

logo

NTDB id 543 H702 RS02375 WP 160172984.1  
NTDB id 406276 GPA00 RS02030 WP 232524224.1  
NTDB id 544 H702 RS02380 WP 039696235.1  
consensus

MIEIWFIIITMLLNFGVIVGILFQQITKVKLTFLLEWVLIIFLQAVSFFMNPQKYSMVALVLMKDISVIFCLLSVSFH  
.....  
MIEIVVFIITMLLNFGVIVGILFQQITKVKLTFLLEWVLIIFLQAVSFFMNPQKYSMVALVLMKDISVIFCLLSVSFH

0  
0  
80

logo

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NTDB id 406276 GPA00 RS02030 WP 232524224.1  
NTDB id 544 H702 RS02380 WP 039696235.1  
consensus

HNPKIGIRYHIFYALYPINLYMILHEVYCYIIFAIFSIQLTSLTMTSPSVGKMIIGMITAVIIPPIFYLLSKWLNIDISN  
.....MYYLVSRWLNIDISN  
.....MTSPSVGKMIIGMITAVIIPPIFYLLSKWLNIDISN  
HNPKIGIRYHIFYALYPINLYMILHEVYCYIIFAIFSIQLTSLTMTSPSVGKMIIGMITAVIIPPIFYLLSKWLNIDISN  
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15  
36  
160

logo

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NTDB id 544 H702 RS02380 WP 039696235.1  
consensus

VRKTLKKNYLSARALRFVNVLLLLFYPGMECFGAIAPFEKMSMNRNIYRAVIFIFYELLFIFLYLNFRHGQEQKNEELLRN  
SQQSKHTEPKIFNIINILMVSYFLFDAIIVKPFHNAD.NDAIRGIVAFIYLLILLFVFLFYLNFRHGQEQKNELLRN  
VRKTLKKNYLSARALRFVNVLLLLFYPGMECFGAIAPFEKMSMNRNIYRAVIFIFYELLFIFLYLNFRHGQEQKNEELLRN  
VRKTLKKNYLSARALRFVNVLLLLFYPGMECFGAIAPFEKMSMNRNIYRAVIFIFYELLFIFLYLNFRHGQEQKNEELLRN  
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94  
116  
240

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consensus

QEMELAALENYSKHVESLYQEVRSFRHDYANVLMSLKMGIDQGNLDDIKKIYDEITADSTKLKVNKFDLTRLANITDSG  
QEMELAALENYSKHVESLYQEVRSFRHDYANVLMSLKMGIDQGNLDDIKKIYDEITADSTKLKVNKFDLTRLANITDSG  
QEMELAALENYSKHVESLYQEVRSFRHDYANVLMSLKMGIDQGNLDDIKKIYDEITADSTKLKVNKFDLTRLANITDSG  
QEMELAALENYSKHVESLYQEVRSFRHDYANVLMSLKMGIDQGNLDDIKKIYDEITADSTKLKVNKFDLTRLANITDSG  
!!!!!!!!\*!!!!!!!!!!!!!!!!!!!!

174  
196  
320

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consensus

VKSLMSAKFLHAENQGIENSLEVAEEMGTPSPKIPPLISYIRILSILFDNAIEGALESAPKISVANFYQDGFVFMENSTK  
VKSLLSAKFLHAENRGIENSLEVAEPMKNPAIPLISYIRILSILFDNAIEGALESENPKIAVANFYQDGFVFMENSTK  
VKSLMSAKFLHAENQGITISLEVAEEMGTPKIPLISYIRILSILFDNAIEGALESAPRISVANFYQDGFVFMENSTK  
VKSLMSAKFLHAENQGITISLEVAEEMGTPKIPLISYIRILSILFDNAIEGALESAPRISVANFYQDGFVFMENSTK  
!!!!!!\*!!!!!!!!!!!!!!!!!!!!

254  
276  
400

logo

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NTDB id 544 H702 RS02380 WP 039696235.1  
consensus

EKSVDLGGKIFERGYSTKGENRGLGLATLMDFQDDYENLSVETSSLDYKFTQWRVYEKSR  
EKSVDLGGKIFERGYSTKGENRGLGLATLMDFQDDYENLSVETSSLDYKFTQWRVYEGKNG  
EKSVDLGGKIFERGYSTKGENRGLGLATLMDFQDDYENLSVETSSLDYKFTQWRVYEA...  
EKSVDLGGKIFERGYSTKGENRGLGLATLMDFQDDYENLSVETSSLDYKFTQWRVYEA...  
!!!!!!\*!!!!!!!!!!!!!!!!!!!!

315  
337  
458

ⓧ non conserved  
ⓧ similar  
ⓧ ≥ 50% conserved