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NTDB id 1193 PAKAF RS26665 WP 003161249.1
NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
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Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169
Sequence 1	E	A	S	S	V	D	V	S	D	D	K	R	A	R	V	V	N	L	K	D	A	G	A	F	T	T	R	V	E	G	N	V	F	I	L	K	I	N	N	I	Q	S	T	A	S	P	V	K	A	S	P	A	A	S	V	S	A	P	I	K	P	K	P	Y	V	P	A	G	R	A	I	R	N	I	D	F	Q																																																																																												
Sequence 2	N	T	R	S	V	T	T	S	E	A	K	R	A	R	V	V	N	L	K	D	A	G	A	F	T	T	R	V	E	G	N	V	F	I	L	K	I	N	N	I	Q	S	T	A	S	P	V	K	A	S	P	A	A	S	V	S	A	P	I	K	P	K	P	Y	V	P	A	G	R	A	I	R	N	I	D	F	Q																																																																																												
Sequence 3	E	A	S	S	V	D	V	S	D	D	K	R	A	R	V	V	N	L	K	D	A	G	A	F	T	T	R	V	E	G	N	V	F	I	L	K	I	N	N	I	Q	S	T	A	S	P	V	K	A	S	P	A	A	S	V	S	A	P	I	K	P	K	P	Y	V	P	A	G	R	A	I	R	N	I	D	F	Q																																																																																												
Sequence 4	E	A	S	S	V	D	V	S	D	D	K	R	A	R	V	V	N	L	K	D	A	G	A	F	T	T	R	V	E	G	N	V	F	I	L	K	I	N	N	I	Q	S	T	A	S	P	V	K	A	S	P	A	A	S	V	S	A	P	I	K	P	K	P	Y	V	P	A	G	R	A	I	R	N	I	D	F	Q																																																																																												
Sequence 5	E	A	S	S	V	D	V	S	D	D	K	R	A	R	V	V	N	L	K	D	A	G	A	F	T	T	R	V	E	G	N	V	F	I	L	K	I	N	N	I	Q	S	T	A	S	P	V	K	A	S	P	A	A	S	V	S	A	P	I	K	P	K	P	Y	V	P	A	G	R	A	I	R	N	I	D	F	Q																																																																																												

Sequence	254	254	236	235	235
RGEKGEGLVVDLSDPTLSPDIQEQQGKIRLDFAKTQLPDLALRVRLDVKDFATPVQFVNSAQSDRTSITIEPSGLYDYLVIYQTD	254	254	236	235	235
RGEKGEGLVVDLSDPTLSPDIQEQQGKIRLDFAKTQLPDLALRVRLDVKDFATPVQFVNSAQSDRTSITIEPSGLYDYLVIYQTD	254	254	236	235	235
RGAQGEGLVVDLQGTINTPVDVQQGSKVVRFPGIIKIPTHLARRLNNTDFATPVASIDSYNDGSGNVISIQSTGSYEYMAVQAE	236	236	236	235	235
RGSQGEGLVVDLGSNTTPVDVQQGSKVVRITIGTKIPTHLARRLNVNDFATPVSSIDAYNDKGVGVITIQSSGSYEYMAVQAE	235	235	235	235	235
RGSQGEGLVVDLGSNTTPVDVQQGSKVVRITIGTKIPTHLARRLNVNDFATPVSSIDAYNDKGVGVITIQSSGSYEYMAVQAE	235	235	235	235	235

NKLTSIKRPQDKNVTSLKKNQNYTGKLSLDFQDIEVRRVLQLLADFTGILNVAADS VQGNITLRLKDV PWDQALDIILKTKN
 RLVTPMTTTEAERRKKNQNYTGKLSLDFQDIEVRRVLQLLADFTGILNVAADS VQGNITLRLKDV PWDQALDIILKTKN
 NRLT VSIKPMTTTEAERRK KDNFA YTG EKLSLNFQDIDVRSVLQLIADFTD LNLVASD TVQGNITLRLQNVPWDQALD LVLKTKG 339
 NRLT VSIKPMTTTEAERRK KDNFA YTG EKLSLNFQDIDVRSVLQLIADFTD LNLVASD TVQGNITLRLQNVPWDQALD LVLKTKG 339
 NKLTISLKR PQDNV. RLNS KNNQNYTGKKISLDFQDIEVRRVLQLLADFTNIMMV TADSVQGNITLRLKDV PWDQALDIILKTKN 320
 NKLTISLKR PQDKN. VTSLYKTPNYSGNKLSLDFQDIEVRRVLQLLADFTGINMVAADS VQGNITLRLKDV PWDQALDIILKTKN 319
 NKLTISLKR PQDKN. VTSLYKTPNYSGNKLSLDFQDIEVRRVLQLLADFTGINMVAADS VQGNITLRLKDV PWDQALDIILKTKN 319

LDKRRNGNVIWIAPVDELIKREEQEAKAVAQSYKLAPLQTEYQLKYAKAADIMKLITQGTTNNGNQLQFQSVRSSSTSGGHTSGGGTSTSNTLNTGV
LDKRRKLGNVLLVAPADEIAARERQELEAQQQIAELAPLRRELITQVNYAKAADIAKLFQSVISDGGQEG..... 407
LDKRRKLGNVLLVAPADEIAARERQELEAQQQIAELAPLRRELITQVNYAKAADIAKLFQSVISDGGQEG..... 407
LDKRRNGNVIWIAPVSELIKSEEEAKAIAQSTKLAPLQTEYILLKYAKAADIEKLITQGRNSGTSNSN.....TNGSATV 396
LDKRRNGNVIWIAPVAELIKAEEEEAKAVAQSVKLAPLQTEYIQLKYAKAGDIMGLITQGSNNSNGLQHTSGGGTSTSNTLNTGV 404
LDKRRNGNVIWIAPVAELIKAEEEEAKAVAQSVKLAPLQTEYIQLKYAKAGDIMGLITQGSNNSNGLQHTSGGGTSTSNTLNTGV 404

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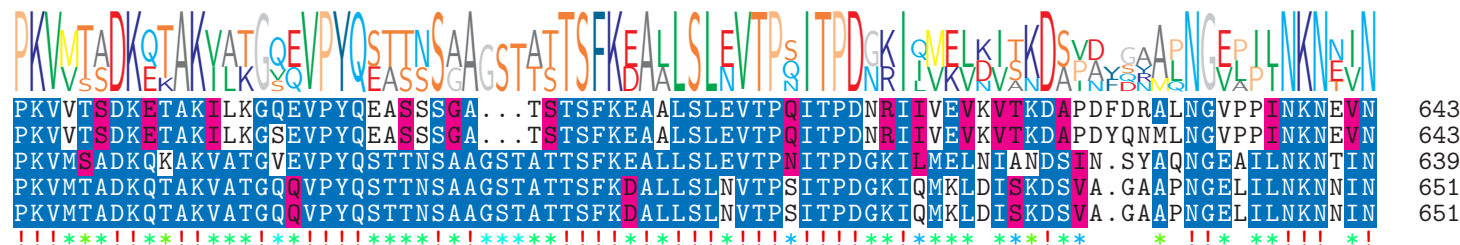
logo

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