

logo

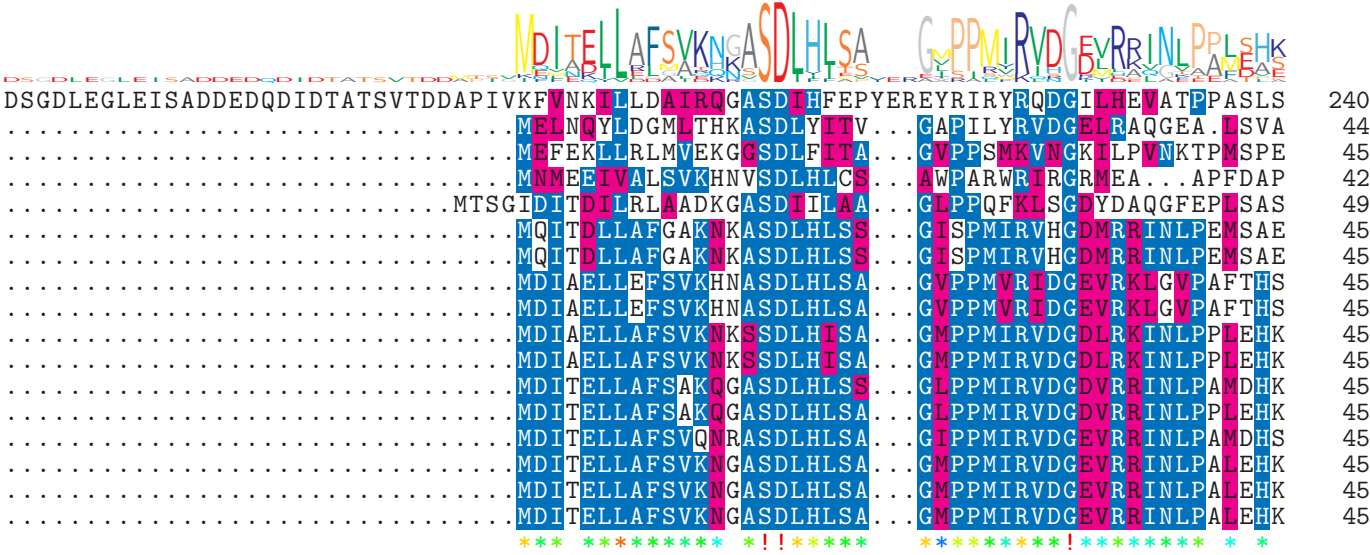
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYIVKNKILSAEQIALTAAGNFGVPMLDINCIDVGTI	80
NTDB id 1177 A1552VC RS01165 WP 000422572.1		0
NTDB id 1203 PSJM300 01605 AFN76401.1		0
NTDB id 176486 A4R37 RS13445 WP 001546096.1		0
NTDB id 1307 DR RS10055 WP 010888596.1		0
NTDB id 1086 NMV RS00245 WP 002218487.1		0
NTDB id 1116 NGFG RS10615 WP 003690200.1		0
NTDB id 1185 GTF74 RS11940 WP 000350195.1		0
NTDB id 1176 A1552VC RS01160 WP 000350195.1		0
NTDB id 1283 ACE17W RS02630 WP 010947729.1		0
NTDB id 1259 GC085 RS10305 WP 010947729.1		0
NTDB id 1202 PSJM300 01600 AFN76400.1		0
NTDB id 1194 PAKAF RS01995 WP 003084552.1		0
NTDB id 1020 ACIAD RS04210 WP 011182164.1		0
NTDB id 1060 ABD1 RS04380 WP 000355489.1		0
NTDB id 1040 HON27 RS13360 WP 000355489.1		0
NTDB id 1081 FDQ49 RS05335 WP 006581387.1		0
consensus		

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NTDB id 1251 GC085 RS07725 WP 011946523.1	PVNLVNEKLIKRIHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE	160
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NTDB id 1307 DR RS10055 WP 010888596.1		0
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NTDB id	1251	GC085	RS07725	WP	011946523.1
NTDB id	1177	A1552VC	RS01165	WP	000422572.1
NTDB id	1203	PSJM300	01605	AFN	76401.1
NTDB id	176486	A4R37	RS13445	WP	001546096.1
NTDB id	1307	DR	RS10055	WP	010888596.1
NTDB id	1086	NMV	RS00245	WP	002218487.1
NTDB id	1116	NGFG	RS10615	WP	003690200.1
NTDB id	1185	GTF74	RS11940	WP	000350195.1
NTDB id	1176	A1552VC	RS01160	WP	000350195.1
NTDB id	1283	ACE17W	RS02630	WP	010947729.1
NTDB id	1259	GC085	RS10305	WP	010947729.1
NTDB id	1202	PSJM300	01600	AFN	76400.1
NTDB id	1194	PAKAF	RS01995	WP	003084552.1
NTDB id	1020	ACIAD	RS04210	WP	011182164.1
NTDB id	1060	ABD1	RS04380	WP	000355489.1
NTDB id	1040	HON27	RS13360	WP	000355489.1
NTDB id	1081	FDQ49	RS05335	WP	006581387.1
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NTDB id	1202	PSJM300	01600	AFN	76400.1
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NTDB id 1081 FDQ49 RS05335 WP 006581387.1
consensus

Accession	Protein	Length
AVRDDFTNQGLIELGFKEADLVNLKLYKAVGCEQCTSGYR	GRVCLFEVLPMTKEIGQLIMSGGN..SLDIKLQSEGM	548
.....DKNGKGRHGVFEVLLNSPRIADLIRRGELHELKATMARSQEVGMQ		313
.....TPDGKGRRAVIEVLINTPLAADLIRKGEVHELKGLMKRSTDLGMQ		315
.....D.KQEGRVALFELLVNTPAVGNLIREGKTHQLLHVITQTGQQVGM		311
.....RADGQGRVLAYEILLANPAVRALIREGKTFQITSVMTQTGAAREGMV		319
.....THDGNGRVASHEILIANPAVRNLIRENKITQINSVLQTGQASGMQ		315
.....THDGNGRVASHEILIANPAVRNLIRENKITQINSVLQTGQASGMQ		315
.....R.VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGAAHGMQ		314
.....R.VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGAAHGMQ		314
.....K.NKGGRVAAL EIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGMQ		314
.....K.NKGGRVAAL EIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGMQ		314
.....K.VGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGSLSGMQ		314
.....K.IGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGSLSGMQ		314
.....K.EGGGRVAAHEIMIGIPAIRNLIREGKVAQMYSIIQTGATHGMT		314
.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGMT		314
.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGMT		314
.....K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGANHGMT		314

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Sequence	Score
TIFQSGIEKVKEGITTIEEVNRVTVD	574
TFDQALYQLVVDKTISEQDALHSADSANDLRLMLKTKRGDD.YGSG..SLQNVKI...DME	368
TFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLGSETD.GEHLTSVVSQGLTL...EMSDDDPGRSFR	381
TFQQSYQQRVGEGRLL	326
TMDAYLAGLFRRHLLITYDKGLERAIDPKEFARLANDASAGLGGASMTPAAPPVPAYNSASSSSTGRGGDFGRGAAAPATP	399
TMDQSLQSLVRQGGLIAPEVARRRQAQNSESMFSF	347
TMDQSLQSLVRQGGLIAPEAARRRAQNSESMFSF	347
TMEQNAKQLIARGVVDAQEVQSKIYDLKAF	345
TMEQNAKQLIARGVVDAQEVQSKIYDLKAF	345
TLDQHLTELVNKNIISKHTAHEAALNK.SLF	344
TLDQHLTELVNKNIISKHTAHEAALNK.SLF	344
TLDSCCLKGLIAKGLISRDSAKEKAKQP.ENF	344
TLDMCLKGLVAKGLISRREAREKAKIP.ENF	344
TLDQSLKQLIAKGIINLPTARAVAKSP.ESF	344
TLDQSLKGLVARGVISPQRTARTAAKQP.ESFL	345
TLDQSLKGLVARGVISPQRTARTAAKQP.ESFL	345
TLDQSLKGLVSRGVISPQRTARTAAKQP.ESFL	345

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NTDB id 176486 A4R37 RS13445 WP 001546096.1		326
NTDB id 1307 DR RS10055 WP 010888596.1	AAPAAGRSEPGRAGGFGRR	418
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NTDB id 1116 NGFG RS10615 WP 003690200.1		347
NTDB id 1185 GTF74 RS11940 WP 000350195.1		345
NTDB id 1176 A1552VC RS01160 WP 000350195.1		345
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NTDB id 1040 HON27 RS13360 WP 000355489.1		345
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved