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NTDB id 1073 ABD1 RS00865 WP 015451369.1	MLTQLSSHHYHTLKVWYLVQHSLSVSFKKIIDYFGNCEK.ATQPDGLAKWSSSLGLHANHLKRVNEFQTTQG	69
NTDB id 1043 HON27 RS16615 WP 168727007.1	MLTQLSSHQYHTLKVWYLVQHSLSVSFKKIIDYFGNCEK.ATQPDGLAKWSSSLGLHANHLKRVNEFQTPQG	69
NTDB id 114 BSU 16110 NP 389493.1	MDQAAVCLTICRINQLLSPSLILKWWKADP.....SMSLTSPVLQTVTRDQIKAAA...L.....KNE	55
NTDB id 626 LCA RS04960 WP 011374694.1	MLTKNQLLLVHLAAGFGTISELRLAAWLSTSHNWALSALETIAQIARLPERY.....W.....PTF	56
NTDB id 599 KW2 RS05940 WP 021037268.1	MITNFDLFRW..KKAGMTNGLVKNLLKFFRKY.DRKISLRQMGGVAQV..KS.....I.....PNF	51
NTDB id 525 SMSK321 RS06295 WP 000705298.1	MKITNYEIYKL.KKSGLTNQILKVLEYGENV.DQELLGLDIADISGC..RN.....P.....AVF	52
NTDB id 267 KZH43 RS05590 WP 000705306.1	MKITNYEIYKL.KKSGLTNQILKVLEYGENV.DQELLGLDIADISGC..RN.....P.....AVF	52
NTDB id 226 SPD RS05990 WP 000705306.1	MKITNYEIYKL.KKSGLTNQILKVLEYGENV.DQELLGLDIADISGC..RN.....P.....AVF	52
NTDB id 192 SPR RS05715 WP 000705306.1	MKITNYEIYKL.KKSGLTNQILKVLEYGENV.DQELLGLDIADISGC..RN.....P.....AVF	52
NTDB id 157 SP RS06205 WP 000705306.1	MKITNYEIYKL.KKSGLTNQILKVLEYGENV.DQELLGLDIADISGC..RN.....P.....AVF	52
NTDB id 497 SM12261 RS05565 WP 000705318.1	MKITNYEIYKL.KKSGLTNQVLALEYGENV.DQELLGLDIAEISGC..RN.....P.....AVF	52
NTDB id 367357 FHI56 RS07745 WP 004182435.1	MNNFELFKL.KAAGLTNLNILNILDYQKTQ.DRKLSLRDMAVVSKS..KN.....A.....VLF	50
NTDB id 407 SMU RS04605 WP 002262865.1	MDNFQLFKL.KKAGLTNLNILNIIIDYEERT.QKSLSLRDMAVVSKN..KK.....P.....LIF	50
consensus	* ***** ** ***** * * * * * *	

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NTDB id 1073 ABD1 RS00865 WP 015451369.1	QAQFEQLVQVVRQHT...DFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQ.PQIAIVGSRKPSPHGRQVAYDFAY	144
NTDB id 1043 HON27 RS16615 WP 168727007.1	QAQFEQLVQVVRQHT...DFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQ.PQIAIVGSRKPSPHGRQVAYDFAY	144
NTDB id 114 BSU 16110 NP 389493.1	IEQFYPKLPRVLAAYREQQIN.TIPISSKQYFPWLKSIYDPPAVLFAKGMTLLSKGRKIGIVGTRNPTAYGKQVNVNHLTK	135
NTDB id 626 LCA RS04960 WP 011374694.1	QASFPSTTLQRQCIDHEVRTTILTDKDYPRQLLETYLPVLLFYRGDLRLLLKQ.PCLAVVGARQATHYSKQSLLEQLLQ	135
NTDB id 599 KW2 RS05940 WP 021037268.1	IEQYKNQDV.KKLRADYKKFSSSILDDLYPERLREIYNPPVLIFYQGNIDLLKN.PKLAIVGSRLAGQSGIKSVQKIVT	129
NTDB id 525 SMSK321 RS06295 WP 000705298.1	MERYFQIDD.AHLEKEFKKIPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRSCKQGAKSVEKIIQ	130
NTDB id 267 KZH43 RS05590 WP 000705306.1	MERYFQIDD.AHLSKEFKKFPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVIQ	130
NTDB id 226 SPD RS05990 WP 000705306.1	MERYFQIDD.AHLSKEFKKFPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVIQ	130
NTDB id 192 SPR RS05715 WP 000705306.1	MERYFQIDD.AHLSKEFKKFPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVIQ	130
NTDB id 157 SP RS06205 WP 000705306.1	MERYFQIDD.AHLSKEFKKFPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVIQ	130
NTDB id 497 SM12261 RS05565 WP 000705318.1	MERYFQIDD.AHLEKEFKKFPFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVIQ	130
NTDB id 367357 FHI56 RS07745 WP 004182435.1	MEKYKSLDI.KQLKEQFDHFPTLSIFDKEYPIELKYTYNPPVLLYYQGNLDLLSK.PKLAVVGARKCSETGKQSVRKIVS	128
NTDB id 407 SMU RS04605 WP 002262865.1	MEHYKNLDS.KALRKEFNRFPSLSILDKEYPLELKNIYNPPVLLFYQGDLDLLAR.PKLAVVGSRNASQMGVAAVKKIIQ	128
consensus	** * *** * ** ***** ***** !! *! ***** !*****!*****!* *****!?! * *	

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NTDB id 1073 ABD1 RS00865 WP 015451369.1	YLSEKGGFFISSGLAYGIDEAAHQGAS.AHQRTIAVTGTGLDITTPAQNKKLAHEYILAQNGAITTEFLPGTPPLQGHFPRR	223
NTDB id 1043 HON27 RS16615 WP 168727007.1	YLSEKGGFFISSGLAYGIDEAAHQGAS.THQRTIAVTGTGLDITTPAQNKKLAHEYILAQNGAITTEFLPGTPPLQGHFPRR	223
NTDB id 114 BSU 16110 NP 389493.1	EICRKGWVIVSGLASGIDGMSHAASIKAKGRTIGVIAAGGFQHIYPRENQLADHM.AKHHTLLSEHPPETKPPQKWHFPMR	214
NTDB id 626 LCA RS04960 WP 011374694.1	GLT.A.TTIIISGLAQGADAMAHEVALQRGLAPIGVIGTGINCYPQNEHLQQVV.AEKGLLLSEYALGTPARRYQFPAR	212
NTDB id 599 KW2 RS05940 WP 021037268.1	ELN.QSFTIVSGLAKGIDTASHLSAIKTKTPTIAVIGTGLDIFYPLENRKIQEYL.AKYQLVLSEYSLGEKPLKYHFPER	207
NTDB id 525 SMSK321 RS06295 WP 000705298.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.SNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 267 KZH43 RS05590 WP 000705306.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.GNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 226 SPD RS05990 WP 000705306.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.GNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 192 SPR RS05715 WP 000705306.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.GNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 157 SP RS06205 WP 000705306.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.GNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 497 SM12261 RS05565 WP 000705318.1	GLE.NELVIVSGLAKGIDTAAHMAALQNGGKTIAVIGTGLDVFPKANKRLQDYI.GNDHLVLSEYCPGEQPLKFHFPPAR	208
NTDB id 367357 FHI56 RS07745 WP 004182435.1	ELG.NHFTIVSGLACGIDTCAHMEALKNKGNITIAVIGTGLDVYPKANKALQDYM.AKNHVLVLEYCPGEQPLKYHFPER	206
NTDB id 407 SMU RS04605 WP 002262865.1	DLS.KQFVIISGLARGIDTAAHLASLSKSGATIAVIGTGLDVHYPKENRRRLQDYI.AKNHLLVSEYEAQSQPLKYHFPER	206
consensus	* * *!!!!!!*!!!!***** *****!*****!*****!* *****!**********!!!!	

