

FINAL PREDICTION

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1: (in) 18-34 (2.46)
 2: 62-78 (2.48)
 3: 90-111 (3.96)
 4: 118-134 (-0.17)
 5: 163-187 (0.22)
 6: 196-220 (3.56)
 7: 258-274 (0.38)
 8: 323-339 (1.51)
 9: 741-763 (0.91)
 10: 838-859 (0.78)

10	20	30	40	50	60
+++++IIIIIXXXXXXXXXXOOOO-----					
MLSRLFRMHGLFVASHPWEVIVGTVTLTICMMSNMFTGNKICGWNYECPKFEEDVLSS					
70	80	90	100	110	120
-OOOXXXXXXXXXIIII+++++IIIIIXXXXXXXXXXXXXXOOOO-----OOO					
DIIILTITRCIAILYIFQFQNLRLGSKYILGIAGLFTIFSSVFVSTVVIHFLDKELTG					
130	140	150	160	170	180
OXXXXXXXXXIIII+++++IIIIIXXXXXXXXXXXXXX					
LNEALPFFLLIDLRSRSTLAKFALSSNSQDEVRENIARGMAILGPTFTLDALVECLVIG					
190	200	210	220	230	240
XXXOOO-----OOOXXXXXXXXXXXXXXXXXIIII+++++					
VGTMSGVRQLEIMCCFGCMSVLANYFVFMFTFFPACVSLVLELSRESREGRPIWQLSHFAR					
250	260	270	280	290	300
+++++IIIIIXXXXXXXXXXOOOO-----					
VLEEEENKPNPVTQVRKMIMSLGLVLVHAHSRWIADPSPQNSTADTSKVSLGLDENVSKR					
310	320	330	340	350	360
-----OOOXXXXXXXXXIIII+++++					
IEPSVSLWQFYLSKMISMIDIEQVITLSLALLLAVKYIFFEQTETESTLSLKNPITSPVVT					
370	380	390	400	410	420
+++++					
QKKVPDNCCRREPLVRNNQKCDSEETGINRERKVEVIKPLVAETDTPNRATFVVGNS					
430	440	450	460	470	480
+++++					
SLLDTSVSLVTQEPEIELPREPRNEECLQILGNAEKGAKFLSDAEIIQLVNAKHIPAYK					
490	500	510	520	530	540
+++++					
LETLMETHERGVSIRRQLLSKKLSEPSSLQYLPYRDYNSLVMGACCENVIGYMPIPVGV					
550	560	570	580	590	600
+++++					
AGPLCLDEKEFQVPMATTEGCLVASTNRCRAIGLGGASSRVLADGMTRGPVVRPRAC					
610	620	630	640	650	660
+++++					
DSAEVKAWLETSEGFVIKEAFDSTSRFARLQKLHTSIAGRNLIRFQSRSGDAMGMNMI					
670	680	690	700	710	720

+++++
SKGTEKALSKLHEYFPEMQILAVSGNYCTDKKPAAINWIEGRGKSVVCEAVIPAKVVREV

730 740 750 760 770 780
+++++IIIIXXXXXXXXXXXXXXXXXOOO-----
LKTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITL

790 800 810 820 830 840
-----OOO
MEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLAR

850 860 870 880 890
OXXXXXXXXXXXXXXXXXIIII+++++
IVCGTVMAGELSLMAALAAGHLVKSHMIHNRSKINLQDLQGACTKKTAAA

--- Key:
+ : Inside loop
- : Outside loop
O : Outside helix cap
X : Central transmembrane helix segment
I : Inside helix cap
