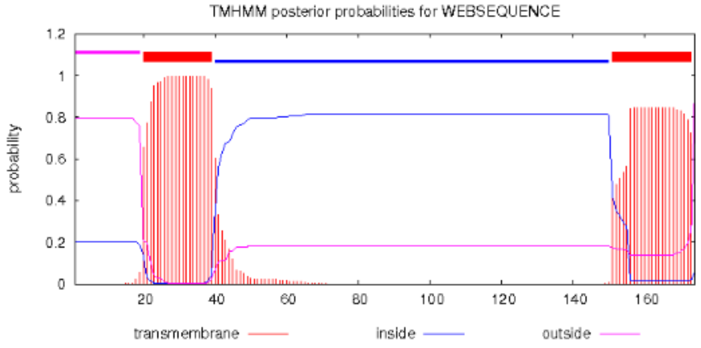
ATGGTGGGCTGCAGTCCGTGCCGGCTGCTCCCAGAAAAGATGTCTTGGAAGAGGTGTAGCGCCCTGGCCTTTGGGGT
AGCTGTCTTGGCGCTGTCRGCGGTCCTCACTTTCTTGTTCTGCCAGCAAGTCGTGGGTTCCGTGGTGGCAATGAACT
GCTCGGTGGGGCTGGCACAGCTGGAGGAGGCACTGGCCAACACCAACCAGTCCCTCACCGAAGCCCGCGGGCAGAGG
GATGCCTGCAGGAAGAGGCTGGGTATGCTGGAGGGGAAATCCTTGGAGCTGGAGCAGGCACTCGCCAATATAACCCA
GCTGCAAGAGGAGAACAAGGCRCTCAAGACAGAGGTGGCCCAGCAGCAGAGGCAGCTGCAGGACCTGCAGAGCAGCA
GGGACAACCTCCAGCTGCAGAACCAGCTCCTGCAGAACCGCCTGCAGGACATGAAGAGACAGCACTCAGGTGGGAAC
AGGCTCTCGGCAGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

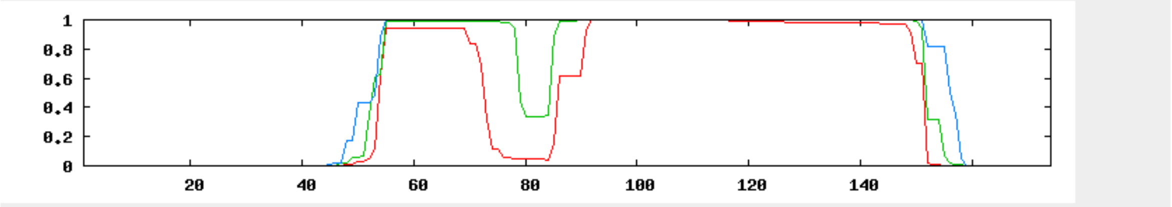
MVGCSPCRLLPEKMSWKRCSALAFGVAVLALSAVLTFLFCQQVVGSVVAMNCSVGLAQLEEALANTNQSLTEARGQR
DACRKRLGMLEGKSLELEQALANITQLQEENKALKTEVAQQQRQLQDLQSSRDNLQLQNQLLQNRLQDMKRQHSGGN
RLSAVSLSLLALLLPGMLLL

possible GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Falco peregrinus (Peregrine falcon)

nucleotide sequence

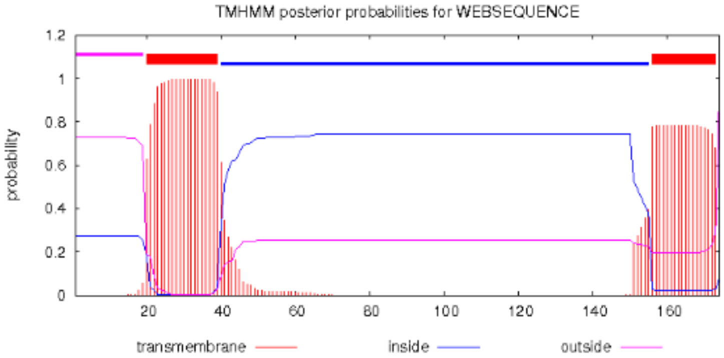
ATGGTGGGCTGCAGTCCGTGCCGGCTGCTCCCAGAAAAGATGTCTTGGAAGAGGTGTAGCGCCCTGGCCTTTGGGGT
AGCTGTCTTGGTGCTGTCGGCGGTCCTCACCTTCTTGTTCTGCCAGCAAGTCGTGGGTTCCGTGGTGGCAATGAACT
GCTCGGTGGGGCTGGCACAGCTGGAGGAGGCACTGGCCAACACCAACCAGTCCCTCACCGAAGCCCGCGGGCAGAGG
GATGCCTGCAGGAAGAGGCTGGGTATGCTGGAGGGGAAATCCTTGGAGCTGGAGCAGGCACTCGCCAATATAACCCA
GCTGCAAGAGGAGAACAAGGCGCTCAAGACAGAGGTGGCCCAGCAGCAGAGGCAGCTGCAGGACCTGCAGAGCAGCA
GGGACAAGCTCCAGCTGCAGAACCAGCTCCTGCAGAACCACCTGCAGGACATGAAGAGACAGCACTCAGGTGGGAAC
AGGCTCTCGGCAGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

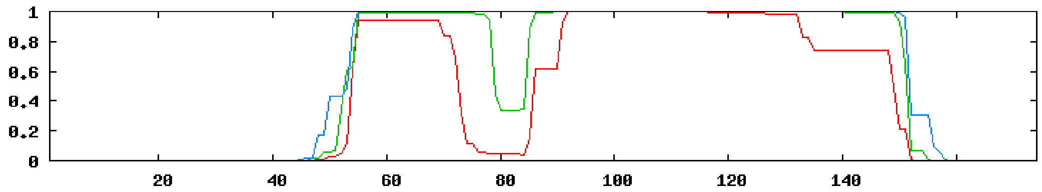
MVGCSPCRLLPEKMSWKRCSALAFGVAVLVLSAVLTFLFCQQVVGSVVAMNCSVGLAQLEEALANTNQSLTEARGQR
DACRKRLGMLEGKSLELEQALANITQLQEENKALKTEVAQQQRQLQDLQSSRDKLQLQNQLLQNHLQDMKRQHSGGN
RLSAVSLSLLALLLPGMLLL

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Falco subbuteo (Eurasian hobby)

nucleotide sequence

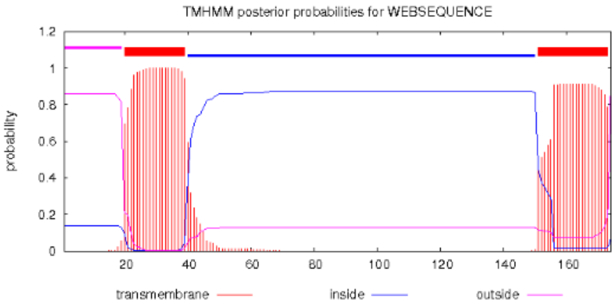
ATGGTGGGCTGCAATCCGTGCCRGCTGCTCCCAGAAAAGATGTCTTGGAAGAGGTGTAGCGCCCTGGCCTTTGGGGT
AGCTGTCTTGGTGCTGTCGGCGGTCCTCACCTTCTTGTTCTGYCAGCAAGTYGTGGGTTCCGTGGTGGCAATGAACT
GCTCGGTGGGGCTGGCACAGCTGGAGGAGGCACTGGCCAACACCAACCAGTCCCTCACCGAAGCCCGCGGGCAGAGG
GATGCCTGCAGGAAGAGGCTGGGTATGCTGGAGGGGAAATCCTTGGAGCTGGAGCAGGCACTCGCCAATATAACCCA
GCTGCAAGAGGAGAACAAGGCGCTCAAGACAGAGGTGGCCCAGCAGCAGAGGCAGCTGCAGGACCTGCAGAGCAGCA
GGGACGAGCTCCAGCTGCAGAACCAGCTCCTGCAGAACCGCCTGCAGGACATGAAAAGACAGCACTCAGGTGGGAAC
AGGCTCTCGGCAGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCTCCGGGATGCTCCTCCTGTGA

amino acid sequence

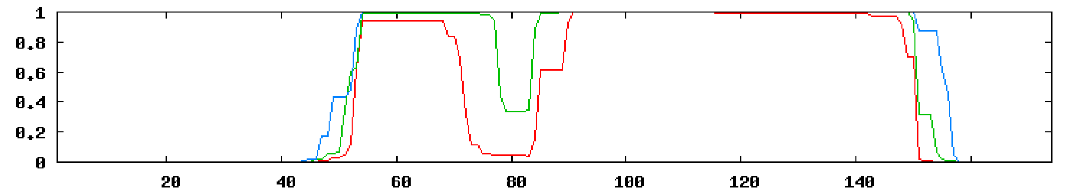
MVGCNPCXLLPEKMSWKRCSALAFGVAVLVLSAVLTFLFCQQVVGSVVAMNCSVGLAQLEEALANTNQSLTEARGQR
DACRKRLGMLEGKSLELEQALANITQLQEENKALKTEVAQQQRQLQDLQSSRDELQLQNQLLQNRLQDMKRQHSGGN
RLSAVSLSLLALLLSGMLLL

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Falco tinnunculus (Common kestrel)

nucleotide sequence

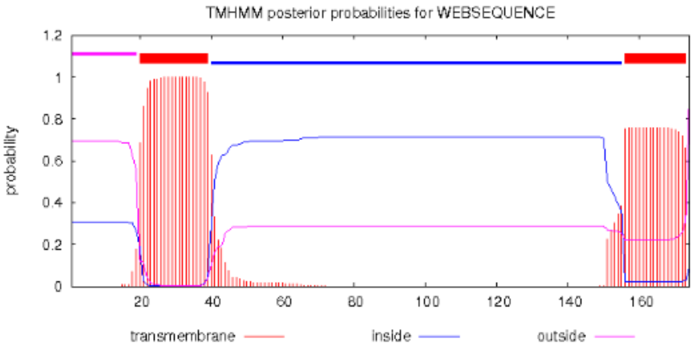
ATGGTGGGCTGCAGTCCGTGCCGGCTGCTCCCAAAAAAGATGTCTTGGAAGAGGTATAGCGCCCTGGCCTTTGGGGT
AGCTGTCTTGGTGCTGTCGGCAGTCCTCACCTTCTTGTTCTGCCAGCAAGTCGTGGGTTCCGTGGTGGCAATGAACT
GCTCGGTGGGGCTGGCACAGCTGGAAGAGGCACTGGCCAGCACCAACCAGTCCCTCACCGAAGCCCGCGGGCAGAGG
GATGCCTGCAGGAAGAGGCTGGGTATGCTGGAGGGGAAATCCTTGGAGCTGGAGCAGGCACTCGCCAATATAACCCA
GCTGCAAGAGGAGAACAAGGCGCTCAAGACAGAGGTGGCCCAGCAGCAGAGGCAGCTGCAGGACCTGCAGAGCAGCA
GGGACAAGCTCCAGCTGCAGAACCAGCTCCTGCAGAACCACCTGCAGGACATGAAGAGACAGCACTCAGGTGGGAAC
AGGCTCTCGGCCGTGTCCCTCAGCCTCCTGGCTCTCCTCCTCCCCGGGATGCTCCTCCTGTGA

amino acid sequence

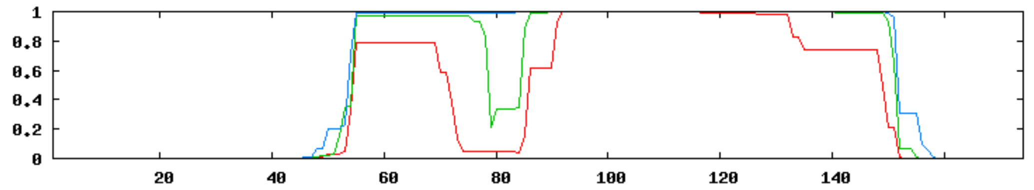
MVGCSPCRLLPKKMSWKRYSALAFGVAVLVLSAVLTFLFCQQVVGSVVAMNCSVGLAQLEEALASTNQSLTEARGQR
DACRKRLGMLEGKSLELEQALANITQLQEENKALKTEVAQQQRQLQDLQSSRDKLQLQNQLLQNHLQDMKRQHSGGN
RLSAVSLSLLALLLPGMLLL

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Aquila chrysaetos canadensis (Golden eagle)

nucleotide sequence

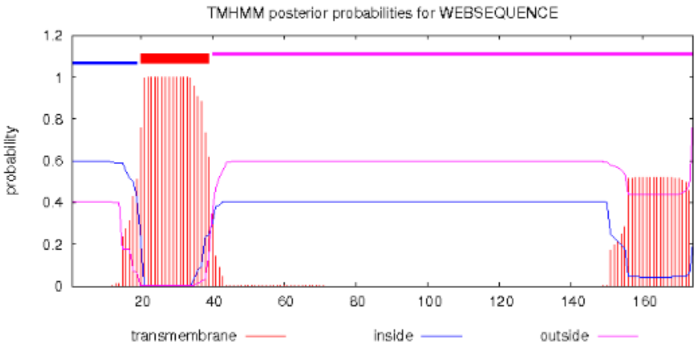
ATGGAGGGCTGCAGCTCACACCGGTTGCCCCGAGCCAGGCAAGCTTGGAAGATATACATGGCCGTGGTCTTCTGCGT
GGTCGTTGTGGTGCCGGCGGTAGTCCTCACCACCATGTTCTGCCAGCCCACCGCAGACTCCGCGATGGCGGGGAATT
GCTCGGTGAGGCTGGAGTGGCTGGRGGAGGCGCTGGCTGTCACCAACCGGTCCCTCACCGAAGCCCACCAGCAGTGG
GAAGTCTGCAGGAATAAGCTGGGTGAGCTGGAGGGGCAAGCCTCGGAGCTGGAGCAGGTGCTCGCCAGGGTAACCCA
GCTGCAAGAGGAGAACGGGAAGCTCAAGGCAGAGGTGGCCCAACAGCAGAATCAGTTGCAGGACCTGGAGAGCATCA
GGAACGAGCTCCAGCTGCAGAACGAGCACCTGCAGAAGGAGCTCCAGGACATGAGGAGCCAGCACTCGGGTGGGAAC
AGGTTCCCGGCCGCGTCCCTCAGCCTCCTGGTTCTCCTCCTCCCTGGGATGCTCCTCCTATGA

amino acid sequence

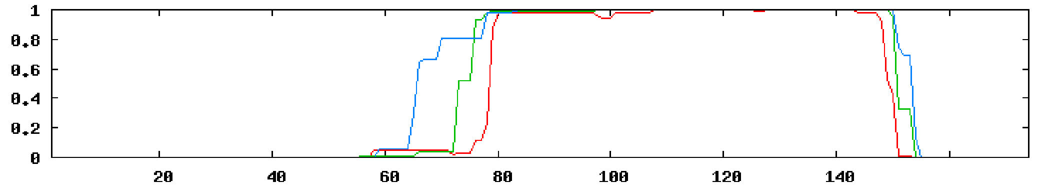
MEGCSSHRLPRARQAWKIYMAVVFCVVVVVPAVVLTTMFCQPTADSAMAGNCSVRLEWLXEALAVTNRSLTEAHQQW
EVCRNKLGELEGQASELEQVLARVTQLQEENGKLKAEVAQQQNQLQDLESIRNELQLQNEHLQKELQDMRSQHSGGN
RFPAASLSLLVLLLPGMLLL

potential GPI site at position 151(red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Haliaeetus leucocephalus (Bald eagle)

nucleotide sequence

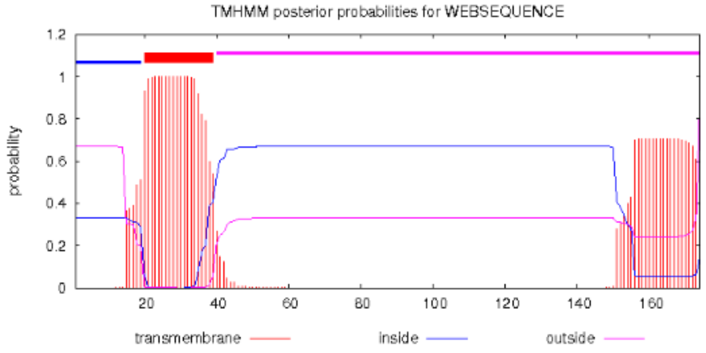
```
ATGGAGGGCTGCAGCCCACACTGGTTGCCCCGAGCCAAGCAAGCTTGGAAGATACACGTGGCCGTGGTCTTCTGTGT
GGTCGTTGTGGCGCTGGCGGTAGTCCTCACCACCATGTTCTGCCAGCCGGCCGCAGTCCCTGCGATGGTGGGGAATT
GCTCAGTGAGGCTGGAGTGGCTGGAGGAGGCGCTGGCTGTCACCAACCGGTCCCTCACGGAAGCCCACCACCAGTGG
GAAGTCTGCAGGAATAAGCTGGGTGAGCTGGAGGGGCAAGCCTCGGAGCTGGAGCAGGCTCTTGCCAGGGTAACCCA
GCTGCAAGAGGAGAATGGGAAGCTCAAGGCAGAGGTGACCCAGCAGCAGAATCAGCTGGAGGACCTGGAAAGCAGCA
GGAATGAGCTCCAGCTGCAGAACGAGCACCTGCAGAAGGAACTCCAGGACTTGAGGAGCCAGCACTCGGGTGGGAAC
AGGCTCCTTGCCACGTCCCTCAGCCTCCTGGTTCTCCTCCTCCCTGGGATGCTCCTCCTGTGA
```

amino acid sequence

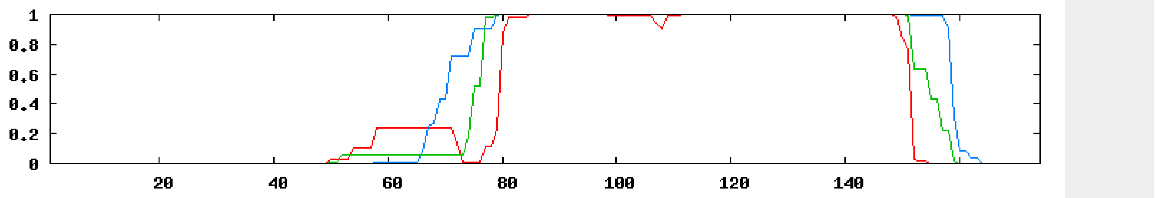
```
MEGCSPHWLPRAKQAWKIHVAVVFCVVVVALAVVLTTMFCQPAAVPAMVGNCSVRLEWLEEALAVTNRSLTEAHHQW
EVCRNKLGELEGQASELEQALARVTQLQEENGKLKAEVTQQQNQLEDLESSRNELQLQNEHLQKELQDLRSQHSGGN
RLLATSLSLLVLLLPGMLLL
```

potential GPI site at popsition 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Pandion haliaetus (Osprey)

nucleotide sequence

```
ATGGAGGGCTGCAGCCCACACCAGTTGCACCGAGGCAGGCAAGCTTGGAAGWTATACGTGGCTGTGGTCTTCTACGT
GGTCGTTGTGGTGCTGGTGGCAGCCCTCACCACCATGTTCTGCCAGCCAGCTACAGGCTCTGCGATGGCAAGGAATT
GCTCAGTGAGGCTGGAGTGGCTGGAGGAGGCGTTGGCCATCACCAACCAGTCCCTCACCGAAGCCCACAGGCAGTGG
GAAGTCTGCAGGAATAATCTGGGTGAGCTGGAGGGGAAAGCCTCGGAGCTGGAGCAGGTGCTTGCCAGGATATCCCA
GCTGCAAGAGGAGAACGGGAAGCTCAAGACAGAGGTGGCCCAGCAGCAGAAGCAGTTAGAGGACCTGGAGAGCAGCA
GGAATGAGCTCCAGCTGCAGAACCAGCACCTGCAGAAGGAGCTCCGGGACATRAGGAGCCAGCACTCGGGTGGGAAT
GGGCTCCCAGCTGCATCCCTCAGCCTCCTGGTTCTCCTCCTCCCCGGGATGCTCCTCCTGTGA
```

amino acid sequence

```
MEGCSPHQLHRGRQAWKXYVAVVFYVVVVVLVAALTTMFCQPATGSAMARNCSVRLEWLEEALAITNQSLTEAHRQW
EVCRNNLGELEGKASELEQVLARISQLQEENGKLKTEVAQQQKQLEDLESSRNELQLQNQHLQKELRDXRSQHSGGN
GLPAASLSLLVLLLPGMLLL
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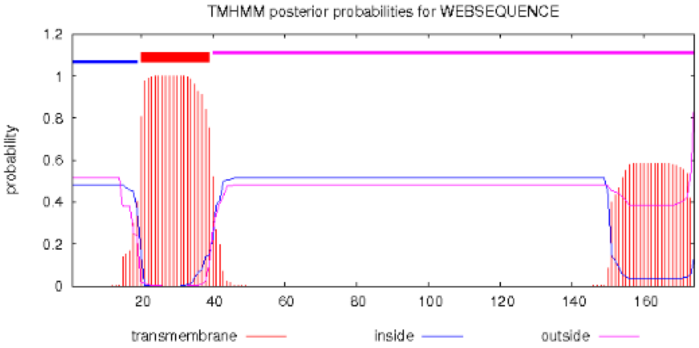
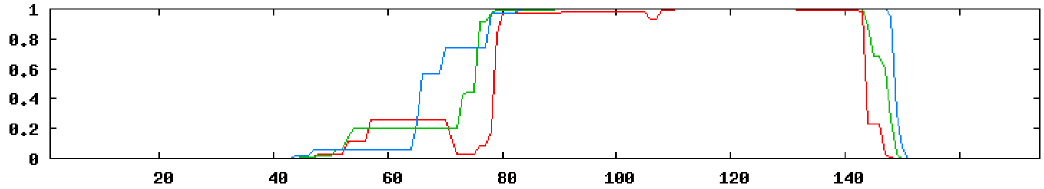
potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Accipiter virgatus (Besra)

nucleotide sequence

ATGGCCGTGGTCTTCTGCGTGGTCGTTGTGGCGCTGACGGTAGCCCTCACCACCATTTTCTGCCAGCCGGCCGCAGT
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GCGCTTGCCAGGATAAACCAGCTGCAAGAGGAGAACGGGAAGCTCAAGGCAGAGGTGGCCCAGCAGCAGAATCAGTT
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GCCAGCACTCAGGTGGGAACCGGCTCCCAGCTGCGTCCCTCAGCCTCCTGGTTCTCCTCCTCCCTGGGATGCTCCTC
CTATGA

amino acid sequence

MAVVFCVVVVALTVALTTIFCQPAAVPAMVRNCSVRLEWLEEALAFTNRSLTEAHQQWEVCRNKLGELEGRASELEQ
ALARINQLQEENGKLKAEVAQQQNQLEDLESSRNELQLQNKHLQNKLQYMRSQHSGGNRLPAASLSLLVLLLPGMLL
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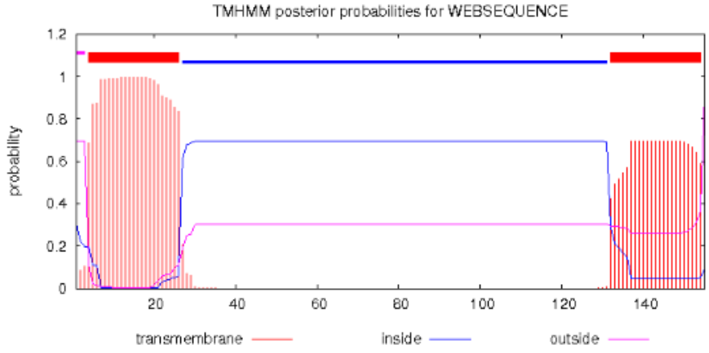
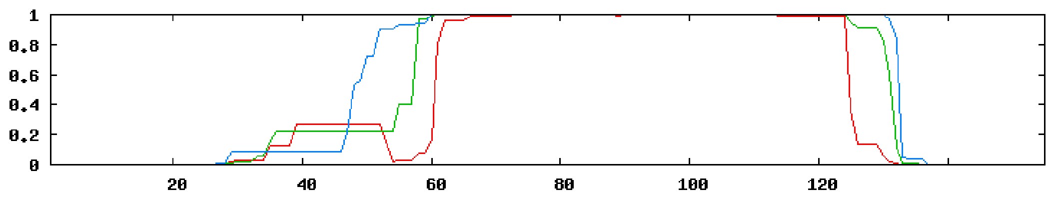
potential GPI site at position 132 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Aegypius monachus (Cinereous vulture)

nucleotide sequence

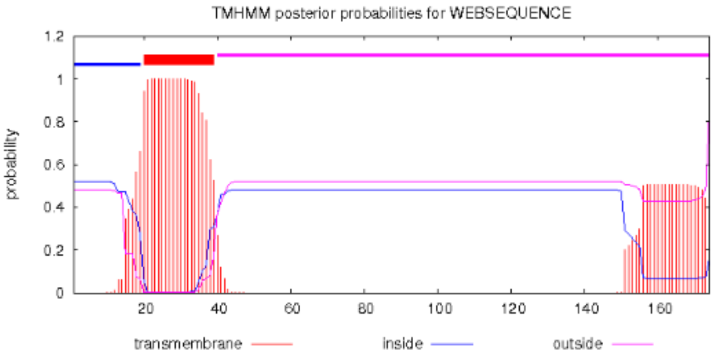
ATGGAGGGCTGCAGACCACAGTGGTCGCCCCGAGCCAGCCAAGCTTGGAAGATATACGTGGCCGTGGTCTTCTGCGT
GGTCGTTGTGGTGCCGGCGGCAGTCCTCACCACCATGTTCTGCCAGCCGGCCGCAGACTCTGCGATGGCGGGGAATT
GCTCAGTAAAGCTGGAGTGGCTGGAGGAAGCGCTGGCTGTCACCAACCGGTCCCTCACCGAAGCCCACCGGGAGTGG
GAAGTCTGCAGGAATAAGCTGGGTGAGCTGGAGGGGCAAGCCTCGGAGCTGGAGCAGGTGCTCGCCAGGGTAACCCA
GCTGCAAGAGGAGAATGGGAAGCTCAAGGCAGAGGTGGCCCGGCAGCAGAAGCAGTTGGAGGACCTGGAGAGCAGCA
GGAACAAGCTCCAGCTGCAGAACGAGCACCTGCAGAAGGAGCTCCAGGACATGAGGAGCCAGCACTCGGGTGGGAAC
AGGCTCCCGGCCGCATCCCTCAGCCTCCTGGTTCTCCTCCTCCCTGGGATGCTTCTCCTGTGA

amino acid sequence

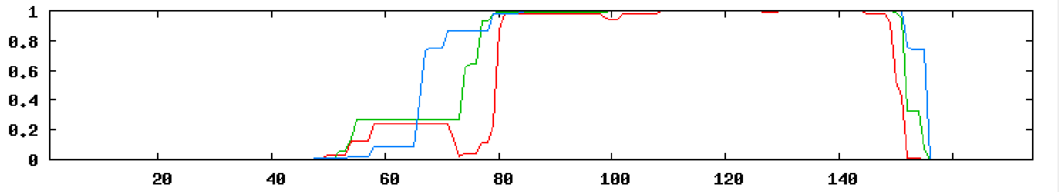
MEGCRPQWSPRASQAWKIYVAVVFCVVVVVPAAVLTTMFCQPAADSAMAGNCSVKLEWLEEALAVTNRSLTEAHREW
EVCRNKLGELEGQASELEQVLARVTQLQEENGKLKAEVARQQKQLEDLESSRNKLQLQNEHLQKELQDMRSQHSGGN
RLPAASLSLLVLLLPGMLLL

potential GPI site at position 151 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Columbiformes

Patagioenas fasciata monilis (band-tailed pigeon)

nucleotide sequence

```
ATGGCGGACAAGCCGGCGTGGGGCGCGTACGCGGCCGTGGCCATCGGGGTGGTCGCCGTGGTGCTGGCGGTGACGCT
CCCCGCCATGCTCTGCCAGCGGGACACGGGCTCCGTGGTGCCCGGGGACACAGCGTGGGGGGCGACACAGCTGGAGG
AGGCGCTTGCCAGGGTGGCCCAGTTGCAAGAGCAGAACCAGGTGCTCAGGGCAGAGTTGGCCCAGCAGCAGGAGCAG
CTGGGGGACCTGCAGATCATCAGGGACAGGATCCAGCTGGAGAACGAGCGCCTGCAGAAGAAGCTGCAGGGCACAGG
AAGCGAGGACTGGGGTGGGACCTGGCTCTGGATCATCATCCTGGGTGTCCTGGTTTGGAAGTGGCTCCGCTGA
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amino acid sequence

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MADKPAWGAYAAVAIGVVAVVLAVTLPAMLCQRDTGSVVPGDTAWGATQLEEALARVAQLQEQNQVLRAELAQQQEQ
LGDLQIIRDRIQLENERLQKKLQGTGSEDWGGTWLWIIILGVLVWKWLR
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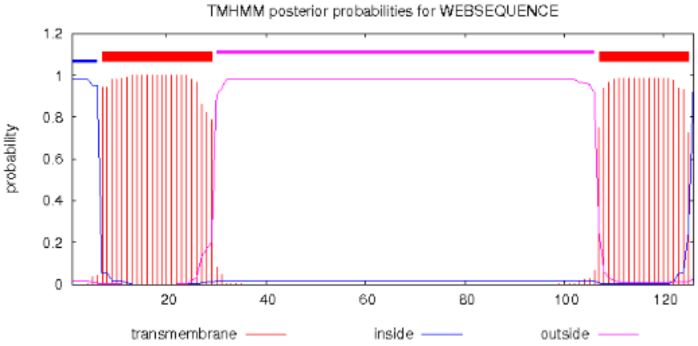
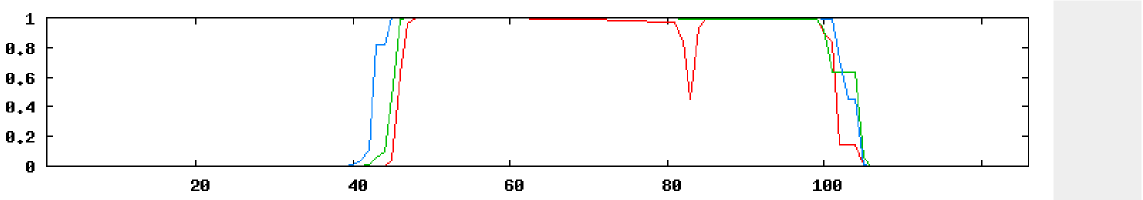
TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Columba livia (common pigeon)

nucleotide sequence

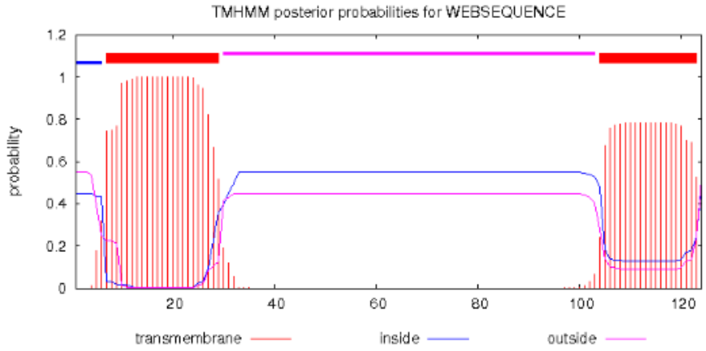
ATGGCGGACAAGCCGGCGTGGGGCACGTACGCGGCCGTGGCCATCGGGGTGGCCGCCGTGCTGCTGGCGGTGACGCT
CCCCGCCATGCTCTGCCAGCGGGACACACGCTCCGTGGAGGCCGGGGACACAGCGTGGGGGGCGACACAGCTGGAGG
AGGCGCTTGCCAGGGTGGCCCAGTTGCAAGAGCAGAACCAGCTGCTCAGGGCAGAGATGGCGCGGCAGCAGGAGCAG
CTGGGGGACCTGCAGATCATCAGGGACAAGCTGGAGAAGGAGTGCCTGCAGAAGCAGCTCCAGGGCACAAGGAGCGA
GGACTGGGGTGGGACTTGTGTCTGGATCCTCATTCTGCTTGTCCTGGTTTGGAAGTGGGTCTGCTGA

amino acid sequence

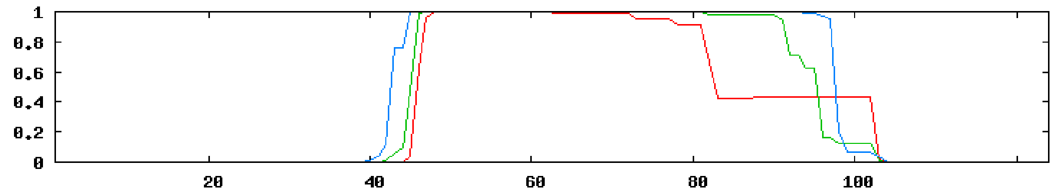
MADKPAWGTYAAVAIGVAAVLLAVTLPAMLCQRDTRSVEAGDTAWGATQLEEALARVAQLQEQNQLLRAEMARQQEQ
LGDLQIIRDKLEKECLQKQLQGTRSEDWGGTCVWILILLVLVWKWVC

potential GPI site at position 100 (red)

TM prediction



CC prediction



Under the sequence are the probabilities abbreviated to first digit for windows of 14, 21 and 28 residues and the corresponding heptads.

Figure S2
Alignment of BST-2 sequences from Galliformes in fasta format.

```
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GAGCCGGGG------------------CCGGGATCAGAGGAGCTGGCATGGCTGCAGGGG
GTGCAGCAG---------------------AGGCTATGGGTGCAGGTGGGTGCGTTGGGG
CAGGAGTTGGCTGCCACCAATAAATCCCTCGCTGCGCTGGTCGGGGCCACCAACAGGTCC
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GAGCCGGGG------------------CCGGGATCAGAGGAGCTGGCACGGCTGTACAGG
GTGCAGCAG---------------------AGGCTGTGGGTGCAGGTGGGTGCGTTGGGG
CAGGAGTTGGCTGCCACCAACAAGTCCCTCGCTGCGCTGGTCGGGGCCACCAACAGGTCC
CTCGCTGAGATGCACAAGCAGTGGGACAGCTGCAGGAGTCAACTGGATACGGTGCAAAGG
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CAGGTCCGTAGGCTGTCGAACTGGATCTGGGAGATAAAGAGCAGCAGATCCAGCGGGAGC
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Figure S3
Alignment of BST-2 sequences from Passeriformes in fasta format.

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