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NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1

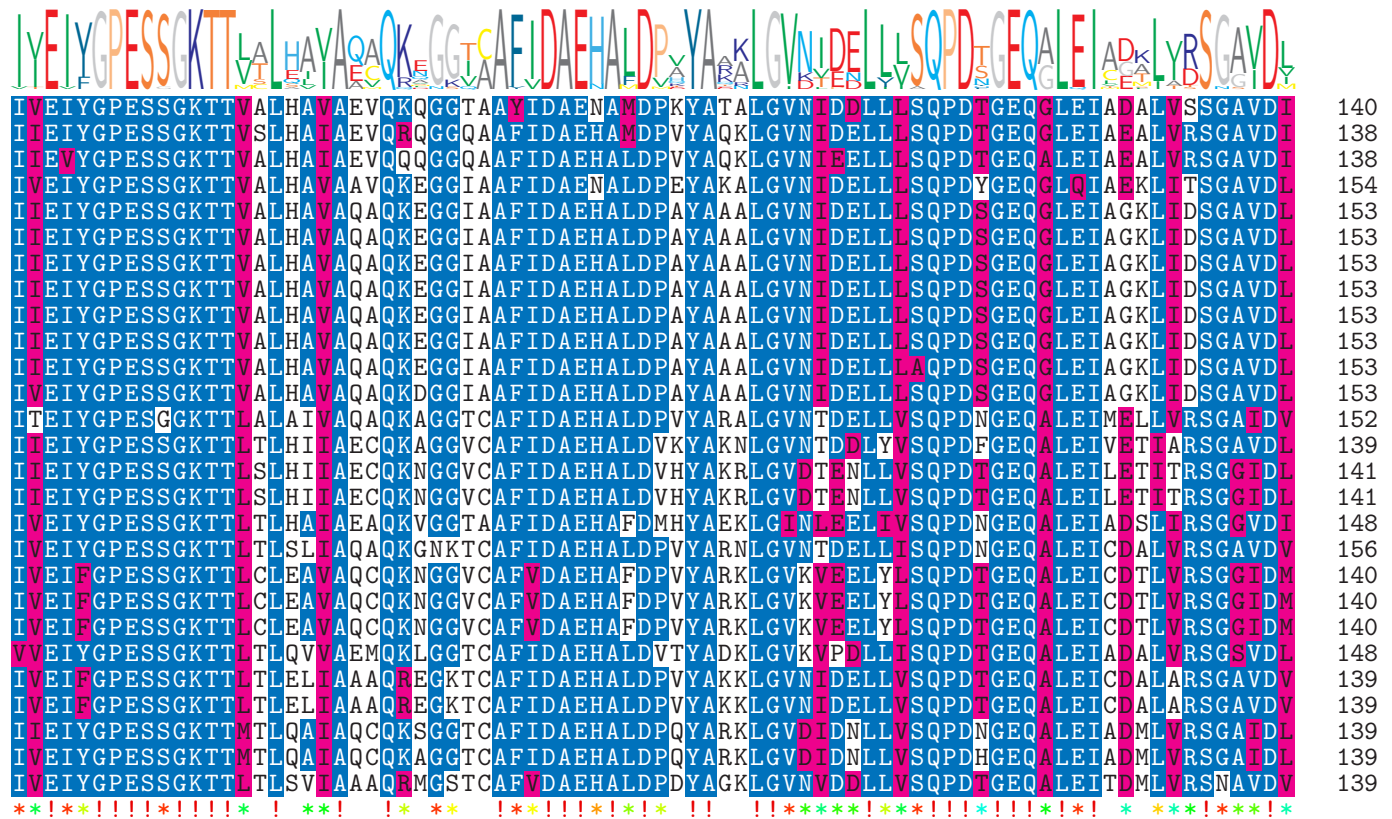
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MAKD	ER	QA	AL	DA	AL	KK	IE	KN	FG	KG	SIM	R	MG	EK	.V	D	T	Q	V	S	T	V	S	SGSL	AL	DE	AL	GV	GGY	P	R	GR																																						
MS	DR	QA	AL	DM	AL	KQ	IE	KQ	FG	KG	SIM	K	L	GE	Q	.A	E	R	R	I	S	T	V	S	SGSL	AL	D	VAL	GV	GGY	P	R	GR																																					
MS	DR	QA	AL	DM	AL	KQ	IE	KQ	FG	KG	SIM	K	L	GE	Q	.T	D	T	R	I	S	T	V	S	SGSL	AL	D	TAL	G	IG	GY	P	R	GR																																				
MATKK		K	T	N	F	D	D	I	T	K	K	Y	G	A	E	R	D	K	A	L	A	D	A	L	K	K	I	E	K	D	F	G	K	S	I	M	R	L	G	E	A	.A	N	Q	K	V	S	V	S	SGSL	AL	D	I	A	L	G	A	G	G	Y	P	K	R	G	R					
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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logo

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NTDB id 115 BSU 16940 NP 389576.2	SVRLDVRRAEQLKQGN.....DV	MGNKTKIKVVKNKVAPPFRTAEVDIMYGGGISKEGEIIDLTGELDIV	QKSGSWYSYE	292
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NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKEAFVEIMYGGGISKTGELLKIASDLDI	IKKAGAWYSYK	311
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKEAFVEIMYGGGISKTGELLKIASDLDI	IKKAGAWYSYK	311
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSS	IGKETKIKVVKNKVAPPFKEAEVEIMYGGGISRTGELVKIASDLDI	IKKAGAWFSYN	311
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKEAFVEIIMYGGGISRTGELVKIASDLGI	IKKAGAWYSYN	311
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTVKIKTVKNKVAAPFKEVELALVYGGKGFQDLSDLVGLAADM	DIKKAGSFYSYG	307
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKIVAT....L.KQNEEP	IGNRVKVVKNKVAPPFRQAEFDVDMFGEGLSREGEIDYGVKLDIV	DKSGAWFSYK	294
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA....L.KQNEQH	IGNRAKAKVVKNKVAPPFREAEFDIMFGEGISKEGEIIDYGVKLDIV	DKSGAWLSYQ	296
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVVKNKVAPPFKSAEFDIMYGGGVSKVGEILDVATDLDI	IKKSGSWFSYQ	307
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGEI	IGSETKVVKNKVAPPFREVQFDIMYGGGISRMNELLILAEANGFI	IKKSGAWFSYD	310
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGISWEGELIDIGVKNDI	INKSGAWYSYN	294
NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGISWEGELIDIGVKNDI	INKSGAWYSYN	294
NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGISWEGELIDIGVKNDI	INKSGAWYSYN	294
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS....I.KKGEV	VGNETKVVKNKVAPPFREAIQFDILYGGAGVSREGEIIDLGVEAKV	VVEKSGAWYSYN	302
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPFKEANTQIMYGGGFNREGELIDLGVKHKM	VVEKSGAWYSYN	293
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVKNKMAPPFKEAIFQILYGGKGVNQLGELVDLAVQQN	DIVQKAGAWYSYQ	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVVKNKVAPPFRQAEFQILYGGKIYRNGEIIDLGVQQGL	LVEKSGAWAYK	293
consensus	*!!**!*~	*~**~*****!!*!!*!!*!!*~	*~*****!!*!!*!!*!!*~	*****~

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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EERLGGGRENASKQFLKENTDLREIAFFVRDHHGIGEDSGVEDTE..DSTLQD.....	343
EERLGGGRENASKQFLKENTDLREIAFFVRDHHGIGEDSGVEDTE..DSTLQD.....	348
DEKIGQGAEKAKNYLKEHQDVFEIDHDKVRAAHGLDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAADNPEIFDEIDHQRVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAADNPEVFAEIDHQRVVRVQFGLIDGEEIAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	382
DERIGGQKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGMI.....SGSEDDE..GEE.....	343
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGMI.....SGSEDDE..GEE.....	347
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGMI.....SGSEDDE..GEE.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNS.....VLKATASDSNDES DVEEF..SEEEL..	372
GA KIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GER..PEE.....	348
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GA KIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GER..PEE.....	348
GERIGQGRDNCREFLRNAAELAR E IENKVR EHLGVTPMG....AV.TLAEVEED.....	352
GD KIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVEFGAV..PEEF.....	354
GD KIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVEFGAV..PEEF.....	354
GN KIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEE EEPD..LL..LES.....	349
GN KIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEE EEPD..LL..LES.....	349
GS KIGQGGKANAAKYLENPEIQEIEQQIRAKLLVTSAN....TKATPVAEDLADAD..I.....	347

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved