

logo

			MYNKAELMKQAWNCFNDSNVWLSDEWISYTDKEK		TFSVCLKAAWSKAKEEIEKSK		56
Acr00188	type	II-A	MYNKAELMKQAWNCFNDSNVWLSDEWISYTDKEK		TFSVCLKAAWSKAKEEIEKSK		56
Acr00187	type	II-A	MYNKAELMKQAWNCFNDSNVWLSDEWISYTDKEK		TFSVCLKAAWSKAKEEIEKSK		56
Acr00181	type	II-A	MFNKAELMKQAWNCFNDSNVWLSDEWISYTDKEK		TFSVCLKAAWSKAKEEIEKSK		56
Acr00315	type	VI-A	MEKIKLCLRLNND		ELITTDKDEW		29
Acr00148	type	II-A	MSIKLLDEFLKKHNKTRYQLSKLTGISQNTLNDYNKKELNKYSVSFLRALSMCTGISTFDVFI				63
Acr00052	type	I-D	MEFEEELKSLVDKFFKD		KTIIRLNLRFDEKEVITYDQFQ		38
Acr00213	type	II-A	MGYIGTKRSERSQDAIEDYEVPLNHFNKDLIQAFIDENEAYDTLTKTKVRLWKEVAPRAGATSWHHTGTYYNKTDHYSLEKVADELQNGDEWEEQFKAYVKEEQ				105
Acr00013	type	I-D	MRNMGVQDIPNELIKLSEKYVKIVGE		RKNIFKTLRKKSIEKKIIEKFKFC		51
consensus			* ** * *		* * * *		

logo

			KESKHIAKSEELKAWNWAERKGLRFLNSDDEKFTSVKDETQHFGLS		VWACAMKAVKLHNDLFPQTAA		125
Acr00188	type	II-A	KESKHIAKSEELKAWNWAERKGLRFLNSDDEKFTSVKDETQHFGLS		VWACAMKAVKLHNDLFPQTAA		125
Acr00187	type	II-A	KESKHIAKSEELKAWNWAERKGLRFLNSDDEKFTSVKDETQHFGLS		VWACAMKAVKLHNDLFPQTAA		125
Acr00181	type	II-A	KEIKHISKSEELKAWNWAERKGLRFLNSDDEKFTSVKDETQHFGLS		VWACAMKAVKLHNDLFPQTAA		125
Acr00315	type	VI-A	RHRGKVSSIEQFNWKIPGNKLQKALEYSFDELYKFKQKENARETD				74
Acr00148	type	II-A	ELAELEKSYDDAGFKHLLNKYKLSFPAQEFELYCLIKFDSANIEVL		PFTFNRFENEHVNTEKDVCKALENAITVLKEKKNEL		149
Acr00052	type	I-D	EIIRBGDLLHRYSDDEKITSDEVYREYRENSIIDYWKDN		KIHIVEIDFWRSS		90
Acr00213	type	II-A	ETATSEPVFSLVIKVIWGGSMKRPKLVGHEVVMGVKKEGWLHAVSKATQSKYKLSANKVEMQKHYSLEDYSALTKDFPEFKAQKRAINKMKEMYN				202
Acr00013	type	I-D	DIIPLYILENIIKPNIVFEYSFEKSYKNKSEKIEVITKARLKFKYENY		ELKLLSVKFEKSINIS		116
consensus			* * ** ** * * * *		*		

- non conserved
- similar
- ≥ 50% conserved