

SUPPLEMENTARY MATERIAL 2

New predictions of OT/VP receptor amino acid sequences together with corresponding results of transmembrane helix (TM) predictions (see summary of sequences in Table 1). TM predictions were made using the TMHMM Server v. 2.0 available at <http://www.cbs.dtu.dk/services/TMHMM/> (see section 2.1). Identified DRY/DRH/DRC motifs have been highlighted.

ABBREVIATIONS

Aca: *Anolis carolinensis* (anole lizard)

Cmi: *Callorhinchus milii* (elephant shark)

Dre: *Danio rerio* (zebrafish)

Gac: *Gasterosteus aculeatus* (stickleback)

Gga: *Gallus gallus* (chicken)

Mdo: *Monodelphis domestica* (opossum)

Oan: *Ornitorhynchus anatinus* (platypus)

Ola: *Oryzias latipes* (medaka)

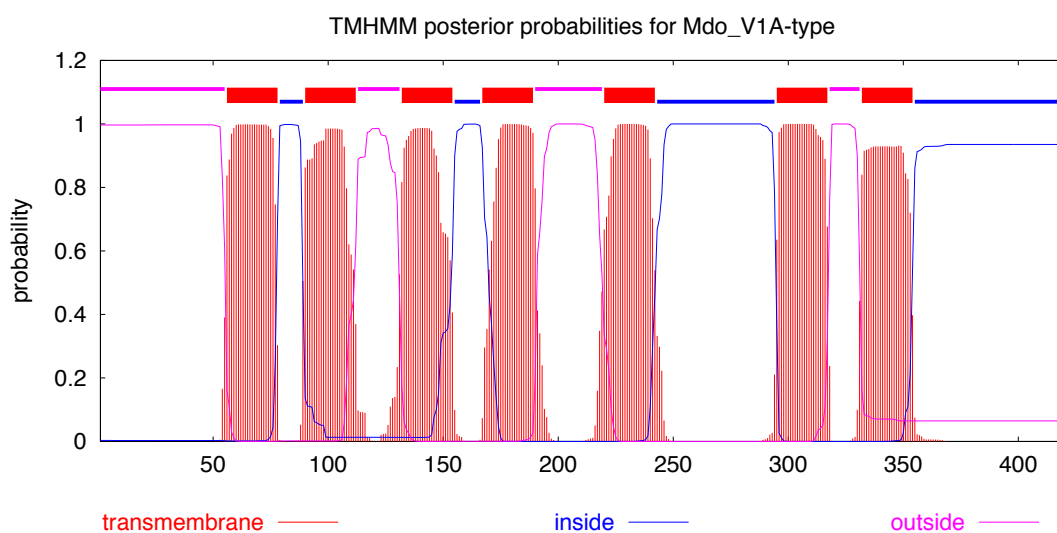
Tru: *Takifugu rubripes* (fugu)

Xtr: *Silurana (Xenopus) tropicalis* (frog)

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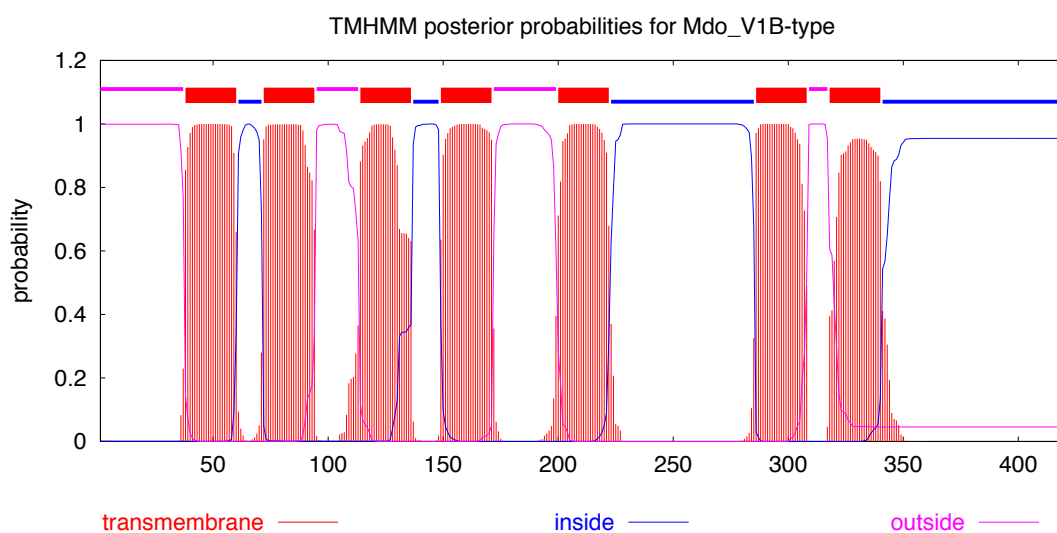
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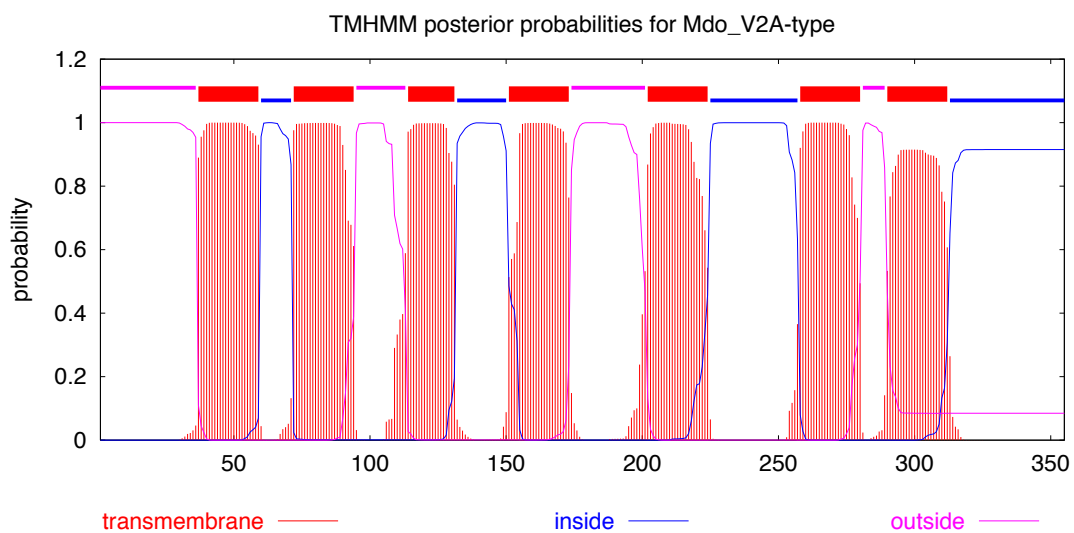
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*



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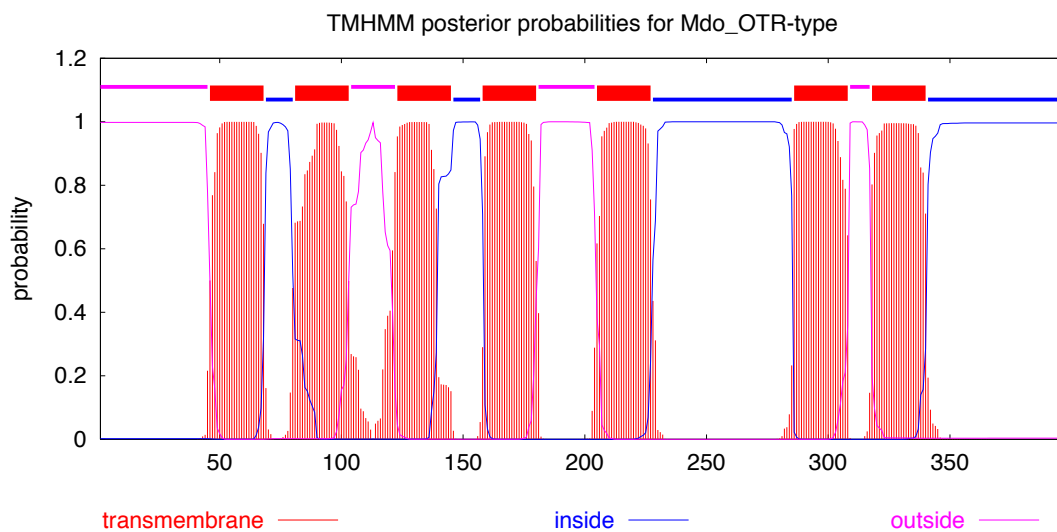
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Note: This sequence was predicted from two *Monodelphis domestica* traces in the NCBI trace archive (<http://www.ncbi.nlm.nih.gov/Traces/trace.cgi?>). The ambiguous residues marked with the character ^X are likely the result of sequencing errors in the original trace (TI number: 368796670).

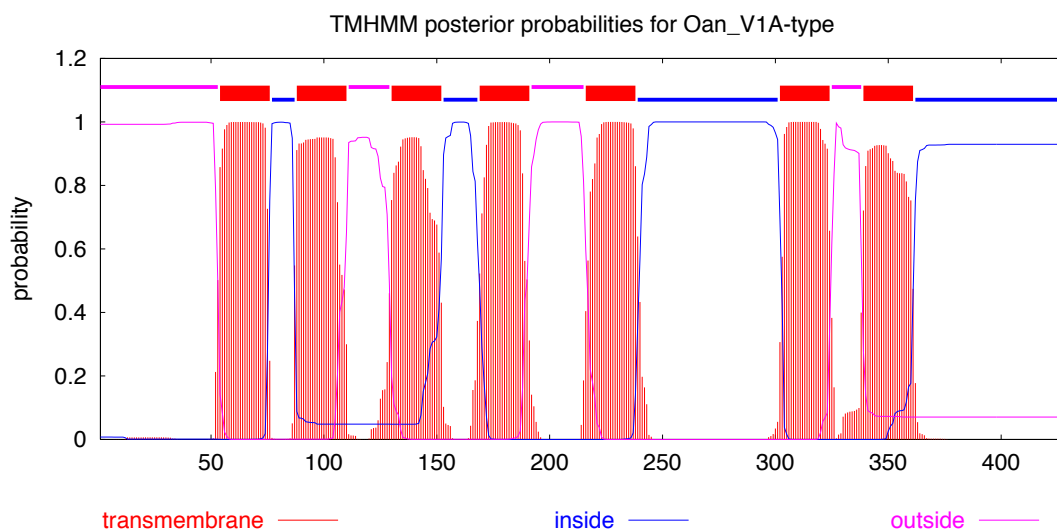
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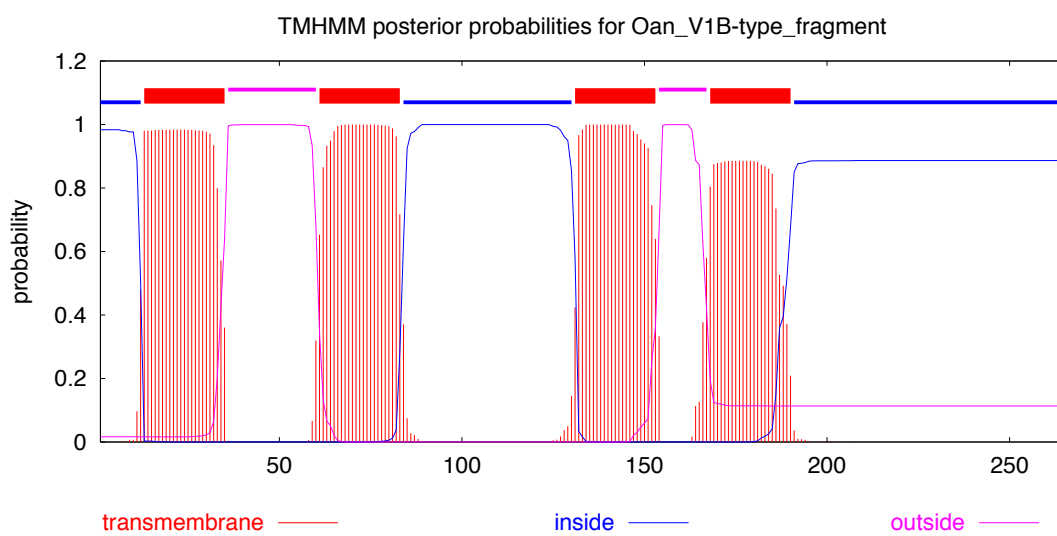
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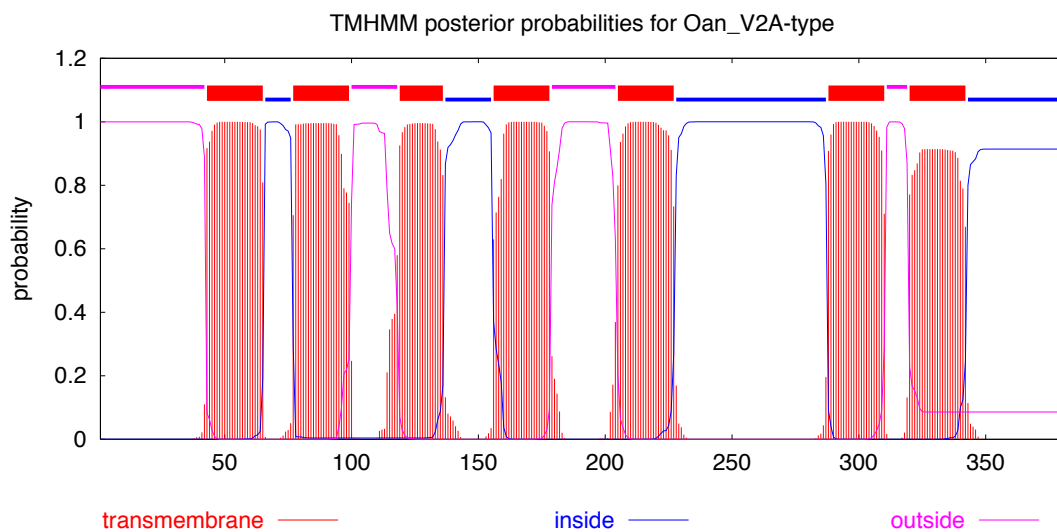
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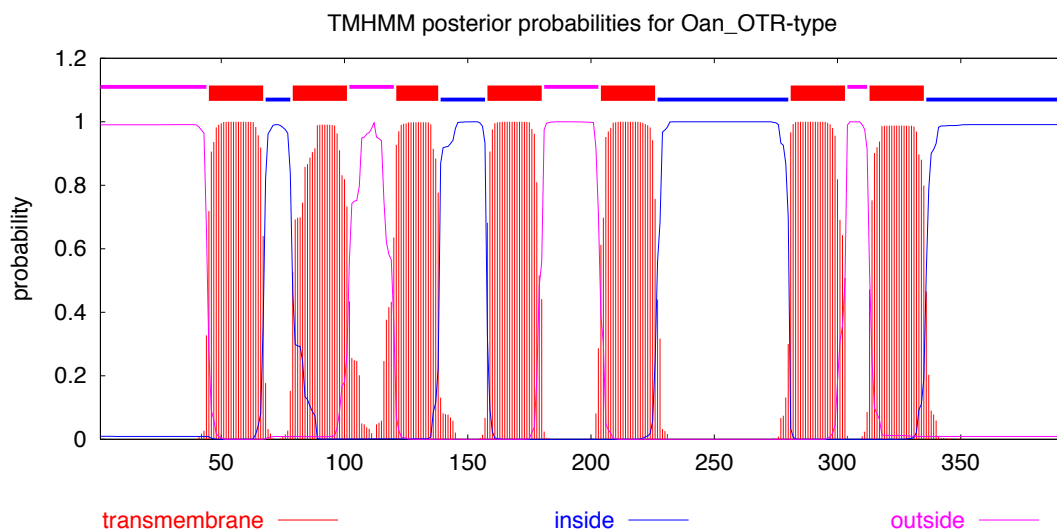
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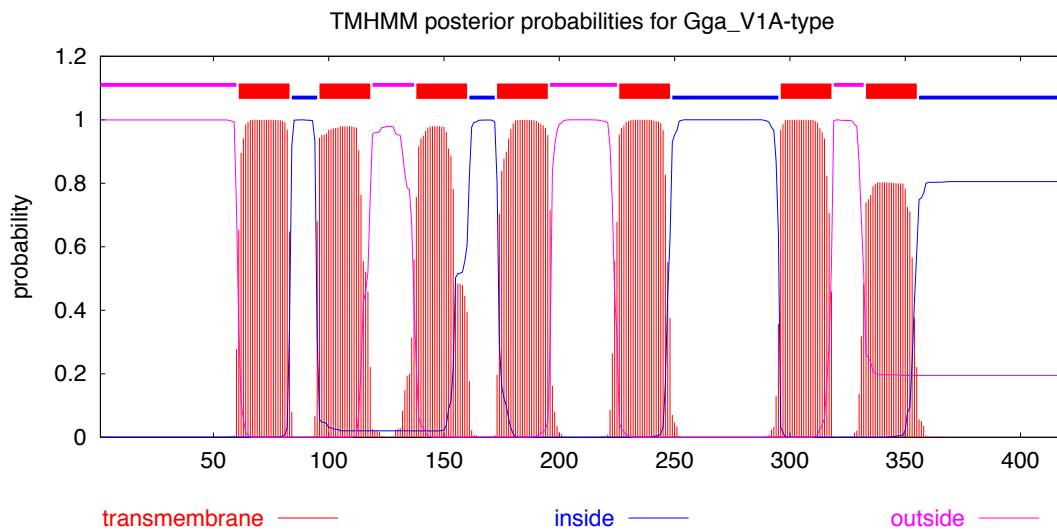
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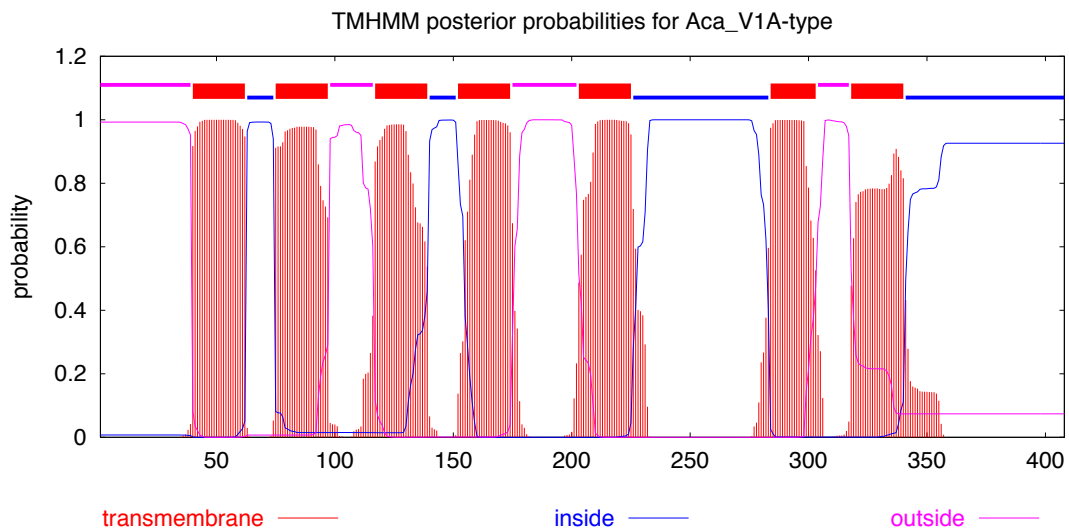
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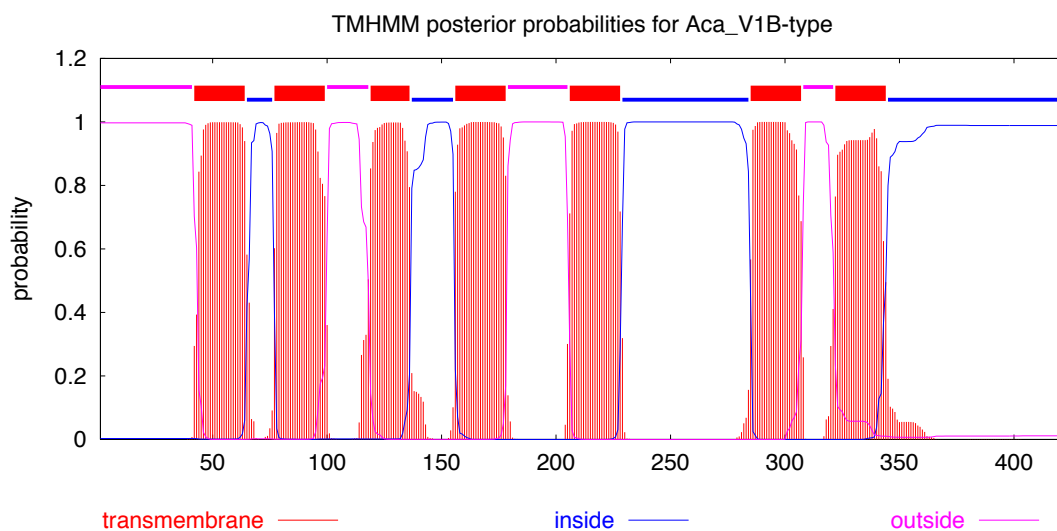
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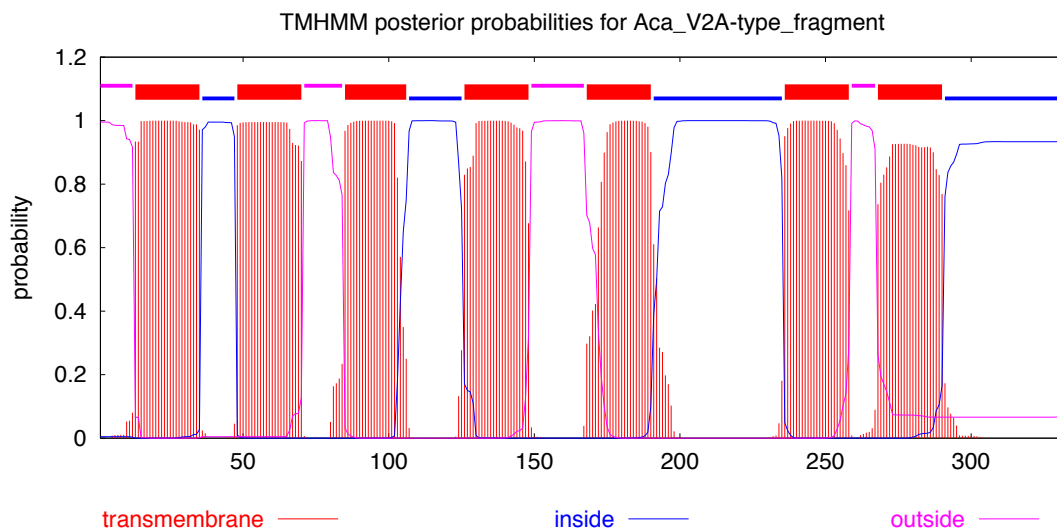
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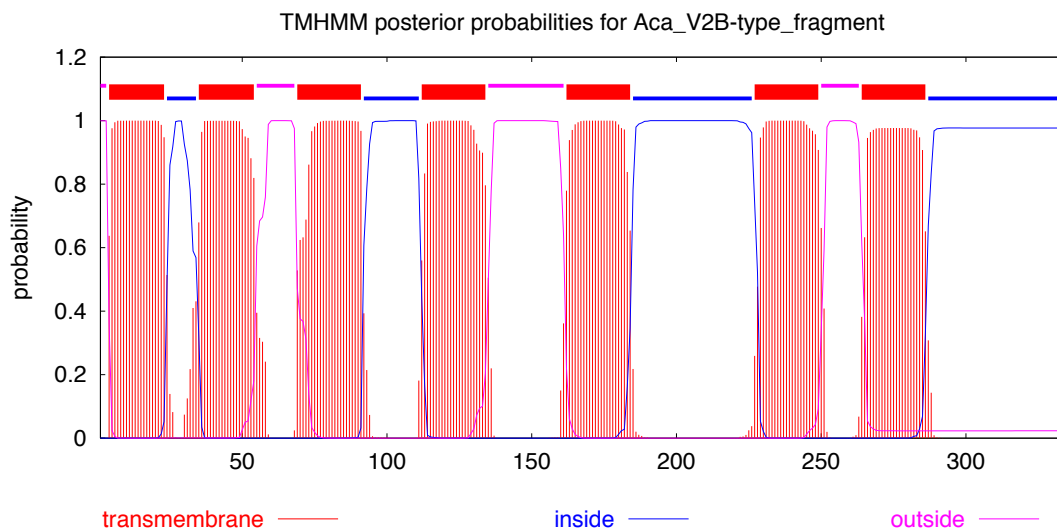
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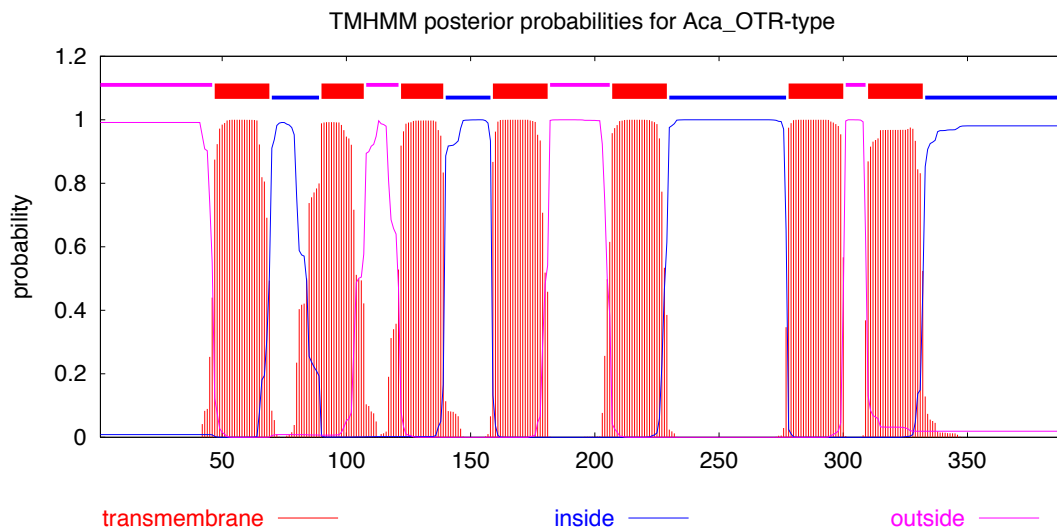
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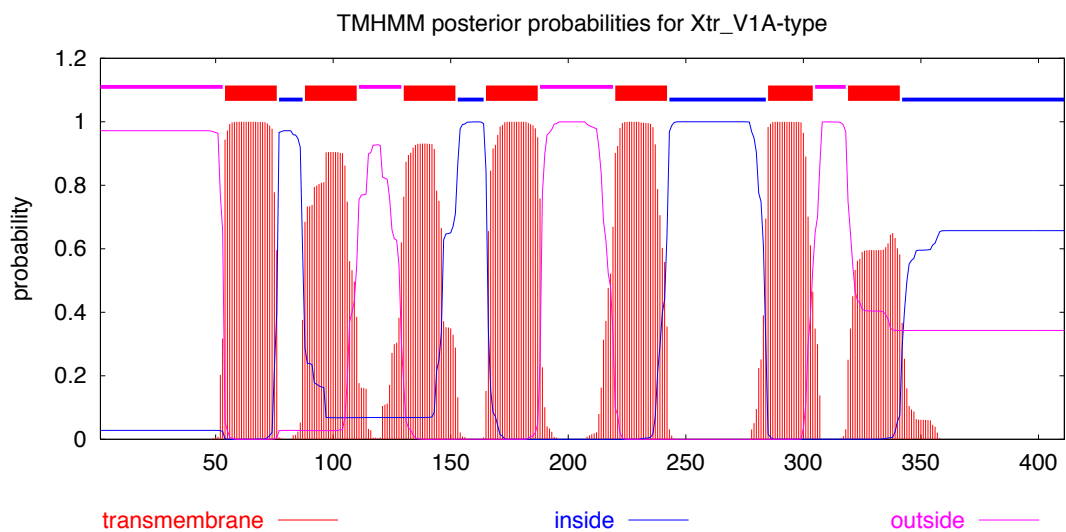
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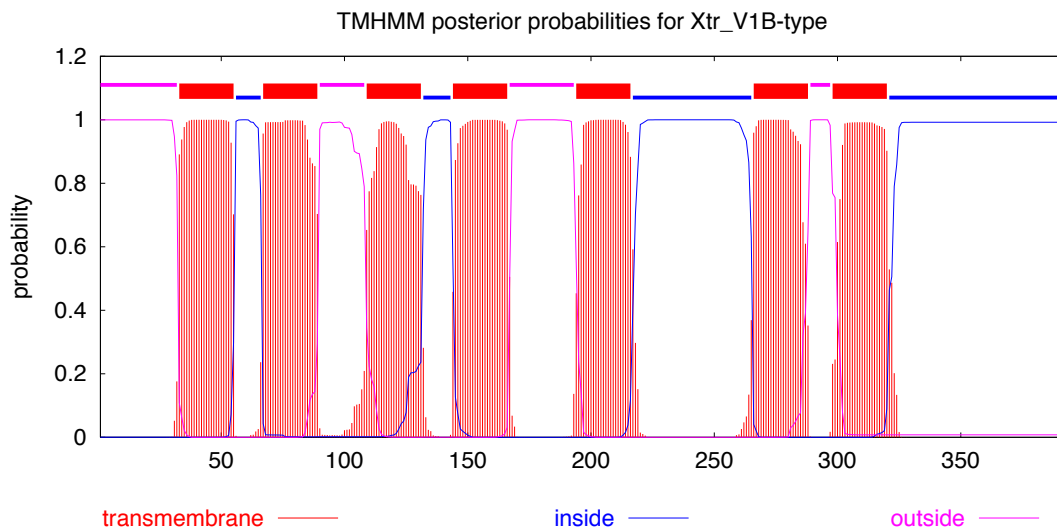
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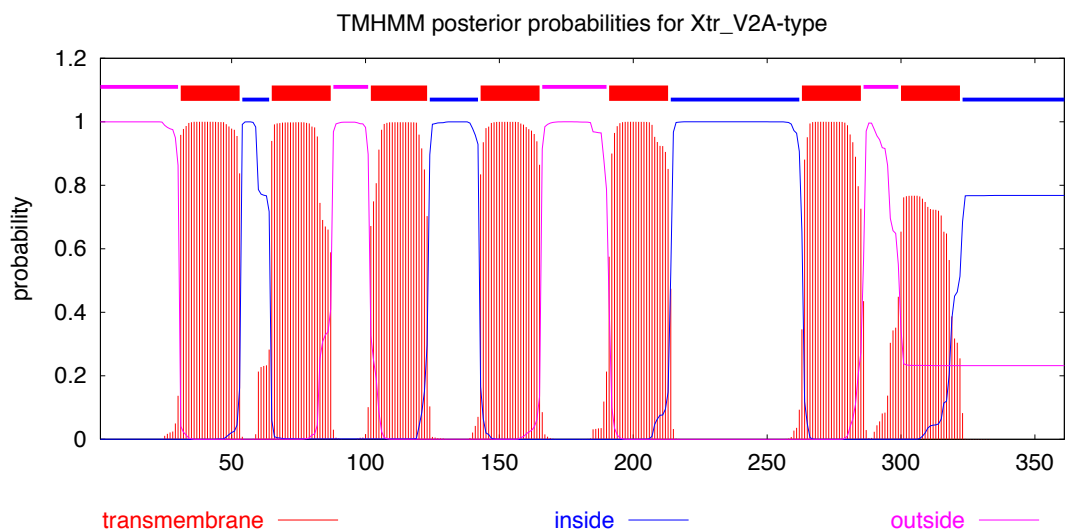
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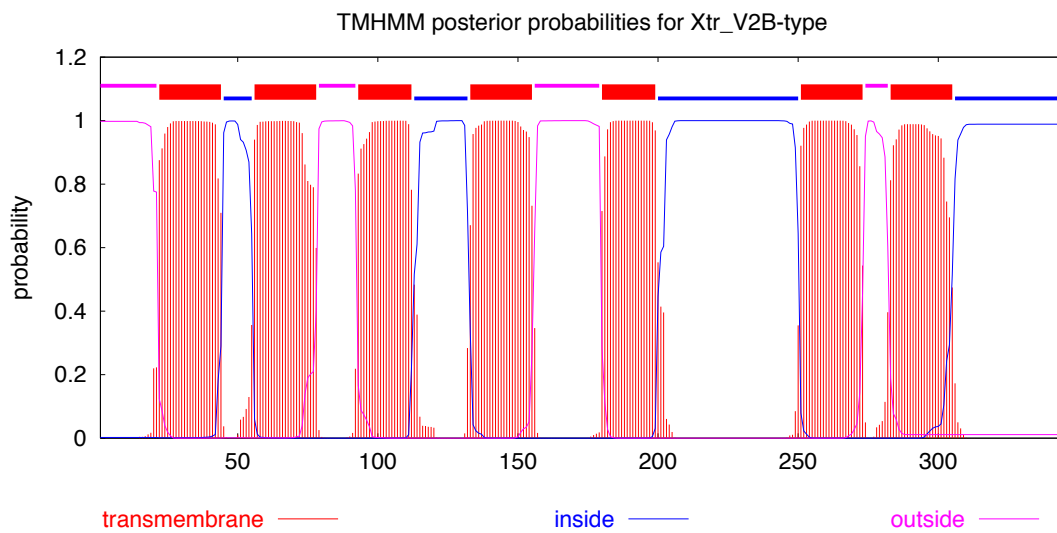
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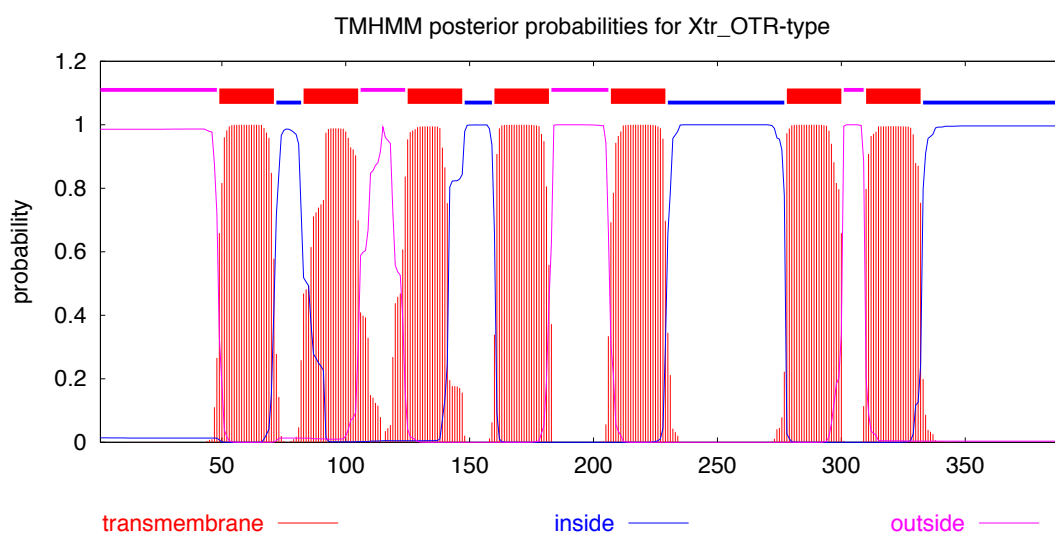
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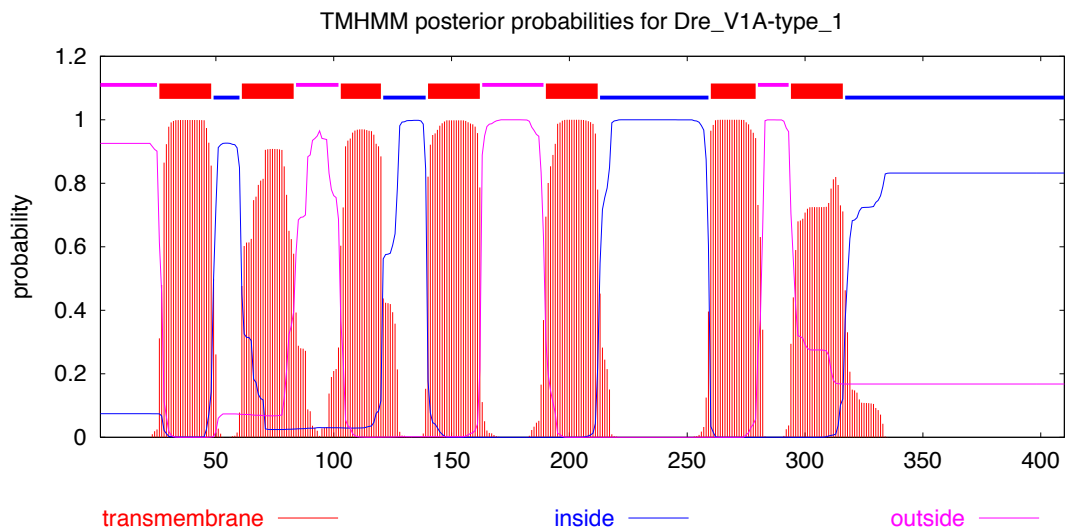
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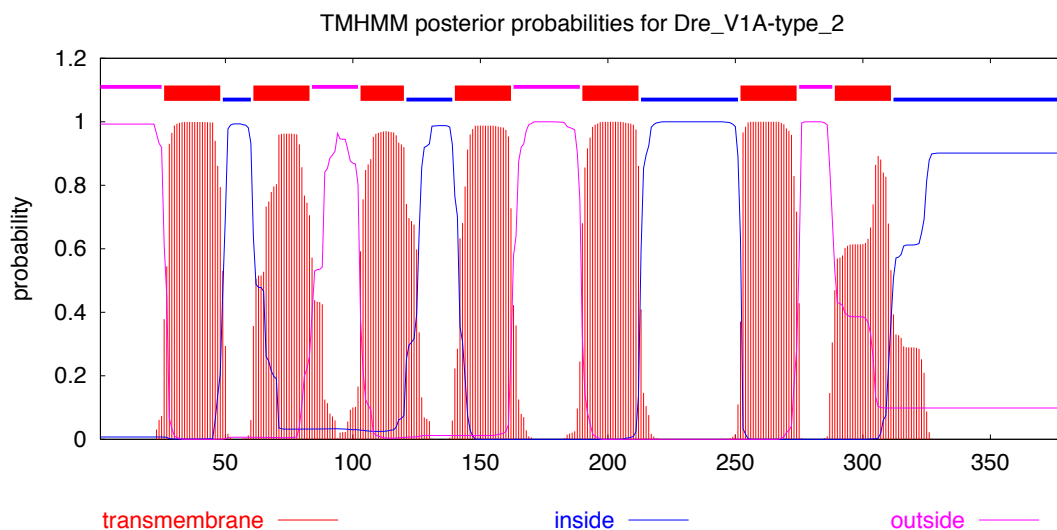
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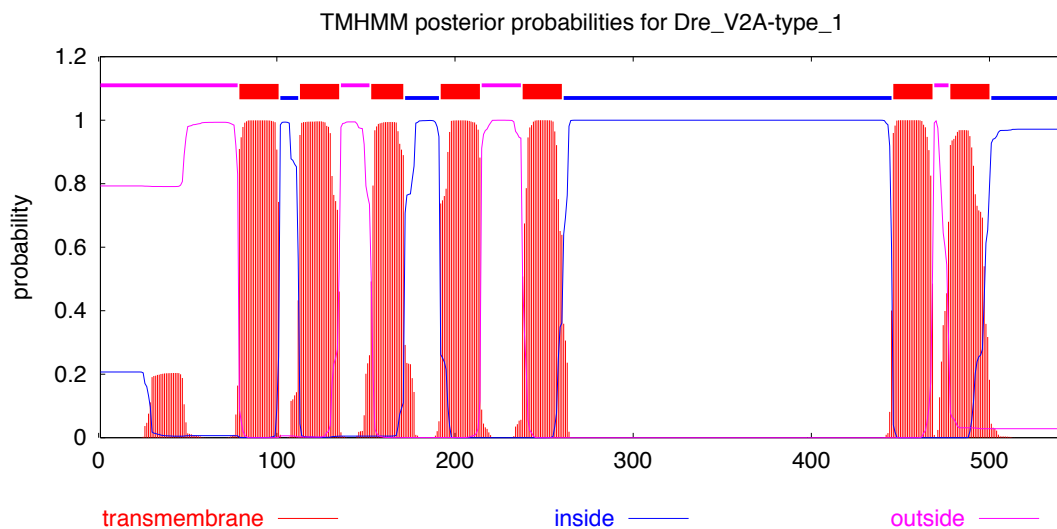
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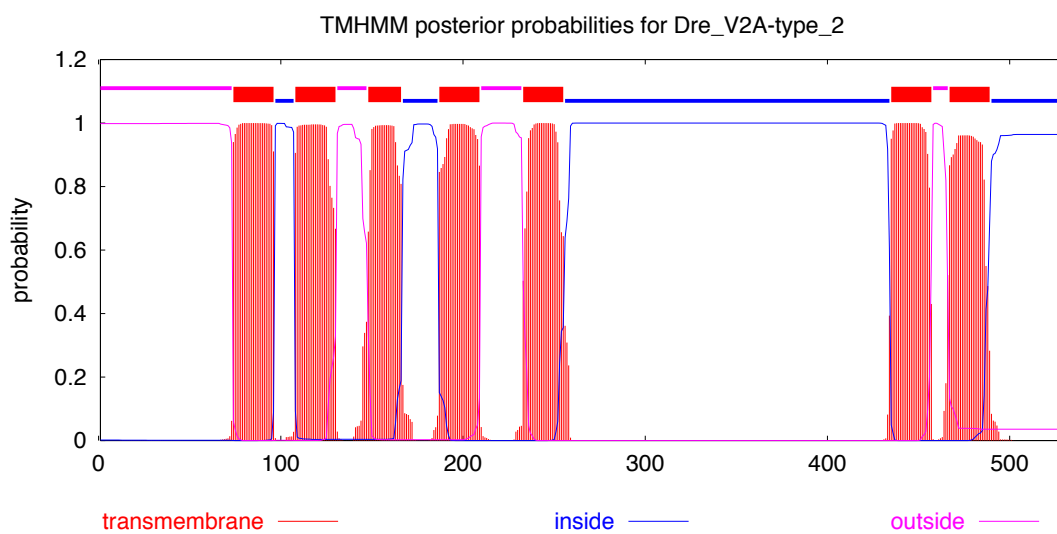
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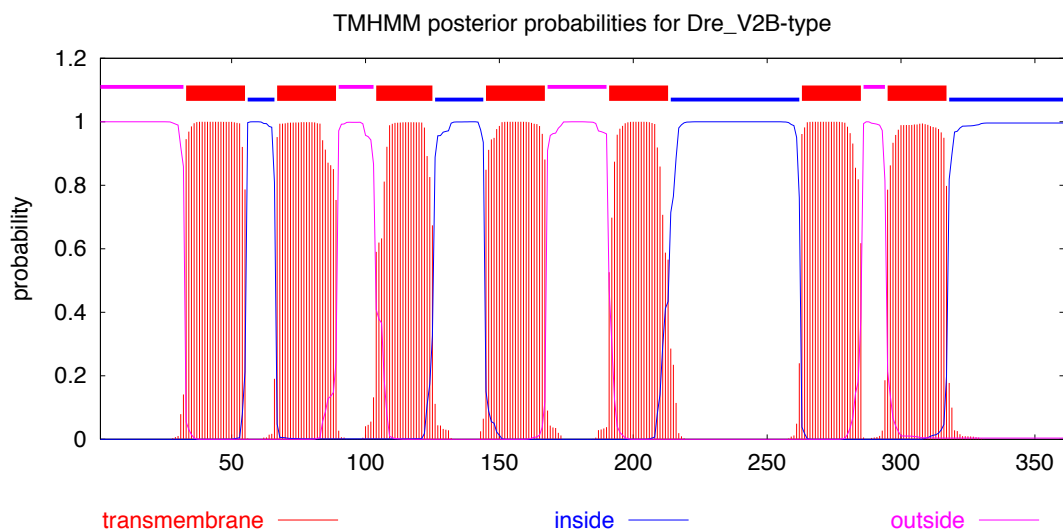
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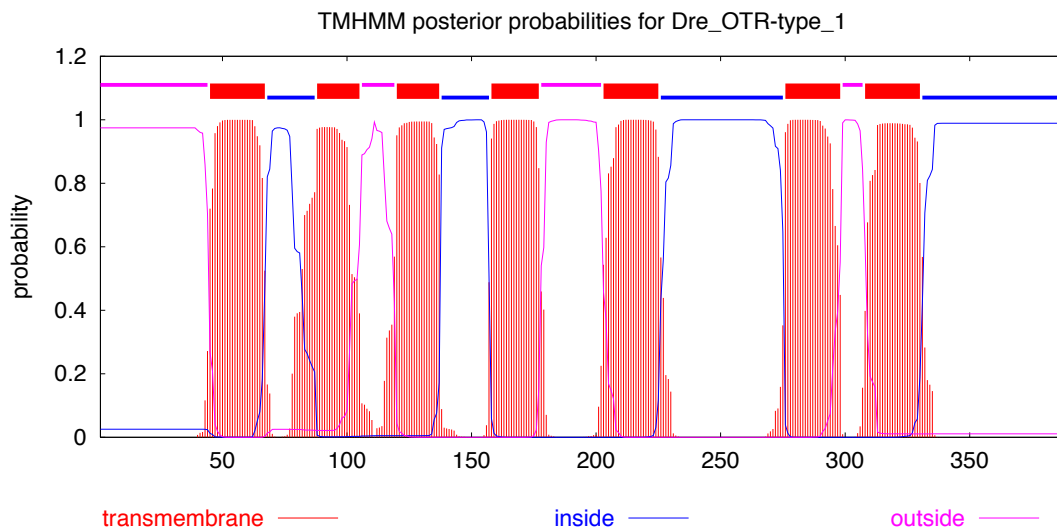
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R*



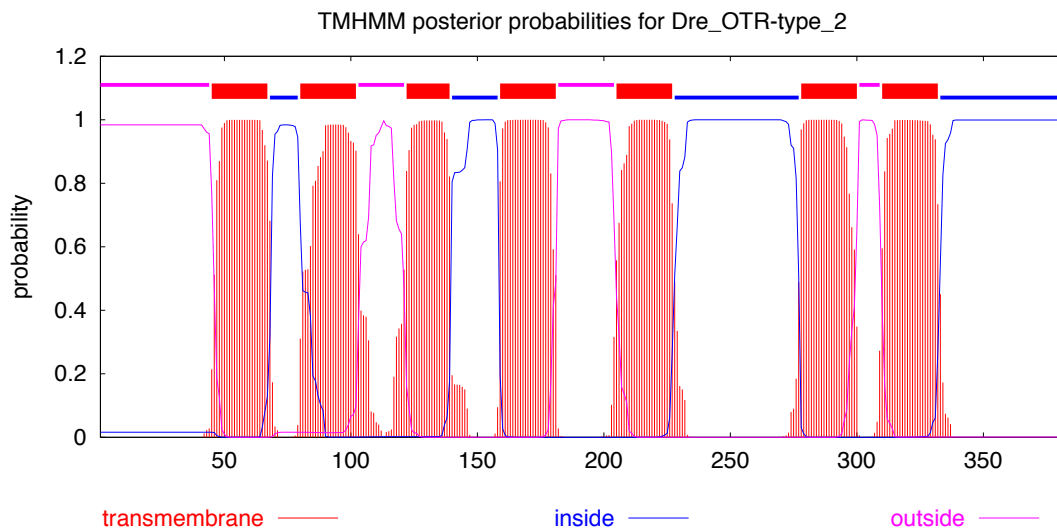
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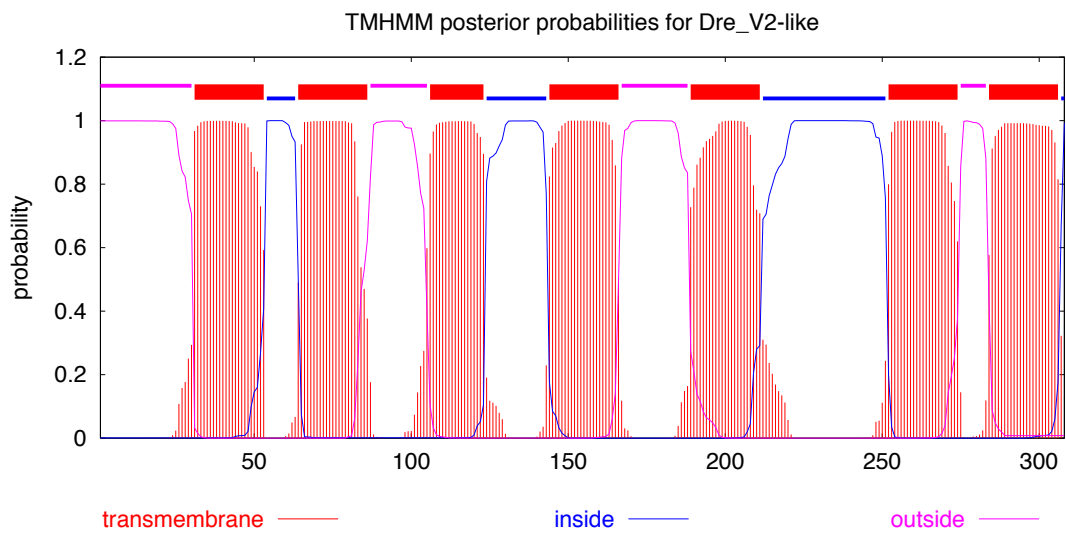
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RDQCLSLTPRPTKGAALSRVSSVKLISKAKIRTVKMTFVIVMAYIICWTPFFFVQMWSAW
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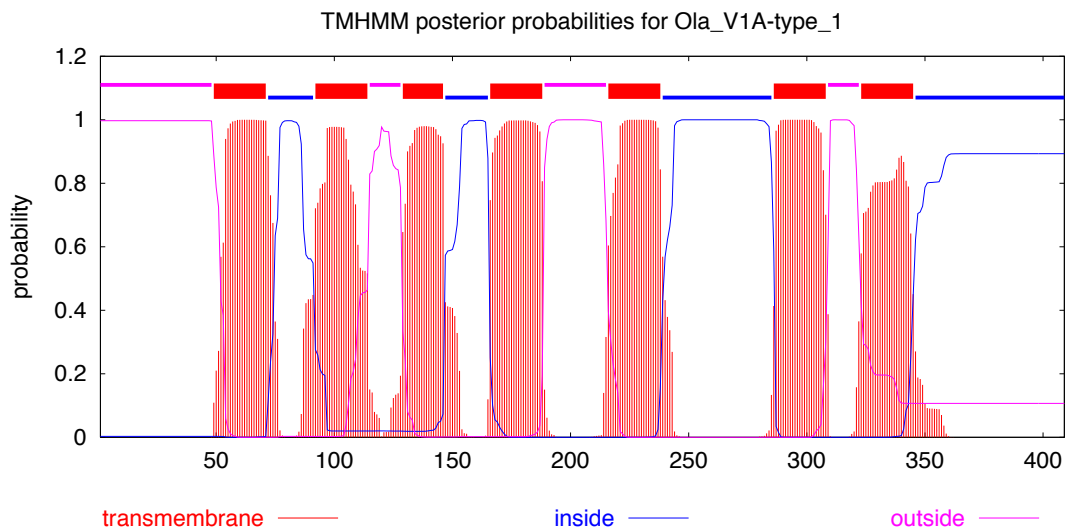
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FIEPWGGRIYITWITLSVFVLP AVILMFCQIKICAGIYFNMKRKALQGSAGDGRSSTKGI
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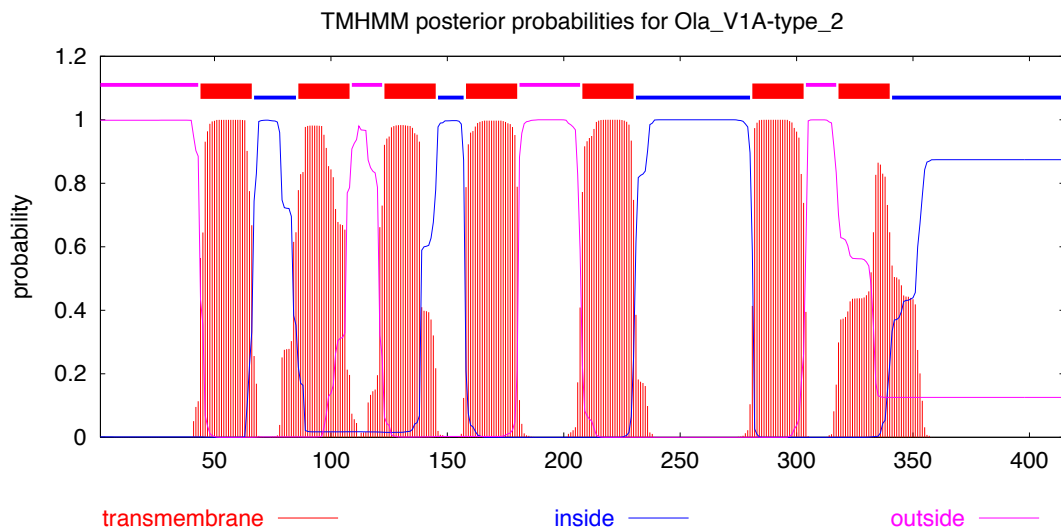
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SIWKNIKYKKRKT TAGASNKNGLIGKNSVSSVTTISRACLRTVKMTFVIVLAYIVCWSPF
FIVQMWSVWDENFLWDDSDNTAVTLSALLASLNSCCNPWIYMIFSGHLLQDFVHCFSCCR
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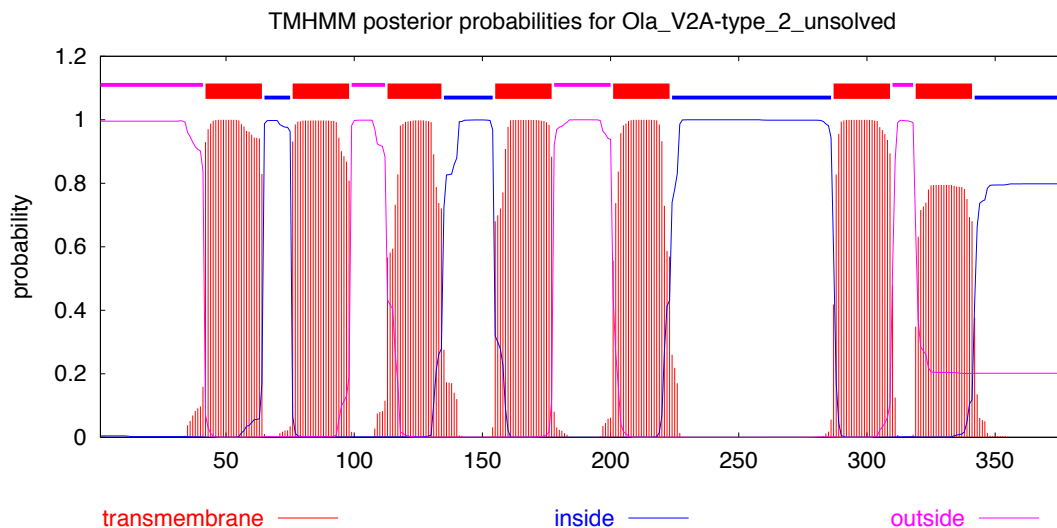
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SLSEVRPGSAVYDCWGHFMEPWGLRAYITWITAGIFLLPVAILVFCYGFICRTIWMNIKY
KTRRKRTDAAEGATTNGVLSRSSVSSVSTISRACLRTVKMTFVIVLAFVVCWAPFFTVQM
WSVWDQTFSWDDSENTTVTL SALLASLNSCCNPWIYMI FSGHLLSDFFSGLPCCRRLKIQ
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>Ola_V2A_2_unsolved

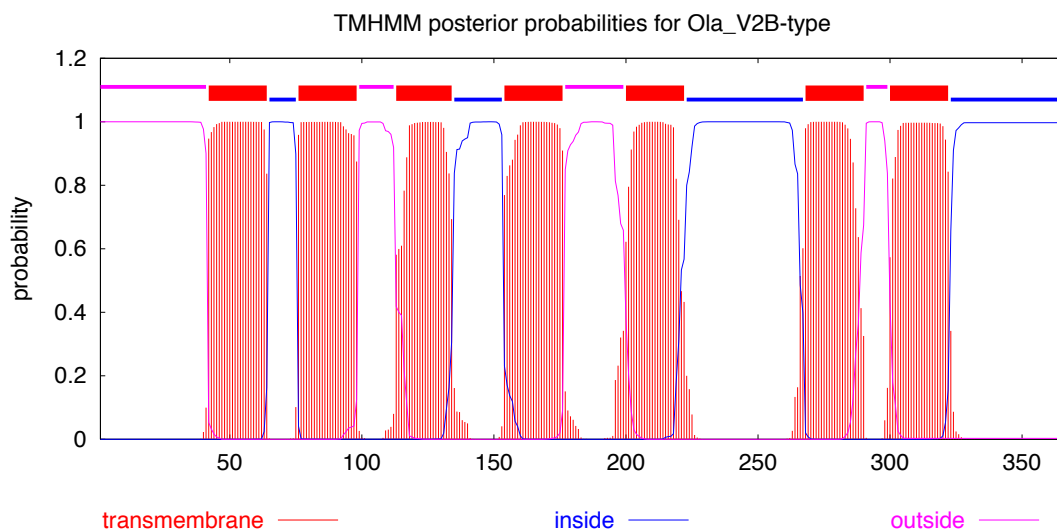
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Note: The sequence has been cut between the residues VSS and CGQ (underlined above) due to interrupted reading frame in the genomic sequence and the absence of canonical splice sites. This excluded region encodes part of the intracellular loop 3 (IL3) that is expanded in the identified teleost V2A sequences.

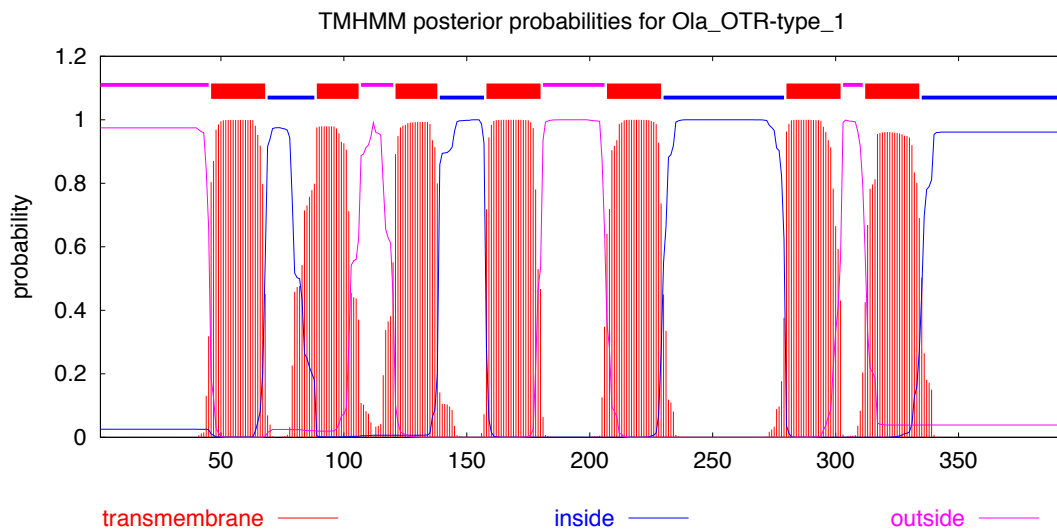
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SKGVALPSRASGVASMSKARVKTLKITVIVLAYIICWAPFFTVQLWSAWDTHAPKETAT
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NISESK*



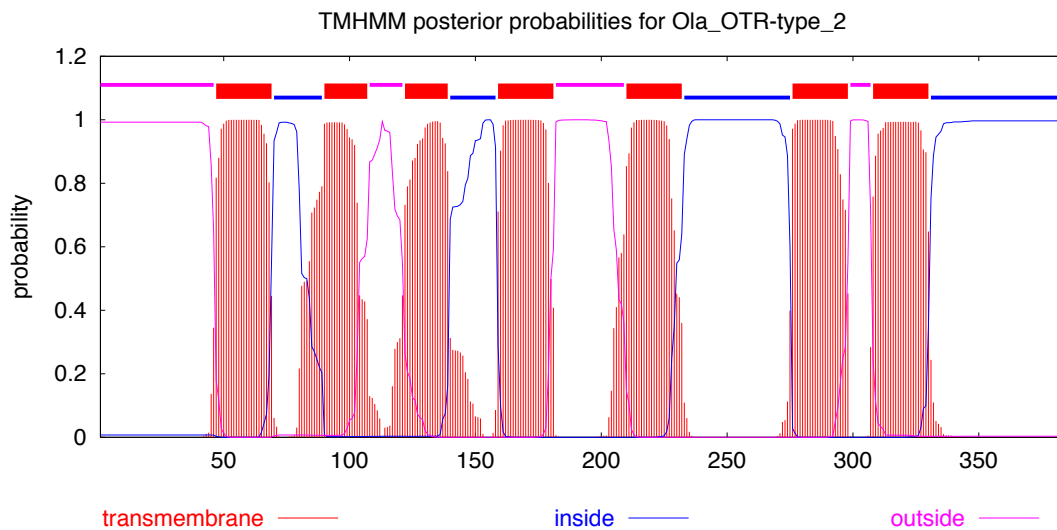
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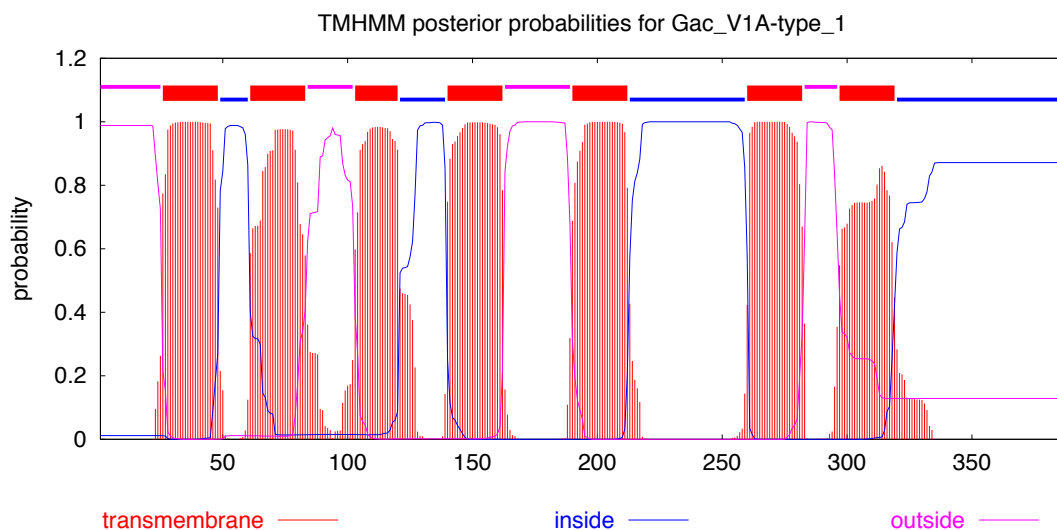
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YLQVVGMFASTYMLVLMVDRC LAICLPFRFVNKRKDRICVIASWMLSLVFSAPQAYIFS
LKEVGNGVYDCWGDFVHPWGAKAYITWMSLSIYILPVAILGICYGLICFKIWENINMKTR
RDRFVAVTSKGTHPLSRVSSVRLISKAKIRTVKMTFVVVIAIYVCWTPFFFFVQMWSAWDP
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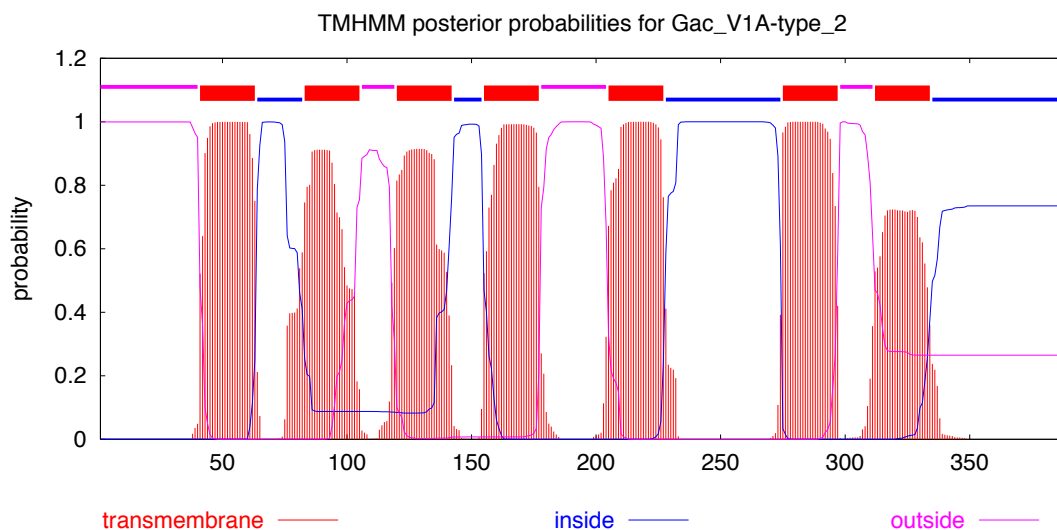
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VEPWGAKAYITWITVGIFLVPVVILMLCYGFICHSIWKNIKYKKTKSTAGSANRNGFIGK
NSVSSITTISRACLRTVKMTLVIVLAYIVCWAPFFTVQMWSVWDDNFQWADSENTAVTLS
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>Gac_V1A_2

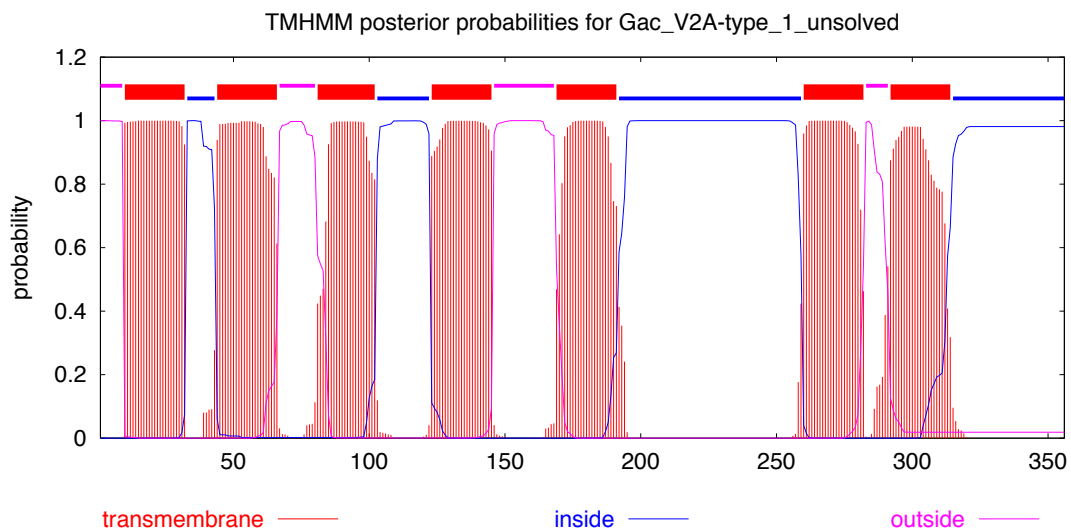
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RRPAEAPGTGALSRSVSGVGNISRAKLRTVKMTFVIVLAYVVCWAPFFTVMWSVWDKS
FSFADSESTTVTL**X**ALLASLNSCNPWIYMFSGHLLSDLPCRRLAGTMRLQDSDSSLR
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Note: The ambiguous residue marked with the character **X** is likely the result of a sequencing or assembly error in the genome sequence causing a frame shift.

>Gac_V2A_1_unsolved

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SRWNTPVMVAWGLALVLSIPQVFIFSRSEVSAGEFDCWGRFAEPWGLKAYITWMTVAVFV
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PASPPPSITKAMSKTVRMTLVIVLVYTICWSPFFIVQLWAAWDPNPASHTGVAFTILMLL
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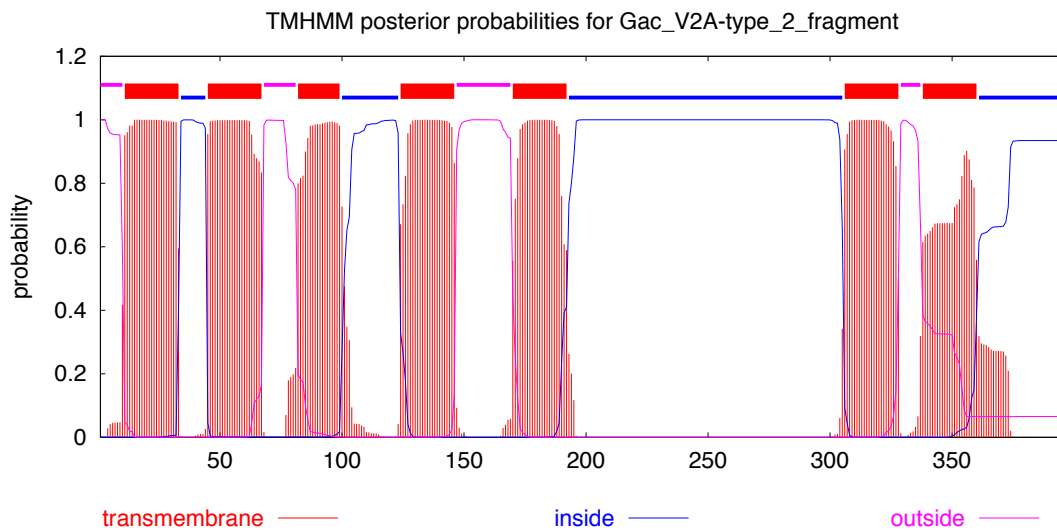


Note: The sequence has been cut between the residues SER and QTL (underlined above) due to interrupted reading frame in the genomic sequence and the absence of canonical splice sites.

This excluded region encodes part of the intracellular loop 3 (IL3) that is expanded in the identified teleost V2A sequences.

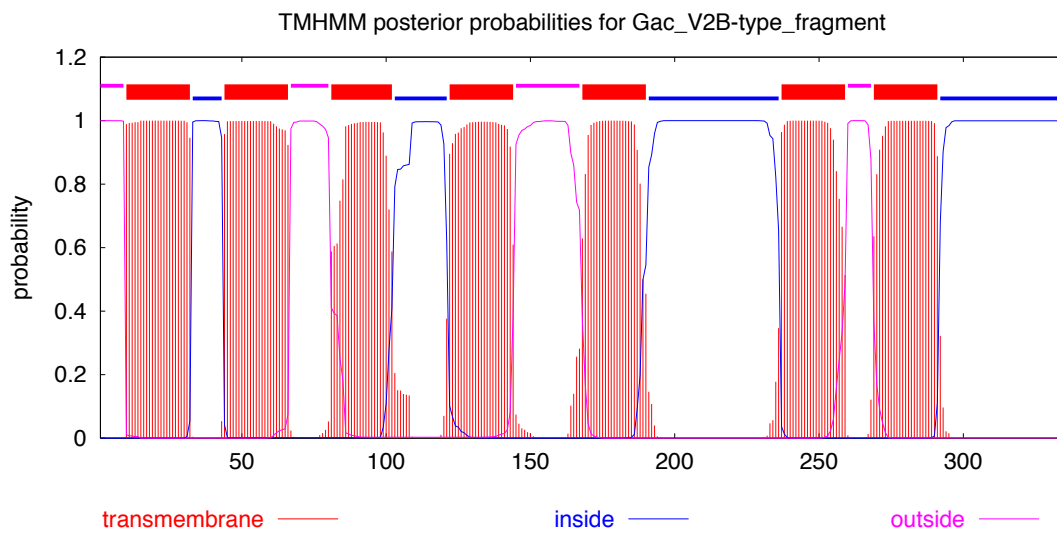
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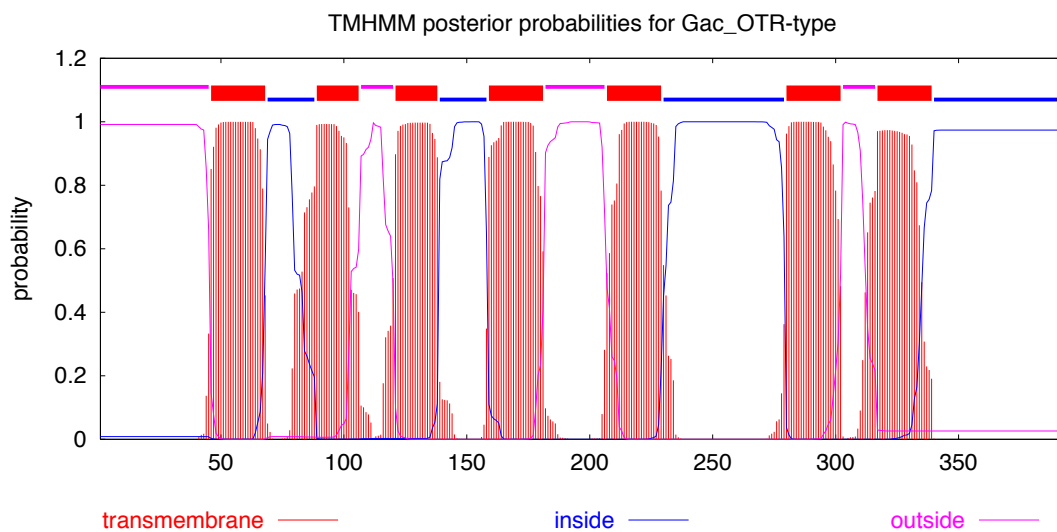
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PVITVVFQVRIICRAIQMNLHQKTAGLQGRAGHPAPSRGSGVAGMSKARVKTLKMTVVIV
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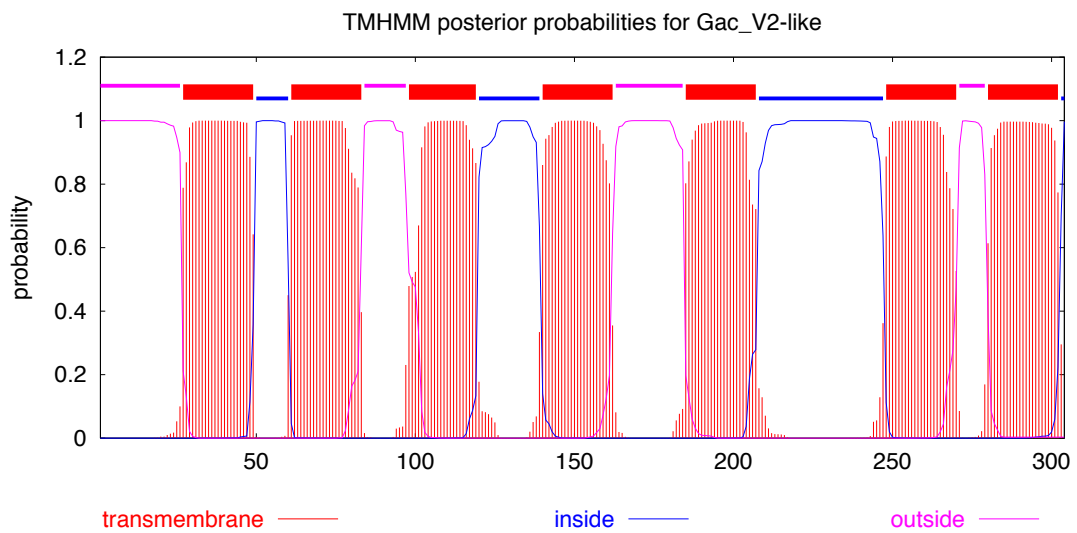
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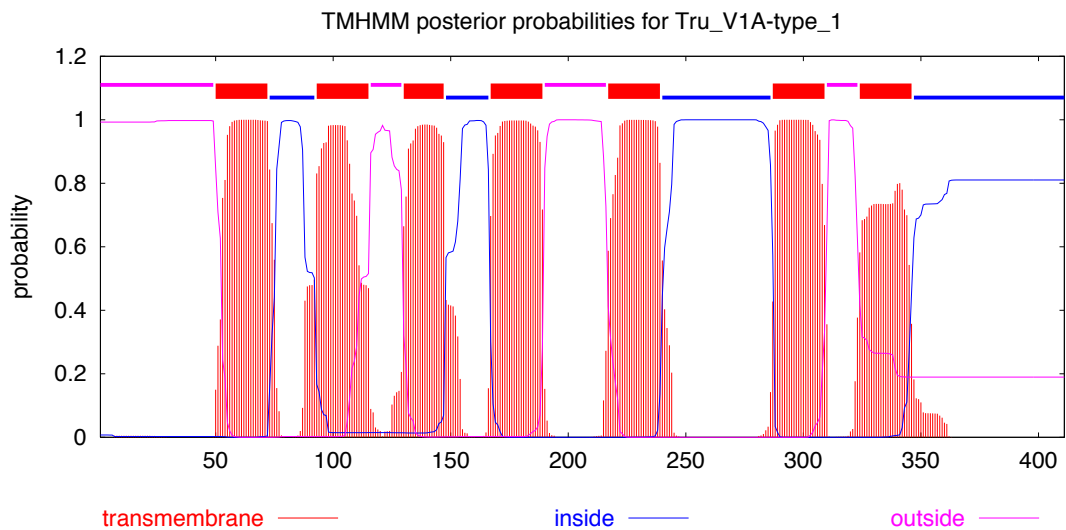
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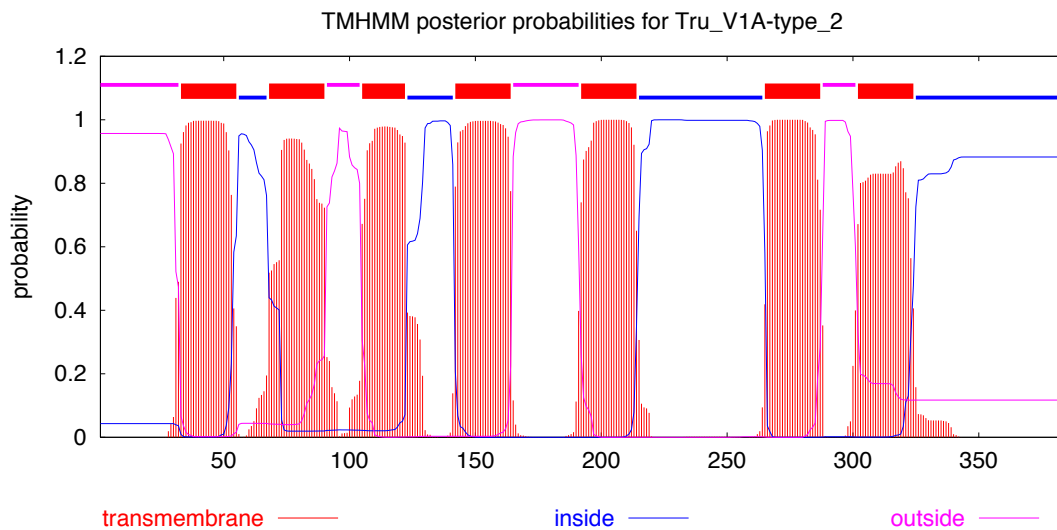
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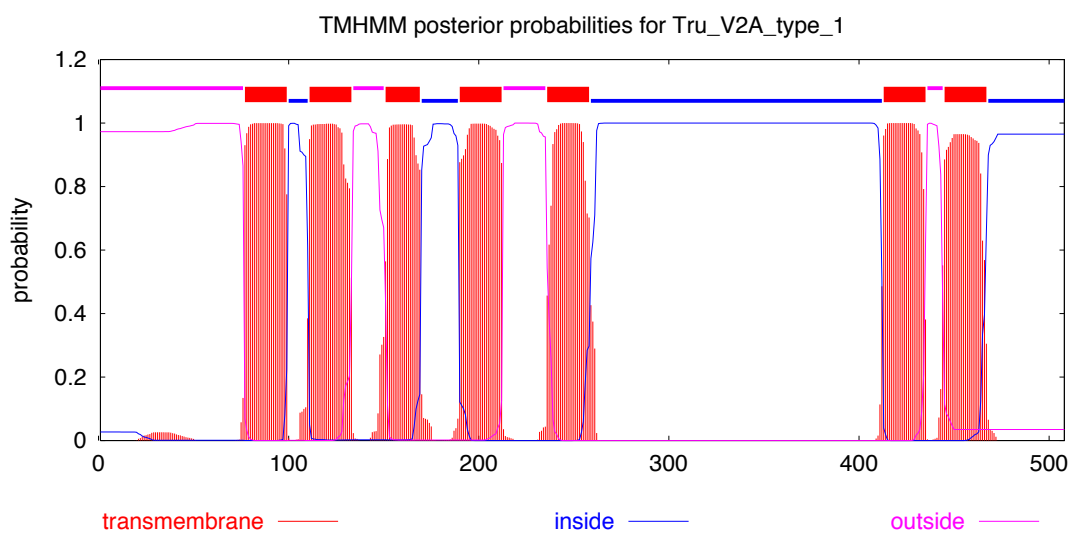
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HFVEPWGLRAYITWMTAGIFVVPVAALVFCYGFICRTIWKNLKCKTQRKSVEAVAEATGA
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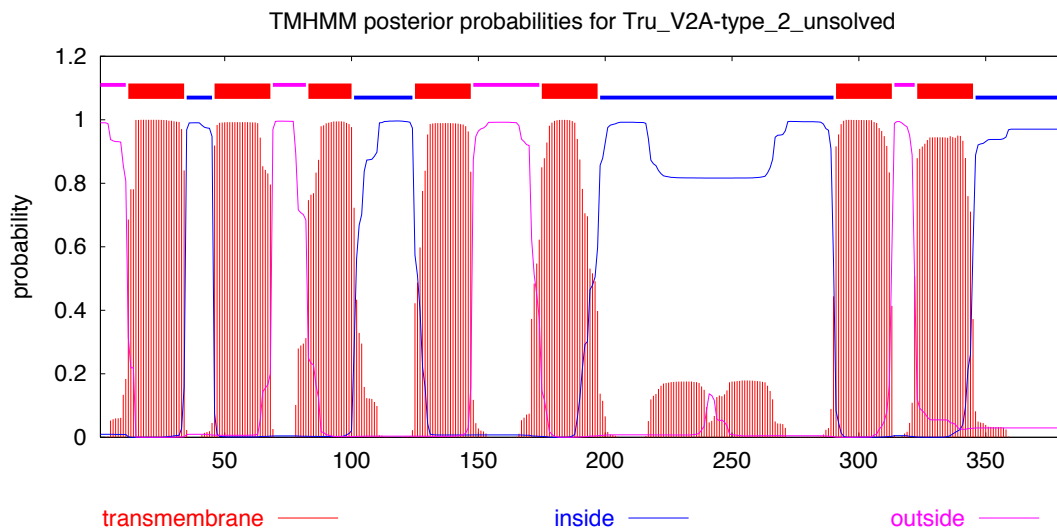
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MTVAVFLLPALIITICQIRIFREIHNNIYLKSERMVVAELKKNEIFFRFHGFKKEDERAR
ERRRASGGGGREGRGGHAVKGVNNNPHNNSNNSGAPPTVQHSSCHGDHATTSAAPVQQQ
QILNGSDCPESYTSYGITPGSPRCSIDYAPPHSPSIPPPSITKAMSKTVRMTLVIVLVYT
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>Tru_V2A_2_unsolved

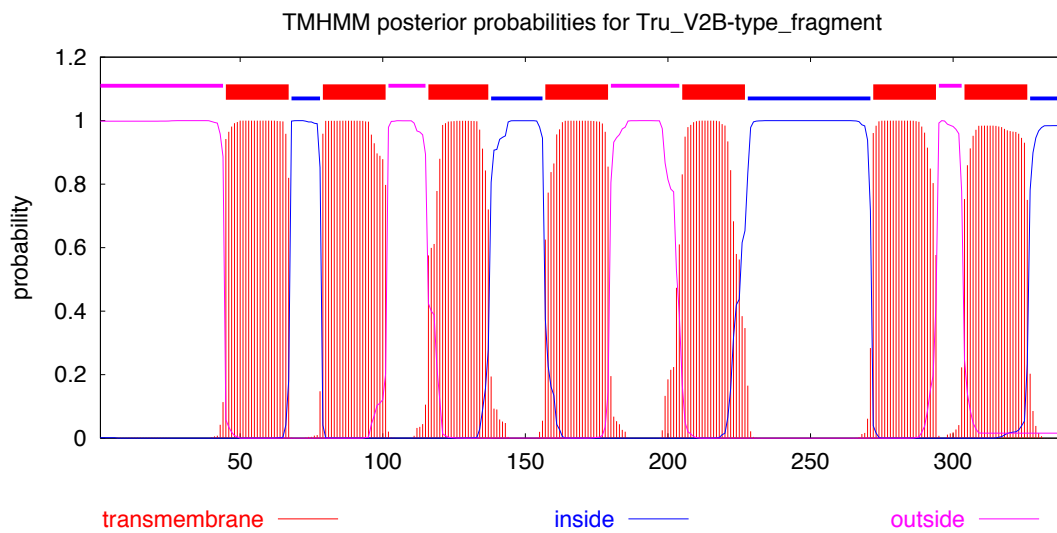
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RRPRRRGSVPAEFSATHSSSS*



Note: The sequence has been cut between the residues SAL and VTA (underlined above) due to interrupted reading frame in the genomic sequence and the absence of canonical splice sites. This excluded region encodes part of the intracellular loop 3 (IL3) that is expanded in the identified teleost V2A sequences. Additionally, a frame-shift was identified in the last predicted exon. This frame-shift is likely due to a sequencing or assembly error since the whole exon could be predicted. The ambiguity at the residue affected by the frameshift is represented by the character X highlighted in yellow above.

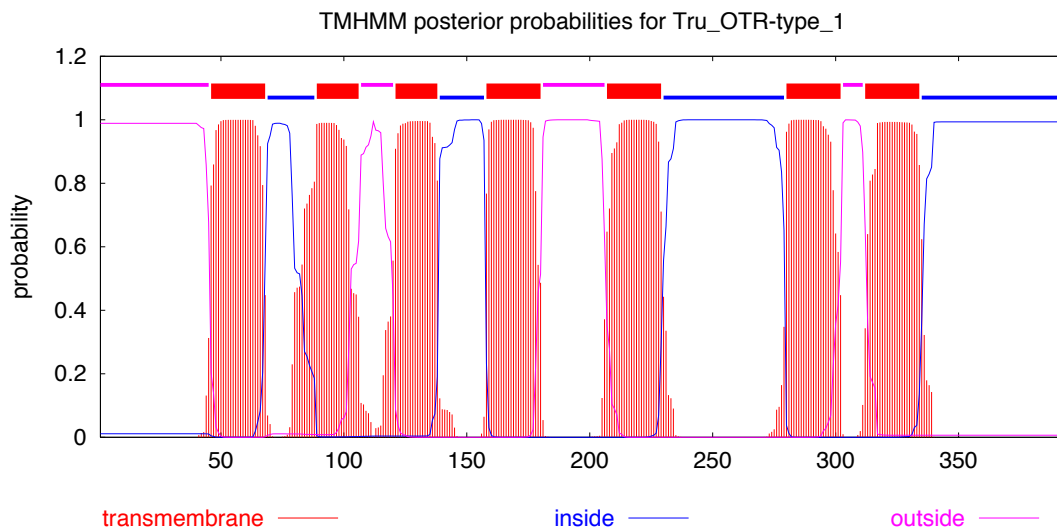
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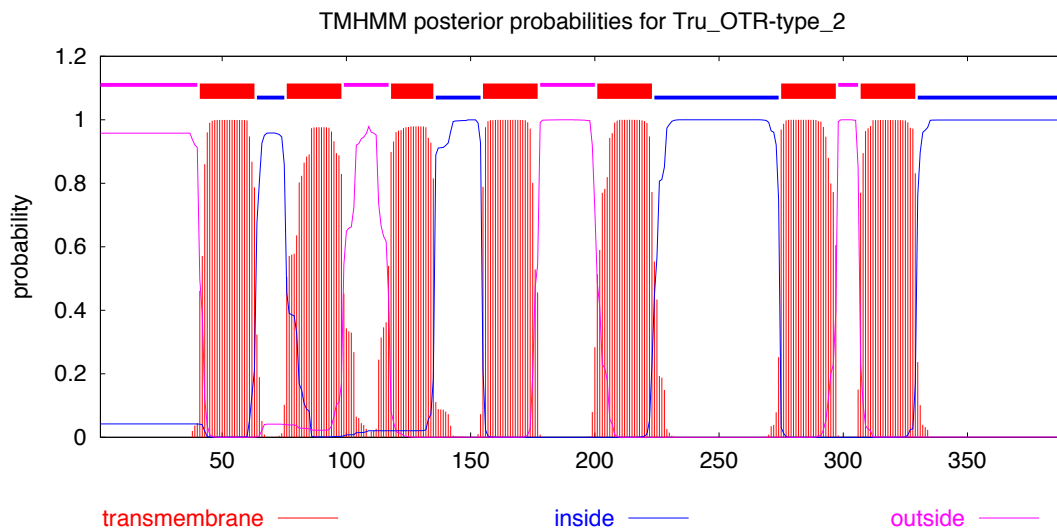
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REVGSAGSGVYDCWGD FVKP WGAKAYITWISLTIIYIIPVAILSVCYGLISFKIWQNFRLK
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>Tru_OTR_2

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GSGVYDCWGDVQPWGTKAYITWMSLSIYIIPVAILCVCYGLICFKIWKNFNVKTSRDRF
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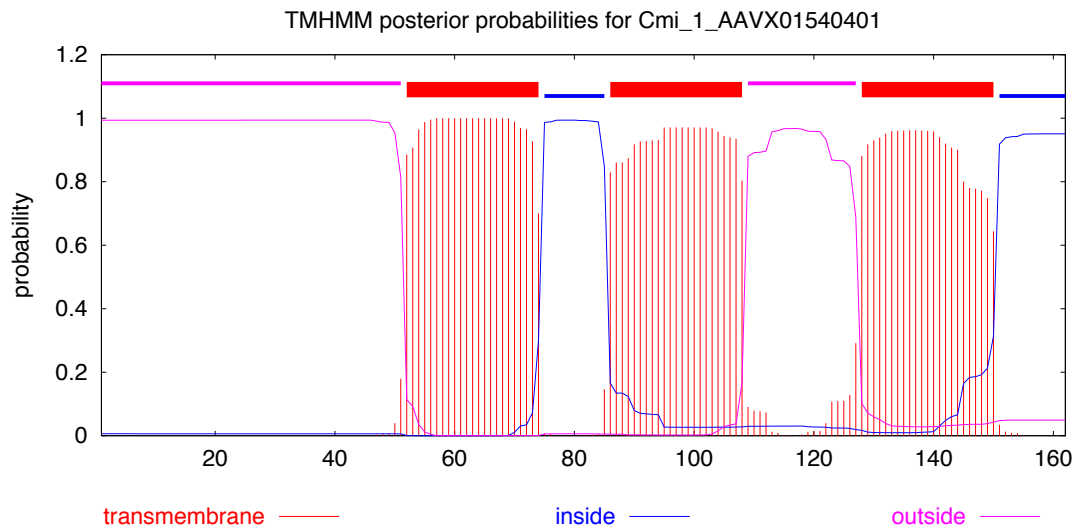


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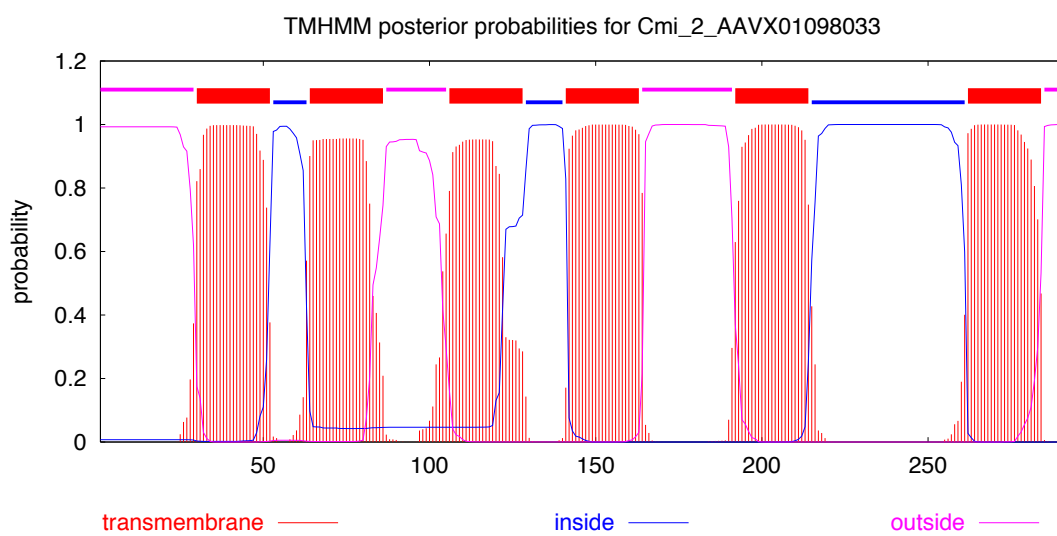
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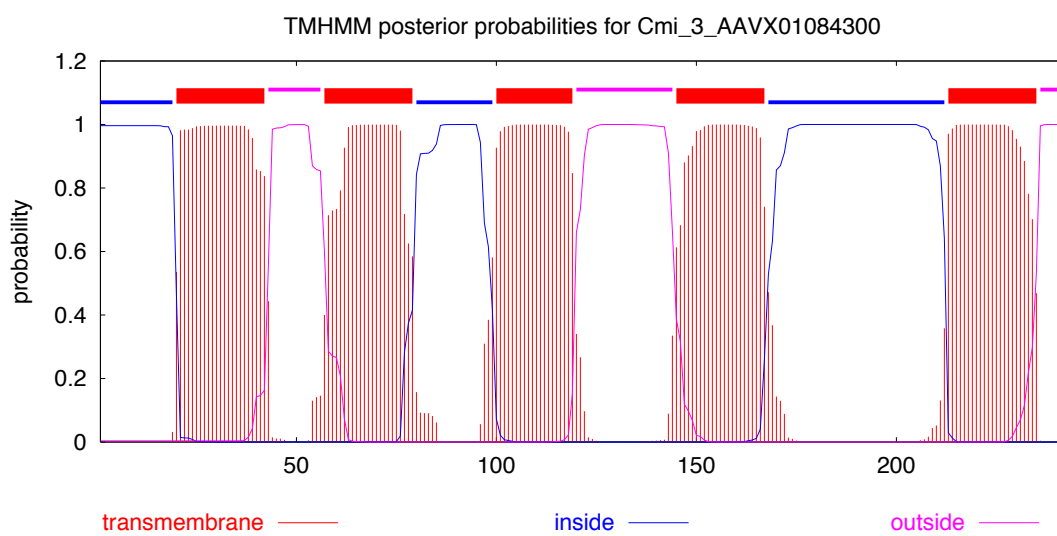
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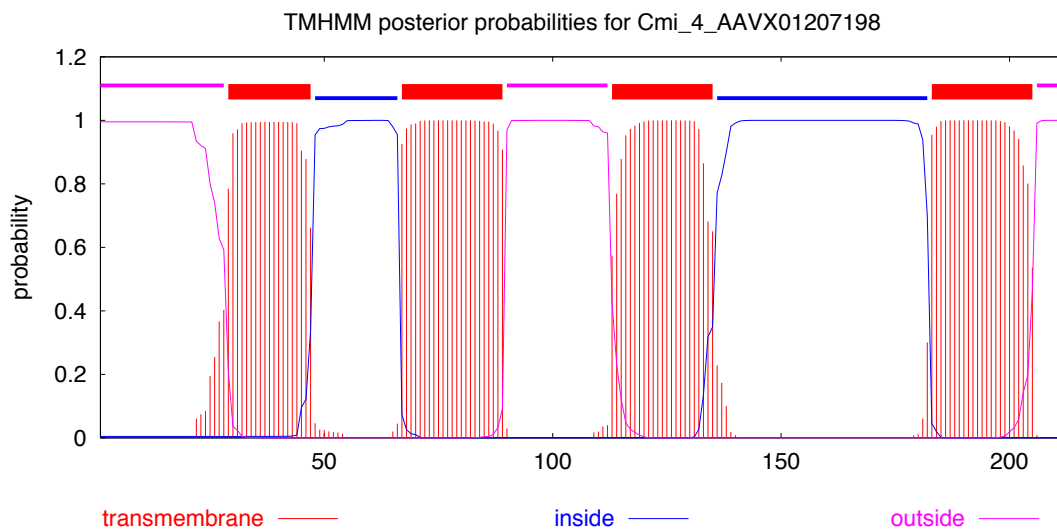
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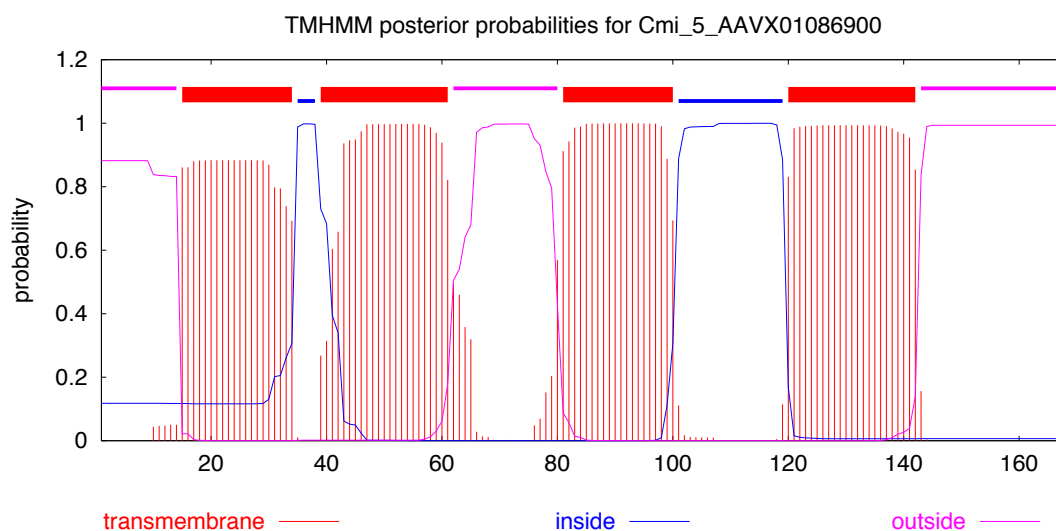


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Note: The ambiguous residue marked with the character **X** is likely the result of a sequencing error in the original genomic scaffold.