

“Revisiting annotation of *Schistosoma mansoni* Micro-Exon Gene (MEG) family”

Štěpánka Nedvědová ^{1,2,3}, Davide De Stefano ¹, Olivier Walker ¹, Maggy Hologne ¹, Adriana Erica Miele ^{1,4*}

¹ UMR 5280 Institute of Analytical Sciences, Université de Lyon, CNRS, Université Claude Bernard Lyon 1, Villeurbanne, France

² Department of Chemistry, Faculty of Agrobiological Sciences, Czech University of Life Sciences, Prague, Czech Republic

³ Department of Zoology and Fisheries, Center of Infectious Animal Diseases, Czech University of Life Sciences, Prague, Czech Republic

⁴ Department of Biochemical Sciences, Sapienza University of Rome, Rome, Italy

*corresponding author. eMail: adriana.miele@univ-lyon1.fr

Supplementary Material

Supplementary Table S1: Summary of sequences and primary structure characteristics of MEG proteins analysed in this study.

Supplementary Figure S1: Multiple alignment of MEG proteins by MUSCLE

Supplementary Table S1: Summary of sequences and primary structure characteristics of MEG proteins analysed in this study. Parameters such as molecular weight (MW), aliphatic index and gravity index have been calculated by ProtParam on the EXPASY server.

Chromosome number	Gene identifier and name in WBPS	GenBank ID / GenBank protein seq.	UniProt ID	MW (g/mol)	pI	Aliphatic index	Gravy Index	Protein Sequence
1	<i>Smp_085840.1</i> <i>MEG-4</i> <i>Antigen 10.3</i>	8347941	C4QKE8	12908	4.86	89.16	-0.45	MNFLTLYVTLVYTILSVYSDIEPRIQKEYYYNLHENNSQ ANHNFHEMPEYDDQLPDFPHKQLEEEQNPFHKLSEVL NSGSVVPLWLVNPIYYVLELFPRAISYYFN
1	<i>Smp_124000.1</i> <i>MEG-14</i> <i>isoform 3</i>	AOL57991.1	A0A1C9A1H6	14354	10.31	80.5	0.1	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST STHGATSTAKPAASTPPKAAATSTIKPTVTPKAAATSTI KPTVTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAA AAVPIVLGVIGEVIGFILQYIAS
1	<i>Smp_124000.1</i> <i>MEG-14</i> <i>isoform 6</i>	AOL57994.1	A0A1C9A1I5	13820	10.19	76.99	0.05	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST THGATSTAKPAASTPPKAAATSTIKPTVTPKAAATSTTE PTVTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAA AVPIVLGVIGEVIGFILQ
1	<i>Smp_124000.1</i> <i>MEG-14</i> <i>isoform 7</i>	AOL57995.1	A0A1C9A1J0	14760	10.56	74.72	-0.06	MNRFFWTVTQRTILLVIICNLNTMKATSANSRTHGATST RTHGATSTAKPAASTPIKPTVTPKAAATSTTEPTVTPK AAATSTTEPTVTTSKPSAKPAASNTAKPAASTPKKPHDE RAVLAAAAPVIVLGVIGEVIGFILQ
1	<i>Smp_124000.2</i> <i>MEG-14</i>	AAN17279.1	Q8ITD5	15822	10.4	79.04	0.09	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST STHGATSTAKPAASTPPKAAATSTIKPTVTPKAAATSTI KPTVTPKAAATSTIKPTVTTSKPSAKPAASNTAKPAAS TPKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
1	<i>Smp_124000.2</i> <i>MEG-14</i> <i>isoform 1</i>	AOL57989.1	A0A1C9A1I1	14267	10.31	81.07	0.11	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST STHGATSTAKPAASTPPKAAATSTIKPTVTPKAAATSTI KPTVTTKPSAKPAASNTAKPAASTPKKPHDERAVLAAA AVPIVLGVIGEVIGFILQYIAS

1	<i>Smp_124000.2</i> <i>MEG-14</i> <i>isoform 2</i>	AOL57990. 1	A0A1C9A II4	15782	10.16	74.52	0.01	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST RTHGATSTAKP AASTPPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTPKAAA TSTTEPTVT-TKPSPAKPAA SNTAKPAASTPKKPHDERAVLAAAAPIVLGVIGEVIGFI LQYIAS
1	<i>Smp_124000.2</i> <i>MEG-14</i> <i>isoform 3</i>	N/A	A0A5K4E K08	15509	10.03	83.47	0.1	YLLCKKEYSIMNRFFWTVTQCTILLVIICNLNTMKATSA NSRTHGATSTSTHGATSTAKP AASTPPKAAATSTIKPTVTTTPKAAATSTIKPTVTTKPSPA KPAASNTAKPAASTPKKPHDERAVLAAAAPIVLGVIGE VIGFILQYIAS
1	<i>Smp_124000.2</i> <i>MEG-14</i> <i>isoform 4</i>	AOL57992. 1	A0A1C9A II3	15447	10.25	75.33	0.01	MNRFFWTVIQCTILLVIICNLNTMKATSANSRTHGATSTR THGATSTAKP AASTPPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTPKAAA TSTTEPTVTTSKPSPAKPAA SNTAKPAASTPKKPHDERAVLAAAAPIVLGVIGEVIGFI LQ
1	<i>Smp_124000.2</i> <i>MEG-14</i> <i>isoform 5</i>	AOL57993. 1	A0A1C9A II0	14179	10.31	81.65	0.12	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATST THGATSTAKPAASTPPKAAATSTIKPTVTTTPKAAATSTIK PTVTTKPSPAKPAAASNTAKPAASTPKKPHDERAVLAAA VPIVLGVIGEVIGFILQYIAS
1	<i>Smp_165050.1</i> <i>MEG-7</i>	8345678	G4V7W5	13106	10.04	79.74	-0.36	MNTLFRSIFVVVVVYAYFDMANGVPEPPRPDEDAVPV RAKPATPIKISTDKIPVNKTMKIQTTSPSKEKKQKPDPKRY KRSSYQKDKKAKSSSSTLTIGYPILFITTPFVISKFLL
1	<i>Smp_165050.2</i> <i>MEG-7 iso2</i>	N/A	A0A5K4E UJ7	16568	9.88	82.62	-0.43	MSVPIRNLLRNNEYAICKFQYCKHIDNGNYNILQRSIFV VVVVYAYFDMANGVPEPPRPDEDAVPVRAKPATPIKIS TDKIPVNKTMKIQTTSPSKEKKQKPDPKRYKRSSYQKDK KAKSSSSTLTIGYPILFITTPFVISKFLL
1	<i>Smp_176020.1</i> <i>MEG-11</i>	N/A	A0A3Q0K TG4	8635	5.36	81.52	0.03	MKLTHILLICFISLFFTYVQCDGEEEEENEEEEKPPQPDV PHGKHPLLKAFLLAPSWLHMPFSIAGAVAAAYVFYHFY G

1	<i>Smp_243780.1</i> <i>MEG-30</i>	CUS27856.1	A0A0U5K I45	6687	8.14	119.31	0.66	MQVDKFIITYTIVIIAIAIFVSMPEIHAFGIKFFTTTPVPNKG LLDKLLDGLYQFFNRH
1	<i>Smp_243790.1</i> <i>MEG-31</i> <i>protein</i>	CUS27857.1	A0A0U5K FM1	6879	9.39	88.1	-0.21	MHCVLLLLSLFAVCSVIMPTVKSGGSASGGSTEVDLMH KRGKDREDKRRKDYIKELVKNATGT
1	<i>Smp_307220.1</i> <i>MEG-4</i> <i>Antigen 10.3</i>	N/A	A0A5K4F 627	19788	6.73	83.35	-0.64	MNIYLIGILCIVGLIISQGSTANGSPLDDRFNDVNTINKK QFTEEEFSRLINSMLKEYIEDNKKDKHPTQKTTPKPTTP KQINDGTSDKTS DHTHTIKRTPKPTTPKQINDGTSDKPKS IADIFLINKPKVPLWIVNPLYMVEKQIMGYLLEDDDD TLELNLPKYYYDKSI
1	<i>Smp_307220.2</i> <i>MEG-4</i> <i>Antigen 10.3</i>	AAP13803.1	Q86D79	22739	8.43	76	-0.77	MNIYLIGILCIVGLIISQGSTANGSPLDDRFNDVNTINKK QFTEEEFSRLINSMLKEYIEDNKKDKHPTQKTTPKPTTP KQINDGTSDKTS DHTHTIKRTPKPTTPKQINDGTSDKTS DHTHTIKRTPKPTTPKQINDGTSDKPKSIADIFLINKPKVPL WIVNPLYMVEKQIMGYLLEDDDDTLELNLPKYYY DKSI
1	<i>Smp_307220.3</i> <i>MEG-4</i> <i>Antigen 10.3</i>	N/A	A0A5K4F 2K5	20828	7.74	81.37	-0.67	MNIYLIGILCIVGLIISQGSTANGSPLDDRFNDVNTINKK QFTEEEFSRLINSMLKEYIEDNKKDKHPTQKTS DHTHTIK RTPKPTTPKQINDGTSDKTS DHTHTIKRTPKPTTPKQIN DGTSDKPKSIADIFLINKPKVPLWIVNPLYMVEKQIMGYL LEDDDDTLELNLPKYYYDKSI
1	<i>Smp_307240.1</i> <i>MEG-4</i> <i>Antigen 10.3</i>	N/A	A0A5K4F 4B1	22129	9.14	94.17	-0.59	MKLVSISLIGIFSLISQYGYLIDIKHINSPNQKQYVRDK MNLLNEYLTSRNIKKQFTEEEFSRLINSMLKKHIEDKNV DIRIENKKDKHPTQKTS DHTHTIKRTPKPTTPKQINDGT SDKPKSIADFFLINKPKVPLWIVNPLYMVEKQIMGYL LEDDDDTLELNLPKYYYDKSI
2	<i>Smp_171190.1</i> <i>MEG-8</i>	8355812	G4VCW5	20959	9.86	66.86	-0.55	MFTIILIYVLYFIANAKFEHTTSGIRNPSKLSDSNASKTLS LKNLTDHYIHTPQKSNGTSCNGKDTCKLPNPSQKGFT NTTSLPHTQSHNSTVAPSVKPTRQEIPRSGTIVNGTKPT PGKPVVNGTKPTPGKPESFLKRVGDGFFDLFSEQEFHPI NHKSYLFWYLFRTSFLNLKNMKNLLLS

3	MEG-2.1 iso1	ADI31109.1	D7DP78	9792	5.53	86.36	-0.05	MKLSGANCLVVFSLQLLVAFSHCDINDITCNKTVCCAS EDGKKGSLCCEKDGCPSTPDLGLGNYQRHQRMKNYL EEVCENFIYTP
3	MEG-2.1 iso2	ADI31107.1	D7DP76	5641	4.83	103.08	0.51	MKLSGANCLVVFSLQLLVAFSHCDINDITCNKTVCCAS EDGKIGENFIYTP
3	MEG-2.1 iso3	ADH02222.1	D7PD75	2818	7.98	146.15	1.14	MKLSGANCLVVFSLQLLVALSHYTP
3	Smp_122630.1 MEG-1 iso1	N/A	A0A3Q0K KC4	18213	5.34	88.65	-0.09	MANKDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EINIDKDYLCYPTNFSHGLITYCTKSNDERDLLSYEED HIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
3	Smp_122630.1 MEG-1 iso10	ADH02235.1	D7PD88	17319	5.58	87.57	-0.07	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDSIKCIFR EICTYPTNFSHGLITYCTKSNDERDLLSYEEDHIALYVIQ PTNHCQRYEGSSSLVSQKPEKECPFCFD
3	Smp_122630.1 MEG-1 iso11	ADH02236.1	D7PD89	16526	5.58	89.15	-0.07	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EISHGLITYCTKSNDERDLLSYEEDHIALYVIQPTNHCQR YEGSSSSVSQKPEKECPFCFD
3	Smp_122630.1 MEG-1 iso16	ADH02240.1	D7PD93	17523	5.33	86.98	-0.12	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCCIFREINIDK DYLCYPTNFSHGLITYCTKSNDERDLLSYEEDHIALYVI QPTNHCQRYEGSSSLVSQKPEKECPFCFD
3	Smp_122630.1 MEG-1 iso18	ADH02241.1	D7PD94	14425	5.28	98.28	0.06	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCCIFREINIDK DYLCYPTNFSHGLITYCTKSNDERDLLSYEEDHIALYVI QPTNHCQRYEGSSSLVSQKPEKECPFCFD
3	Smp_122630.1 MEG-1 iso5	ADH02230.1	D7PD83	18241	5.34	88.65	-0.09	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EINIDKDYLCYPTNFSHGLITYCTKSNDERDLLSYEED

								HIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
3	<i>Smp_122630.1</i> <i>MEG-1 iso6</i>	ADH02231. 1	D7PD84	16143	5.48	91.88	-0.1	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLTDFIKCIFREINIDKDHLCTYPTNFH GLITYCTKSNDERDLLSYEEDHIALYVIQPTNHCQRYEG SSSLVSQKPEKECPFCFD
3	<i>Smp_122630.1</i> <i>MEG-1 iso8</i>	ADH02233. 1	D7PD86	14480	5.53	95.89	-0.02	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLTDFIKCIFREISHGLITYCTKSNDERD LLSYEEDHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPF CFD
3	<i>Smp_122630.2</i> <i>MEG-1 iso2</i>	N/A	A0A5K4E KN1	18156	6.28	102.53	0.02	MANKDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EINIDKDYLCYPTNFHGLITYCTKSNDERDLLSYEED HIALYVIQPTNHCQRYEGSSIKKRLLESYLIITPI
3	<i>Smp_122630.2</i> <i>MEG-1</i> <i>isoform 1</i>	ADH02226. 1	D7PD79	18184	6.28	102.53	0.02	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EINIDKDYLCYPTNFHGLITYCTKSNDERDLLSYEED HIALYVIQPTNHCQRYEGSSIKKRLLESYLIITPI
3	<i>Smp_122630.2</i> <i>MEG-1</i> <i>isoform 12</i>	ADH02243. 1	D7PD99	16495	6.81	107.21	0.09	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLNRTWFVFNKEICSCLTDFIKCIFR EISHGLITYCTKSNDERDLLSYEEDHIALYVIQPTNHCQR YEGSSIKKRLLESYLIITPI
3	<i>Smp_122630.2</i> <i>MEG-1</i> <i>isoform 14</i>	ADH02238. 1	D7PD91	16112	6.27	107.45	0.04	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKLTDFIKCIFREINIDKDYLCYPTNFH GLITYCTKSNDERDLLSYEEDHIALYVIQPTNHCQRYEG SSIKKRLLESYLIITPI
3	<i>Smp_122630.2</i> <i>MEG-1</i> <i>isoform 17</i>	ADH02242. 1	D7PD95	15394	6.27	106.41	0.02	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWR KDIDWLILTKGGKCIFREINIDKDYLCYPTNFHGLITY CTKSNDERDLLSYEEDHIALYVIQPTNHCQRYEGSSIKK RLLESYLIITPI
3	<i>Smp_138060.1</i>	N/A	A0A3Q0K	16404	4.81	57.55	-0.32	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNC

	<i>MEG-3 Grail family</i>		MS0					GILCSGTIGPQTFYCYLGCSHNATKQSEFDNCKTKCDGG VQLTKEACLSNCGLITTHPELCAVCGGNDGGSFICLY NCDQEHTDPRKDGADGSEDFDKCKTKCYKMAGQ
3	<i>Smp_138060.1 MEG-3.3 isoform 1</i>	ADH02209. 1	D7PD62	16403	5.07	57.55	-0.32	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNC GILCSGTIGPQTFYCYLGCSHNATKQSEFDNCKTKCDGG VQLTKEACLSNCGLITTHPELCAVCGGNDGGSFICLY NCDQKHTDPRKDGADGSEDFDKCKTKCYKMAGQ
3	<i>Smp_138060.1 MEG-3.3 isoform 2</i>	ADH02210. 1	D7PD63	16153	4.81	55.78	-0.37	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNC GILCSGTIGPQTFYHYFSTKQSEFDNCKTKCDGGVQLT KEACLSNCGLITTHPELCAVCGGNDGGSFICLYNCDQ EHTDPRKDGADGSEDFDKCKTKCYKMAGQ
3	<i>Smp_138060.1 MEG-3.3 isoform 3</i>	ADH02211. 1	D7PD64	15542	4.7	57.34	-0.35	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNC GILCSGTIGPQTFYSTKQSEFDNCKTKCDGGVQLTKEAC LSNCGLITTHPELCAVCGGNDGGSFICLYNCDQEHTD PRKDGADGSEDFDKCKTKCYKMAGQ
3	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2</i>	ADH02200. 1	D7PD53	14811	5.6	60.72	-0.17	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHSGL CSGSTGPQTFYCYLGCSHNASNQNDFDKCLPKCNGSPQ LTESSCQNDGCRVTTHPELPGIVCGGNVGDSPFLCLYNC DQGNGSGNFDECKTKCYLMAGR
3	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2/1</i>	GB PS : ADH02199. 1	D7PD52	15769	5.39	57.1	-0.26	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHNEYV TRYCGGLCSGSTGPQTFYCYLGCSHNASNQNDFDKCLP KCNGSPQLTESSCQNDGCRVTTHPELPGIVCGGNVGDSP FPLCLYNC DQGNGSGNFDECKTKCYEMAGR
3	<i>Smp_138070.1 MEG-3.2 (Grail) isoform3</i>	GB PS : ADH02201. 1	D7PD54	15208	5.39	57.17	-0.3	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHNEYV TRYCTGPQTFYCYLGCSHNASNQNDFDKCLPKCNGSPQ LTESSCQNDGCRVTTHPELPGIVCGGNVGDSPFLCLYNC DQGNGSGNFDECKTKCYEMAGR
3	<i>Smp_138070.1 MEG-3.2 (Grail) isoform6</i>	ADH02204. 1	D7PD57	14794	5.62	55.88	-0.27	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHNEYV TRYCGGLCSGSTGPQTFYCYLGCSHNASNQNDFDKCLP KCNGQNDGCRVTTHPELPGIVCGGNDGGSFICLYNCD QGNGSGNFDECKTKCYEMAGR

3	<i>Smp_138070.1</i> <i>MEG-3.2</i> <i>(Grail)</i> <i>isoform9</i>	ADH02207. 1	D7PD60	14500	5.42	54.62	-0.34	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHNEYV TRYCGGLCSGSTGPQTFYCYLGCSHNASNQNDFDKCLP KCNGQND CGRVTTHPEL CGIVCGGNDGGSFPICLYNCD QGNGSGNFDECKTKCYEMAGR
3	<i>Smp_138070.2</i> <i>MEG-3.2</i> <i>(Grail)</i> <i>isoform1</i>	N/A	A0A5K4E PC8	17562	7.16	68.01	-0.22	RTTTHRLVKMLFVALILIISLHSFDCVFTARETQQECVRH CGGHNEYVTRYCGGLCSGSTGPQTFYCYLGCSHNASN QNDFDKCLPKCNGSPQLTESSCQND CGRPH TLN CVVSF VVEMLETHFHCVCITAIEMVRETLTNVKQSATKWRDG EFP
3	<i>Smp_138080.1</i> <i>MEG-3 (Grail)</i>	N/A	A0A3Q0K MU6	17152	5.44	50.99	-0.67	MLFVALILIISLHSFDCVFTAQETRDAERECKKHCEGNN EYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDDFDK CLPKCNDRVQLTEENCRDDCGRVTSHHEL CGDVCGGN HGGSFPLCLYNCDQEHPREYERGYDKCKTKCYAMEGR
3	<i>Smp_138080.1</i> <i>MEG-3.1</i> <i>(Grail)</i> <i>isoform1</i>	ADH02196. 1	D7PD49	16404	5.07	57.55	-0.32	MLFVALILIISLHSFDCVFTAQETRDAERECKKHCEGNN EYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDDFDK CLPKCNDRVQLTEENCRDDCGRVTSHHEL CGDVCGGN HGGSFPLCLYNCDQEHPREYERGYDKCKTKCYAMEGR
3	<i>Smp_138080.1</i> <i>MEG-3.1</i> <i>(Grail)</i> <i>isoform2</i>	ADH02197. 1	D7PD50	14569	5.39	55.04	-0.44	MLFVALILIISLHSFDCVFTAQETRDAERECKKHCEGNN EYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDDFDK CLPKCNDRVQLTEENCRNDCGRVTSHHEL CGDVCGGN HGGSFPLCFFQSSSSDK
3	<i>Smp_138080.1</i> <i>MEG-3.1</i> <i>(Grail)</i> <i>isoform3</i>	ADH02198. 1	D7PD51	16615	5.77	47.07	-0.74	MLFVALILIISLHSFDCVFTAQETRDAERECKKHCEGNN EYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDDFDK CLPKCNDRVQLTEENCRNDCGRVTSHHESCGDVCGGN HGGSFPLCSYNCDQEHPREYER GKT KRYAMEGR
3	<i>Smp_159800.1</i> <i>MEG-2</i> <i>(ESP15)</i> <i>family</i>	8347467	C4QG05	9095	7.53	95.06	0.03	MCLTIFYVIHLLAIFSDSTEWVITCNKTTCCDEDGNSKIC CVGNDCKDVIKPRSSGADDLNLFLRKRGMAYKLGEILK KLN
3	<i>Smp_159800.1</i> <i>MEG-2.4</i>	ADH02216. 1	D7PD69	8971	6.52	96.3	0.05	MCLTIFYVIHLLAIFSDSTEWVITCNKTTCCDEDGNSKIC CVGNDCKDVIKPRSSGADDLNLFLRKRGMAYKLGEILK

	<i>isoform 1</i>							KLN
3	<i>Smp_159830.1</i> <i>MEG-2</i> <i>(ESP15)</i> <i>family</i>	N/A	A0A3Q0K R24	7734	5.07	87.54	-0.05	MCLTIFYVIHLLAIFSDSNEWVITCNKTTCCDEDKNSKIC CVGNDCKDVIKPRSSGADDFDLLKLNPS
3	<i>Smp_180310.1</i> <i>MEG-2</i> <i>(ESP15)</i>	8340871	C4QPR6	8646	7.54	50.68	-0.58	MERFKSSYFYFEIYLLCFTETVCCESDGGKAGSLCCEKN GCSVPSGTHDLLSENYRRHQRMKNYLKEVCKYFK
3	<i>Smp_180320.1</i> <i>MEG-2</i> <i>(ESP15 iso1)</i>	8340874	C4QPR8	11165	7.57	73.02	-0.22	MHGIWCKVPVSVVIWIHSTLFQFTFKVIFYELKQNNTFPL PGDGWTITCNETYCCENTDNGKLCDDGEYCSASISKLD PPFSNCFQYVFS
3	<i>Smp_180320.2</i> <i>MEG-2</i> <i>(ESP15 iso2)</i>	N/A	A0A3Q0K TV3	10983	6.87	73.79	-0.2	MHGIWCKVPVSVVIWIHSTLFQFTFKVIFYELKQNNTFPL PGDGWTITCNETYCCENTDNGKLCDDGEYCSASISNHQ DLTKHQQLLMSKKFKII
3	<i>Smp_180330.1</i> <i>MEG-2</i> <i>(ESP15)</i> <i>family</i>	8340875	C4QPR9	5497	10.37	103.54	-0.35	QKAISRPFVAVIKMVVTVDNPELTLKNYLRKAQMIDKL REAVQKLGGR
3	<i>Smp_180340.1</i> <i>MEG-2</i> <i>(ESP15)</i>	8340876	C4QPS0	4895	9.9	84.09	0.14	MTAKGSVAMASFVLVYDPSVAVKNYRQQVLMATKIKE VCQKFRG
3	<i>Smp_326790.1</i> <i>MEG-1</i>	N/A	A0A5K4F 8B3	22040	5.12	79.09	-0.3	MAKSDLILTPYQVFILPCILIFWSLFLIVFKSDGSGTWRR DIDWFILTQGKQIQRIWFVFNETEEVCSCVTGFEKCNIRE IIAANYSPIIHNEEKKNISNREKDYLCTCPTYFNHGVITY CTKSNEYKDSLQYEDDFMDL FVKKHNDKDDCQHYGGY SSLEYRNPEKVCPCFYEEITQCSIWETLS
3	<i>Smp_326790.2</i> <i>MEG-1</i>	N/A	A0A5K4F 8U8	21198	5.24	80.56	-0.34	MAKSDLILTPYQVFILPCILIFWSLFLIVFKSDGSGTWRR DIDWFILTQGKQIQRIWFVFNETEEVCSCVTGFEKCNIRE IIAANYSPIIHNEEKKNISNREKDYLCTCPTYFNHGVITY CTKSNEYKDSLQYEDDFMDL FVKKHNDKDDCQHYGGY

								SSLEYRNPEKEITQCSIWETLS
3	<i>Smp_326790.3</i> <i>Uncharacterized</i>	N/A	A0A5K4F AB4	19957	5.23	65.33	-0.67	MYYPYFLVSIFDSLQNSYIKQSGTWRRDIDWFILTQG KQIQRIWFVFNETEEVCSCVTGFEKCNIREIIAANYSPIIH NEEKKNISNREKDYLCTCPTYFNHGVTYCTKSNEYKD SLQYEDDFMDLFVKKHNKDDCQHYGGYSSLEYRNPEK EITQCSIWETLS
3	<i>Smp_336990.1</i> <i>Uncharacterized</i>	N/A	A0A5K4F DB9	9393	6.68	82.17	-0.07	MKLSGANCLVVFSLQLLVAFSHCDISDITCNKTVCCAS EDGKTGSLCCEKDGCPSTPDLFLENYRRHRRMKNYLEE VCKYYI
3	<i>Smp_345100.1</i> <i>MEG-2.2</i> <i>isoform1</i>	N/A	A0A5K4F FX0	13413	9.64	96.52	-0.37	MYCQSFTLLNRDYISNVTKQSKHRLYNTMKLSGANCLV VFSLQLLVAFSHCKLMSHNMQQDSSLRQKTVKKVRTE ERWLSNTPDLLLGNVQRHQRMKNYLEEVQILHIYYI
3	<i>Smp_345100.1</i> <i>MEG-2.2</i> <i>isoform2</i>	ADH02224. 1	D7PD77	9336	7.5	87.37	0.02	MKLSGATCLVVFSLQLLVAFSHCDISAITCNKTVCCASE DGKTGSLCCEKDGCPSTPDLFLENYRRHRRMKNYLEEV CKYYI
4	<i>Smp_158890.1</i> <i>MEG-16 iso1</i>	N/A	A0A3Q0K QX7	12759	10.12	78.68	-0.18	MFYCRVLIITSFMIFLLGTANCDIIDVLSLLFGNGNKN RRNRNRGGDSGGLSDFLTSLFDWNGDGYRGS GFNFYD FLSLFFGLNKKDNRNRRRYRSGGGGGNGGLIRLFFAR
4	<i>Smp_158890.2</i> <i>MEG-16 iso2</i>	N/A	A0A5K4E U45	11802	9.91	72.21	-0.32	MFYCRVLIITSFMIFLLGTANCDIIDDKNIRNRNRGGDS GGLSDFLTSLFDWNGDGYRGS GFNFYDFLSLFFGLNKK DNRNRRRYRSGGGGGNGGLIRLFFAR
5	<i>Smp_152580.1</i> <i>MEG-5</i>	8345024	G4LYD1	8884	9.36	112.28	0.05	MRRNYLLLYICII VFILLKEINASGRQPKFVNVDTDGNLR SGGSSDISDMFGQNKTLGTAFKTLHNLWDLLKQSLGL P
5	<i>Smp_152590.1</i> <i>MEG-10</i>	N/A	A0A3Q0K Q39	6127	7.74	59.29	0.04	MTLLLIQSCHCGSSGSTEAGSNGTNSKGWWPKFLGWA NTFCTFITFSNTIQNFIYG
5	<i>Smp_152590.2</i> <i>MEG-10 iso2</i>	8345025	G4LYD0	6056	7.74	58.55	0.01	MTLLLIQSCHCGSSGSTEAGSNGTNSKGWWPKFLGWAN TFCTFITFSNTIQNFIYG
5	<i>Smp_152630.1</i> <i>MEG-12</i>	N/A	A0A3Q0K Q41	5050	8.1	60.24	-0.18	GENYEQLLQPKAYGIWSLFSYFYKTFKVFCVSNMVN WIFG

5	<i>Smp_243730.1</i> <i>MEG-10.2</i> <i>protein</i>	CUS27851. 1	A0A0U5K JN7	7428	5.96	88.44	0.36	MISLLLFGLLLLQSCLYCSSDNENAGTTTEKPTSFWKRF FDFNFICTLNQTWSTIRNFFGIAL
5	<i>Smp_243750.1</i> <i>MEG-27 iso1</i>	CUS27853. 1	A0A0U5K IV9	6701	5.99	95.64	0.26	MNLIQTLLWMIFMMIMNLTNEIKWVNCSHELNEHTSET SLRGWIHTVFSFLFHNH
5	<i>Smp_243750.1</i> <i>MEG-27 iso2</i>	N/A	A0A5K4F 014	6800	6.38	95.64	0.18	MNLIQTLLWMIFMMIMNLTNEIKWVNCSHELNEHTSET SLRRWIHTVFSFLFHNH
6	<i>Smp_123100.1</i> <i>MEG-32.1</i>	CUS27858. 1	A0A0U5K EW2	8861	9.3	118.72	0.61	MYYRHYLLAIINVIVLSTMIQYVIGGSIFGDDTSTTKNM TTTTKASSANSLEVSOLAISSISMIVIGLINGHLRRFIF
6	<i>Smp_123200.1</i> <i>MEG-32.2</i>	CUS27859. 1	A0A0U5K J28	9879	6.63	102.81	0.26	MKETTVMHHYHHPNHRLLTVISAIVLLTIVHDVKGS GLFDDDITTRTTAPTSTSGSVSSFQVSWLALSSVFMIVLG LINSYTERSIF
6	<i>Smp_127990.1</i> <i>MEG 13 iso1</i>	N/A	A0A3Q0K LA7	14352	4.19	58.46	-0.41	MDITYSWCIICLINLLLNGKLGQAQEDNYTEDSTTDPTT FDNTTIVTSTTTEFNNTTIVTSTTTEFNNTTIVTSTTTEFTNK PKVENSTTDGTTYTTTTPSHFSTSTSTNDATNSKFQRIFY MIVGLISLMAIN
6	<i>Smp_127990.2</i> <i>MEG 13 iso2</i>	N/A	A0A5K4E L02	13790	4.27	60.8	-0.39	MDITYSWCIICLINLLLNGKLGQAQEDNYTEDSTTDNTT VTSTTTEFNNTTIVTSTTTEFNNTTIVTSTTTEFTNKPKVE NSTTDGTTYTTTTPSHFSTSTSTNDATNSKFQRIFYMIVGL ISLMAIN
6	<i>Smp_172180.1</i> <i>MEG-8</i>	8340626	G4VLP3	15839	9.07	58.5	-0.47	MNTVTLGLFCIAICLIGINAGTVSKPTATVKPQPVNKMN TTPVHQEESFWRMWNSTSMFGSSDSSGTNNKDTK SPNPNTTEAKSLSLKERIMNKFNSIFGEEYPPKDSDFE ERLWMLFKHCFLNFKNLAKIFST
6	<i>Smp_243740.1</i> <i>MEG-26</i> <i>protein</i>	CUS27852. 1	A0A0U5F Z31	8252	7.75	129.45	0.25	MDISKILLGSLFLLSVIILQEVNGQKGNRVIFNVEELILNL WKNLYERLADTFKCLSPLPESIGGKKNKSCYP
6	<i>Smp_243760.1</i> <i>MEG-28</i>	CUS27854. 1	A0A0U5K KP6	7864	10.01	110.76	0.44	MNTIVRYYLILFIITTEIQNIRSAFKKRPPASFVILENMTS TDRFRKLLYHCFTSFSTWMLLGG
6	<i>Smp_243770.1</i>	CUS27855.	A0A0U5K	7636	6.7	129.86	0.94	MLNKLLLQLFILVTIIIIHDVKCGGEEETTTTTLPTTTSVAI

	<i>MEG-29 protein</i>	1	LL2					KGTISAYTVMMGLSIYVIHSFIVFKMM
7	<i>Smp_010550.1 Uncharacterized MEG-15 iso4</i>	N/A	A0A3Q0KC91	16111	9.94	86.31	-0.44	MLNRFIVILVVFVVGIVTFDQVQQRDPPTNNTITHTTNHYVVGKLSHHNTVPAKTTRKSQHPNTTPSHTDKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
7	<i>Smp_010550.2 Uncharacterized MEG-15 iso2</i>	N/A	A0A5K4E9M7	18948	10.26	81.08	-0.52	MLNRFIVILVVFVVGIVTFDQVQKTNNTITHTTNHYVVGKLSHHNTVPAKTTRKSQHTTATARHHNTLKTTLSHHNTVPAKTTRKSQHPNTTPSHTDKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
7	<i>Smp_010550.3 Uncharacterized MEG-15 iso1</i>	8353067	G4VMN2	19569	10.33	78.72	-0.59	MLNRFIVILVVFVVGIVTFDQVQQRDPPTNNTITHTTNHYVVGKLSHHNTVPAKTTRKSQHTTATARHHNTLKTTLSHHNTVPAKTTRKSQHPNTTPSHTDKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
7	<i>Smp_010550.4 Uncharacterized MEG-15 iso3</i>	N/A	A0A5K4E9G8	16045	9.94	87.73	-0.37	MLNRFIVILVVFVVGIVTFDQVQQRDPPTNNTITHTTNHYVVGKLSHHNTVPAKTTRKSQHTTATASHTDKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
7	<i>Smp_125320.1 MEG-9</i>	N/A	A0A3Q0K KW2	6818	5.31	86.61	0.36	MIISCQFITGFVVHESSTEGQNHEELAAAAGAHFLQFLNGCFLNMDNLKLVFPG
ZW	<i>Smp_163710.1 MEG-6</i>	8355717	G4VTX1	7549	12.14	98.77	-0.66	MVQNPKN TKKINRTIRRSTKTVIVITDRVQNVLGHRLHHRIPTIKRSKSHGINKNETVSNLFP

Supplementary Figure S1. Multiple alignment of the 87 sequences of MEG products by MUSCLE.

	cov	pid	1 [100
1 A0A0U5KPK6_MEG-28	100.0%	100.0%	-----MNTIVRYYLILF-----	-----
2 A0A0U5F231_MEG-26	51.5%	1.9%	-----MD-ISKILGSLFLL-----SVIILQEVNQGKGNRVI-FNVNELI---LNL-----WKN-LYERLAD-----	-----
3 C4QKE8_MEG-4	71.2%	2.5%	-----MN-FLTLY-----VTLVYTI-----LSVYSIDIEPRIQKEYYYN-LHENNSQANHNKFHEMPE-----KKDKHP-----	-----
4 A0A5K4F4B1_MEG-4	100.0%	5.6%	MKLVSIISLIGIFSLISQEYG-----YLI--DIKHINSPNQKQYVRDKMNLLE-YLTSRNI-KKQFTTEEF SRLINSMK-----KHIED--	-----
5 A0A5K4F2K5_MEG-4	98.5%	4.4%	-----MNIYLIGIL-CIVGL-----IISQGSTANGSPLDDRFNDVNTINKKQFTTEEF SRLINSMKKEYIEDNKKDKHPTQKT	-----
6 A0A5K4F627_MEG-4	98.5%	4.6%	-----MNIYLIGIL-CIVGL-----IISQGSTANGSPLDDRFNDVNTINKKQFTTEEF SRLINSMKKEYIEDN-----	-----
7 Q86D79_MEG-4	100.0%	4.0%	-----MNIYLIGIL-CIVGL-----IISQGSTANGSPLDDRFNDVNTINKKQFTTEEF SRLINSMKKEYIEDNKKDKHPTQKT	-----
8 A0A3Q0FQX7_MEG-16	98.5%	1.7%	MFYCRVLIITSEFMIFLLGTAN-C-----DIIDVLSLLFGNGNKNIRRN-----RNRGGDSGGLS-----	-----
9 A0A5K4EU45_MEG-16	92.4%	2.9%	-----MFYCRVLI---I-----TSFMIFLLGTANCDIIDDKNIRRN-----RNRGGDSGGLS-----	-----
10 A0A3Q0KLA7_MEG-13	93.9%	4.5%	-----MDITYSW---CIICL---I-----NLLLNKGLGQAQEDNYTEDSTTDP---TTFDNTT VTSTTTE-----	-----
11 A0A5K4EL02_MEG-13	100.0%	5.6%	-----MDITYSW---CIICL---I-----NLLLNKGLGQAQEDNYTEDSTTDN---TTVTSTTTE-----	-----
12 A0A3Q0KQ39_MEG-10	42.4%	6.9%	-----MTL---LLIQSCHCGS---S-----GSTEAGSNGTNSKGWPKFLGWAN-----	-----
13 G4LYD0_MEG-10	40.9%	6.9%	-----MTL---LLIQSCHCGS---S-----GSTE-GSNGTNSKGWPKFLGWAN-----	-----
14 G4VCW5_MEG-8	98.5%	2.6%	MFT-----IIL-IYVLY---F-----IANAKFEHTTSGIRNPSKLSDSNA---SKTLSLKNLTDHYIHTPQKSNGTSCNGKDT	-----
15 A0A3Q0KKW2_MEG-9	69.7%	5.6%	-----MIISCQ---F-----ITGFVV-----	-----
16 G4VLP3_MEG-8	100.0%	5.0%	-----MN--TVTLGLFCIAIC---L-----IGINAGTVSKPTATVKPQPVNKMN---TPVHQ--EESFWRMWN SFTSMFGSSDSSS-	-----
17 G4V7W5_MEG-7	100.0%	5.2%	-----MN--TL-----F-----RSIFVVVVVYAYFDMANGVPEPPRPVDEDAVP--VRA-----KPATP-----IK-I-	-----
18 A0A5K4EUJ7_MEG-7-iso2	98.5%	2.7%	--MSVIPRNLRLRNEY---AICKFQYCKH--IDNGNYNILQRSIFVVVVVYAYFDMANGVPEPPRPVDEDAVP--VRA-----KPATP-----IK-I-	-----
19 A0A5K4EKN1_MEG-1	95.5%	4.5%	--MANKDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
20 D7PD99_MEG-1	95.5%	4.9%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
21 D7PD79_MEG-1	95.5%	4.5%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
22 D7PD91_MEG-1	95.5%	5.0%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGK-----LTD FIKCI-	-----
23 D7PD95_MEG-1	95.5%	5.2%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGG-----LTKGG-----KCI-	-----
24 D7PD89_MEG-1	98.5%	4.9%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
25 A0A3Q0KKC4_MEG-1	98.5%	4.5%	--MANKDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
26 D7PD88_MEG-1	98.5%	4.7%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDSIKCI-	-----
27 D7PD93_MEG-1	98.5%	4.7%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSC-----CI-	-----
28 D7PD94_MEG-1	98.5%	4.7%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSC-----CI-	-----
29 D7PD83_MEG-1	98.5%	4.5%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGKLNRTWVFVNETKEICSLTDFIKCI-	-----
30 D7PD84_MEG-1	98.5%	5.0%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGK-----LTD FIKCI-	-----
31 D7PD86_MEG-1	98.5%	5.6%	--MANRDLILTP--YQVFILPCFILI---F-----WSLFLIVFKSDGSGTWRKIDWLI---LTKGGK-----LTD FIKCI-	-----
32 A0A5K4FAB4_Uncharacterized	95.5%	2.9%	--M-----YYPYFL--VSI---F-----DSLQNSYIKQSGTWRRDIDWFI---LTQGKQIQRIWVFVNETEEVCSVGTGFEKCN-	-----
33 A0A5K4F8B3_MEG-1	100.0%	3.2%	--MAKSDLILTP--YQVFILPCIIIL---F-----WSLFLIVFKSDGSGTWRRDIDWFI---LTQGKQIQRIWVFVNETEEVCSVGTGFEKCN-	-----
34 A0A5K4F8U8_MEG-1	100.0%	3.4%	--MAKSDLILTP--YQVFILPCIIIL---F-----WSLFLIVFKSDGSGTWRRDIDWFI---LTQGKQIQRIWVFVNETEEVCSVGTGFEKCN-	-----
35 A0A0U5KI45_MEG-30	59.1%	8.6%	-----MQ--VDKFIYTVIIL---A-----IAIFVSMPEIHAFLGK-----	-----
36 A0A5K4E9G8_MEG-15	95.5%	2.8%	-----MLNR--FIVILVFVFGIVT--F-----DNVQQRDPPTNTTITHTTNHYV---GKLSHHNTVPAKTRKSOH-----	-----
37 A0A5K4E9M7_MEG-15	93.9%	1.8%	-----MLNR--FIVILVFVFGIVT--F-----VTFDNVQGTNTTITHTTNHYV---GKLSHHNTVPAKTRKSOHTTATARHHNTLK-	-----
38 A0A3Q0KC91_MEG-15	95.5%	2.8%	-----MLNR--FIVILVFVFGIVT--F-----DNVQQRDPPTNTTITHTTNHYV---GKLSHHNTVPAKTRKSO-----	-----
39 G4VMN2_MEG-15	95.5%	2.3%	-----MLNR--FIVILVFVFGIVT--F-----DNVQQRDPPTNTTITHTTNHYV---GKLSHHNTVPAKTRKSOHTTATARHHNTLK-	-----
40 A0Q3Q0KQ41_MEG-12	39.4%	2.4%	-----GEN--YEQQLQPKAYG---I-----WSLFSYFYKTFK-----	-----
41 A0A5K4EPC8_MEG-3.2	100.0%	1.9%	--RTTTHRLVKML--FVALILIIISLHS---F-----DCVF TA---RETQQECVRHCGGHN---EYVTRYCGGLCSGSTGPTFYCYLGC SHNAS-	-----
42 D7PD63_MEG-3.3	100.0%	4.8%	-----ML--FFALILIIISLHS---F-----DCAF-----TAQQECEKNCKGDN---EYVSPNCGILCSGTIGPQTFYH---YFST-	-----
43 D7PD64_MEG-3.3	100.0%	4.9%	-----ML--FFALILIIISLHS---F-----DCAF-----TAQQECEKNCKGDN---EYVSPNCGILCSGTIGPQTFYH-----T-	-----
44 D7PD62_MEG-3.3	100.0%	4.6%	-----ML--FFALILIIISLHS---F-----DCAF-----TAQQECEKNCKGDN---EYVSPNCGILCSGTIGPQTFYCYLGC SHNAT-	-----
45 A0A3Q0KMS0_MEG-3	100.0%	4.6%	-----ML--FFALILIIISLHS---F-----DCAF-----TAQQECEKNCKGDN---EYVSPNCGILCSGTIGPQTFYCYLGC SHNAT-	-----
46 D7PD57_MEG-3.2	86.4%	3.4%	-----ML--FVALILIIISLHS---F-----DCVF TA---RETQQECVRHCGGHN---EYVTRYCGGLCSGSTGPTFYCYLGC SHNAS-	-----
47 D7PD60_MEG-3.2	86.4%	3.4%	-----ML--FVALILIIISLHS---F-----DCVF TA---RETQQECVRHCGGHN---EYVTRYCGGLCSGSTGPTFYCYLGC SHNAS-	-----
48 D7PD53_MEG-3.2	86.4%	3.4%	-----ML--FVALILIIISLHS---F-----DCVF TA---RETQQECVRHC-----GGHSGGLCSGSTGPTFYCYLGC SHNAS-	-----

49	D7PD52_MEG-3.2	86.4%	3.2%	-----ML--FVALILIIISLHS----F-----DCVFTA---RETQQECVRHCGGHN---EYVTRYCGGLCSGSGTGPQTFYCYLGCSHNAS-
50	D7PD54_MEG-3.2	86.4%	3.4%	-----ML--FVALILIIISLHS----F-----DCVFTA---RETQQECVRHCGGHN---EYVTRYC-----TGPQTFYCYLGCSHNAS-
51	D7PD51_MEG-3.1	84.8%	1.9%	-----ML--FVALILIIISLHS----F-----DCVFTAQETRAERECKKHCEGNN---EYVTRYCGGLCSSNTGPQTFYCYLGCSHNAS-
52	AOA3Q0KMU6_MEG-3	90.9%	1.9%	-----ML--FVALILIIISLHS----F-----DCVFTAQETRAERECKKHCEGNN---EYVTRYCGGLCSSNTGPQTFYCYLGCSHNAS-
53	D7PD49_MEG-3.1	90.9%	1.9%	-----ML--FVALILIIISLHS----F-----DCVFTAQETRAERECKKHCEGNN---EYVTRYCGGLCSSNTGPQTFYCYLGCSHNAS-
54	D7PD50_MEG-3.1	68.2%	2.3%	-----ML--FVALILIIISLHS----F-----DCVFTAQETRAERECKKHCEGNN---EYVTRYCGGLCSSNTGPQTFYCYLGCSHNAS-
55	AOA0U5KIV9_MEG-27	53.0%	3.5%	-----MN--LIQTL-----W-----MIFMMIMNLTNEIKW-----
56	AOA5K4F014_MEG-27	45.5%	4.9%	-----MN--LIQTL-----W-----MIFMMIMNLTNEIKWV-----
57	G4LYD1_MEG-5	53.0%	2.5%	-----MRRNY-LLLYICIIIV----F-----ILLKEINASGRQPKFVNVDTDGNL-----R-SGG--SS-----
58	G4VTX1_MEG-6	65.2%	1.5%	-----MV-----QNPKN-----TKK----IN-----
59	AOA3Q0KTG4_MEG-11	71.2%	4.1%	-----MK--LTHILLICFISFL--F-----FTYVQCDGEEENE-----
60	AOA0U5KLL2_MEG-29	69.7%	4.5%	-----MLNK----LLLQLFILV----F-----T---IIIIHDVKCGGEEET-----
61	AOA0U5KEW2_MEG-32.1	75.8%	1.1%	-----MYYRH--YLLAINVIVLS-----T-----MIQ-YVIGGSIFGDDT-----
62	AOA0U5KJ28_MEG-32.2	78.8%	3.9%	MKETTVMHHYHP--HPNHRLLTVisA-----IVLITIVHDVKGSGGLFDDDIIT-----
63	AOA5K4EK08_MEG-14	100.0%	5.3%	YLLCKKEYSIMNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTPPKAAATSTIKPTVTTP
64	AOA1C9A1H6_MEG-14	100.0%	5.0%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTP-----STIKPTVTTP
65	Q8ITD5_MEG-14	100.0%	4.5%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTPPKAAATSTIKPTVTTP
66	AOA1C9A1I1_MEG-14	100.0%	5.7%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTPPKAAATSTIKPTVTTP
67	AOA1C9A1I0_MEG-14	100.0%	5.8%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTP-----STIKPTVTTP
68	AOA1C9A1I5_MEG-14	100.0%	5.1%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTS---THGATSTAKPAASTP-----STIKPTVTTP
69	AOA1C9A1J0_MEG-14	100.0%	4.9%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTR---THGATSTAKPAASTP-----IKPTVTTP
70	AOA1C9A1I3_MEG-14	100.0%	4.6%	-----MNR--FFWTVIQTILL-----V---IICNLNMTKATSANSRTHGATSTR---THGATSTAKPAASTPPKAAATSTIKPTVTTP
71	AOA1C9A1I4_MEG-14	100.0%	5.2%	-----MNR--FFWTVTQCTILL-----V---IICNLNMTKATSANSRTHGATSTR---THGATSTAKPAASTPPKAAATSTIKPTVTTP
72	C4QPR8_MEG-2	69.7%	2.7%	-----MH--GIWCKVPVSVVI-----WIHSTLFQF---TFKVFYELKQNTFPLP-----
73	AOA3Q0KTV3_MEG-2	81.8%	2.8%	-----MH--GIWCKVPVSVVI-----WIHSTLFQF---TFKVFYELKQNTFPLP-----
74	C4QPR9_MEG-2	62.1%	2.7%	-----QKAISRPFQVAVI-----
75	AOA0U5KJN7_MEG-10.2	48.5%	10.6%	-----MISLLLFGLLLL---Q-----SCLYCSDN---ENAGTTEKPTSF---WKRFFDFFN-----
76	AOA0U5KFM1_MEG-31	42.4%	2.1%	-----MH-----CVLLLLSL-----F--AVCSVIMPTVKSGSASGGSTEV---LMHKGKDR-----
77	C4QPS0_MEG-2	62.1%	3.8%	-----MTA--KGSVAMASFVLV-----Y-----
78	C4QG05_MEG-2	74.2%	5.2%	-----M-----CLTIF-----Y-VIHLLAI-FS--DSTEWVITCN-----
79	D7PD69_MEG-2.4	75.8%	3.6%	-----M-----CLTIF-----Y-VIHLLAI-FS--DSTEWVI-----
80	AOA3Q0KR24_MEG-2	57.6%	8.7%	-----M-----CLTIF-----Y-VIHLLAI-FS--DSNEWVITCN-----
81	C4QPR6_MEG-2	75.8%	1.1%	-----MER--FKSSYF--YFEI-----Y---LLC--FT--ETVCESEDGKAG-----
82	AOA5K4FFX0_MEG-2.2	62.1%	0.8%	MYCQSFTLLNRDYISNVTKQSKHRLYNTMKLSGANCLVVFSLQLLVA-FSHC----KLMSHNMQQDS
83	AOA5K4FDB9_Uncharacterized	74.2%	3.0%	-----MKLSGANCLVVFSLQLLVA-FSHCDIS----DI-----
84	D7PD77_MEG-2.2	74.2%	2.0%	-----MKLSGATCLVVFSLQLLVA-FSHCDIS----AI-----
85	D7DP78_MEG-2.1	92.4%	8.6%	-----MKLSGANCLVVFSLQLLVA-FSHCDIND----ITCNKTV-----
86	D7DP76_MEG-2.1	53.0%	4.8%	-----MKLSGANCLVVFSLQLLVA-FSHCDIND-----
87	D7DP75_MEG-2.1	31.8%	6.8%	-----MKLSGANCLVVFSLQLLVA-LSH-----
	consensus/100%		
	consensus/90%		h.....
	consensus/80%		h.hhhh.h.lh.....h.....tt.t.h.....
	consensus/70%		h.hhhh.shlh.....h.....h.h.....psttph.ptht.....

	cov	pid	101		200
1	A0A0U5KPK6_MEG-28	100.0%	100.0%	-----IITTIEI--QNIRSAFKRPPASFVILENMTSTDRFRKLLYHCFT---SF	
2	A0A0U5FZ31_MEG-26	51.5%	1.9%	-----TFKCLLSPLPESIGGKNN-----	
3	C4QKE8_MEG-4	71.2%	2.5%	-----YDDQLPDFPHKQLEE-----EQNPFHKLSVLENSGVS-----VPLWLVIPIYYVLELF	
4	A0A5K4F4B1_MEG-4	100.0%	5.6%	KNVDIRI-----IENKDKKHPQT-----KTS DHTTIKRTTPKPTTPKQINDGTS DKPKSIADFFLINKPKVPLWIVNPLYMVEKF	
5	A0A5K4F2K5_MEG-4	98.5%	4.4%	SDTHT-----IKRTPKPTPKQINDGTS DKTS DHTTIKRTTPKPTTPKQINDGTS DKPKSIADIFLINKPKVPLWIVNPLYMVEKF	
6	A0A5K4F627_MEG-4	98.5%	4.6%	TQK-----TTPKPTTPKQINDGTS DKTS DHTTIKRTTPKPTTPKQINDGTS DKPKSIADIFLINKPKVPLWIVNPLYMVEKF	
7	Q86D79_MEG-4	100.0%	4.0%	PKPTTPKQINDGTS DKTS DHTTIKRTTPKPTTPKQINDGTS DKTS DHTTIKRTTPKPTTPKQINDGTS DKPKSIADIFLINKPKVPLWIVNPLYMVEKF	
8	A0A3Q0KQX7_MEG-16	98.5%	1.7%	-----DFLTSLFDWNGDGYRSGGFNFYDFL---SLFFGLNKKDNRRNRRYRSGGGGGNGGL	
9	A0A5K4EU45_MEG-16	92.4%	2.9%	-----DFLTSLFDWNGDGYRSGGFNFYDFL---SLFFGLNKKDNRRNRRYRSGGGGGNGGL	
10	A0A3Q0KLA7_MEG-13	93.9%	4.5%	-----FNNTTVTSTTTEFNN-----TTVTSTTTEFTNPKVENSTTDG---TTYTTTSPHFSTSTSTNDATNSKFQRI	
11	A0A5K4EL02_MEG-13	100.0%	5.6%	-----FNNTTVTSTTTEFNN-----TTVTSTTTEFTNPKVENSTTDG---TTYTTTSPHFSTSTSTNDATNSKFQRI	
12	A0A3Q0KQ39_MEG-10	42.4%	6.9%	-----TFCTFITFSNTIQNFIYG-----	
13	G4LYD0_MEG-10	40.9%	6.9%	-----TFCTFITFSNTIQNFIYG-----	
14	G4VCW5_MEG-8	98.5%	2.6%	CKLP-----NPSQKGFNTTSLPH-----TQSHNSTVAPSVPKPTQEI PRSGTIVNGTKPTPGKPVVNGTKPTPGKPEFLKRV	
15	A0A3Q0KKW2_MEG-9	69.7%	5.6%	-----HESSTEGQNHLELAAAAG---AHFLQFLNGC-----FLNM	
16	G4VLP3_MEG-8	100.0%	5.0%	GTNN-----KDTKSPNPNT-----TEAKSLSLKERIMNKFN---SIFGEEYNP PKDSDFTERLWMLFKHCF	
17	G4V7W5_MEG-7	100.0%	5.2%	-----STDKIPVNK-----TMKIQTTPSKEKKQKPD---KRYKRSSYQDKKAKSSSSTLTIGYPIL	
18	A0A5K4EUJ7_MEG-7-iso2	98.5%	2.7%	-----TMKIQTTPSKEKKQKPD---KRYKRSSYQDKKAKSSSSTLTIGYPIL	
19	A0A5K4EKN1_MEG-1	95.5%	4.5%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSS--IKKRL	
20	D7PD99_MEG-1	95.5%	4.9%	FREI-----SHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSS--IKKRL	
21	D7PD79_MEG-1	95.5%	4.5%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSS--IKKRL	
22	D7PD91_MEG-1	95.5%	5.0%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSS--IKKRL	
23	D7PD95_MEG-1	95.5%	5.2%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSS--IKKRL	
24	D7PD89_MEG-1	98.5%	4.9%	FREI-----SHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
25	A0A3Q0KKC4_MEG-1	98.5%	4.5%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
26	D7PD88_MEG-1	98.5%	4.7%	FREI-----CTYPT-----HIALYVIQPT-NHCQRYEGSSSSVSQKP	
27	D7PD93_MEG-1	98.5%	4.7%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
28	D7PD94_MEG-1	98.5%	4.7%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
29	D7PD83_MEG-1	98.5%	4.5%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
30	D7PD84_MEG-1	98.5%	5.0%	FREI-----NIDKDYLCYPT-----NFSHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
31	D7PD86_MEG-1	98.5%	5.6%	FREI-----SHGLITYCTKSNDERDLSYEED---HIALYVIQPT-NHCQRYEGSSSSVSQKP	
32	A0A5K4FAB4_Uncharacterized	95.5%	2.9%	IREIIAANYSPIIHNEEKKNISNREKDYLCCTP-----YFNHGVITYCTKSNEYKDSLQYEDD---FMDLFVKKHNKDDCQHGGYSSLEYRNP	
33	A0A5K4F8B3_MEG-1	100.0%	3.2%	IREIIAANYSPIIHNEEKKNISNREKDYLCCTP-----YFNHGVITYCTKSNEYKDSLQYEDD---FMDLFVKKHNKDDCQHGGYSSLEYRNP	
34	A0A5K4F8U8_MEG-1	100.0%	3.4%	IREIIAANYSPIIHNEEKKNISNREKDYLCCTP-----YFNHGVITYCTKSNEYKDSLQYEDD---FMDLFVKKHNKDDCQHGGYSSLEYRNP	
35	A0A0U5KI45_MEG-30	59.1%	8.6%	-----FFTTTPVPNKGLLDKLLD---GLYQFFNRH-----	
36	A0A5K4E9G8_MEG-15	95.5%	2.8%	-----TTATASHTDKTVQKKCLNKMT PQDL---ISLFLSLIPQIKTIEFSQENLLKLATI	
37	A0A5K4E9M7_MEG-15	93.9%	1.8%	TTLS-----HHNTVPAKTTRKSQH-----PNTTPSHTDKTVQKKCLNKMT PQDL---ISLFLSLIPQIKTIEFSQENLLKLATI	
38	A0A3Q0KC91_MEG-15	95.5%	2.8%	-----H-----PNTTPSHTDKTVQKKCLNKMT PQDL---ISLFLSLIPQIKTIEFSQENLLKLATI	
39	G4VMN2_MEG-15	95.5%	2.3%	TTLS-----HHNTVPAKTTRKSQH-----PNTTPSHTDKTVQKKCLNKMT PQDL---ISLFLSLIPQIKTIEFSQENLLKLATI	
40	A0Q3Q0KQ41_MEG-12	39.4%	2.4%	-----VFCVSNMVN-----WIFG-----	
41	A0A5K4EPC8_MEG-3.2	100.0%	1.9%	NQND-----FDKCLPKCNGSPQL-----TESSQNDCGRVTHPELNCV---VSFVVEMLBTHFHCVCITAI REMVRETL	
42	D7PD63_MEG-3.3	100.0%	4.8%	KQSE-----FDNCKTKCDGGVQLT-----KEACL SNCGLITTHPELCAVCGGNDG---GSFPICLYNCDQEHTDPRKDGADGSEDF	
43	D7PD64_MEG-3.3	100.0%	4.9%	KQSE-----FDNCKTKCDGGVQLT-----KEACL SNCGLITTHPELCAVCGGNDG---GSFPICLYNCDQEHTDPRKDGADGSEDF	
44	D7PD62_MEG-3.3	100.0%	4.6%	KQSE-----FDNCKTKCDGGVQLT-----KEACL SNCGLITTHPELCAVCGGNDG---GSFPICLYNCDQEHTDPRKDGADGSEDF	
45	A0A3Q0RMS0_MEG-3	100.0%	4.6%	KQSE-----FDNCKTKCDGGVQLT-----KEACL SNCGLITTHPELCAVCGGNDG---GSFPICLYNCDQEHTDPRKDGADGSEDF	
46	D7PD57_MEG-3.2	86.4%	3.4%	NQND-----FDKCLPKCNG-----QNDCGRVTHPELCAVCGGNDG---GSFPICLYNCDQGN-----GSGNF	
47	D7PD60_MEG-3.2	86.4%	3.4%	NQND-----FDNCKTKCDGGVQLT-----QNDCGRVTHPELCAVCGGNDG---GSFPICLYNCDQGN-----GSGNF	
48	D7PD53_MEG-3.2	86.4%	3.4%	NQND-----FDKCLPKCNGSPQL-----ESSQNDCGRVTHPELCAVCGGNDG---DSFPLCLYNCDQGN-----GSGNF	
49	D7PD52_MEG-3.2	86.4%	3.2%	NQND-----FDKCLPKCNGSPQL-----ESSQNDCGRVTHPELCAVCGGNDG---DSFPLCLYNCDQGN-----GSGNF	
50	D7PD54_MEG-3.2	86.4%	3.4%	NQND-----FDKCLPKCNGSPQL-----ESSQNDCGRVTHPELCAVCGGNDG---DSFPLCLYNCDQGN-----GSGNF	
51	D7PD51_MEG-3.1	84.8%	1.9%	TQDD-----FDKCLPKCNDRVQLT-----EENCRNDCGRVTHHESCGDVCGGNDG---GSFPLCLYNCDQEHPRE-----EY	
52	A0A3Q0RMU6_MEG-3	90.9%	1.9%	TQDD-----FDKCLPKCNDRVQLT-----EENCRNDCGRVTHHESCGDVCGGNDG---GSFPLCLYNCDQEHPRE-----EY	

53	D7PD49_MEG-3.1	90.9%	1.9%	TQDD-----FDKCLPKCNDRVQLT-----EENCRDDCGRVTSHHELCDGVCVGGNHG---GSFPLCLYNCQEHPRE-----YERGY
54	D7PD50_MEG-3.1	68.2%	2.3%	TQDD-----FDKCLPKCNDRVQLT-----EENCRNDCGRVTSHHELCDGVCVGGNHG---GSFPLCFQSSSSDK-----
55	A0A0U5KIV9_MEG-27	53.0%	3.5%	-----VNCHELNEHTSETSL-----RGWIHTVFSFLFHN-----
56	A0A5K4F014_MEG-27	45.5%	4.9%	-----NCSHELNEHTSETSL-----RRWIHTVFSFLFHN-----
57	G4LYD1_MEG-5	53.0%	2.5%	-----DTSDFMGQNKTLGTAFKTLHLNL--WDLLKQSLGLP-----
58	G4VTX1_MEG-6	65.2%	1.5%	-----RTIRR--ST-KTVIVITDRVQNI-----VLG---HRLHHRIPTIKRSKSHG---INKNETVSNL-----
59	A0A3Q0KTG4_MEG-11	71.2%	4.1%	-----EEEEPPQDPV-----HGKHPLLRKAFLTAPSW--LHMPFSIAGA-----
60	A0A0U5KLL2_MEG-29	69.7%	4.5%	-----TTTTLPT-TTS-----VAIKGTISAYTVMGSL-----IYVI---
61	A0A0U5KEW2_MEG-32.1	75.8%	1.1%	-----STTKNMTTTKASSANSLEVS---WLAISSIS-----MIVIGLI
62	A0A0U5KJ28_MEG-32.2	78.8%	3.9%	R-----TTAP-----TTT-SGSVSSFQVS---WLALSSVF-----MIVLGLI
63	A0A5K4EK08_MEG-14	100.0%	5.3%	KAAA-----TSTIKP-----TVTTKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
64	A0A1C9A1H6_MEG-14	100.0%	5.0%	KAAA-----TSTIKPTVTTTPKAAA-----TSTIKPTVTTSKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
65	Q8ITD5_MEG-14	100.0%	4.5%	KAAA-----TSTIKPTVTTTPKAAA-----TSTIKPTVTTSKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
66	A0A1C9A1I1_MEG-14	100.0%	5.7%	KAAA-----TSTIKP-----TVTTKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
67	A0A1C9A1I0_MEG-14	100.0%	5.8%	KAAA-----TSTIKPTVTTTPKAAA-----TSTIKPTVTTKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
68	A0A1C9A1I5_MEG-14	100.0%	5.1%	KAAA-----TSTIKPTVTTTPKAAA-----TSTTEPTVTTSKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
69	A0A1C9A1J0_MEG-14	100.0%	4.9%	KAAA-----TSTTEPTVTTTPKAAA-----TSTTEPTVTTSKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
70	A0A1C9A1I3_MEG-14	100.0%	4.6%	KAAA-----TSTTEPTVTTTPKAAA-----TSTTEPTVTTSKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
71	A0A1C9A1I4_MEG-14	100.0%	5.2%	KAAA-----TSTTEPTVTTTPKAAA-----TSTTEPTVTTKPSPAKPAASNTAK---PAASTPKKPHDERAVLAAAAPVIVLGI
72	C4QPR8_MEG-2	69.7%	2.7%	-----GDGWTITCNE-----TYCCENTDNGKLCDDGEY---CSASISKLDP-----
73	A0A3Q0KTV3_MEG-2	81.8%	2.8%	-----GDGWTITCNE-----TYCCENTDNGKLCDDGEY---CSASISNHQDLTKHQQL-----
74	C4QPR9_MEG-2	62.1%	2.7%	-----KVVTVVDNPELTLKNYLRK-----AQMI
75	A0A0U5KJN7_MEG-10.2	48.5%	10.6%	-----FICTLNQWTSTIRNFF---GIAL-----
76	A0A0U5KFM1_MEG-31	42.4%	2.1%	-----EDKRRKDYIKELVKNATG-----
77	C4QPS0_MEG-2	62.1%	3.8%	-----DPSAVKKNYRQQ-----VLMATKIKEVCQKFRG-----
78	C4QG05_MEG-2	74.2%	5.2%	-----KTCCDEEDGNS-----KICCVGNDCKDVIKPRSS---GADDLNLFLRKR---MAYKL
79	D7PD69_MEG-2.4	75.8%	3.6%	-----TCNKTTCCD-----EDGNSKICCVGNDCKDVIKPRSS---GADDLNLFLRKRGMAYKLGE---ILKKL
80	A0A3Q0KR24_MEG-2	57.6%	8.7%	-----KTCCDEEDKNS-----KICCVGNDCKDVIKPRSS---GADDLNLFLRKRGMAYKLGE---ILKKL
81	C4QPR6_MEG-2	75.8%	1.1%	-----SLCCEKNGCVSPSGTHDL---LSENYRRHQ---MKNYL
82	A0A5K4FFX0_MEG-2.2	62.1%	0.8%	-----LLRQKTVKKVTEERWLSNTPDL---LLGNYQRHQ---MKNYL
83	A0A5K4FDB9_Uncharacterized	74.2%	3.0%	-----TCNKTVCCASEDGKT-----GS-----LCCEKDGCP--PS-TPDL---FLENYRRHR---MKNYL
84	D7PD77_MEG-2.2	74.2%	2.0%	-----TCNKTVCCASEDGKT-----GS-----LCCEKDGCP--PS-TPDL---FLENYRRHR---MKNYL
85	D7DP78_MEG-2.1	92.4%	8.6%	-----CCASEDGK-----GS-----LCCEKDGCP--PS-TPDL---LLGNYQRHQ---MKNYL
86	D7DP76_MEG-2.1	53.0%	4.8%	-----ITCNKTVCCASEDGKI-----
87	D7DP75_MEG-2.1	31.8%	6.8%	-----
	consensus/100%		
	consensus/90%		p...t.....
	consensus/80%		hhssh.p.tt.h.t.t.....h.....
	consensus/70%		phsspsp.pp.hhs.ptt.....h.h.h..p.p.....h.t..

53	D7PD49_MEG-3.1	90.9%	1.9%	D-----K-----CKTKCYAMEGR-----
54	D7PD50_MEG-3.1	68.2%	2.3%	-----
55	A0A0U5KIV9_MEG-27	53.0%	3.5%	-----
56	A0A5K4F014_MEG-27	45.5%	4.9%	-----
57	G4LYD1_MEG-5	53.0%	2.5%	-----
58	G4VTX1_MEG-6	65.2%	1.5%	F-----P-----
59	A0A3Q0KTG4_MEG-11	71.2%	4.1%	-----VAAYVFYHFG-----
60	A0A0U5KLL2_MEG-29	69.7%	4.5%	-----HSFIVFKMM-----
61	A0A0U5KEW2_MEG-32.1	75.8%	1.1%	N-----GHLRRFIF-----
62	A0A0U5KJ28_MEG-32.2	78.8%	3.9%	N-----SYTERSIF-----
63	A0A5K4EK08_MEG-14	100.0%	5.3%	G-----E-----VIGFILQYIAS-----
64	A0A1C9A1H6_MEG-14	100.0%	5.0%	G-----E-----VIGFILQYIAS-----
65	Q8ITD5_MEG-14	100.0%	4.5%	G-----E-----VIGFILQYIAS-----
66	A0A1C9A1I1_MEG-14	100.0%	5.7%	G-----E-----VIGFILQYIAS-----
67	A0A1C9A1I0_MEG-14	100.0%	5.8%	G-----E-----VIGFILQYIAS-----
68	A0A1C9A1I5_MEG-14	100.0%	5.1%	G-----E-----VIGFILQ-----
69	A0A1C9A1J0_MEG-14	100.0%	4.9%	G-----E-----VIGFILQ-----
70	A0A1C9A1I3_MEG-14	100.0%	4.6%	G-----E-----VIGFILQ-----
71	A0A1C9A1I4_MEG-14	100.0%	5.2%	G-----E-----VIGFILQYIAS-----
72	C4QPR8_MEG-2	69.7%	2.7%	-----PFSNCFQYVFS-----
73	A0A3Q0KTV3_MEG-2	81.8%	2.8%	-----LMSKKFKII-----
74	C4QPR9_MEG-2	62.1%	2.7%	D-----K-----LREAVQKLGGR-----
75	A0A0U5KJN7_MEG-10.2	48.5%	10.6%	-----
76	A0A0U5KFM1_MEG-31	42.4%	2.1%	-----T-----
77	C4QPS0_MEG-2	62.1%	3.8%	-----
78	C4QG05_MEG-2	74.2%	5.2%	G-----E-----ILKKLN-----
79	D7PD69_MEG-2.4	75.8%	3.6%	N-----
80	A0A3Q0KR24_MEG-2	57.6%	8.7%	-----
81	C4QPR6_MEG-2	75.8%	1.1%	K-----E-----VCK--YFK-----
82	A0A5K4FFX0_MEG-2.2	62.1%	0.8%	E-----E-----VQLLHIYYI-----
83	A0A5K4FDB9_Uncharacterized	74.2%	3.0%	E-----E-----VCK--YYI-----
84	D7PD77_MEG-2.2	74.2%	2.0%	E-----E-----VCK--YYI-----
85	D7DP78_MEG-2.1	92.4%	8.6%	E-----E-----VCENFIYTP-----
86	D7DP76_MEG-2.1	53.0%	4.8%	-----GENFIYTP-----
87	D7DP75_MEG-2.1	31.8%	6.8%	-----YTP-----
	consensus/100%		
	consensus/90%		
	consensus/80%		h.....
	consensus/70%		h.hhh.....