



MHHTIARVNAFNAKAFANAKDCYKKVRAWHLLNKPKHAFPPMONTPALDNGLAALYELRGCKEDAHILSILSRLYLYGAWRNTLGIYQLDEEIIKDKCELDPDTP

100

Sequence	Position
SQLVESIKKLIQKDTVGIEFTSKEP	83
RQTIEEIKKLLQSDVGVEINEREP	83
...IDTVQRLIQENIIGKEKVSFENS	78
SQIETIQKLLMSITEIGKVVNFENS	84
NAEFNVGQPKTENNTISIVDEKEP	98
GAKFDIDQ.FETENKTLKLEVEPKP	97
NAEYNIGQPEETVNDTTLVEIKLGKP	97
GIALHLNLWCSVNVLSTGTFLNLSLSNSLIALVFALLIGVTLH	111
GIALHLNLWCSVNVLSTGTFLNLSLSNSLIALVFALLIGVTLH	111
GIALHLNLWCSVNVLSTGTFLNLSLSNSLIALVFALLIGVTLH	111
IETITDFDMVIFDLVTDLGRVDLAEH	77
IETINDFDMVKFDLVTDLGRVELAEH	77
SQLESYKKFFEDQTAKEMVVFSEF	84
SIFNLPLPDCWCVYVDISSAQIATEDGVAKHIKGFWAIYDI	210

LINEVFAEYEFYFIIEVRYR		
LYNESSEPNFDDQVSLKFEKATKEMKQKFNELYEFRFMFTLGIVSLVILLIALVYSTISVSKPVLSEIYFKIAFFAVIIGIAVPVANWLRKKMIITVFGCY		
IVIESHFN..VERIFVDLIQLIRYPR.....		107
IIIESHFN..VERIFIMSIQLIRYPR.....		107
IIIESHFN..VERIFIDSIQLIRYPR.....		102
IVIESYRN..IERIFIKSIQLIRYPR.....		108
YYTKVCTGG.KTTFFIKKIEVE..LNIQENTNEL.....		129
EYNKVSVGG.ETTYFVNKEVE..LNTSEEFMNLFF.....		129
YYTKVSTCD.ETTYFVNKIEFETEENIQKYFNELKKYVNELF.....		138
NTNNAVPAENLFDYAYYYLEVNGKNAQAKNFQSLYFFFRNMFTLGIVSIVILIIALVYSTITSVGKDVLSSEIVFKIAFFAVIIGIAVPVANWLRKKMIITVFGCY		216
NTNNAVPAENLFDYAYYYLEVNGKNA.....		137
NTNNAVPAENLFDYAYYYLEVNGKNAQAKNFQSLYFFFRNMFTLGIVSIVILIIALVYSTITSVGKDVLSSEIVLKIAFFAVIIGIAVPVANWLRKKMIITVFGCY		216
EIDYVPFAE.VIEAVEEMLEA.....		97
AIDYVTFAE.IIEAVEEMLEA.....		97
KMLLVYYKD.TDKIYNRIDCWRETSFLNEDEEDNI.....		119
WLCVAEPDITYKGLPVSRREITRPKHSINKKTGAFVTPSEPFIYQIGERLGSEVRRYQSIIDGEQKRNRPHTKRPHIRRGHWGHWYWGQTGQAKEFRVRWQPAVFW		315
* * * * *		

logo

		<div>YADRVHSTNK</div>	
Acr00014	type I-D	.....	107
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Acr00022	type I-D	.....	138
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Acr00334	type VI-B	.....	137
Acr00335	type VI-B	YADRVHQTNK	226
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Acr00114	type I-F	.....	97
Acr00046	type I-D	.....	119
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consensus			

- non conserved
- similar
- ≥ 50% conserved