



Sequence	Position	Score
MN. NV TLEYS VVT	1	36
MN. NV TLEYS VVT	2	36
MTKFTSSVTT	3	33
MTKFTSSVTT	4	33
MSHASHNGEAPKRIEA	5	49
MTTFTSIVTT	6	33
MTTFTSIVTT	7	33
MTTFTSIVTT	8	33
MCLIWRHASHNGEAPTRIEA	9	53
MTTFTSIVTT	10	33
MTTFTSIVTT	11	33
MTTFTSIVTT	12	33
MTTFTSIVTT	13	33
MSTQYTYQQIAEDFRLWSEYV	14	85
DTAGEMSKDEF	15	85
NSLSTEDKVRLQVEAFGEEK	16	85
SPKFTKVTT	17	85
MTTITIAIEV	18	34
MKKIEMIEISQNRQNLTAFL	19	84
HIS.EIKAINA	20	84
KLADGVDVDKKSFDEICSI	21	93
LEQYQAKQS	22	93
NRWALNIPDENRNTAAWHPRTYLFSYDKDKA	23	93
INLNTNVLG	24	94
NSGIKKRIIDYPSKREVI	25	94
IANFPRAIADLV	26	94
MMEELMEKIKEFLDGKNAEYNI	27	94
GQPEETVNDTTLVEIKLGKPIELTENEYEKLSDLLRFLG	28	94
FRPTDIWENRV	29	94
NSLNVRSYKGVDF	30	94
DKNNDQ	31	94

EAYGVS	VP	SAWVEEMNAKAAQLKDG	EMLNVSHEA	
LYMSEKTLNRSD	LDTPDSEVLATREAAANLQPG	EWLTVVSHSIAA	75	
YSYKLNKRS	LDPDSEVLATREAAENLQPG	EWLTVVSHSIAA	75	
EAYGIN	VPQEVIDDLNLKAEQLKDG	EWLNVQHEA	67	
EAYGIN	VPQDVIDDLNLKAEQLKDG	EWLNVQHEA	67	
EAYGVS	VPSAVVEEMNAKAAQLKDG	EWLNVSHEA	83	
EAYGVS	VPSAVVEEMNAKAAQLKDG	EWLNVSHEA	67	
EAYGVS	VPSAVVEEVNAKAAQLKDG	EWLNVSHEA	67	
EAYGVS	VPTAVVEEMNAKAAQLKDG	EWLNVSHEA	67	
EAYGVS	VPTAVVEEMNAKAAQLKDG	EWLNVSHEA	87	
EAYGVS	VPTAVVEEMNAKAAQLKDG	EWLNVSHET	67	
EAYGVS	VPSAVTEEMNAKAAQLKDG	EWLNVSHEA	67	
EAYGVS	VPSSVVEEMNAKAAQLKDG	EWLNVSHEA	67	
EAYGVS	VPSAVVEEMNAKAAQLKDG	EWLNVSHEA	67	
EAYGVA	VPINIAARIQAQAELNAG	EWLLVEHEA	119	
EFTIER	GDFTSIDKDEAEHVKILN	KIQDIIHGYS	69	
CSHGYN.EI	YKYSPPDHEAYLFYCKGGGQ	QLNKLIAENGRFM	124	
LTMKDYLQSLSHNCCNDFNDETEQLYQYLRSTKDNRRVD	EFLKYEFVTVRYFNDDKKF	151		
..VRIYYTK	VSTIGDETTTFVNKIEFETE	ENIKQYFNELKKYVNELF	138	

- X non conserved
- X similar
- X > 50% conserved