

logo

			MKINNDIKELILEYVSRYFKFENDFYKLPGIKFTDAN	WQKFKNGET	STEKMGAARVN	
Acr00203	type	II-A	.....MKINNDIKELILEYVSRYFKFENDFYKLPGIKFTDAN	.....WQKFKNGET	.....STEKMGAARVN	57
Acr00202	type	II-A	.....MKINNDIKELILEYVSRYFKFENDFYKLPGIKFTDAN	.....WQKFKNGET	.....STEKMGAARVN	57
Acr00201	type	II-A	.....MKINDDIKELILEYMSRYFKFENDFYKLPGIKFTDAN	.....WQKFKNGET	.....DIEKMGAARVN	57
Acr00099	type	I-F	.....MSYLLSNGQ	.....MSYLLSNGQ	.....IIAKTSAT...	17
Acr00100	type	I-F	.....MSYLLSNGQ	.....MSYLLSNGQ	.....IVAKTSAT...	17
Acr00097	type	I-F	.....MARIAPN.....EDSTMS.....TAVIIFNSS	.....TAVIIFNSS	.....VAAVVDTE...	30
Acr00098	type	I-F	.....MVAIATYNVFNNGSGWLEPILLRTMKMN.....IAYIIRNNI	.....IAYIIRNNI	.....VLAIVSTG...	44
Acr00311	type	V-A	MHHTIARMNAFNKAFANAKDCYKKMQAWHLLNKPKEAFFPMQNTPALDNGLAALYELRGKEDAHILSILSRLYLYGAWRNTLGIYQLDEEIIKDCKELPDDTPT	.....AFENIDCWY	.....LSSMKDS...	105
Acr00200	type	II-A	.....MAYGKSRYSYRKRFSNRSNKQRREYAQEMDRLEK	.....AFENIDCWY	.....LSSMKDS...	51
consensus			.....* *.....* * * *	.....* * * *	.....* * * *	

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			AMLDCLFEDFELAMIGKAAQINYYIDNSIKLNMPFYAYYDMFKK	QLLINWLKNNRDDVIGGTGRMYTASCN	
Acr00203	type	II-A	AMLDCLFEDFELAMIGKAAQINYYIDNSIKLNMPFYAYYDMFKK	.....QLLINWLKNNRDDVIGGTGRMYTASCN	127
Acr00202	type	II-A	AMLDCLFEDFELAMIGKAAQINYYIDNSIKLNMPFYAYYDMFKK	.....QQLIKWLKNNRDDVIGGTGRMYTASCN	127
Acr00201	type	II-A	AMLDCLFDDFELAMIGKAAQINYYNDNSIKMNPFFITYYDMFKK	.....QQLIKWLKNNRDDVIGGTGRMYTASCN	127
Acr00099	type	I-F	.....LASQSVAFSGTRVAEEINAGRQNNLVN	.....AQHATIG.NGKTWDAKWA	62
Acr00100	type	I-F	.....LASQSVAFSGTRVSEETNAGRKNLVN	.....AQRATIG.NGKTWDAKWA	62
Acr00097	type	I-F	.....IANGANVTFTSTVTKEETNANRDNLVN	.....AQNGKIS.RAKRWGNEAS	75
Acr00098	type	I-F	.....LPNCTEIQYSHEKTHEETDANRDYNLVN	.....AKSAKIS.RAQRWEKEAS	89
Acr00311	type	V-A	SIFLNLPDWCYVVDISSAQIATFDDGVAKHIGFWAIYDIVEMNGINHDVLDVFVDDTDDNVYVPQPFILSSGQSVAEVL	.....DYGASLFDDDTSTNTLIKGLLPYLL	210
Acr00200	type	II-A	.....AYKDFCKYEIRLSNHSADNKYHDLNGLLVN	.....IKASKLNFVDIENKLDKIEKID	107
consensus			.....* * * * * * * * * * * * * * * *	.....* * * * * * * * * *	

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			WLCVAEPDITYKGLPVISREELTRPKHSINKKTGAVTPSEPFYIYQIGERLGSEVRRYQSIIDGQKRNRPHTKRPHIRRGHWGHGYWQGTGQAKEFRVRWQPAVFV	
Acr00203	type	II-A	.....YIANAYLEVALESSSLGSCSYMIMQMRFKDYSKGQEPGPSGRKRNRLIEWIENNLENIR	183
Acr00202	type	II-A	.....YIANAYLEVALESSSLGSCSYMIMQMRFKDYSKGQEPGPSGRKRNRLIEWIENNLENIR	183
Acr00201	type	II-A	.....YIANAYLEVALESSSLGSCSYMIMQMRFKDYSKGQEPGPSGRKRNRLIEWIENNLENIR	183
Acr00099	type	I-F	.....KLENGRMASEINP.....GEFFIA	81
Acr00100	type	I-F	.....KLEDGRMASEINP.....GEFFIA	81
Acr00097	type	I-F	.....KCE..YFCREINP.....TEFFIK	92
Acr00098	type	I-F	.....KCS..ASAVEINP.....LEFLIVD	107
Acr00311	type	V-A	WLCVAEPDITYKGLPVISREELTRPKHSINKKTGAVTPSEPFYIYQIGERLGSEVRRYQSIIDGQKRNRPHTKRPHIRRGHWGHGYWQGTGQAKEFRVRWQPAVFV	315
Acr00200	type	II-A	.....KLLLDKYRFINATN....LEHDIKCYKKGFKTKKEVI	140
consensus			.....* * * * * * * * * * * * * * * *	

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			NSGRVSS	
Acr00203	type	II-A	.....NSGRVSS	183
Acr00202	type	II-A	.....NSGRVSS	183
Acr00201	type	II-A	.....NSGRVSS	183
Acr00099	type	I-F	.....NSGRVSS	81
Acr00100	type	I-F	.....NSGRVSS	81
Acr00097	type	I-F	.....NSGRVSS	92
Acr00098	type	I-F	.....NSGRVSS	107
Acr00311	type	V-A	NSGRVSS	322
Acr00200	type	II-A	.....NSGRVSS	140
consensus			.....NSGRVSS	

 non conserved  
 similar  
  $\geq 50\%$  conserved