

logo

NTDB id 1347 HI 0435 AAC22094.1	MNSGLSRLGIALLAAMFAPALLAADLEKLDVAALPGDRVELKLQFDEPVAAAPRGYTI EQPARIALDLPGVQNKLGTKNRE	0
NTDB id 1373 NTHI RS02645 WP 011272046.1		0
NTDB id 1465 ASU2 RS06170 WP 014991934.1		0
NTDB id 1381 A4U84 RS02010 WP 021113424.1		0
NTDB id 67805 AABE55 RS19340 WP 002431761.1		0
NTDB id 1433 BW25113 RS17570 WP 000815987.1		0
NTDB id 1193 PA5040 NP 253727.1	MNSGLSRLGIALLAAMFAPALLAADLEKLDVAALPGDRVELKLQFDEPVAAAPRGYTIEQPARIALDLPGVQNKLGTKNRE	80
NTDB id 1186 GTF74 RS01320 WP 000788426.1		0
NTDB id 1175 A1552VC RS12105 WP 000788426.1		0
NTDB id 1408 DSB67 RS13980 WP 010643500.1		0
consensus		

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NTDB id 1347 HI 0435 AAC22094.1	LSVGNTRSVTVWEAKDRTRLIINLTALSSYTTRVEGNNLFVVVGNSPAGASVASAAPVKASPAPASYAQPIKPKPYVPAG	0
NTDB id 1373 NTHI RS02645 WP 011272046.1		0
NTDB id 1465 ASU2 RS06170 WP 014991934.1		0
NTDB id 1381 A4U84 RS02010 WP 021113424.1		0
NTDB id 67805 AABE55 RS19340 WP 002431761.1		0
NTDB id 1433 BW25113 RS17570 WP 000815987.1		0
NTDB id 1193 PA5040 NP 253727.1	LSVGNTRSVTVWEAKDRTRLIINLTALSSYTTRVEGNNLFVVVGNSPAGASVASAAPVKASPAPASYAQPIKPKPYVPAG	160
NTDB id 1186 GTF74 RS01320 WP 000788426.1	MKNGLKT..YVAQTW.....LTLWVGLALCAS.....S....MVFSAESATA	36
NTDB id 1175 A1552VC RS12105 WP 000788426.1	MKNGLKT..YVAQTW.....LTLWVGLALCAS.....S....MVFSAESATA	36
NTDB id 1408 DSB67 RS13980 WP 010643500.1	MKMRHGLTLTPRKLTGL.....FSLWFSLLLAP.....FVAEEVQS	37
consensus		

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NTDB id 1347 HI 0435 AAC22094.1	NQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVV	0
NTDB id 1373 NTHI RS02645 WP 011272046.1		0
NTDB id 1465 ASU2 RS06170 WP 014991934.1		0
NTDB id 1381 A4U84 RS02010 WP 021113424.1		0
NTDB id 67805 AABE55 RS19340 WP 002431761.1		0
NTDB id 1433 BW25113 RS17570 WP 000815987.1		0
NTDB id 1193 PA5040 NP 253727.1	RAIRNIDFQRGEKGEKNVVIDLSDPTLSPDIQEQQGKIRLDFAKTQLPDALRVRLDVKDFATPVQFVNASDAQSDRTSITI	240
NTDB id 1186 GTF74 RS01320 WP 000788426.1	NQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVV	116
NTDB id 1175 A1552VC RS12105 WP 000788426.1	NQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPSTQLVV	116
NTDB id 1408 DSB67 RS13980 WP 010643500.1	NSLKSIDFRTNKDKDAVIVVELVSPAAIVDIKRVQEGLSIDLLNTSVKDDQLYLLDVKDFSTVVESVEVFRDTSITRLVA	117
consensus		

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NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
consensus

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Protein	Sequence	Length
MDGA1_MOUSE	MKKYFLKCGYFLVFCFLPLLVF.....ANPKTDNERFFTRLSQLAQLAQTLLEQLAFQQDVNLVIGDILENKISL	68
MDGA1_MOUSE	MKKYFLKCGYFLVFCFLPLLVF.....ANPKTDNECFRLFRLSQLAQLAQTLLEQLAFQQDVNLVGMERGEINISL	68
MDGA1_MOUSE	MKRMILLFF.....ILPPVIAHAFSISLKNAPTAKILSYLAEHGKNIVLSDNIETNTTL	56
MDGA1_MOUSE	MRYLFLFFA.....TFPVLANQQISLSIRNAPTAELISYLAEETGKNITISDEIKDTKNF	56
MDGA1_MOUSE	MKQWIAAILMMA.....LPVAQAAKPAKVTLVVDVDPVAQVLQALAEQERQNVVSPDVSGLVSL	60
MDGA1_MOUSE	MKQWIAAILLML.....IPGVAAKPKVTLVMDVDPVAQVLQALAEQERKNLVVSPDVSGTVSL	60
MDGA1_MOUSE	EPSGLYDYLVTQDNRLLTISIKPMTTEDAERRKKDNFAYTGEKLSLNFQDIDVRSVLQLIADFTDLNLVASDVTVGQNTTL	320
MDGA1_MOUSE	TVDGEFQHDYTLKGKYLEVVISKLLK.ADEKPKPKSVLEKEGKLISINFQDIPVRNVLQLIADYNGFNLVVSDSVVGNTTL	195
MDGA1_MOUSE	TVDGEFQHDYTLKGKYLEVVISKLLK.ADEKPKPKSVLEKEGKLISINFQDIPVRNVLQLIADYNGFNLVVSDSVVGNTTL	195
MDGA1_MOUSE	YIDEDYSHDYRLTGRYLEVKGKLLK.ANEKAPDKSILDKEGKLISINFQDIPVRNVLQLIADYNGFNLVVSDSVEGNTTL	196

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RLNVPMQV DILLKSKG DKKR DGNVY LIAPKQ ELK RERQQL EAKRL ELPPE EENFED ENHRYVY FSDIADVMEITSG
 KLNNDIMPRLLQIIIAKSKHLTLNKKDDGIYYINGSSQSGK...GQV.AGNLTTNEPHLVSHTVKLHFAKASELMKSIIT.. 140
 KLNNDIMPRLLKIIIAKSKHLTLNKKDGVVYYINGSSQSGK...GQV.AGNLTTNEPHLVSHTVKLHFAKASELMKSIIT.. 140
 RIENSNFDSVLKSIIRANKLTSAYENQIYFIHGKKDDK...DPNRGLNELLLPKPLITKTIKLDYAKAAEVIESIT.. 129
 RVEKSHFDEILNSLIKTHQLNLKKENGIIYITHQAQEHK...QHT.TAQLVNALPKLITKTIKLHYSKASEVIESIT.. 128
 HLIDVPWKQALQTVVKSAGLVSRRQEGNIIHHSAAWQNENAAARQEAQEARRLASLPVEHRAITQLYADAAELAKA... 135
 HLTDPVPWKQALQTVVKSAGLITRQEGNIIHHSIAWQNNNIAARQEAQARAQANLPLENRSITLQYADAGELAKA... 135
 RLQNPWDQDALDVLVLTIKGLDKRKLGNLVLVAPADETIAA.RERQELAQKQIAELAPLRRELIQVNYAKAAADIAKLFQSV 399
 RLDGVPWQQVLDIILQVKGLDKRV DGNVIL IAPKEELDLD.REKQALEKARLAEELGDLKSEIITKINFAKASDIAAMIIGG. 273
 RLDGVPWQQVLDIILQVKGLDKRV DGNVIL IAPKEELDLD.REKQALEKARLAEELGDLKSEIITKINFAKASDIAAMIIGG. 273
 RLDGVPWQQVLDIILQVKGLDKRV DGNVIL IAPKDELDLD.REKQQLKQLEKEITGE LSSEIITKVNFAKASDIAEMING. 274
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Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
...TSGS	T	S	G	S	L	L	S	P	A	G	S	I	F	D	D	R	S	N	L	L	V	I	Q	D	E	P	R	S	V	Q	N	I	K	K	L	I	A	E	M	D	K	P	I	E	Q	I	A	E	A	R	I	V	T	I	D	E	S	L	K	E	L	G	V	R	W	G	I	F	N	P	T	E	N																											
...TSGS	T	S	G	S	L	L	S	A	G	S	I	T	F	D	D	R	S	N	L	L	V	I	Q	D	E	P	R	F	V	Q	N	I	K	K	L	I	A	E	M	D	K	P	I	E	Q	I	A	E	A	R	I	V	T	I	D	E	S	L	K	E	L	G	V	R	W	G	I	F	N	P	T	E	N																											
...KGS	K	G	S	G	N	F	L	S	E	N	G	L	H	F	D	D	R	S	N	L	L	I	K	D	S	P	E	S	M	K	N	I	V	K	L	R	N	L	D	R	P	T																																																										

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NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
consensus

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NTDB id 1347 HI 0435 AAC22094.1	AGETLEALKQKSEGKK..	445
NTDB id 1373 NTHI RS02645 WP 011272046.1	AGETLEALKQKSAGKK..	445
NTDB id 1465 ASU2 RS06170 WP 014991934.1	SEKQQISS.HSLQKLPPK	431
NTDB id 1381 A4U84 RS02010 WP 021113424.1	SEKIGA EK.QK.....	420
NTDB id 67805 AABE55 RS19340 WP 002431761.1	SE.....	412
NTDB id 1433 BW25113 RS17570 WP 000815987.1	SE.....	412
NTDB id 1193 PA5040 NP 253727.1	NQAIAIGR.....	714
NTDB id 1186 GTF74 RS01320 WP 000788426.1	Q.....	571
NTDB id 1175 A1552VC RS12105 WP 000788426.1	Q.....	571
NTDB id 1408 DSB67 RS13980 WP 010643500.1	Q.....	580
consensus		



-  non conserved
-  similar
-  ≥ 50% conserved