

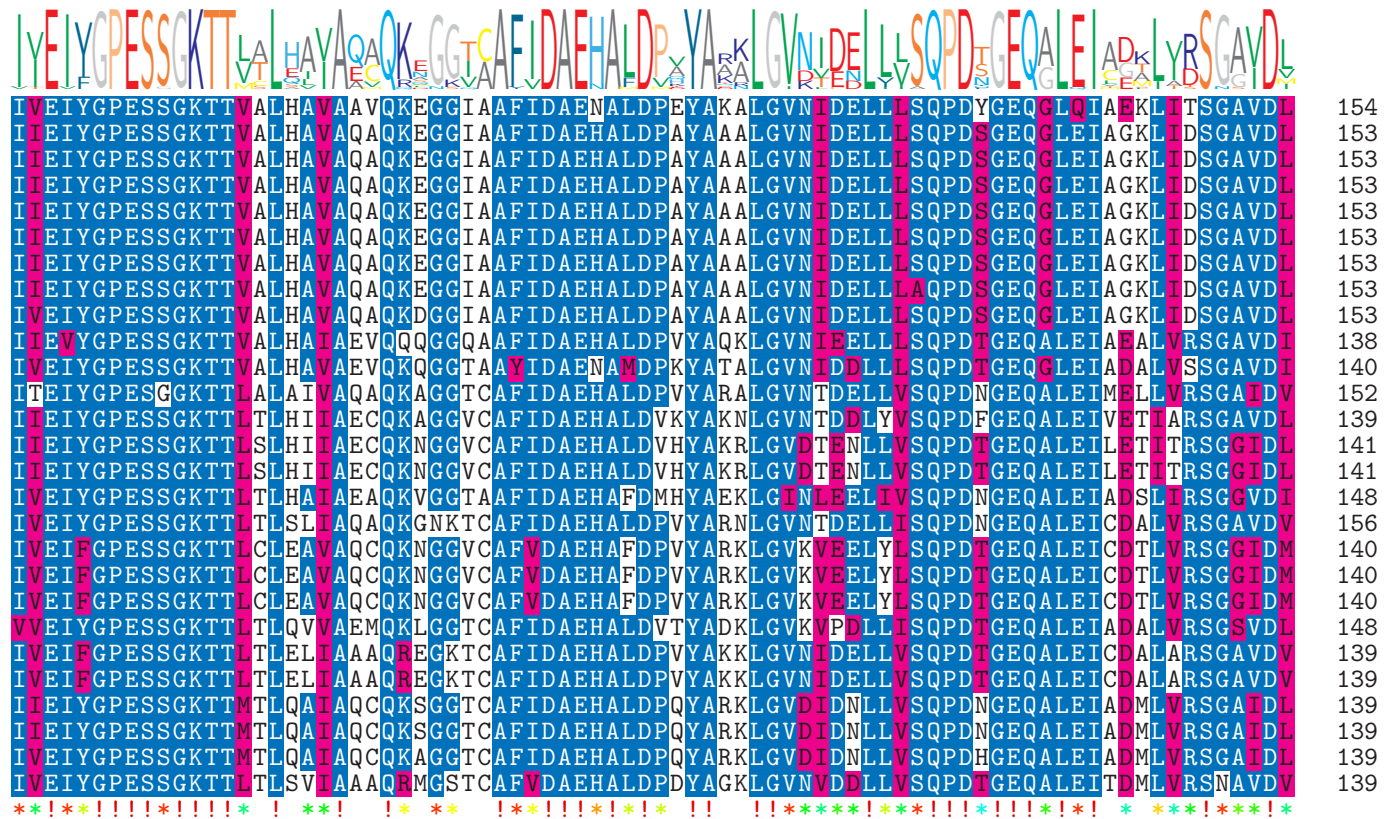
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NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 159 SP RS09750 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
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NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKK....PKKLDEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFG	DERRKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQ	VMSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFG	DERKKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQ	VMSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTR	ISTVPSGSLALD	TALGIGGY	PRGR			58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKK	IEKNFGKGSIMRMGEK	.VDTQVSTVSSGSLAL	DEALGVGGY	PRGR				60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	QIEKAFGKGSIMKLGAE	.SKLDVQV	VSTGSLSLDL	ALGVGGI	PRGR		72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKTFGKGTILRLGDK	.EVEQ	IDSIGTGSVGLDL	ALGIGGV	PKGR			59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEK	IDAISTGSLGLDL	ALGIGGV	PKGR		61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEK	IDSISTGSLGLDL	ALGIGGV	PKGR		61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTS	PNDDKKKALA	AVLEKLDKTYGKGTVMKLG	DGTVDH	NIEVIPSGSLGLDL	ALGVGGY	PKGR		68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQ	VEPEQKKQALEA	AALAQIEKQFGKGSIMKLG	QT.EQLD	IESVSTGSLGLDL	ALGIGGL	PMGR		76
NTDB id 1130 NGFG RS03960 WP 003688695.1	MSDDKSKALAA	AALAQIEKSFGKGAIMKMDGS	QREENLEVISTGSLGLDL	ALGVGGL	PRGR				60
NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAA	AALAQIEKSFGKGAIMKMDGS	QREENLEVISTGSLGLDL	ALGVGGL	PRGR				60
NTDB id 1123 OK783 RS03845 WP 003688695.1	MSDDKSKALAA	AALAQIEKSFGKGAIMKMDGS	QREENLEVISTGSLGLDL	ALGVGGL	PRGR				60
NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAAS	MSAEKQKALAA	AALAQIEKQFGKGSIMKMD	A.EVEP	VQVSTGSLGLD	VALGVGGL	PRGR		68
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAA	ALGQIEKQFGKGSIMRLG	DN.RAMD	VETISTGSLSLD	I	ALGAGGL	PMGR		59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAA	ALGQIEKQFGKGSIMRLG	DN.RAMD	VETISTGSLSLD	I	ALGAGGL	PMGR		59
NTDB id 92576 QMN04 RS07390 WP 000344169.1	MDENKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAA	ALGQIEKQFGKGAVMRMG	DH.DRQA	IPSISTGSLGLD	I	ALGIGGL	PKGR		59
consensus	***	***	*	***!	***!	***!	***!	***!	

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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

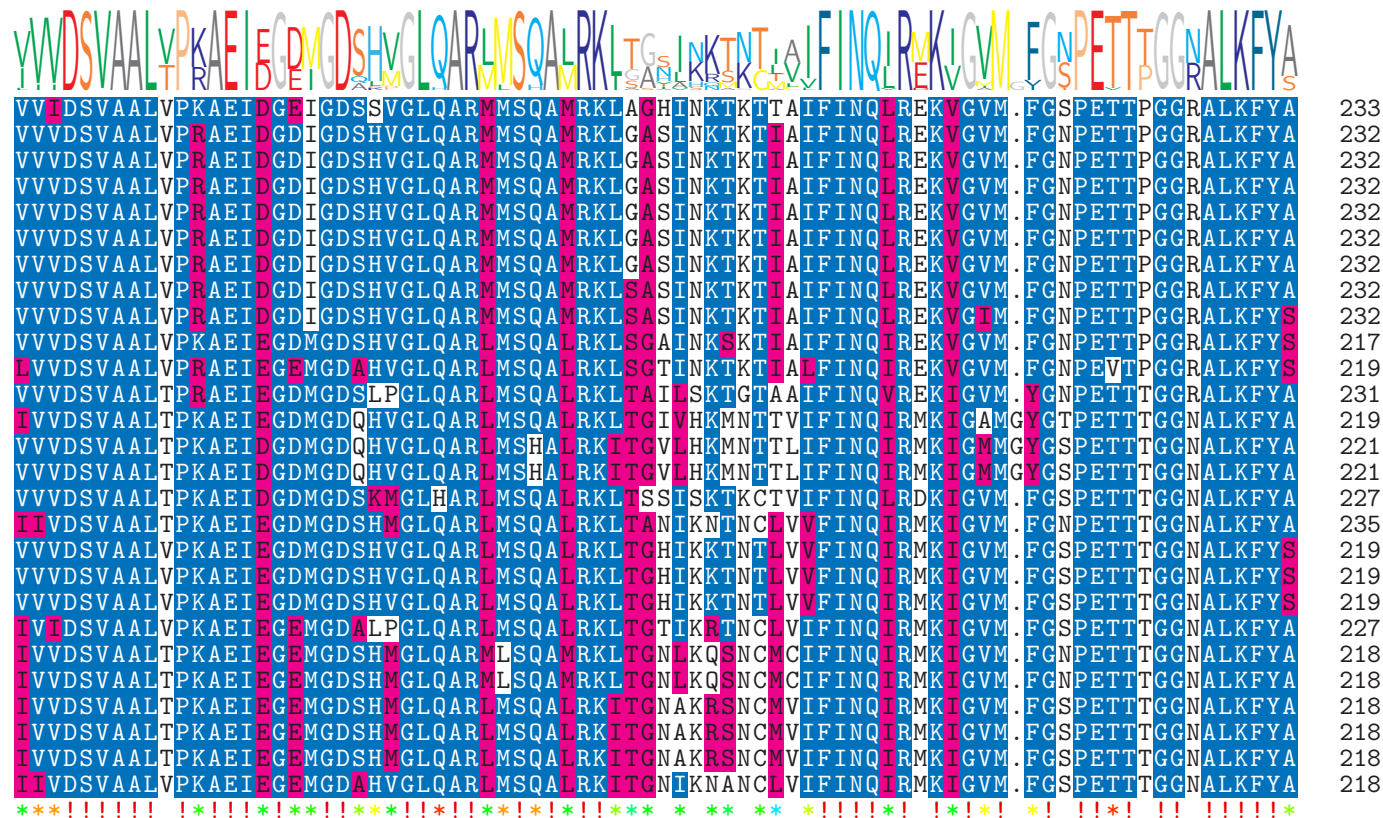
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGQGS E NAKKYLA E HP E IF D EIDDKVRSK F GLIDGEEVSEQDTE.NKKD EPKKEEA..VNEEVPLDLGDEL	382
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DEKIGQGS E NAKKYLA D N P EV F D E IDHQRV V Q F GLIDGEEIAE.....SKKD EAAQVDS..VNEEVTLDLGDEL	378
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GEKIGQGS E NAKK F LAD N P E IF D DIDHKVRV V Q V GLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EE R LGQGR E NAK Q FL K EN K DIM L MI Q EQ I REHYGLDNNGVVQQQAEE.TQEEL.E..FE.E.....	348
SERIGQGR E NAK N YLAD H D E VE D EVRLK 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 D VM A AIRAGNAGEAPALAPAPA A PEAAEA.....	363
DKKLGGGR E NA K FL K EN P E I AD E IT K AIQNS M G I EGMISGS..EDDEGE. E	343
DKKLGGGR E NAKALL K ED K ALAD E IT L K I KES I GSNEEIMPL..PDEPLE.. E ME.....	347
DKKLGGGR E NAKALL K ED K ALAD E IT L K I KES I GSNEEIMPL..PDEPLE.. E ME.....	347
DTKLGGGR D TV K EL I K D N P EL A E E LEAK I REKLQAK.....	343
GTKIGQG K NNAV K VL K EN P E I AD K LE Q EIR N TL A SN P NSVLK..ATASDSND E SDVEEFSE.....EEL.....	372
GAKIGGQ K DNVR V WL K EN P E I SD E IDAK I RAL N GV E MHITEG..TQDET.....GERPE.....E.....	348
GAKIGGQ K DNVR V WL K EN P E I SD E IDAK I RAL N GV E MHITEG..TQDET.....GERPE.....E.....	348
GAKIGGQ K DNVR V WL K EN P E I SD E IDAK I RAL N GV E MHITEG..TQDET.....GERPE.....E.....	348
GE R IGG R DN C REFL R EN A EL A RE I EN K V R EHL G VT P MGAV..TLAEEVEED.....	352
GDKIGQG K ANACKY L KEN P E I AK T L D KK L REMLLN P EN M QL I .AETSSAAD V FE G AV P E.....EF.....	354
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logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE	388
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consensus

 non conserved
 similar
 ≥ 50% conserved