




Protein	Sequence	Score
1	MNLKKVKRIIDMFFKEK...NLNE...LTLAFKRPLIVSENEYN...ELVGRPNLSFVD....KD	52
2	MGFREVKRILNIFLKDE...NIEE...LTLKFENPLKITLDEYN...ELTRNFKLIDAK....ND	52
3	MNGNEIVEEILEFLNKKGAKFDIDQ.F..ETENKTLKLEVEFPKPIILTETEYDMLYDLLKSLGFYPVNGAENKIN	73
4	MDYEEVIQTIKEFFNSKNAEFNVGQPQ...KTENNTISIVDFKEPIELTEEYDLDYDFLDNLGFGYPINGAENQVN	74
5	MNTQLLKQI...IFNSK...EEEIFEPEPLVLSKSKQMLEI...FCKPHHNVLVNRGDLWT	51
6	MKAQLPKQILKQI...IFNSKNAEEEIFEPEPMLTKSQVREV...FGRPKSIITAN.GDLWT	56
7	MKTQLLKQ...IFNSQKAEIEELKEPLKLSRSQVLELLQMFGKQVRSIITSRGDIWT	55
8	MLYYSKRLKILRHEKIKRYCKRMKKDLNIRFYIMYISDQKMTNENVKKIRKIIDF..FINSSDKEKEINFEKPLLTRGETIEI...LCMPKNSILTRFDLWT	100
9	MSFSYISISDKKMISENVKKLKEMINS..FIKSEEKEKEIFENPYLILNLSKETIEA...FGRKNSILTRFDLWI	71
10	MERLSIYELLSFVVGLVIMIELMNFSAEYVFGK.AP..LITAGNLSDSLFFFAIALFIGCLIHIT..FRLIKRKWYQKLACTPM	80
11	MDRLSIYELLSFVVPGVIMIELINFSAEYVFGK.DR..LITAGNLSDGLLFFFAIALFIGCLIHIT..FRLIKRKWYKKLAYKPI	80
12	MDEIDDLSDLPMPRFIWGFAVIANKGGDVMHDEFEY..LTHTRSPRFTCRVVELEDMPADSED....SGIDGRIVHHD....DP	74
13	MDDMDEIDDLSDLPMPRFIWGFAVIANKGGDVMHDEFEY..LTHTRSPRFTCRVVELEDMPADSED....SGIDGRIVHHD....DP	77
14	MDDMDEIDDLSDLPMPRFIWGFAVIANKGGDVMHDEFEY..LTHTRSPRFTCRVVELEDMPADSED....SGIDGRIVHHD....EP	77
15	MDDMDELDDLSDLPMPRFIWGFAVIANKGGDVMHDEFEY..LTHTRSPRFTCRVVELEDMPADSED....SGIDGRIVHHD....EP	77
16	MEFEDLDVVLYVFFENP...EMKSFEFEFKQLFETTESGLRYLIGVPDSRNKIKNNN..EIIIE	58
17	MEKQDLEKIESDIINDWTEADDLDDALDFLMKEKVSEFKIKFKDPLKVTEEEYRELLGNYSNIVSSNG..ITID	74
18	MHICKSEVKGMSMQNLSQLESYMKKF..FEDQTAKEVMVLFSEPIVITEEEYRQLIS..GGRYIAGTNYGMINE	72
19	MIYYIKDLKVKGKIFENLMNKEAVEGLITFLKKAEFEIYSRENYSKYNKWFEMWKSPTSSSLVFWKNYSFRCHLLFVIEKDGECLGIPASVFESVLQIYLDAPF	103
20	MFKEF...LEKCLRYGNLYILEETGDR....KKVKRISKRHGKVTEA	40
21	MTNIIMVKNRMVNTVVRKEVTKLYYDIKRFNDPNAKKLILKYDKPTIVRKSAFFS..WIAGTCTIYEHENTYYYEDD	75
22	MDEGTLINILTGPADKPLWFEFIGIGVTISLAAGWYLRAFGAWEKQK.KRELELQHKQRKLEIKLQFEKQRYEHELKAAEGVWPLLAYFSLWEND	96
23	MKLIIVEEETNYKNLVNYTKLTNESHNILVNRLISEYITKPYELRLDLRSERYSNRDLIEFKFMLEYCKEALQDIKELAN	80

Sequence	Score
PWVLSDEFVYYELSNLTVLKLIYYFKEK..G....FIHILEIDLFREKR.....	95
CWISINMFMYYDLSKTVLKLIIHFYSDY..D....TINVYEINLFHEKR.....	95
EYVGYKNYTGIEEFENDAGDKIWL EYNKVS VGGETTYFVK NVEVELNTEEFMNLFF.....	129
NYIGYKSWGVDEFENDDGD EIVYYTKVCTGGKTTFFIKKIEVELNIQENTNEL.....	129
EVLFYDSGVKIVL...IHDNKFRIHKIKVIGNEGKS.....	85
EVLFYDSGVKIVI...IQDNKFRIHKIKMVRG.....	86
ELLFYDSGVKIVITYEIQDNKIG.IHKIKMVRG.....	87
ELLIYDD.FKIIIIYENSDDKVFKIYKIKLMKN.....	132
NLLFFDK.YKILLVIYENPDDKKFIIHKIKLIKN.....	103
DKMKNDEYITEILP..HLKEIYRANKGISATENISNGSVFDTAYYYLEAQGKISQAKNFQSIYFLFRNIVTLSLFLVPVSVIFLLASFFMNDCKLSGKIITIVIG	183
NETENNAYIKGIFT..TLKEEYSKIHNINSIDEIS.....KLN..IFEAVIT	123
DRMFYITDIGMALVNFQLFDKLPDKGKLLK NVCDEAIANWMLRREFLDDEEDEA.....	127
DRMFYITDIGMALVNFQLFDKLPDKGKLLK NVCDEAIANWMLRREFLDDEEDEA.....	130
DRMFYITDIGMALVNFQLFDKLPDKGKLLK KVCDEAIANWMLRREFLDDEEDEA.....	130
DRMFYITDIGMALVNFQLFDKLPDKGKLLK KVCDEAIANWMLRREFLDDEEDEA.....	130
EFIYYQNDDIVTKLIFYYTGTNR IYIRKIYG.....WKEKRLESEDEE.....	102
QYTYDEDDDI MYKLEFTYRKEDNKIYIYEVQG.....WREKKK.....	112
IFEFHESQKQYVKKMLLVYYKDTDKIYINRIDCWRETSFLNDEEDNI.....	119
APDTKELFVEVCNLYECLADVTTVVEHFEAEESA WHKLT HNETEVSKRVYSKDDDELLKYIPEFLDTIATNKKSQKYNQIQGKIQEINKEIATLYESSEDIYIFTEY	208
SVLLFDSGTKRTTINEIYLSNQGYFIIRDQKR.....LKLEKFK.....	79
FGQYVEMKLDYEERKKEDVIEISKIILSRLSK.....	107
KSVFVKRGDHWYFRQEQQGREYILALSENFFNKG YGVFMPGPAKENLYHFRGMIYKLLQDSKSN GNDNNEVLLKNQSMVQKKDKQAAPNKKSV EQLKDEINASLRN	201
SDEAYETDEAFEAVFRQLFEEVISNPDTVLKAFHSYTSFLEENK.....	124

logo

Acr00039	type I-D	.....	95
Acr00036	type I-D	.....	95
Acr00024	type I-D	.....	129
Acr00023	type I-D	.....	129
Acr00026	type I-D	.....	85
Acr00028	type I-D	.....	86
Acr00027	type I-D	.....	87
Acr00029	type I-D	.....	132
Acr00030	type I-D	.....	103
Acr00338	type VI-B	TLVIGGISSVIAQWFRVKMTDRIFGLYYAELTHHKK	219
Acr00323	type VI-B	T.....	124
Acr00274	type II-C	.....	127
Acr00275	type II-C	.....	130
Acr00269	type II-C	.....	130
Acr00265	type II-C	.....	130
Acr00043	type I-D	.....	102
Acr00044	type I-D	.....	112
Acr00046	type I-D	.....	119
Acr00316	type VI-A	VSNLYRESAKLEQHSKQILKE.....	229
Acr00318	type VI-A	.....	79
Acr00020	type I-D	.....	107
Acr00324	type VI-B	MLQKSEIDLD.....	211
Acr00216	type II-A	.....	124
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved