```
logo                                        MTIKVLFVDDHEMVRIGISSYLSTQSDIEVVGEGASGKEAIAKAHELKPDLILMDLLMEDMDGVEATTQIKKDLPQIKVLMLTS
                                            MTKVNIVIIDDHQLFREGVKRILDFEPTFEVVAEGDDGDEAARIVEHYHPDVVIMDINMPNVNGVEATKQLVELYPESKVIILSI
NTDB id 20529 SAV RS10310 WP 000153535.1    .MTIKVLFVDDHEMVRIGISSYLSTQSDIEVVGEGASGKEAIAKAHELKPDLILMDLLMEDMDGVEATTQIKKDLPQIKVLMLTS   84
NTDB id 4 SA RS09755 WP 000153535.1         .MTIKVLFVDDHEMVRIGISSYLSTQSDIEVVGEGASGKEAIAKAHELKPDLILMDLLMEDMDGVEATTQIKKDLPQIKVLMLTS   84
NTDB id 83 BSU 35490 NP 391429.1            MTKVNIVIIDDHQLFREGVKRILDFEPTFEVVAEGDDGDEAARIVEHYHPDVVIMDINMPNVNGVEATKQLVELYPESKVIILSI   85
consensus                                    ********!!!***!*!****!******!!!*!!**!*!!********!!***!!**!****!!!!!*!*****!**!!**!**

logo                                        FIEDKEVYRALDAGVDSYILKTTSAKDIADAVRKTSRGESVFEPEVLVKMRNRMKKR                AELYEMLTERE
                                            HDDENYVTHALKTGARGYLLKEMDADTLIEAVKVVAEGGSYLHPKVTHNLVNEFRRLATSGVSAHPQHEVYPEIRRPLHILTRRE
NTDB id 20529 SAV RS10310 WP 000153535.1    FIEDKEVYRALDAGVDSYILKTTSAKDIADAVRKTSRGESVFEPEVLVKMRNRMKKR..................AELYEMLTERE   152
NTDB id 4 SA RS09755 WP 000153535.1         FIEDKEVYRALDAGVDSYILKTTSAKDIADAVRKTSRGESVFEPEVLVKMRNRMKKR..................AELYEMLTERE   152
NTDB id 83 BSU 35490 NP 391429.1            HDDENYVTHALKTGARGYLLKEMDADTLIEAVKVVAEGGSYLHPKVTHNLVNEFRRLATSGVSAHPQHEVYPEIRRPLHILTRRE   170
consensus                                   ******!**!!**!***!*!!***!*****!!*****!*!***!*!*****!*****                ******!!*!!

logo                                        MEILLLIAKGYSNQEIASASHITIKTVKTHVSNILSKLEVQDRTQAVIYAFQHNLIQ
                                            CEVLQMLADGKSNRGIGESLFISEKTVKNHVSNILQKMNVNDRTQAVVVAIKNGWVEMR
NTDB id 20529 SAV RS10310 WP 000153535.1    MEILLLIAKGYSNQEIASASHITIKTVKTHVSNILSKLEVQDRTQAVIYAFQHNLIQ..   209
NTDB id 4 SA RS09755 WP 000153535.1         MEILLLIAKGYSNQEIASASHITIKTVKTHVSNILSKLEVQDRTQAVIYAFQHNLIQ..   209
NTDB id 83 BSU 35490 NP 391429.1            CEVLQMLADGKSNRGIGESLFISEKTVKNHVSNILQKMNVNDRTQAVVVAIKNGWVEMR   229
consensus                                   *!*!***!*!*!!**!*****!**!!!!*!!!!!!!*!**!*!!!!!!**!*******
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X non conserved

X similar

X $\geq$ 50% conserved