

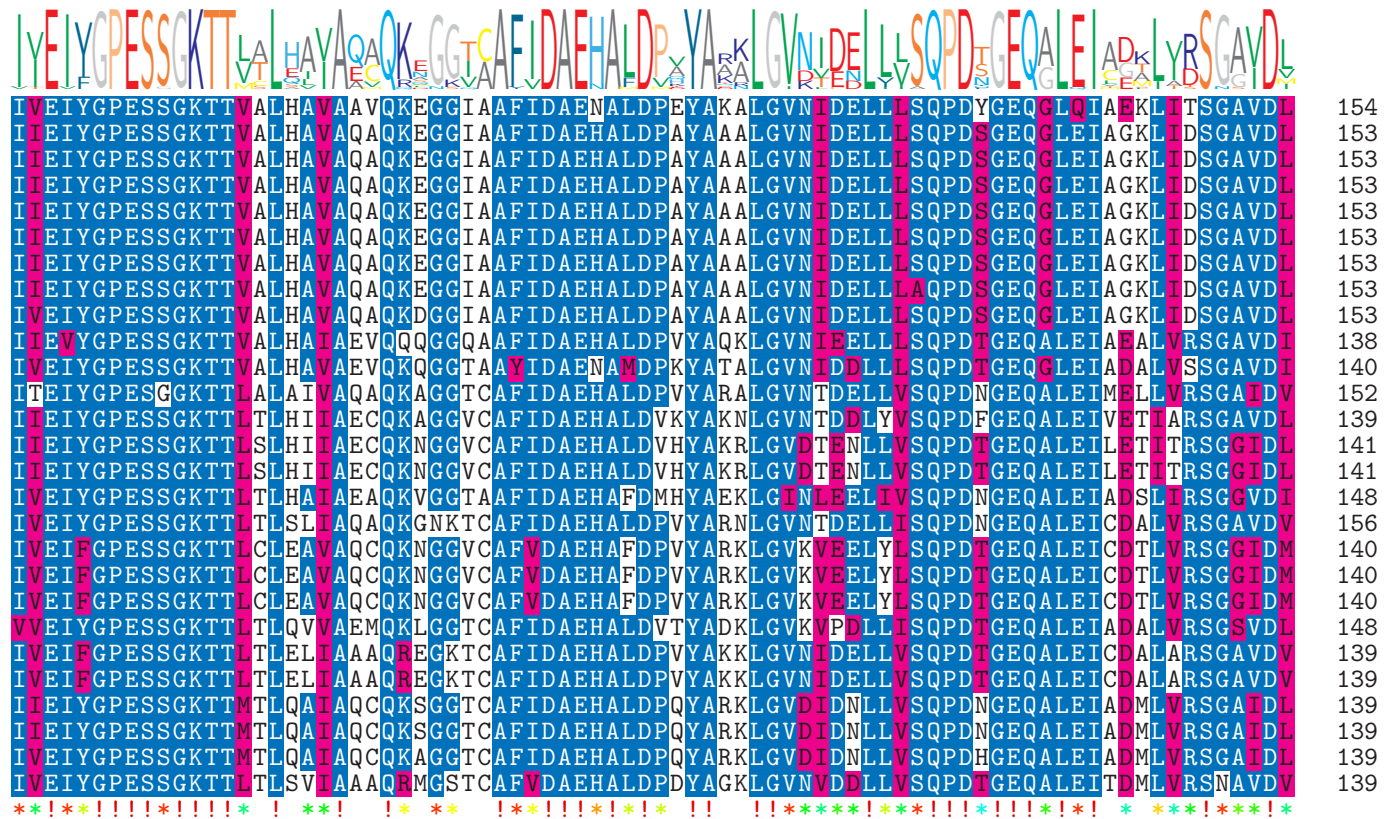
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK.....KTNFDDITKKYGA	ERDKALADALALIEKD	FGKGSIMRLGEA	.ANQKVS	VSSGSLALD	I	ALGAGGY	PKGR	74	
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK.....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQV	MSSGSLALD	I	ALGSGGY	PKGR	73	
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK.....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQV	MSSGSLALD	I	ALGSGGY	PKGR	73	
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKK.....LKKNEEITKKFG	DERRKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQV	MSSGSLALD	I	ALGAGGY	PKGR	73	
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTRI	STVPSGSLALD	T	ALGIGGY	PRGR	58		
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDA	ALKKIEKNFGKGSIMRMGEK	.VDTQV	STVSSGSLALDE	A	LGVGGY	PRGR	60		
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	SQIEKAFGKGSIMKLGAE	.SKLDVQV	VSTGSLSLD	I	ALGVGG	IPRGR	72	
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NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTS	PNDDKKKALAAVLEK	LDKTYGKGTVMKLG	DGTVDHNI	EVIPS	GSLGLD	I	ALGVGG	YPKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQ	VEPEQKKQALEAALA	QIEKQFGKGSIMKLGQT	.EQLDIES	VSTGSLGLD	I	ALGIGGL	PMGR	76	
NTDB id 1130 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALA	QIEKSFGKGAIMKMDGS	QREENLEVIST	GSLGLD	I	ALGVGGL	PRGR	60		
NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALA	QIEKSFGKGAIMKMDGS	QREENLEVIST	GSLGLD	I	ALGVGGL	PRGR	60		
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAAS	MSAEKQKALAAALA	QIEKQFGKGSIMKMDA	.EVEPVQV	VSTGSLGLD	V	ALGVGGL	PRGR	68	
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAALG	QIEKQFGKGSIMRLGDN	.RAMDVET	ISTGSLSLD	I	ALGAGGL	PMGR	59		
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NTDB id 361933 FDM99 RS13190 WP 000344167.1	MDENKSKALQAALS	QIEKQFGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59		
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALS	QIEKQFGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59		
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQAALS	QIEKQFGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59		
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALG	QIEKQFGKGAVMRMGDH	.DRQAIPS	ISTGSLGLD	I	ALGIGGL	PKGR	59		
consensus	***	***	*	***!	!!	*****	*	***!!*!!*!!*!!*!!	!!	***!!

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NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 625 LCA RS02525 WP 011374196.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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NTDB	id	600	KW2	RS01765	WP	011675413.1	VV	IDSVAAL	V	PKAEID	G	H	IGDSS	V	GLQAR	M	MSQAM	R	K	L	G	A	S	I	N	K	T	K	T	T	A	I	F	I	N	Q	L	R	E	K	V	G	V	M	.	F	G	S	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	.	233												
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NTDB	id	453	Spy49	1753c	ACI62003.1	VV	DSVAAL	V	RAEID	G	D	IGDSH	V	GLQAR	M	MSQAM	R	K	L	S	A	S	I	N	K	T	K	T	T	A	I	F	I	N	Q	L	R	E	K	V	G	V	M	.	F	G	N	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	.	232													
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NTDB	id	625	LCA	RS02525	WP	0011374196.1	L	V	DSVAAL	V	RAEID	E	G	M	G	D	A	H	V	G	L	Q	A	R	L	M	S	Q	A	L	R	K	L	S	G	T	I	N	K	T	K	T	I	A	I	F	I	N																												

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NTDB id 1205 PSJM300 05545 AFN77183.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGGGS E NAKKYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTE.NKKD EPKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS E NAKKYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTE.NKKD EPKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS E NAKKYLA D N P EV F AEIDHQVVRVQ F LIDGEEAAE.....SKKD EVAQVDS..VNEEVTLDLGDEL	378
DEKIGGGS E NAKKYLA D N P EV F DEIDHQVVRVQ F LIDGEEIAE.....SKKD EAAQVDS..VNEEVTLDLGDEL	378
GEKIGGGS E NAKRYLADHP Q L F DEIDRKVRVK F GLLEESEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGGGS E NAKK F LAD N P E IF D IDHKVVRVQ Y GLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EE R LGQGG R ENAK Q FL K EN K DIM L MIQE Q IREHYGLDNNGVVQQQAEE.TQEEL.E..FE.E.....	348
SERIGQGG R ENAKNYLAD H ED V ED V RLK V RAAY G ISDVPEEDLP T TE.DE.QI.N..ILPDDST....EE.....	355
DERIGQG K EKT I AY I A E R P EME Q EIDR V MAA I RAG N AGEAPALAPAPA A PEAAEA.....	363
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DKKLGGG R ENAKALL K ED K ALADEITLK I KES I GSNEEIMPL..PDEPLE.. E ME.....	347
DKKLGGG R ENAKALL K ED K ALADEITLK I KES I GSNEEIMPL..PDEPLE.. E ME.....	347
DTKLGGG R DT V KEL I K D N P ELAE E LEAK I REKLQAK.....	343
GTKIGQG K NNAV K VLKEN P E I AD K LE Q EIR N TLAS N PN S VLK..ATASDSND E SDVEEFSE.....EEL.....	372
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GE R IGGQ R DN C REF L REN A ELAR E IE N K V REHL G VT P MGAV..TLAEEVEED.....	352
GDKIGGQ K ANACKY L KEN P E I AK T L D KK L REML L N P EN M QLI..AETSSAAD V FE G AV P E.....EF.....	354
GDKIGGQ K ANACKY L KEN P E I AK T L D KK L REML L N P EN M QLI..AETSSAAD V FE G AV P E.....EF.....	354
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GNKIGGQ K NNVIR Y FE E NN Q IA E E I ERN I REQL L T T GT N GA V ..Q.I.EDEE E PD..L L L ES.....	349
GNKIGGQ K NNVIR Y LE E N P Q I STE I E A VI R EQ L L T KAS D Q T A..A.HDETEE E PD..L L ES.....	349
GS K IGGQ K ANA A KY L EN P E I Q E IE Q Q I RA K LL V TSAN T KA..TPVAEDLAD..I.....	347

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1						387
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE					388
NTDB id 228 SPD RS09265 WP 001085462.1	EIEIEE					388
NTDB id 194 SPR RS08825 WP 001085462.1	EIEIEE					388
NTDB id 159 SP RS09750 WP 001085462.1	EIEIEE					388
NTDB id 527 SMSK321 RS11065 WP 001085454.1	EIEIEE					384
NTDB id 499 SM12261 RS08315 WP 078228268.1	EIEIEE					384
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NTDB id 1205 PSJM300 05545 AFN77183.1						347
consensus						

-  non conserved
-  similar
-  ≥ 50% conserved