```
logo
O56773    MSKGLIHPSAIRSGLVDLEMAEETVDLVHKNLADSQAHLQGEPLNVDSLPEDMRKMRLTNAPSEREIIEEDEEEYSSEDEYYLSQGQDPMVPFQNFLDELGTQIVRRMKS   110
Q5VKP1    MSKGLIHPSAIRSGLVDLEMAEETVDLVHKNLADSQAHLQGEPLNVDSLPEDMRKMRLTNAPSEREIIEEDEEEYSSEDEYYLSQGQDPMVPFQNFLDELGTQIVRRMKS   110
P0C569    MSKDLVHPSLIRAGIVELEMAEETTDLINRTIESNQAHLQGEPLYVDSLPEDMSRLRIEDKSRRTKTEEEERDEGSSEEDNYLSEGQDPLIPFQNFLDEIGARAVKFLKT   110
P06747    MSKIFVNPSAIRAGLADLEMAEETVDLINRNIEDNQAHLQGEPIEVDNLPEDMGRLHLDDGKSPNPGEMAKVGEGKYREDFQMDEGEDPSLLFQSYLDNVGVQIVRQIRS   110
consensus !!!** *!!*!! !***!!!!!!!*!!    *  * !!!!!!!!**!!*!!!!!*  *** ******* *****! ***  **** !*!!***!!**!!**!***!*****

logo
O56773    GDGFFKIWSAASEDIKGYVLSTFMKPETQATVSKPTQTDSLSVPRPSQGYTSVPRDKPSNSESQGGGVKPKKVQKSEWTRDTDEISDIEGEVAHQVAESFSKKYKFPSRS   220
Q5VKP1    GDGFFKIWSAASEDIKGYVLSTFMKPETQATVSKPTQTDSLSVPRPSQGYTSVPRDKPSNSESQGGGVKPKKVQKSEWTRDTDEISDIEGEVAHQVAESFSKKYKFPSRS   220
P0C569    GEGFFRVWSALSDDIKGYVSTNIMTSGERDTKSIQIQTEPTASVSSGNESRHDSESMHDPNDKKDHTPDHDVVPDIESSTDKGEIRDIEGEVAHQVAESFSKKYKFPSRS   220
P06747    GERFLKIWSQTVEEIISYVAVNFPNPPGKSSEDKSTQTTGRELKKETTPTPSQRESQSSKARMAAQTASGPPALEWSATNEEDDLS.VEAEIAHQIAESFSKKYKFPSRS   219
consensus ! *!***!!*****!**!!** **************!!****************  ********** **********************!*!*!!!*!!!!!!!!!!!!!!!

logo
O56773    SGIFLWNFEQLKMNLDDIVKTSMNVPGVDKIAEKGGKLPLRCILGFVSLDSSKRFRLLADTDKVARLMQDDIHNYMTRIEEIDHN   305
Q5VKP1    SGIFLWNFEQLKMNLDDIVKTSMNVPGVDKIAEKGGKLPLRCILGFVSLDSSKRFRLLADTDKVARLMQDDIHNYMTRIEEIDHN   305
P0C569    SGIFLWNFEQLKMNLDDIVKAAMNVPGVERIAEKGGKLPLRCILGFVALDSSKRFRLLADNDKVARLIQEDINSYMARLEEAE..   303
P06747    SGILLYNFEQLKMNLDDIVKEAKNVPGVTRLARDGSKLPLRCVLGWVALANSKKFQLLVESNKLSKIMQDDLNRYTSC.......   297
consensus !!!*!*!!!!!!!!!!!!!!!* *!!!!!* *!**!*!!!!!!*!!*! !**!!*!*!!****!*****!*!* *!**********
```

X non conserved

X ≥ 50% conserved