

MEKFSLYDFLAIIILPGIAFIVVFRIIFSSLHLSLPVDIPLGLESTIVYALICGAVLYVLSFSLVKLFPRRLFGLYRHVADLYQKMKALHPIMNDTLNRQAE 100

MEKFSLYDFLAIIILPGIAFIVVFRIIFSSLHLSLPVDIPLGLESTIVYALICGAVLYVLSFSLVKLFPRRLFGLYRHVADLYQKMKALHPIMNDTLNRQAE 100

MEKFSLYDFLAIIILPGIAFIVVFRIIFSSLHLSLPVDIPLGLESTIVYALICGAVLYVLSFSLVKLFPRRLFGLYRHVADLYQKMKALHPIMNDTLNRQAE 100

MEKFSLYDFLAIIILPGIAFIVVFRIIFSSLHLSLPVDIPLGLESTIVYALICGAVLYVLSFSLVKLFPRRLFGLYRHVADLYQKMKALHPIMNDTLNRQAE 100

MEKFSLYDFLAIIILPGIAFIVVFRIIFSSLHLSLPVDIPLGLESTIVYALICGAVLYVLSFSLVKLFPRRLFGLYRHVADLYQKMKALHPIMNDTLNRQAE 100

.....MKYEVLNQIVN 11

.....MKFKELKELVN 11

.....MSYFYGNIGERKISFKEVKKIID 23

.....MAKTLHELID 10

.....MGPGKKEKIIIM 11

.....MSTQYTYQQIAE 12

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Sequence	Position	Score
MI...NSFIKSEEK...EKEIEFNPLYLILNKSET.IEA...FGREK...NSILTTTFDLWI...NLLFFDK...YKI	81	
II...DFFINSSDK...EKEINFEKPLLILTRGET.IEI...LGMPK...NSILTTTFDLWT...ELLIYDD...FKI	110	
...IFNSK...EEIEFEEPVLVLSKSQM.LEI...FGKPH...HNVLVNRGDLWT...EVLFYDSG...VKI	62	
...IFNSKNA...EEIEFEEPVMLTKSQV.REV...FGRPK...SIITAN.GDLWT...EVLFYDSG...VKI	67	
...IFNSQKA...EEIEELKEPKLSRSQV.LELLQMFGKVQ...RSIITSFGDIWT...ELLFYDSG...VKI	66	
...MFFKEKNLD...ELTLAFKRSILILTENEY.NEL...VRRPN...LSFIDK...DPWIT...SDEFVYYELSN...KVVKL	72	
...MFFKEKNLD...ELTLAFKRPLIITENEY.NEL...VKRPN...LSFEDK...DPWVT...SDEFVYYELSN...RVVKL	72	
...MFFKEKNLN...ELTLAFKRPLIVSENEY.NEL...VGRPN...LSFVDK...DPWVL...SDEFVYYELSN...TLVKL	72	
RWGLGKIYLSSEEFQCSEEKEKIRMLQSDFYDRMWYRLDFRGKLGSAKSFQCYIFFFRHSFWGLVLISLILLSYKLLAYIPACDMEDIGRREYSIDIAVPI	200	
RWGLGKIYLSSEEFQCSEEKEKIRMLQSDFYDRMWYRLDFRGKLGSAKSFQCYIFFFRHSFWGLVLISLILLSYKLLAYIPACDMEDIGWREYSIDIAVPI	200	
QWGLGKIYLSSEEFQCSEEKEKIRMLQSDFYDRMWYRLDFRGKLGSAKSFQCYIFFFRHSFWGLVLISLILLSYKLLAYIPACDMEDIGWREYSIDIAVPI	200	
RWGLGKIYLSSEEFQCSEEKEKIRMLQSDFYDRMWYRLDFRGKLGNAKSFQCYIFFFRHSFWGLVLISLILLSYKLLAYIPACDMEDIGWREYSIDIAVPI	200	
QWGLGKIYLSSEEFQCSEEKEKIRMLQSDFYDRMWYRLDFRGKLGNAKSFQCYIFFFRHSFWGLVLISLILLSYKLLAYIPACDMEDIGWREYSIDIAVPI	200	
...QVFEDSTVD...ELQLRFREDVEVSPEEF.KQL...IGQGT...LVTGTEDYGVIT...DIYEWECK...RYVKM	72	
...IFSNAEIK...EIIIKTNDSTIELSGDEF.YEL...TKDKK...FVNTSVKNAIFT...VEFEQNE...FTKF	68	
...LFFEDSNIQ...ELSLKFISFEINEEDY...RQLIELAFSQFI...YPLNDN...IEI	70	
...DFFKSQDK...QLVIFYFAEKVEVDEAEF.KEL...VGNYVP.IDFVVTGKVNVD...LYYIINKG...YVEI	68	
AN...PYYYIREAQG...QWAACNAKTMPAAKRAAVRAQM...FQGTD...VWVGSVVGEVIEP...VALIKRHPDA...LNM	75	
DFRLWSEYVDTAGEMSKDEFNSLSTEDKVRILQVEAFGEKSPKFSKTVTTKPD.FDGFQFYIEAG...RDFDGDAYTEAYG...VAVPT	94	

logo

Acr00030	type I-D	LVIYE.....NPDDKKFIHKKIKLIK.....	103
Acr00029	type I-D	ITIIYE.....NSDDKVFKIYKIKLMKN.....	132
Acr00026	type I-D	VL.....IHDNKIFRIHKKIKVIGNEGKS.	85
Acr00028	type I-D	VI.....IQDNKIFRIHKKIKMVRG.....	86
Acr00027	type I-D	VITYE.....IQDNKIG.IHKKIKMVRG.....	87
Acr00038	type I-D	IIHY.....FKEDGFINILEIDLFREKR...	95
Acr00037	type I-D	IIHY.....FKEDDIIINILEIDLFREKR...	95
Acr00039	type I-D	IIYY.....FKEKGFIHILEIDLFREKR...	95
Acr00325	type VI-B	MILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	238
Acr00329	type VI-B	MILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	238
Acr00328	type VI-B	MILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	238
Acr00327	type VI-B	MILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	238
Acr00326	type VI-B	MILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	238
Acr00048	type I-D	LI VY.....YKKDEKYYVMEIQMWREIKL..	96
Acr00040	type I-D	LFKY.....EEIDDIIAYVKEIKMWREV....	90
Acr00032	type I-D	RINT.....MELTDNEKDLLYEIQIVRTKKL..	96
Acr00031	type I-D	GYIK.....KEQGKYQLSIHAYKECEQQ.	92
Acr00112	type I-F	SSRG.....RWVELDPAHCSVGDFGRI....	97
Acr00063	type I-E, I-F	NTAAR.....IQAQAAELNAGEWLVEHEA...	119
consensus		* * * * * * * * * * * * * * * * * * * *	

- ⓧ non conserved
- ✕ similar
- ⓧ ≥ 50% conserved