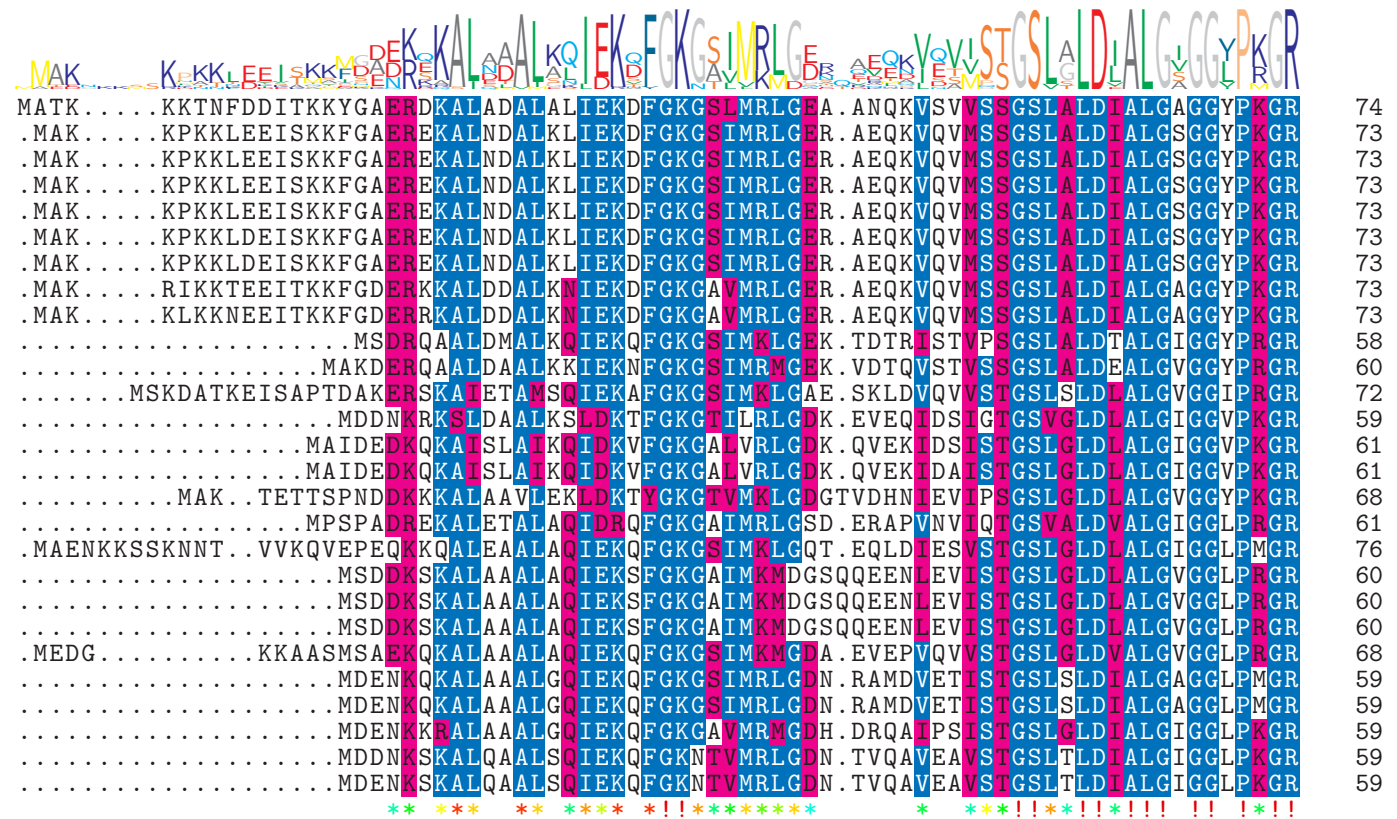


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

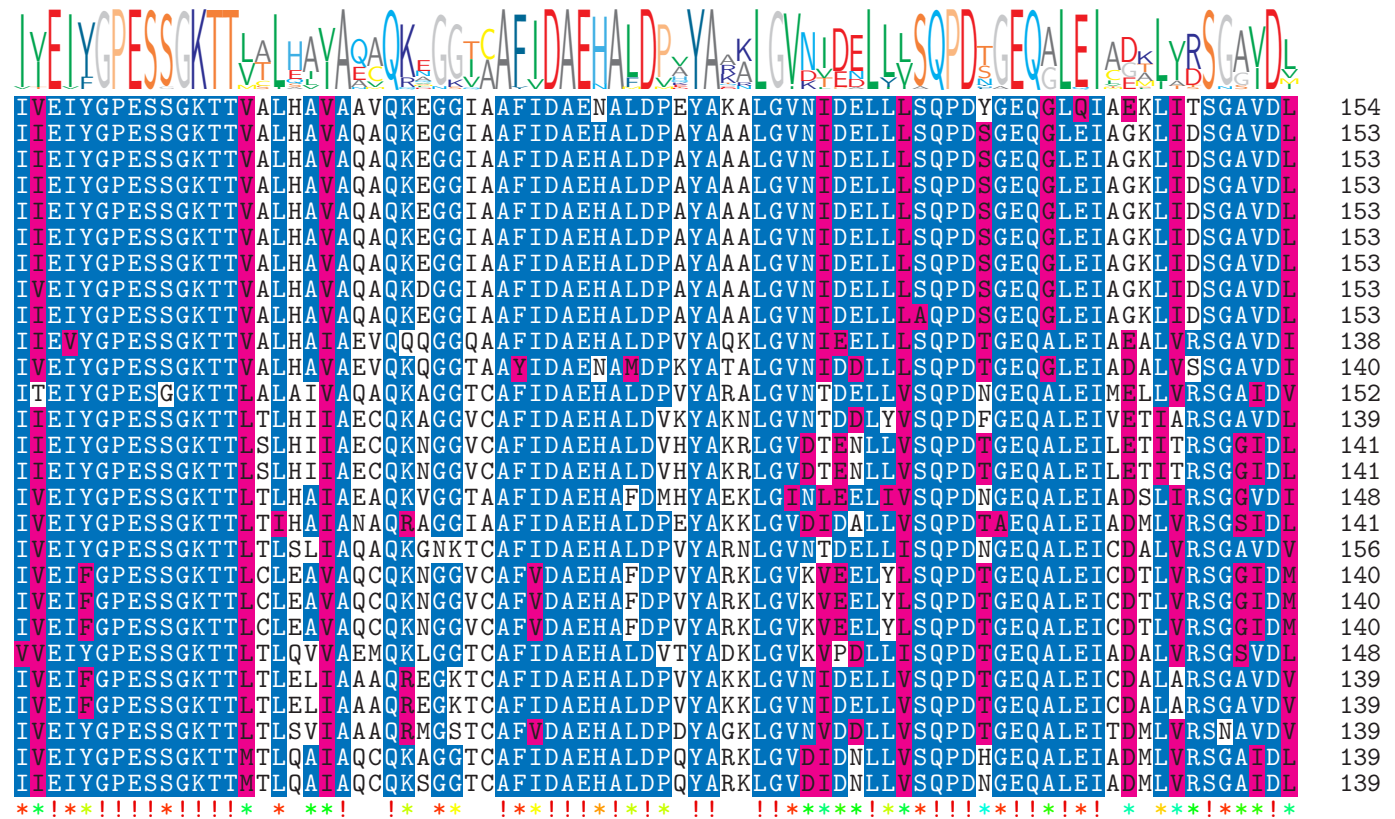
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NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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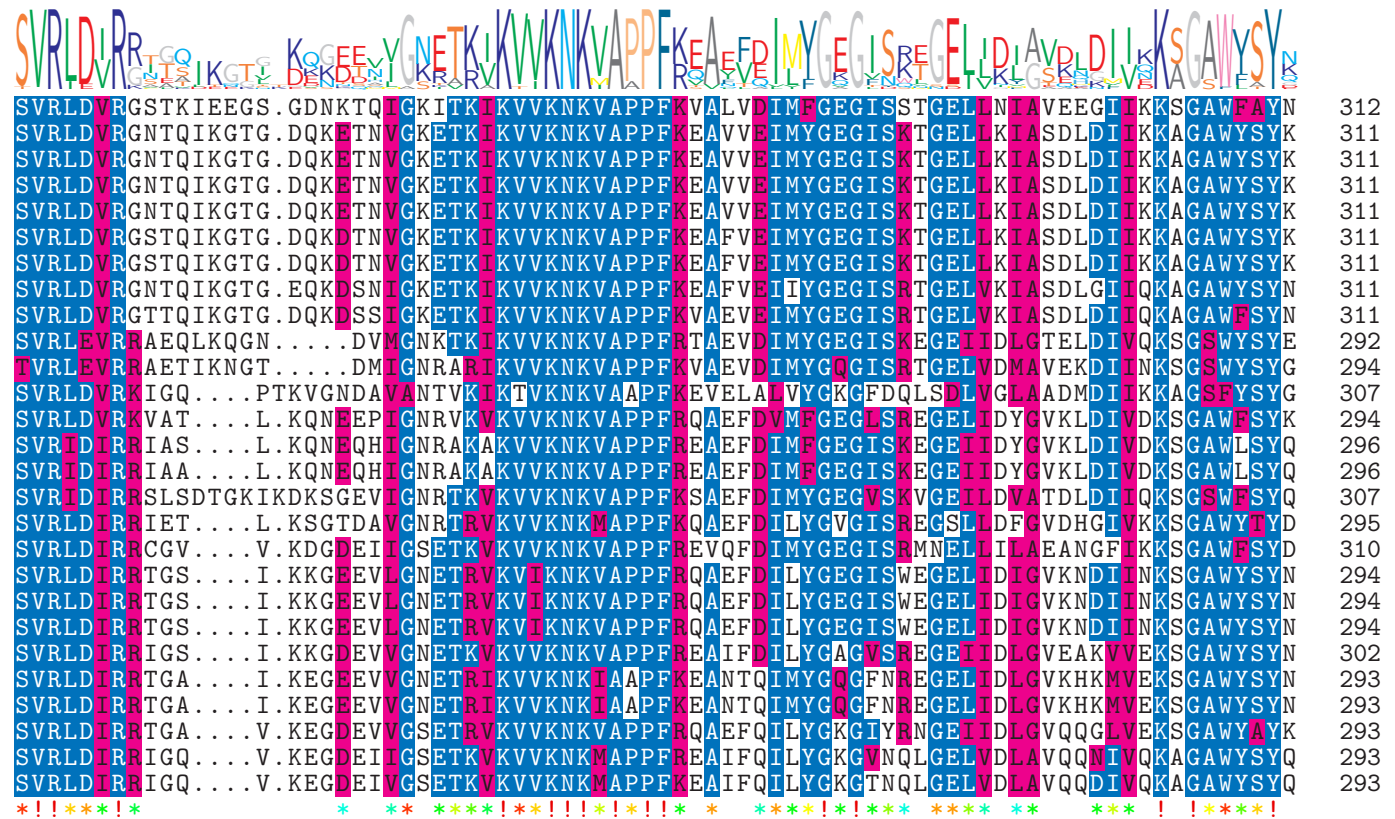


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NTDB	id	269	KZH43	RS08665	WP	001085462.1	VV	DSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	228	SPD	RS09265	WP	001085462.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	194	SPR	RS08825	WP	001085462.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	159	SP	RS09750	WP	001085462.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	527	SMSK321	RS11065	WP	001085454.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	499	SM12261	RS08315	WP	078228268.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	GAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
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NTDB	id	453	Spy49	1753c	ACI	62003.1	VV	VDSVAALVP	RA	EID	GD	IGDSHVGLQARMMSQAMRKL	SAS	INKTKT	TTA	IFINQLREK	VGV	M	FGNPETT	P	GG	RALKFYA	232					
NTDB	id	115	BSU	16940	NP	389576.2	VV	VDSVAALVP	KA	EIE	GDM	GDSHVGLQARLMSQALRKLS	GA	INKS	KT	IA	IFINQIREK	VGV	M	FGNPETT	P	GG	RALKFY	S	217			
NTDB	id	625	LCA	RS02525	WP	001374196.1	L	VVDSVAALVP	RA	EIE	GEM	GDAHVGLQARLMSQALRKLS	SGT	INKTKT	IA	IFINQIREK	VGV	M	FGNPEV	TP	GG	RALKFY	S	219				
NTDB	id	1313	DR	RS12030	WP	010888966.1	VV	VDSVAAL	TP	RA	EIE	GDM	GDSLPLGLQARLMSQALRKLT	AIL	LSKT	GTAA	IFINQVREK	IG	V	M	YGNPETT	T	GG	RALKFYA	231			
NTDB	id	1245	Cj1673c	YP	002345041.1	I	VVDSVAAL	TP	KA	EIE	GDM	GDAQHVGLQARLMSQALRKLT	IG	IVHKMNT	TV	IFINQIRMK	IG	AMGY	YGT	PETT	T	GG	NALKFYA	219				
NTDB	id	1211	C694	RS00795	WP	000963128.1	VV	VDSVAAL	TP	KA	EID	GDM	GDAQHVGLQARLMSHALRK	IT	GV	LHKMNT	TL	IFINQIRMK	IG	MMGY	YGS	PETT	T	GG	NALKFYA	221		
NTDB	id	1214	NCTC11637	00359	SQJ	03206.1	VV	VDSVAAL	TP	KA	EID	GDM	GDAQHVGLQARLMSHALRK	IT	GV	LHKMNT	TL	IFINQIRMK	IG	MMGY	YGS	PETT	T	GG	NALKFYA	221		
NTDB	id	1334	RAOC	RS04870	WP	004918236.1	VV	VDSVAAL	TP	KA	EID	GDM	GDSKMLGLHARLMSQALRKLT	VSS	ISKTKCT	V	IFINQLRDK	IG	V	M	FGSPETT	T	GG	NALKFYA	227			
NTDB	id	370857	FK523	RS05670	WP	027464767.1	I	V	IDSVAALVP	RA	EIE	GEM	GDSHVGLQARLMSQALRKLAG	G	LNQT	QT	TM	IFINQLREK	IG	V	F	FGSPETTS	G	GK	ALKFYA	220		
NTDB	id	1389	A4U84	RS07560	WP	021112712.1	I	V	DSVAAL	TP	KA	EIE	GDM	GDSHMLGLQARLMSQALRKLT	AN	IKNTN	CL	V	V	FINQIRMK	IG	V	M	FGNPETT	T	GG	NALKFYA	235
NTDB	id	1130	NGFG	RS03960	WP	003688695.1	VV	VDSVAALVP	KA	EIE	GDM	GDSHVGLQARLMSQALRKLT	G	HIKKT	NTL	V	V	FINQIRMK	IG	V	M	FGSPETT	T	GG	NALKFY	S	219	
NTDB	id	1124	NGFG	RS03960	WP	003688695.1	VV	VDSVAALVP	KA	EIE	GDM	GDSHVGLQARLMSQALRKLT	G	HIKKT	NTL	V	V	FINQIRMK	IG	V	M	FGSPETT	T	GG	NALKFY	S	219	
NTDB	id	1123	OK783	RS03845	WP	003688695.1	V																					

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NTDB id 600 KW2 RS01765 WP 011675413.1
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQVRVQFGLIDGEEAAE...SKKDE...AAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEEKSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAIYIAERPMEQEIRDRVMAAIRAGNAGEAPALA...PAPAAP..EAAE.....A.....	363
DKKLGGGRENKSAFLKENPEIADIEITKATIQNSMGIEGMISGSEDD.....EGE..E.....	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDE.....PLE..EME.....	347
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDE.....PLE..EME.....	347
DTKLGGGRDITVKELIKDNPELAELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGT.....QDETGD..ERPE....E.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGT.....QDETGD..ERPE....E.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGT.....QDETGD..ERPE....E.....	348
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GSKIGGQKANAACKYLEENPEIGQEIEQQIRAKLLVTSANTKATPVAEDLADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTAA.HDETEEEPDLL....ES.....	349
GNKIGGQKNNVIRIYFENNQIAEIERNIREQLLTTGTNGAVQ.I.EDEEEPDLL....LE.....S.....	349

logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349
consensus		

 non conserved
 similar
 ≥ 50% conserved