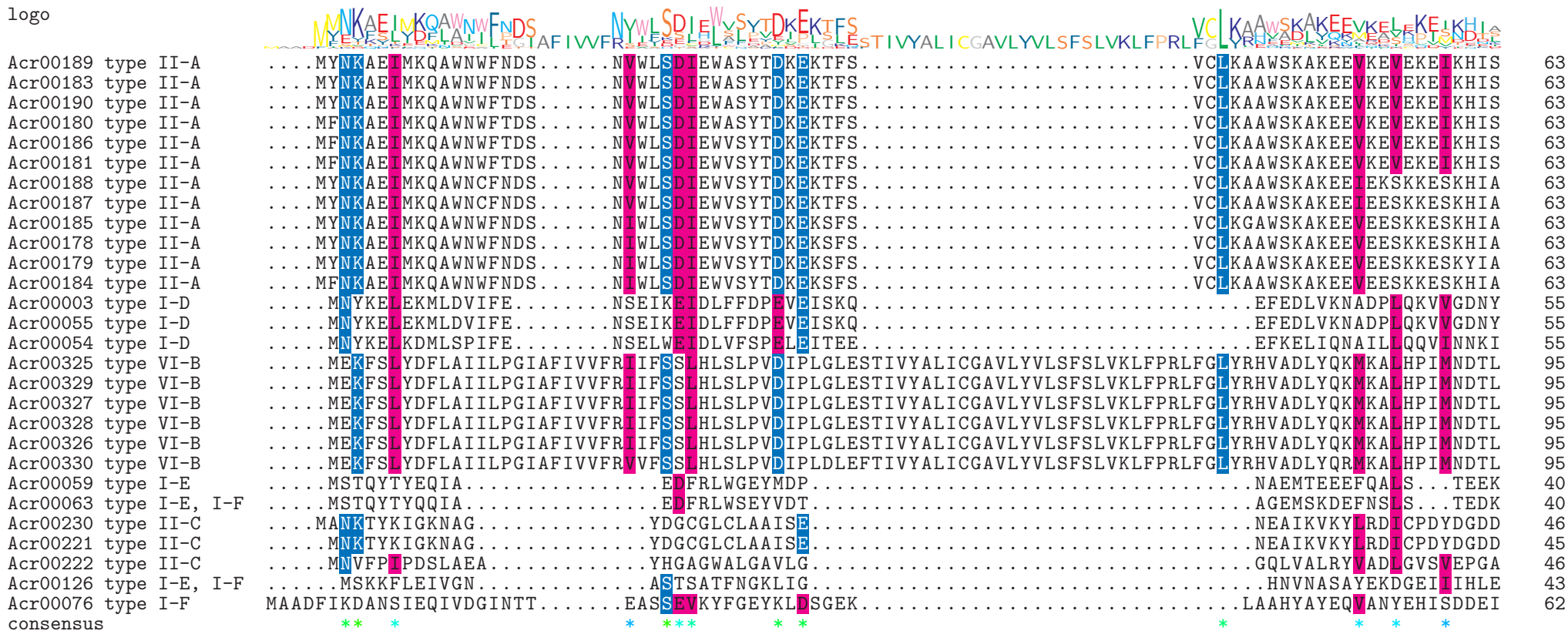


logo



Sequence logo for the protein sequence. The logo shows the conservation of amino acids at each position. The sequence is: KSE ELKAN NRE QEEB GLCK IYLS EEEF CQSEE KEK I RML QSD FYDRM I AERK LGL LFN I SDDEK FTSV D ETK L N FGL SVW ACAM KAVK L HN PACDM. The logo highlights several conserved regions, including the N-terminal KSE ELKAN NRE QEEB, the central AERK LGL LFN I SDDEK FTSV D, and the C-terminal ETK L N FGL SVW ACAM KAVK L HN.

Acr00189	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00183	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHS.....	117
Acr00190	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00180	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00186	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00181	type II-A	KSE.	ELKAWN.....	WAERKLGLRFNISDDEKFTSVKD...ETKQHFGLSVWACAMKAVKLHN.....	117
Acr00188	type II-A	KSE.	ELKAWN.....	WAERKLGLRFNISDDEKFTSVKD...ETKQHFGLSVWACAMKAVKLHN.....	117
Acr00187	type II-A	KSE.	ELKAWN.....	WAERKLGLRFNISDDEKFTSVKD...ETKQHFGLSVWACAMKAVKLHN.....	117
Acr00185	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00178	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSLWACAMKAVKLHN.....	117
Acr00179	type II-A	KSE.	ELKAWN.....	WAERKLGLRFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00184	type II-A	KSE.	ELKAWN.....	WAERKLGLHFNISDDEKFTSVKD...ETKINFGLSVWACAMKAVKLHN.....	117
Acr00003	type I-D	IT..	ETFEW.....	W...EFENQY...LEFELDYYVK...DEKIF.....VLEMHF.....	90
Acr00055	type I-D	IT..	ETFEW.....	W...EFENQY...LEFELDYYVK...DEKIF.....VLEMHF.....	90
Acr00054	type I-D	YS..	DIFYEW.....	W...EFENQY...LKLQVKYYKD...TEKIY.....LRELYF.....	90
Acr00325	type VI-B	NR..	QAERWGLGKIYLSEEEFCQSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGSAKSFCYYFFF...RHSFWGLVLISLILLSYKLLAYI...PACDM	185
Acr00329	type VI-B	NR..	QAERWGLGKIYLSEEEFCQSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGSAKSFCYYFFF...RHSFWGLVLISLILLSYKLLAYI...PACDM	185
Acr00327	type VI-B	NR..	QAERWGLGKIYLSEEEFCQSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGNAKSFCYYFFF...RHSFWGLVLISLILLSYKLLAYI...PACDM	185
Acr00328	type VI-B	NR..	QAERWGLGKIYLSEEEFCQSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGSAKSFCYYFFF...RHSFWGLVLISLILLSYKLLAYI...PACDM	185
Acr00326	type VI-B	NR..	QAERWGLGKIYLSEEEFCQSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGNAKSFCYYFFF...RHSFWGLVLISLILLSYKLLAYI...PACDM	185
Acr00330	type VI-B	NR..	QAERWGLGRIYLSEEEYCRSEEKEKIRMLQSDFYDRM	WYRLDFRGKLGNAKSFCYYFFF...RHSFLGLVLISLILLSYKLLAYI...PACE	185
Acr00059	type I-E	VAM.	QVEAFG.....	AEA.....	52
Acr00063	type I-E, I-F	VRL.	QVEAFG.....	EESPKPFSTKVTTKPDFDGFFQFYIEAGRDFDGDAYTEAYGVAVPTNIAARIQAQAEL	107
Acr00230	type II-C	KAE.	DWLRWG.....	TDSRVK....AAALEMEQYAY.....TSVGMA	79
Acr00221	type II-C	KAE.	DWLRWG.....	TDSRVK....AAALEMEQYAY.....TSVGMA	78
Acr00222	type II-C	AGVQAVRA	WIE.....	SPGAAP....VVRELQALGR.....VTIGMCS.....	80
Acr00126	type I-E, I-F	TNG..	SRWK.....	SSPEVR....MTKEEYDSFCE.....KQSRPLFVRGIEL.....	80
Acr00076	type I-F	KT..	HLQELK.....	SKDAHFDMMNESLQIAKQFCSK.....CET.....	94
consensus		*	*	* ** *	

logo

			DLFPQTAA	
			EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL	
Acr00189	type II-A	..	DLFPQTAA	125
Acr00183	type II-A	..	HLFPQTAA	125
Acr00190	type II-A	..	DLFPQTVA	125
Acr00180	type II-A	..	DLFPQTAA	125
Acr00186	type II-A	..	DLFPQTAA	125
Acr00181	type II-A	..	DLFPQTAA	125
Acr00188	type II-A	..	DLFPQTAA	125
Acr00187	type II-A	..	DLFPQTAA	125
Acr00185	type II-A	..	DLFPQTAA	125
Acr00178	type II-A	..	DLFPQTAA	125
Acr00179	type II-A	..	DLFPQTAA	125
Acr00184	type II-A	..	DLFPQTAA	125
Acr00003	type I-D	WRKIRK	96
Acr00055	type I-D	WRKIRKLE	98
Acr00054	type I-D	WREVKK	96
Acr00325	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00329	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00327	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00328	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00326	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00330	type VI-B	EDIGWREYSDIAVPIMILSALFVFLAQWFRIKMVEKMYWTFYISLIEQENSNL		238
Acr00059	type I-E		52
Acr00063	type I-E, I-F	NAGEWLLVEHEA		119
Acr00230	type II-C	...CWEFVEL		86
Acr00221	type II-C	...CWEFVEL		85
Acr00222	type II-C	...GWQFVEQ		87
Acr00126	type I-E, I-FFGAEALLS		88
Acr00076	type I-F		94
consensus		*		

- ☐ non conserved
- similar
- ≥50% conserved