

logo

NTDB id 39398 HIBPF RS00285 WP 013525419.1
NTDB id 1359 HI 0061 AAC21739.1
consensus

85
85

logo

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consensus

VTFKIQEILHQDDYQTLIATATL^ANNLQEQRIFLNWKAKEVPQLSEI^WQAEISLR^SLSARLNFGGFDRQQWYFSKGITAF^YGTVKS
 VTFKIQEILHQDDYQTLIATATL^ANNLQEQRIFLNWKAKEVPQLSEI^WQAEISLR^SLSARLNFGGFDRQQWYFSKGITAF^YGTVKS
 VTFKIQEILHQDDYQTLIATATL^ENNLQEQRIFLNWKAKEVPQLSEI^WQAEISLR^SLSARLNFGGFDRQQWYFSKGITAV^GGTVKS

170
170

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AVKIANVSSLRAEKLQQVRKQTEGLSLQGLLIAAFGERAWLDKTTWSIYQQSNTAHLIAISGLHIGLAMGIGFCLARWQVFEP
AVKIANVSSLRAEKLQQVRKQTEGLSLQGLLIAAFGERAWLDKTTWSIYQQSNTAHLIAISGLHIGLAMGIGFCLARVVQVFCP
AVKIANVSSLRAEKLQQVRKQTEGLSLQGLLIAAFGERAWLDKTTWSIYQQSNTAHLIAISGLHIGLAMGIGFCLARVVQVFP

255
255

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TRFIHPYFPLVF^GSVLFALIIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQL^LFT^LVVGFL^LFC^DPL^MPLSV^SFW^LSCGAVG^C
 TRFIHPYFPLVF^GSVLFALIIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQL^LFT^LVVGFL^LFC^DPL^MPLSV^SFW^LSCGAVG^C
 TRFIHPYFPLVF^GSVLFALIIYAYLAGFSVPTFRAISALVFVLFIQIMRRHYSPIQL^LFT^LVVGFL^LFC^DPL^MPLSV^SFW^LSCGAVG^C

340
340

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L L W R Y V P F S L F Q W K N R P F S P K V R W I F S L F H L Q F G L L L F F T P L Q L F L F N G L S L S G F L A N F M A V P I Y S F L L V P L I L F A V F T N G T M
 L L W R Y V P F S L F Q W K N R P F S P K V R W I F S L F H L Q F G L L L F F T P L Q L F L F N G L S L S G F L A N F M A V P I Y S F L L V P L I L F A V F T N G T M
 L L W R Y V P F S L F Q W K N R P F S P K V R W I F S L F H L Q F G L L L F F T P L Q L F L F N G L S L S G F L A N F M A V P I Y S F L L V P L I L F A V F T N G T M
 *

425
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FSNQLANKLAEGITGLISVFQGNW^{FN}VSFNLAL^{GL}LTALCAGIFMLII^{WR}IYREPEISSSNWQIKRAKFFTLNLSKPLLKNERIN^V
 FSWQLANKLAEGITGLISVFQGNW^{FN}VSFNLAL^{GL}LTALCAGIFMLII^{WR}IYREPEISSSNWQIKRAKFFTLNLSKPLLKNERIN^V
 FSWQLANKLAEGITGLISVFQGNW^{LT}VSFNLAL^{GL}LTALCAGIFMLII^{WN}IYREPEISSSNWQIKRAKFFTLNLSKPLLKNERIN^V

510
510

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The figure displays a sequence logo for a protein segment, likely a transmembrane domain, comparing three different sequences. The sequences are aligned horizontally, with each column representing a specific position. The top sequence is L R C S F G I I L L C F M I L L F K Q = S K P T W Q V D T L D V G Q G L A T L I V K N G K G I L Y D T G S S W R G G S M A E I L P Y L Q R E G I V L E K L I L S H D D. The middle sequence is L L C S F G I I L L C F M I L L F K Q F S K P T W Q V D T L D V G Q G L A T L I V K N G K G I L Y D T G S S W R G G S M A E I L P Y L Q R E G I V L E K L I L S H D D. The bottom sequence is L R C S F G I I L L C F T I L L F K Q L S K P T W Q V D T L D V G Q G L A T L I V K N G K G I L Y D T G S S W R G G S M A E I L P Y L Q R E G I V L E K L I L S H D D. The logo uses color coding to highlight differences between the sequences at various positions.

595
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680
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765
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consensus



788
788

-  non conserved
-  similar
-  $\geq 50\%$ conserved