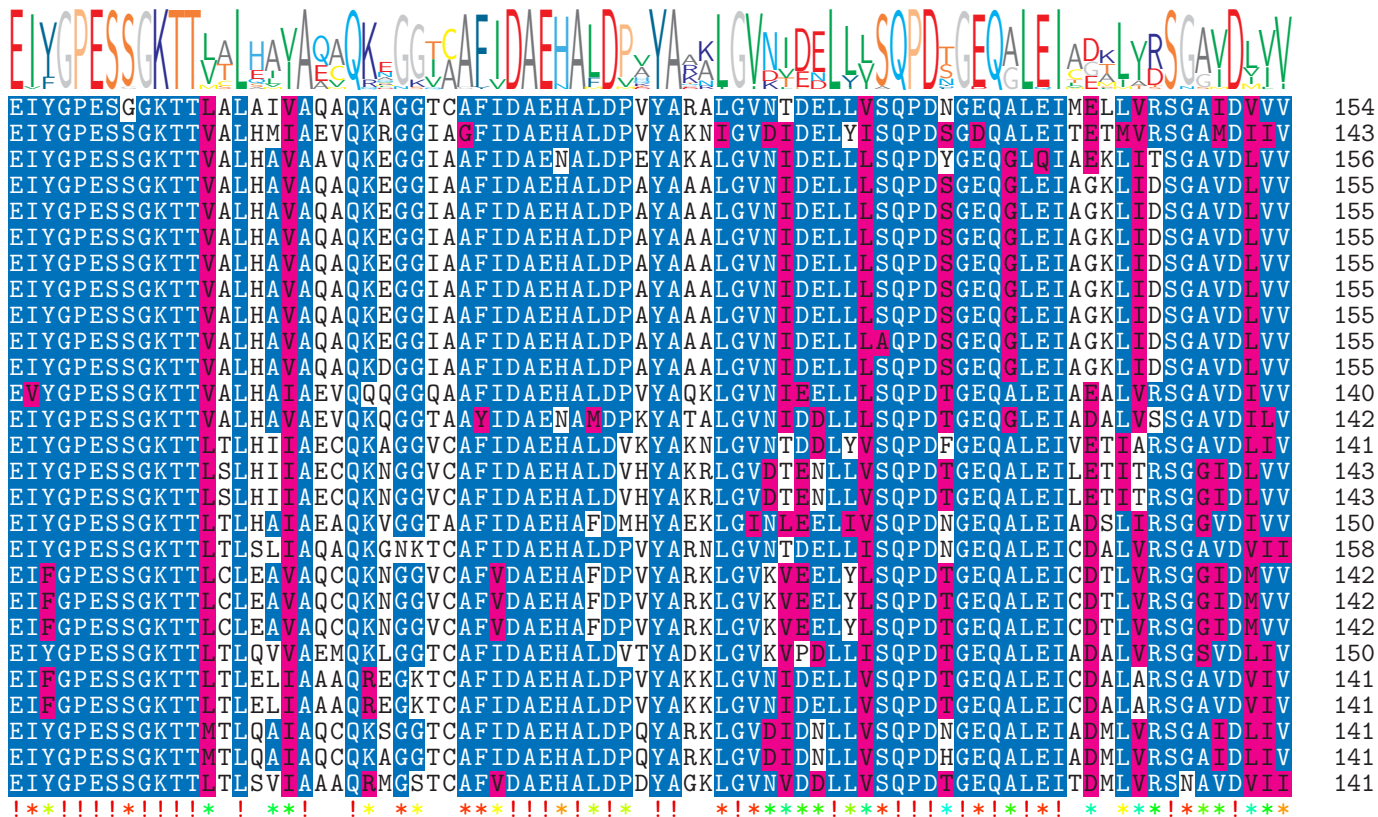


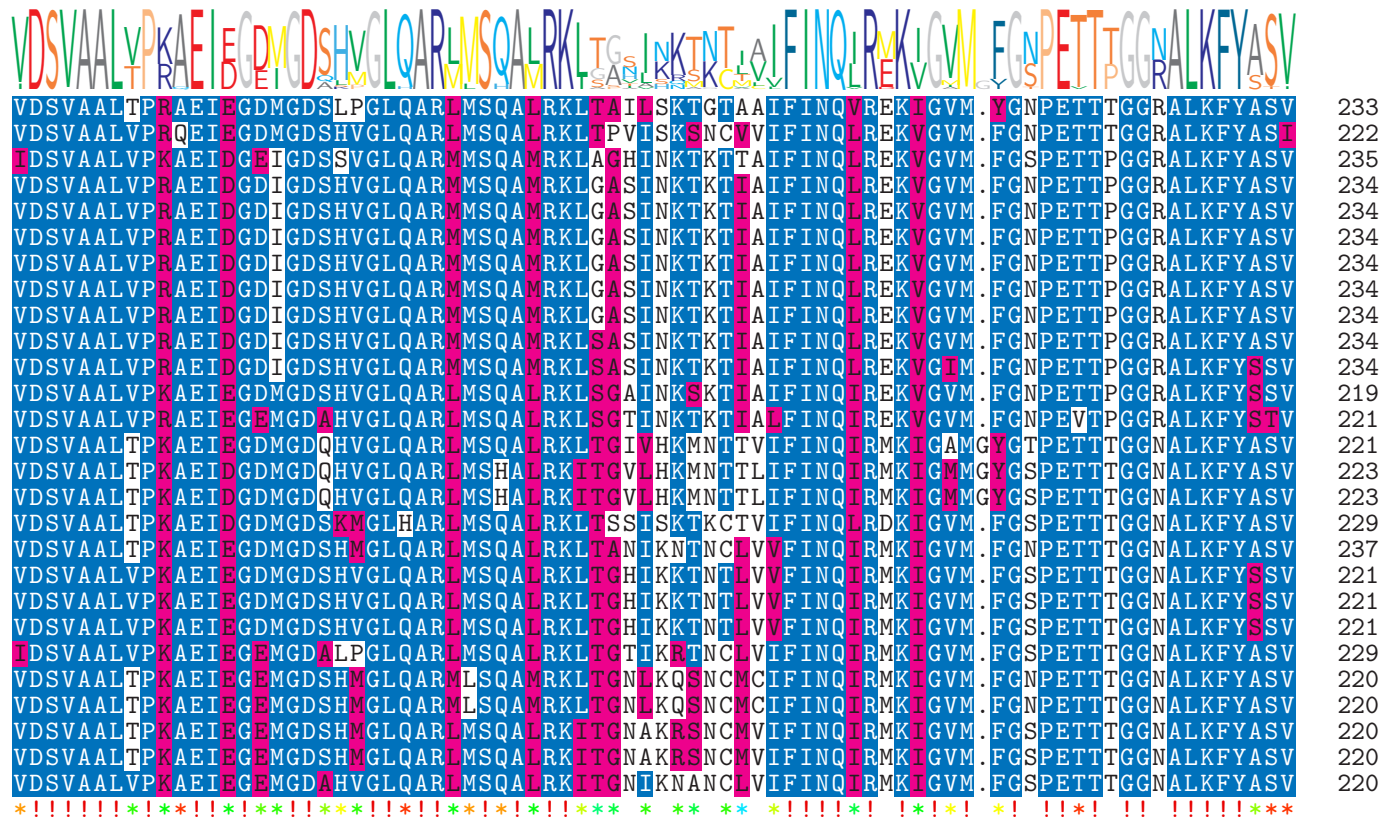
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NTDB id 109153 ACGG81 RS08045 WP 390107741.1	MAGDDKLKALDAALAK	IEKDFGKGAVMKLGD	AAANVS	VETVPT	GSLSLD	IALGLGGV	PKGRI	I	63
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NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAK...KPKKLEEISKKFGAER	EKALNDALKLIEKDFGKCSIMRLG	ERA.EQKVQVMSSGSLALD	IALSGGYP	PKGRI	V			75
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NTDB id 159 SP RS09750 WP 001085462.1	.MAK...KPKKLEEISKKFGAER	EKALNDALKLIEKDFGKCSIMRLG	ERA.EQKVQVMSSGSLALD	IALSGGYP	PKGRI	V			75
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAK...RIKKTEEITKKFGDER	RKALDDALKNIEKDFGKGAVMRLG	ERA.EQKVQVMSSGSLALD	IALGAGGY	PKGRI	V			75
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQ	FGKCSIMKLG	EKT.DTRI	STVPSGSLALD	TALGIGGY	PRGRI			60
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKKIEK	NFGKCSIMRM	CEKV.DTQV	STVSSGSLALDEAL	GVGGYP	PRGRIV			62
NTDB id 1245 Cj1673c YP 002345041.1	MDENKRRKSLDAALKSLDK	TFGKCTILRL	CDK.EVEQ	IDSIGTGSVGLD	IALGIGGV	PKGRI			61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKATSLATKQID	KVFGKGALVRL	CDK.QVEK	IDAISTGSLGLD	IALCIGGV	PKGRI			63
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKATSLATKQID	KVFGKGALVRL	CDK.QVEK	IDAISTGSLGLD	IALCIGGV	PKGRI			63
NTDB id 1334 RA0C RS04870 WP 004918236.1	MAKTETTSPNDKKK	KALAAVLEKLDKTY	GKCTVMKLC	DGTVDHNI	EVIPS	GSLGLD	IALGVGGY	PKGRI	70
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKALAAALGQIEK	QFGKGAVMRMG	DH.DRQA	IPSI	STGSLGLD	IALCIGGL	PKGRI		61
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consensus



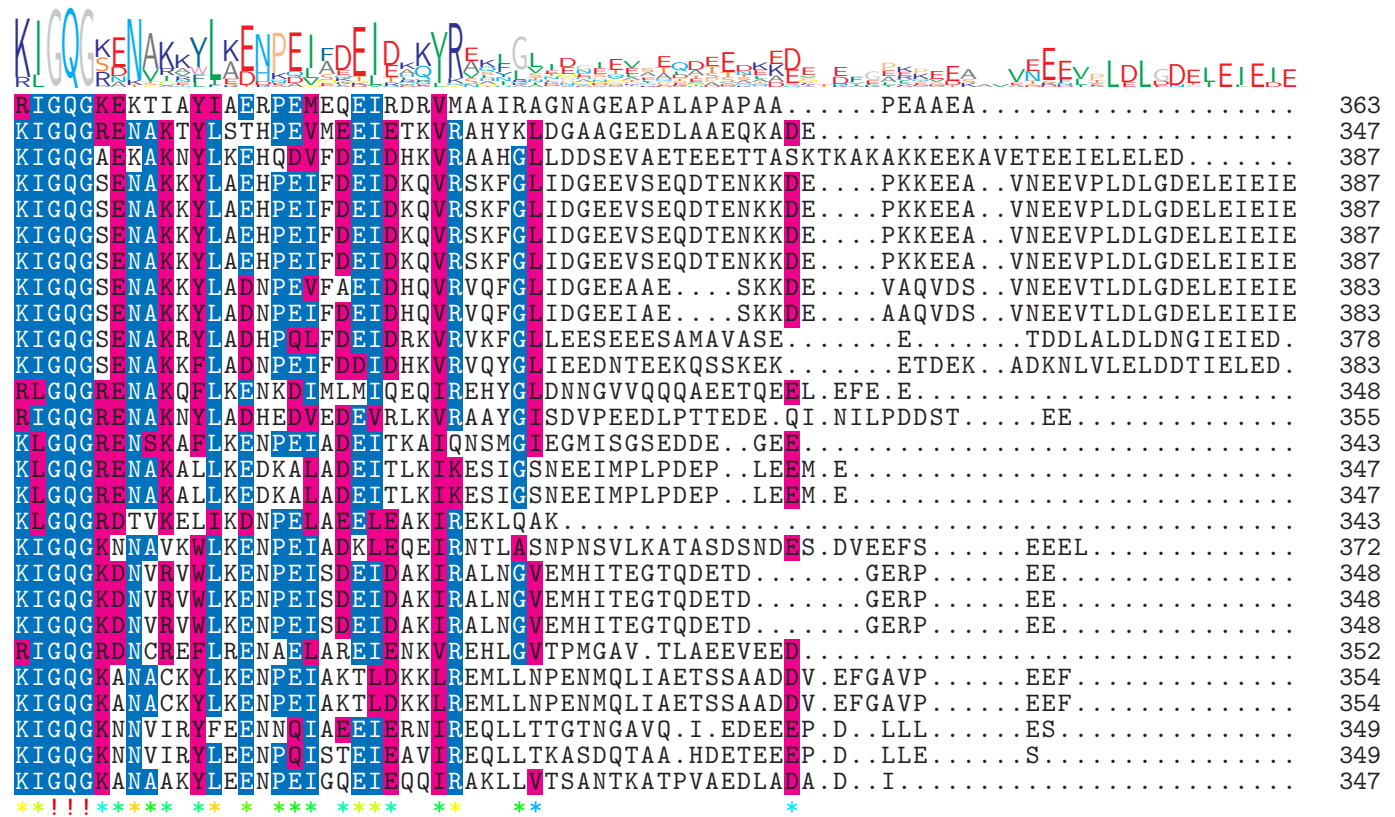
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consensus



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NTDB id 159 SP RS09750 WP 001085462.1	RLDVRGNTQIKGTG.DQKEITNVGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDLDIINKAGAWYSYKDE	313
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consensus	!***!* * * * * !**!!*!*!!* * * * * !**!* * * * * !**!* * * * * !**!* * * * *	

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consensus



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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved