

## ANNEXES

**Annex A - Summary of sequences and primary structure characteristics of MEG proteins analysed in this study.** Molecular weight (MW in Da), aliphatic index and gravy index have been calculated by ProtParam on the EXPASY server.

<b>UniProt ID</b>	<b>Gene name (WBPS) and annotated name(s)</b>	<b>MW (g/mol)</b>	<b>pI</b>	<b>Aliphatic index</b>	<b>Gravy Index</b>
C4QKE8	<i>Smp_085840.1 MEG-4 Antigen 10.3</i>	12908	4.86	89.16	-0.45
A0A1C9A1H6	<i>Smp_124000.1 MEG-14 isoform 3</i>	14354	10.31	80.5	0.1
A0A1C9A1I5	<i>Smp_124000.1 MEG-14 isoform 6</i>	13820	10.19	76.99	0.05
A0A1C9A1J0	<i>Smp_124000.1 MEG-14 isoform 7</i>	14760	10.56	74.72	-0.06
Q8ITD5	<i>Smp_124000.2 MEG-14</i>	15822	10.40	79.04	0.09
A0A1C9A1I1	<i>Smp_124000.2 MEG-14 isoform 1</i>	14267	10.31	81.07	0.11
A0A1C9A1I4	<i>Smp_124000.2 MEG-14 isoform 2</i>	15782	10.16	74.52	0.01
A0A5K4EK08	<i>Smp_124000.2 MEG-14 isoform 3</i>	15509	10.03	83.47	0.1
A0A1C9A1I3	<i>Smp_124000.2 MEG-14 isoform 4</i>	15447	10.25	75.33	0.01
A0A1C9A1I0	<i>Smp_124000.2 MEG-14 isoform 5</i>	14179	10.31	81.65	0.12
G4V7W5	<i>Smp_165050.1 MEG-7</i>	13106	10.04	79.74	-0.36
A0A5K4EUJ7	<i>Smp_165050.2 MEG-7 iso2</i>	16568	9.88	82.62	-0.43
A0A3Q0KTG4	<i>Smp_176020.1 MEG-11</i>	8635	5.36	81.52	0.03
A0A0U5KI45	<i>Smp_243780.1 MEG-30</i>	6687	8.14	119.31	0.66
A0A0U5KFM1	<i>Smp_243790.1 MEG-31 protein</i>	6879	9.39	88.1	-0.21
A0A5K4F627	<i>Smp_307220.1 MEG-4 Antigen 10.3</i>	19788	6.73	83.35	-0.64
Q86D79	<i>Smp_307220.2 MEG-4 Antigen 10.3</i>	22739	8.43	76	-0.77
A0A5K4F2K5	<i>Smp_307220.3 MEG-4 Antigen 10.3</i>	20828	7.74	81.37	-0.67
A0A5K4F4B1	<i>Smp_307240.1 MEG-4 Antigen 10.3</i>	22129	9.14	94.17	-0.59
G4VCW5	<i>Smp_171190.1 MEG-8</i>	20959	9.86	66.86	-0.55

D7DP78	<i>MEG-2.1 iso1</i>	9792	5.53	86.36	-0.05
D7DP76	<i>MEG-2.1 iso2</i>	5641	4.83	103.08	0.51
D7DP75	<i>MEG-2.1 iso3</i>	2818	7.98	146.15	1.14
A0A3Q0KKC4	<i>Smp_122630.1 MEG-1 iso1</i>	18213	5.34	88.65	-0.09
D7PD88	<i>Smp_122630.1 MEG-1 iso10</i>	17319	5.58	87.57	-0.07
D7PD89	<i>Smp_122630.1 MEG-1 iso11</i>	16526	5.58	89.15	-0.07
D7PD93	<i>Smp_122630.1 MEG-1 iso16</i>	17523	5.33	86.98	-0.12
D7PD94	<i>Smp_122630.1 MEG-1 iso18</i>	14425	5.28	98.28	0.06
D7PD83	<i>Smp_122630.1 MEG-1 iso5</i>	18241	5.34	88.65	-0.09
D7PD84	<i>Smp_122630.1 MEG-1 iso6</i>	16143	5.48	91.88	-0.1
D7PD86	<i>Smp_122630.1 MEG-1 iso8</i>	14480	5.53	95.89	-0.02
A0A5K4EKN1	<i>Smp_122630.2 MEG-1 iso2</i>	18156	6.28	102.53	0.02
D7PD79	<i>Smp_122630.2 MEG-1 isoform 1</i>	18184	6.28	102.53	0.02
D7PD99	<i>Smp_122630.2 MEG-1 isoform 12</i>	16495	6.81	107.21	0.09
D7PD91	<i>Smp_122630.2 MEG-1 isoform 14</i>	16112	6.27	107.45	0.04
D7PD95	<i>Smp_122630.2 MEG-1 isoform 17</i>	15394	6.27	106.41	0.02
A0A3Q0KMS0	<i>Smp_138060.1 MEG-3 Grail family</i>	16404	4.81	57.55	-0.32
D7PD62	<i>Smp_138060.1 MEG-3.3 isoform 1</i>	16403	5.07	57.55	-0.32
D7PD63	<i>Smp_138060.1 MEG-3.3 isoform 2</i>	16153	4.81	55.78	-0.37
D7PD64	<i>Smp_138060.1 MEG-3.3 isoform 3</i>	15542	4.70	57.34	-0.35
D7PD53	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2</i>	14811	5.60	60.72	-0.17
D7PD52	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2/1</i>	15769	5.39	57.1	-0.26
D7PD54	<i>Smp_138070.1 MEG-3.2 (Grail) isoform3</i>	15208	5.39	57.17	-0.3

D7PD57	<i>Smp_138070.1 MEG-3.2 (Grail) isoform6</i>	14794	5.62	55.88	-0.27
D7PD60	<i>Smp_138070.1 MEG-3.2 (Grail) isoform9</i>	14500	5.42	54.62	-0.34
A0A5K4EPC8	<i>Smp_138070.2 MEG-3.2 (Grail) isoform1</i>	17562	7.16	68.01	-0.22
A0A3Q0KMU6	<i>Smp_138080.1 MEG-3 (Grail)</i>	17152	5.44	50.99	-0.67
D7PD49	<i>Smp_138080.1 MEG-3.1 (Grail) isoform1</i>	16404	5.07	57.55	-0.32
D7PD50	<i>Smp_138080.1 MEG-3.1 (Grail) isoform2</i>	14569	5.39	55.04	-0.44
D7PD51	<i>Smp_138080.1 MEG-3.1 (Grail) isoform3</i>	16615	5.77	47.07	-0.74
C4QG05	<i>Smp_159800.1 MEG-2 (ESP15) family</i>	9095	7.53	95.06	0.03
D7PD69	<i>Smp_159800.1 MEG-2.4 isoform 1</i>	8971	6.52	96.3	0.05
A0A3Q0KR24	<i>Smp_159830.1 MEG-2 (ESP15) family</i>	7734	5.07	87.54	-0.05
C4QPR6	<i>Smp_180310.1 MEG-2 (ESP15)</i>	8646	7.54	50.68	-0.58
C4QPR8	<i>Smp_180320.1 MEG-2 (ESP15 iso1)</i>	11165	7.57	73.02	-0.22
A0A3Q0KTV3	<i>Smp_180320.2 MEG-2 (ESP15 iso2)</i>	10983	6.87	73.79	-0.2
C4QPR9	<i>Smp_180330.1 MEG-2 (ESP15 family)</i>	5497	10.37	103.54	-0.35
C4QPS0	<i>Smp_180340.1 MEG-2 (ESP15)</i>	4895	9.90	84.09	0.14
A0A5K4F8B3	<i>Smp_326790.1 MEG-1</i>	22040	5.12	79.09	-0.3
A0A5K4F8U8	<i>Smp_326790.2 MEG-1</i>	21198	5.24	80.56	-0.34
A0A5K4FAB4	<i>Smp_326790.3 Uncharacterized</i>	19957	5.23	65.33	-0.67
A0A5K4FDB9	<i>Smp_336990.1 Uncharacterized</i>	9393	6.68	82.17	-0.07
A0A5K4FFX0	<i>Smp_345100.1 MEG-2.2 isoform1</i>	13413	9.64	96.52	-0.37
D7PD77	<i>Smp_345100.1 MEG-2.2 isoform2</i>	9336	7.50	87.37	0.02
A0A3Q0KQX7	<i>Smp_158890.1 MEG-16 iso1</i>	12759	10.12	78.68	-0.18
A0A5K4EU45	<i>Smp_158890.2 MEG-16 iso2</i>	11802	9.91	72.21	-0.32

G4LYD1	<i>Smp_152580.1 MEG-5</i>	8884	9.36	112.28	0.05
A0A3Q0KQ39	<i>Smp_152590.1 MEG-10</i>	6127	7.74	59.29	0.04
G4LYD0	<i>Smp_152590.2 MEG-10 iso2</i>	6056	7.74	58.55	0.01
A0Q3Q0KQ41	<i>Smp_152630.1 MEG-12</i>	5050	8.10	60.24	-0.18
A0A0U5KJN7	<i>Smp_243730.1 MEG-10.2 protein</i>	7428	5.96	88.44	0.36
A0A0U5KIV9	<i>Smp_243750.1 MEG-27 iso1</i>	6701	5.99	95.64	0.26
A0A5K4F014	<i>Smp_243750.1 MEG-27 iso2</i>	6800	6.38	95.64	0.18
A0A0U5KEW2	<i>Smp_123100.1 MEG-32.1</i>	8861	9.30	118.72	0.61
A0A0U5KJ28	<i>Smp_123200.1 MEG-32.2</i>	9879	6.63	102.81	0.26
A0A3Q0KLA7	<i>Smp_127990.1 MEG 13 iso1</i>	14352	4.19	58.46	-0.41
A0A5K4EL02	<i>Smp_127990.2 MEG 13 iso2</i>	13790	4.27	60.8	-0.39
G4VLP3	<i>Smp_172180.1 MEG-8</i>	15839	9.07	58.5	-0.47
A0A0U5FZ31	<i>Smp_243740.1 MEG-26 protein</i>	8252	7.75	129.45	0.25
A0A0U5KKP6	<i>Smp_243760.1 MEG-28</i>	7864	10.01	110.76	0.44
A0A0U5KLL2	<i>Smp_243770.1 MEG-29 protein</i>	7636	6.70	129.86	0.94
A0A3Q0KC91	<i>Smp_010550.1 Uncharacterized MEG-15 iso4</i>	16111	9.94	86.31	-0.44
A0A5K4E9M7	<i>Smp_010550.2 Uncharacterized MEG-15 iso2</i>	18948	10.26	81.08	-0.52
G4VMN2	<i>Smp_010550.3 Uncharacterized MEG-15 iso1</i>	19569	10.33	78.72	-0.59
A0A5K4E9G8	<i>Smp_010550.4 Uncharacterized MEG-15 iso3</i>	16045	9.94	87.73	-0.37
A0A3Q0KKW2	<i>Smp_125320.1 MEG-9</i>	6818	5.31	86.61	0.36
G4VTX1	<i>Smp_163710.1 MEG-6</i>	7549	12.14	98.77	-0.66



Annex B - Sequences of MEG proteins analyzed in this study.

UniProt ID	Gene name (WBPS) and annotated name(s)	Protein Sequence
C4QKE8	<i>Smp_085840.1 MEG-4 Antigen 10.3</i>	MNFLTLYVTLVYVILSVYSDIEPRIQKEYYYNHLHENNSQANHNKFMPEYDDQLPDFPHKQLEEEQNPFHKLSEVLNSGSVVPLWLVNPIYYVLELFPRAISYYFN
A0A1C9A1H6	<i>Smp_124000.1 MEG-14 isoform 3</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
A0A1C9A1I5	<i>Smp_124000.1 MEG-14 isoform 6</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQ
A0A1C9A1J0	<i>Smp_124000.1 MEG-14 isoform 7</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTRTHGATSTAKPAASTPKPTVTTTPKAAATSTTEPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQ
Q8ITD5	<i>Smp_124000.2 MEG-14</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
A0A1C9A1I1	<i>Smp_124000.2 MEG-14 isoform 1</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
A0A1C9A1I4	<i>Smp_124000.2 MEG-14 isoform 2</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTRTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
A0A5K4EK08	<i>Smp_124000.2 MEG-14 isoform 3</i>	YLLCKKEYSIMNRFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
A0A1C9A1I3	<i>Smp_124000.2 MEG-14 isoform 4</i>	MNRFFWTVIQTILLVIICNLNTMKATSANSRTHGATSTRTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQ
A0A1C9A1I0	<i>Smp_124000.2 MEG-14 isoform 5</i>	MNRFFWTVTQCTILLVIICNLNTMKATSANSRTHGATSTSTHGATSTAKPAASTPKAAATSTIKPTVTTTPKAAATSTIKPTVTTTPKAAATSTTEPTVTTTSKPSAKPAASNTAKPAASTPKKPHDERAVLAAAAPVIVLGVIGEVIGFILQYIAS
G4V7W5	<i>Smp_165050.1 MEG-7</i>	MNTLFRSIFVVVVVYAYFDMANGVPEPPRPVDEDVAVRAKPATPIKISTDKIPVNTMKIQTTPSKEKKQKQPKRYKRSSYQKDKKAKSSSSTLTIGYPILFITTPFVISKFLL
A0A5K4EUJ7	<i>Smp_165050.2 MEG-7 iso2</i>	MSVPIRNLRLNNEYAICKFQYCKHIDNGNYNILQRSIFVVVVVYAYFDMANGVPEPPRPVDEDVAVRAKPATPIKISTDKIPVNTMKIQTTPSKEKKQKQPKRYKRSSYQKDKKAKSSSSTLTIGYPILFITTPFVISKFLL
A0A3Q0KTG4	<i>Smp_176020.1 MEG-11</i>	MKLTHILLICFISLFFTYVQCDGEEEEEENEEKPPQDPVPHGKHPLLRKAFLTA PSWLHMPFSIAGAVAAYVFYHFYG
A0A0U5KI45	<i>Smp_243780.1 MEG-30</i>	MQVDKFIYITVIAIAIFVSMPEIHAFGIKFFTTTPVPNKGLLDKLLDGLYQFFNRH
A0A0U5KFM1	<i>Smp_243790.1 MEG-31 protein</i>	MHCVLLLSLFAVCSVIMPTVKSGGSASGGSTEVDLMHHRGKDREDKRRKDYIKELVKNATGT
A0A5K4F627	<i>Smp_307220.1 MEG-4 Antigen 10.3</i>	MNIYLIGILCIVGLIISQGSTANGSPLDDRFDVNTINKKQFTEEEFSRLINSMLKEYIEDNKKDKHPTQK TTPKPTTPKQINDGTSKTSDDTHTIKRTTPKPTTPKQINDGTSKPKSIADIFLINKPKVPLWIVNPLYMVEKQVQIMGYLLEDDDTLELNLPKYYYDKSI
Q86D79	<i>Smp_307220.2 MEG-4 Antigen 10.3</i>	MNIYLIGILCIVGLIISQGSTANGSPLDDRFDVNTINKKQFTEEEFSRLINSMLKEYIEDNKKDKHPTQK TTPKPTTPKQINDGTSKTSDDTHTIKRTTPKPTTPKQINDGTSKPKSIADIFLINKPKVPLWIVNPLYMVEKQVQIMGYLLEDDDTLELNLPKYYYDKSI
A0A5K4F2K5	<i>Smp_307220.3 MEG-4 Antigen 10.3</i>	MNIYLIGILCIVGLIISQGSTANGSPLDDRFDVNTINKKQFTEEEFSRLINSMLKEYIEDNKKDKHPTQK TSDTHTIKRTTPKPTTPKQINDGTSKTSDDTHTIKRTTPKPTTPKQINDGTSKPKSIADIFLINKPKVPLWIVNPLYMVEKQVQIMGYLLEDDDTLELNLPKYYYDKSI
A0A5K4F4B1	<i>Smp_307240.1 MEG-4 Antigen 10.3</i>	MKLVSISLIGIFSLISQEGYGLIDIKHINSPNQKQYVRDKMNLNEYLTSRNIKKQFTEEEFSRLINSMLKKHIEDKNVDIRIENKDKKHPTQK TSDTHTIKRTTPKPTTPKQINDGTSKPKSIADIFLINKPKVPLWIVNPLYMVEKQVQIMGYLLEDDDTLELNLPKYYYDKSI

G4VCW5	<i>Smp_171190.1 MEG-8</i>	MFTIILYVLYFIANAKFEHTTSGIRNPSKLSDSNASKTSLKLNLDHYIHTPQKS NNGTSCNGKDTCKLPNPSQKGFNTTSLPHTQSHNSTVAPSPKPTRQEIPIRS TIVNGTKPTPGKPVVNGTKPTPGKPEFSLKRVGDGFFDLFSEQEFHPINHKSYLF NFWYLFRTSFLNLKNMKNLLGS
D7DP78	<i>MEG-2.1 iso1</i>	MKLSGANCLVVFSLLQLLVAFSHCDINDITCNKTVCCASEDGKKGSLCCEKDG CPIPSTPDLLGNVQRHQRMKNYLEEVCEFIYTP
D7DP76	<i>MEG-2.1 iso2</i>	MKLSGANCLVVFSLLQLLVAFSHCDINDITCNKTVCCASEDGKIGENFIYTP
D7DP75	<i>MEG-2.1 iso3</i>	MKLSGANCLVVFSLLQLLVALSHYTP
A0A3Q0KKC4	<i>Smp_122630.1 MEG-1 iso1</i>	MANKDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDER DLSYEEDHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD88	<i>Smp_122630.1 MEG-1 iso10</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREICTYPTNFHSHGLITYCTKSNDERDLSYEE DHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD89	<i>Smp_122630.1 MEG-1 iso11</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREISHGLITYCTKSNDERDLSYEEDHIALYVI QPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD93	<i>Smp_122630.1 MEG-1 iso16</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDERDLSY EEDHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD94	<i>Smp_122630.1 MEG-1 iso18</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDERDLSY EEDHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD83	<i>Smp_122630.1 MEG-1 iso5</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDER DLSYEEDHIALYVIQPTNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD84	<i>Smp_122630.1 MEG-1 iso6</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLT DFIKCIFREINIDKDLCTYPTNFHSHGLITYCTKSNDERDLSYEEDHIALYVIQ TNHCQRYEGSSSLVSQKPEKECPFCFD
D7PD86	<i>Smp_122630.1 MEG-1 iso8</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLT DFIKCIFREISHGLITYCTKSNDERDLSYEEDHIALYVIQPTNHCQRYEGSSSLV SQKPEKECPFCFD
A0A5K4EKN1	<i>Smp_122630.2 MEG-1 iso2</i>	MANKDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDER DLSYEEDHIALYVIQPTNHCQRYEGSSIKRLLLESYLIITPI
D7PD79	<i>Smp_122630.2 MEG-1 isoform 1</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDER DLSYEEDHIALYVIQPTNHCQRYEGSSIKRLLLESYLIITPI
D7PD99	<i>Smp_122630.2 MEG-1 isoform 12</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLN RTWVFNETKEICSCCLDFIKCIFREISHGLITYCTKSNDERDLSYEEDHIALYVI QPTNHCQRYEGSSIKRLLLESYLIITPI
D7PD91	<i>Smp_122630.2 MEG-1 isoform 14</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLT DFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDERDLSYEEDHIALYVIQ TNHCQRYEGSSIKRLLLESYLIITPI
D7PD95	<i>Smp_122630.2 MEG-1 isoform 17</i>	MANRDLILTPYQVFILPCFILIFWSLFLIVFKSDGSGTWRKDDIDWLILTKGGKLT DFIKCIFREINIDKDYLCYPTNFHSHGLITYCTKSNDERDLSYEEDHIALYVIQPTNHCQ RYEGSSIKRLLLESYLIITPI
A0A3Q0KMS0	<i>Smp_138060.1 MEG-3 Grail family</i>	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNCGILCSGTIGPQTFYC YLGCSHNATKQSEFDNCKTKCDGGVQLTKEACLNSCGLITTHPELCAVCGGN DGGSPICLYNCDQEHNTDPRKDGADGSEDFDKCKTKCYKMAQG
D7PD62	<i>Smp_138060.1 MEG-3.3 isoform 1</i>	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNCGILCSGTIGPQTFYC YLGCSHNATKQSEFDNCKTKCDGGVQLTKEACLNSCGLITTHPELCAVCGGN DGGSPICLYNCDQKHNTDPRKDGADGSEDFDKCKTKCYKMAQG
D7PD63	<i>Smp_138060.1 MEG-3.3 isoform 2</i>	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNCGILCSGTIGPQTFYF HYFSTKQSEFDNCKTKCDGGVQLTKEACLNSCGLITTHPELCAVCGGNDDGG SPICLYNCDQEHNTDPRKDGADGSEDFDKCKTKCYKMAQG
D7PD64	<i>Smp_138060.1 MEG-3.3 isoform 3</i>	MLFFALILIISLHSFDCAFTAQQECEKNCKGDNEYVSPNCGILCSGTIGPQTFYST KQSEFDNCKTKCDGGVQLTKEACLNSCGLITTHPELCAVCGGNDDGGSPICL YNCDQEHNTDPRKDGADGSEDFDKCKTKCYKMAQG
D7PD53	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2</i>	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHSGGLCSGSGTGPQTFYCYLG CSHNASNQNDQCLPKCNGSPQLTESSQNDCGRVTTPELPGIVCGGNVGD SFPLCLYNCDQGNNGFNDECKTKCYLMAGR
D7PD52	<i>Smp_138070.1 MEG-3.2 (Grail) isoform2/1</i>	MLFVALILIISLHSFDCVFTARETQQECVRHCGGHNEYVTRYCGGLCSGSGTGPQ TFYCYLGCSHNASNQNDQCLPKCNGSPQLTESSQNDCGRVTTPELPGIVCGGNVGD SFPLCLYNCDQGNNGFNDECKTKCYEMAGR

D7PD54	<i>Smp_138070.1 MEG-3.2 (Grail) isoform3</i>	MLFVALILILSHSFD CVFTARETQQECVRHCGGHNEYVTRYCTGPQTFYCYLGCSHNASNQND FDKCLPKCNGSPQLTESSCQND CGRVTTHP ELCGIVCGGNVGD SFPLCLYNCDQGN GSGNFDECKTKCYEMAGR
D7PD57	<i>Smp_138070.1 MEG-3.2 (Grail) isoform6</i>	MLFVALILILSHSFD CVFTARETQQECVRHCGGHNEYVTRYCGGLCSGSTGPQTFYCYLGCSHNASNQND FDKCLPKCNGQND CGRVTTHP ELCGIVCGGNDGGS FPICLYNCDQGN GSGNFDECKTKCYEMAGR
D7PD60	<i>Smp_138070.1 MEG-3.2 (Grail) isoform9</i>	MLFVALILILSHSFD CVFTARETQQECVRHCGGHNEYVTRYCGGLCSGSTGPQTFYCYLGCSHNASNQND FDKCLPKCNGQND CGRVTTHP ELCGIVCGGNDGGS FPICLYNCDQGN GSGNFDECKTKCYEMAGR
A0A5K4EPC8	<i>Smp_138070.2 MEG-3.2 (Grail) isoform1</i>	RTTHRLVKMLFVALILILSHSFD CVFTARETQQECVRHCGGHNEYVTRYCGGLCSGSTGPQTFYCYLGCSHNASNQND FDKCLPKCNGSPQLTESSCQND CGRPH TLNCVVSFVMELE THFHCVCITAI REMVRETLNVKQSATK WRDGEFP
A0A3Q0KMU6	<i>Smp_138080.1 MEG-3 (Grail)</i>	MLFVALILILSHSFD CVFTAQETRDAERECKKHCEGNNEYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDD FDKCLPKCNDRVQLTEENCRDD CGRVTSHELL CGDVCGGNHGGSFPLCLYNCDQEH PREYERGYDKCKTKCYAMEGR
D7PD49	<i>Smp_138080.1 MEG-3.1 (Grail) isoform1</i>	MLFVALILILSHSFD CVFTAQETRDAERECKKHCEGNNEYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDD FDKCLPKCNDRVQLTEENCRDD CGRVTSHELL CGDVCGGNHGGSFPLCLYNCDQEH PREYERGYDKCKTKCYAMEGR
D7PD50	<i>Smp_138080.1 MEG-3.1 (Grail) isoform2</i>	MLFVALILILSHSFD CVFTAQETRDAERECKKHCEGNNEYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDD FDKCLPKCNDRVQLTEENCRND CGRVTSHELL CGDVCGGNHGGSFPLCFQSSSDK
D7PD51	<i>Smp_138080.1 MEG-3.1 (Grail) isoform3</i>	MLFVALILILSHSFD CVFTAQETRDAERECKKHCEGNNEYVTRYCGGLCSSNTGPQTFYCYLGCSHNASTQDD FDKCLPKCNDRVQLTEENCRND CGRVTSHELLS CGDVCGGNHGGSFPLCSYNCDQEH PREYERGKTKRYAMEGR
C4QG05	<i>Smp_159800.1 MEG-2 (ESP15) family</i>	MCLTFYVIHLLAIFSD STEWVITCNKTTCCDEDGNSKICCVGNDCKDVIKPRSSGADDLNLFLRKRGMAYKLG EILKKNL
D7PD69	<i>Smp_159800.1 MEG-2.4 isoform 1</i>	MCLTFYVIHLLAIFSD STEWVITCNKTTCCDEDGNSKICCVGNDCKDVIKPRSSGADDLNLFLRKRGMAYKLG EILKKNL
A0A3Q0KR24	<i>Smp_159830.1 MEG-2 (ESP15) family</i>	MCLTFYVIHLLAIFSDSNEWVITCNKTTCCDEDKNSKICCVGNDCKDVIKPRSSGADDFLLKKNLNSP
C4QPR6	<i>Smp_180310.1 MEG-2 (ESP15)</i>	MERFKSSYFYFEIYLLCFTE TVCCESEDGKAGSLCCEKNGCSVPSGTHDLLSEN YRRHQRMKNYLKEVCKYFK
C4QPR8	<i>Smp_180320.1 MEG-2 (ESP15 iso1)</i>	MHGIWCKVPVSVVIWIHSTL FQFTFKVFYELKQNNTFPLPGDGWTITCNETYC CENTDNGKLCDDGEYCSA SISKLDPPFSNCFQYVFVS
A0A3Q0KTV3	<i>Smp_180320.2 MEG-2 (ESP15 iso2)</i>	MHGIWCKVPVSVVIWIHSTL FQFTFKVFYELKQNNTFPLPGDGWTITCNETYC CENTDNGKLCDDGEYCSA SISNHQDLTKHQQLLMSKFKII
C4QPR9	<i>Smp_180330.1 MEG-2 (ESP15 family)</i>	QKAISQRPFAVIKMMVTVDNPELTLKNYLRKAQMIDKLREAVQKLGGR
C4QPS0	<i>Smp_180340.1 MEG-2 (ESP15)</i>	MTAKGSVAMASVFLVYDPSVAVKNYRQQVLMATKIKEVCQKFRG
A0A5K4F8B3	<i>Smp_326790.1 MEG-1</i>	MAKSDLILTPYQVFILPCHILFWSLF LIVFKSDGSGTWRRDIDWFIL TQGKQIQRI WVFVNETEEVCSCVTGFEKCNIREIIAANYSPIIHNEEKKNISNREKDYLC TPT YFNHGVITYCTKSNEYKDSLQYEDDFMDL FVKKHNKDDCQHYGGYSSLEYR NPEKVC PFCYEEITQCSIWETLS
A0A5K4F8U8	<i>Smp_326790.2 MEG-1</i>	MAKSDLILTPYQVFILPCHILFWSLF LIVFKSDGSGTWRRDIDWFIL TQGKQIQRI WVFVNETEEVCSCVTGFEKCNIREIIAANYSPIIHNEEKKNISNREKDYLC TPT YFNHGVITYCTKSNEYKDSLQYEDDFMDL FVKKHNKDDCQHYGGYSSLEYR NPEKEITQCSIWETLS
A0A5K4FAB4	<i>Smp_326790.3 Uncharacterized</i>	MYYPYFLVSIFDSLQNSYIKQSGTWRRDIDWFIL TQGKQIQRIWVFVNETEEVCSCVTGFEKCNIREIIAANYSPIIHNEEKKNISNREKDYLC TPT YFNHGVITYCTKSNEYKDSLQYEDDFMDL FVKKHNKDDCQHYGGYSSLEYR NPEKEITQCSIWETLS
A0A5K4FDB9	<i>Smp_336990.1 Uncharacterized</i>	MKLSGANCLVVFSLQLLVA FSHCDISDITCNKTVCCASED GKTGSLCCEKDGC PSTPDLFLENYRRHRRMKNYLEEVCKYYYI
A0A5K4FFX0	<i>Smp_345100.1 MEG-2.2 isoform1</i>	MYCQSFTLLNRDYISNVTKQSKHRLYNTMKLSGANCLVVFSLQLLVA FSHCK LMSHNMQDSSLRQKTVKKVRTEERWLSNTPDLLLGN YQRHQRMKNYLEEV QILHIYYI
D7PD77	<i>Smp_345100.1 MEG-2.2 isoform2</i>	MKLSGATCLVVFSLQLLVA FSHCDISAITCNKTVCCASED GKTGSLCCEKDGC PSTPDLFLENYRRHRRMKNYLEEVCKYYYI

A0A3Q0KQX7	<i>Smp_158890.1 MEG-16 iso1</i>	MFYCRVLIITFSMIFLLGTANCDIIDVLSLLFGGNGNKNIRNRNRNGGDSGGLSDFLTSLFDWNGDGYRGSGFNFYDFLSLFFGLNKKDNRNRRYRSGGGGGNGGLIRLFFAR
A0A5K4EU45	<i>Smp_158890.2 MEG-16 iso2</i>	MFYCRVLIITFSMIFLLGTANCDIIDDKNIRNRNRNGGDSGGLSDFLTSLFDWNGDGYRGSGFNFYDFLSLFFGLNKKDNRNRRYRSGGGGGNGGLIRLFFAR
G4LYD1	<i>Smp_152580.1 MEG-5</i>	MRRNYLLLYICIIIVFILLKEINASGRQPKFVNVDTDGNLRSGGSSDISDMFGQNKTLGTAFKTLHNLWDLLKQSLGLP
A0A3Q0KQ39	<i>Smp_152590.1 MEG-10</i>	MTLLLIQSCHCGSSGSTEAGSNGTNSKGWWPKFLGWANTFCTFITFSNTIQNFIYG
G4LYD0	<i>Smp_152590.2 MEG-10 iso2</i>	MTLLLIQSCHCGSSGSTEAGSNGTNSKGWWPKFLGWANTFCTFITFSNTIQNFIYG
A0Q3Q0KQ41	<i>Smp_152630.1 MEG-12</i>	GENYEQQQLQPKAYGIWSLFSYFYKTFKVFCSVSNMNVNWF
A0A0U5KJN7	<i>Smp_243730.1 MEG-10.2 protein</i>	MISLLFLGLLLQSCLYCSSDNENAGTTTEKPTSFWRKFFDFNFICTLNQWTWSTIRNFFGIAL
A0A0U5KIV9	<i>Smp_243750.1 MEG-27 iso1</i>	MNLIQTLLWMIFMMIMNLTNEIKWVNCHELNEHTSETSLRGWIHTVFSFLFHN
A0A5K4F014	<i>Smp_243750.1 MEG-27 iso2</i>	MNLIQTLLWMIFMMIMNLTNEIKWVNCHELNEHTSETSLRRWIHTVFSFLFHN
A0A0U5KEW2	<i>Smp_123100.1 MEG-32.1</i>	MYRHYLLAIINIVLSTMIQYVIGGSIFGDDTSTTKNMTTTTKASSANSLEVSWLAISSIMIVGLINGHLRRFIF
A0A0U5KJ28	<i>Smp_123200.1 MEG-32.2</i>	MKETTVMHHYHHPNHRLLTVISAIVLLTIVHDVKGSGLFDDDTTRTAPTTSGSVSSFQVSWLALSSVFMIVLGLINSYTERSIF
A0A3Q0KLA7	<i>Smp_127990.1 MEG-13 iso1</i>	MDITYSWCIICLINLLNGKLGQAQEDNYTEDSTTDPTTFDNTTSTTTTEFNNTTSTTTTEFNNTTSTTTTEFTNKPKVENSTTDGTTYTTTPSHFSTSTNDATNSKFQRIFYMIVGLISLMAIN
A0A5K4EL02	<i>Smp_127990.2 MEG-13 iso2</i>	MDITYSWCIICLINLLNGKLGQAQEDNYTEDSTTDNTTSTTTTEFNNTTSTTTTEFNNTTSTTTTEFTNKPKVENSTTDGTTYTTTPSHFSTSTNDATNSKFQRIFYMIVGLISLMAIN
G4VLP3	<i>Smp_172180.1 MEG-8</i>	MNTVTLGLFCIAICLIGINAGTVSKPTATVQKQPVNKMNTTPVHQEESPFWRRMWNSTSMFGSSDSSSGTNNKDTKSPNPNTTEAKSLSLKERIMNKFNSIFGEEYNNPKDSDFTERLWMLFKHCFLNFKNLAKIFST
A0A0U5FZ31	<i>Smp_243740.1 MEG-26 protein</i>	MDISKILLGSLFLLSVIILQEVNGQKGNRVIFNVEELILNLWKNLYERLADTFKCLLSPLPESIGGKNSCYP
A0A0U5KKP6	<i>Smp_243760.1 MEG-28</i>	MNTIVRYYLILFIITIEIQNIRSAFKKRPPASVILENMTSTDRFKLLYHCFTSFSTWMLLG
A0A0U5KLL2	<i>Smp_243770.1 MEG-29 protein</i>	MLNKKLLQLFILVTIIHHDVKCGGEEETTTTLPPTTSVAIKGTISAYTVMGLSIYVIHSFIVFKMM
A0A3Q0KC91	<i>Smp_010550.1 Uncharacterized MEG-15 iso4</i>	MLNRFIVILVVFVGVITFDNVQQRDPPTNTTHTTTHNYVGKLSHHNTVPAKTTRKSQHPNTTPSHDTKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
A0A5K4E9M7	<i>Smp_010550.2 Uncharacterized MEG-15 iso2</i>	MLNRFIVILVVFVGVITFDNVQQRDPPTNTTHTTTHNYVGKLSHHNTVPAKTTRKSQHTTATARHNTLKTTLSSHNTVPAKTTRKSQHPNTTPSHDTKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
G4VMN2	<i>Smp_010550.3 Uncharacterized MEG-15 iso1</i>	MLNRFIVILVVFVGVITFDNVQQRDPPTNTTHTTTHNYVGKLSHHNTVPAKTTRKSQHTTATARHNTLKTTLSSHNTVPAKTTRKSQHPNTTPSHDTKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
A0A5K4E9G8	<i>Smp_010550.4 Uncharacterized MEG-15 iso3</i>	MLNRFIVILVVFVGVITFDNVQQRDPPTNTTHTTTHNYVGKLSHHNTVPAKTTRKSQHTTATARHNTLKTTLSSHNTVPAKTTRKSQHPNTTPSHDTKTVQKKCLNKMTPQDLISLLFSLIPQIKTIEFSQENLKLATILEKIFEQQSRVEHSSPTKTPANKIFH
A0A3Q0KKW2	<i>Smp_125320.1 MEG-9</i>	MIISCQFITGFVVHESSTEGQNEELAAAAGAHFLQFLNGCFLNMDNLKLVFPG

G4VTX1

*Smp\_163710.1 MEG-6*

MVQNPKNKKINRTIRRSTKTVIVITDRVQNIVLGHRLHHRIPTIKRSKSHGIN  
KNETVSNLFP



B) Isoform 1a

$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2
51.664	CA	1	25	51.908	CA	7	31	50.682	CA	14	38
37.844	CB	1	25	4.507	HA	7	31	20.212	CB	14	38
4.563	HA	1	25	2.732	HB2	7	31	4.293	HA	14	38
2.674	HB2	1	25	8.202	HN	7	31	1.202	HB	14	38
2.648	HB3	1	25	119.429	N	7	31	8.141	HN	14	38
8.214	HN	1	25	51.822	CA	8	32	116.986	N	14	38
123.395	N	1	25	40.944	CB	8	32	57.089	CA	15	39
59.106	CA	2	26	4.524	HA	8	32	4.279	HA	15	39
39.084	CB	2	26	2.737	HB2	8	32	3.606	HB2	15	39
13.297	CD1	2	26	8.084	HN	8	32	3.540	HB3	15	39
26.258	CG	2	26	119.269	N	8	32	7.980	HN	15	39
4.105	HA	2	26	54.314	CA	9	33	112.339	N	15	39
1.675	HB	2	26	33.206	CB	9	33	54.324	CA	16	40
0.770	HD1	2	26	24.388	CG	9	33	29.060	CB	16	40
1.356	HG2	2	26	4.121	HA	9	33	31.988	CG	16	40
1.006	HG3	2	26	1.672	HB2	9	33	4.220	HA	16	40
7.634	HN	2	26	1.511	HB3	9	33	1.737	HB2	16	40
115.301	N	2	26	1.287	HG2	9	33	1.911	HB3	16	40
8.085	HN	3	27	1.246	HG3	9	33	2.222	HG2	16	40
57.190	CA	3	27	7.748	HN	9	33	8.010	HN	16	40
40.944	CB	3	27	117.263	N	9	33	118.531	N	16	40
4.373	HA	3	27	51.833	CA	10	34	51.963	CA	17	41
2.739	HB2	3	27	68.738	CB	10	34	4.472	HA	17	41
8.083	HN	3	27	21.757	CG	10	34	2.702	HB2	17	41
119.269	N	3	27	4.518	HA	10	34	2.677	HB3	17	41
3.948	HA	4	28	3.948	HB	10	34	8.140	HN	17	41
2.680	HB2	4	28	1.009	HG	10	34	116.921	N	17	41
2.735	HB3	4	28	7.771	HN	10	34	44.611	CA	18	42
8.087	HN	4	28	113.811	N	10	34	3.690	HA2	18	42
117.212	N	4	28	59.503	CA	11	35	7.991	HN	18	42
60.321	CA	5	29	38.307	CB	11	35	105.845	N	18	42
39.084	CB	5	29	4.169	HA	11	35	54.314	CA	19	43
17.446	CD1	5	29	1.772	HB	11	35	33.206	CB	19	43
4.210	HA	5	29	0.786	HG2	11	35	24.406	CG	19	43
1.675	HB	5	29	7.672	HN	11	35	4.121	HA	19	43
0.774	HD1	5	29	115.640	N	11	35	1.670	HB2	19	43
7.648	HN	5	29	59.412	CA	12	36	1.517	HB3	19	43
115.487	N	5	29	4.216	HA	12	36	1.286	HG2	19	43
56.916	CA	6	30	7.770	HN	12	36	1.246	HG3	19	43
68.738	CB	6	30	117.293	N	12	36	7.748	HN	19	43
21.757	CG	6	30	59.663	CA	13	37	117.263	N	19	43
4.411	HA	6	30	4.360	HA	13	37				
3.954	HB	6	30	2.741	HB2	13	37				
1.007	HG	6	30	8.139	HN	13	37				
7.846	HN	6	30	116.961	N	13	37				
117.179	N	6	30								

#res2 corresponds to the numbering of the full-length isoform 1.

C) Isoform 1b

$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2
44.321	CA	1	42	57.165	CA	7	48	55.209	CA	13	54
3.672	HA3	1	42	40.938	CB	7	48	40.938	CB	13	54
8.121	HN	1	42	4.371	HA	7	48	4.605	HA	13	54
111.021	N	1	42	2.741	HB2	7	48	2.746	HB2	13	54
54.459	CA	2	43	2.678	HB3	7	48	8.130	HN	13	54
33.333	CB	2	43	8.034	HN	7	48	117.805	N	13	54
28.710	CD	2	43	116.188	N	7	48	61.628	CA	14	55
24.318	CG	2	43	57.165	CA	8	49	31.150	CB	14	55
4.234	HA	2	43	40.938	CB	8	49	49.475	CD	14	55
1.649	HB2	2	43	4.370	HA	8	49	26.631	CG	14	55
1.509	HB3	2	43	2.746	HB2	8	49	4.363	HA	14	55
1.496	HD2	2	43	2.696	HB3	8	49	1.994	HB2	14	55
1.280	HG2	2	43	8.101	HN	8	49	1.832	HB3	14	55
7.974	HN	2	43	118.102	N	8	49	3.528	HD2	14	55
117.635	N	2	43	54.281	CA	9	50	3.667	HD3	14	55
54.556	CA	3	44	29.333	CB	9	50	1.856	HG2	14	55
33.333	CB	3	44	32.261	CG	9	50	1.797	HG3	14	55
28.710	CD	3	44	4.241	HA	9	50	38.296	CB	15	56
24.318	CG	3	44	1.848	HB2	9	50	13.053	CD1	15	56
4.195	HA	3	44	1.771	HB3	9	50	26.225	CG1	15	56
1.655	HB2	3	44	2.228	HG2	9	50	17.230	CG2	15	56
1.509	HB3	3	44	8.062	HN	9	50	4.326	HA	15	56
1.501	HD2	3	44	119.191	N	9	50	1.723	HB	15	56
1.285	HG2	3	44	54.637	CA	10	51	0.781	HD1	15	56
7.997	HN	3	44	33.333	CB	10	51	1.062	HG12	15	56
118.322	N	3	44	28.710	CD	10	51	0.853	HG2	15	56
44.093	CA	4	45	24.318	CG	10	51	7.954	HN	15	56
3.756	HA2	4	45	4.201	HA	10	51	118.286	N	15	56
3.720	HA3	4	45	1.645	HB2	10	51	61.893	CA	16	57
8.073	HN	4	45	1.509	HB3	10	51	31.150	CB	16	57
106.049	N	4	45	1.494	HD2	10	51	49.475	CD	16	57
56.851	CA	5	46	1.279	HG2	10	51	26.652	CG	16	57
63.849	CB	5	46	7.953	HN	10	51	4.314	HA	16	57
4.321	HA	5	46	117.668	N	10	51	1.977	HB2	16	57
3.569	HB2	5	46	51.764	CA	11	52	1.836	HB3	16	57
3.535	HB3	5	46	41.478	CB	11	52	3.527	HD2	16	57
7.919	HN	5	46	4.491	HA	11	52	3.646	HD3	16	57
112.991	N	5	46	2.686	HB2	11	52	1.854	HG2	16	57
53.366	CA	6	47	2.662	HB3	11	52	1.796	HG3	16	57
42.470	CB	6	47	8.220	HN	11	52	57.230	CA	17	58
25.214	CD1	6	47	117.757	N	11	52	63.809	CB	17	58
23.616	CD2	6	47	44.093	CA	12	53	4.107	HA	17	58
26.236	CG	6	47	3.763	HA2	12	53	3.573	HB2	17	58
4.289	HA	6	47	3.734	HA3	12	53	3.525	HB3	17	58
1.475	HB3	6	47	7.971	HN	12	53	7.703	HN	17	58
0.850	HD1	6	47	104.988	N	12	53	112.950	N	17	58
0.810	HD2	6	47								
1.589	HG	6	47								
8.072	HN	6	47								
120.236	N	6	47								

#res2 corresponds to the numbering of the full-length isoform 1.



## D) Isoform 1c

$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2
57.073	CA	1	58	118.648	N	6	63	7.289	HE21	12	69
63.838	CB	1	58	53.333	CA	7	64	54.894	CA	12	69
4.300	HA	1	58	42.434	CB	7	64	30.833	CB	12	69
3.519	HB	1	58	25.227	CD1	7	64	27.192	CG	12	69
3.521	HB2	1	58	23.602	CD2	7	64	4.195	HA	12	69
7.962	HN	1	58	26.175	CG	7	64	1.489	HB2	12	69
118.789	N	1	58	4.244	HA	7	64	1.652	HB3	12	69
58.711	CA	2	59	1.453	HB2	7	64	3.066	HD	12	69
68.914	CB	2	59	0.844	HD1	7	64	3.068	HD2	12	69
21.353	CG	2	59	0.789	HD2	7	64	1.502	HG2	12	69
4.410	HA	2	59	1.573	HG	7	64	1.436	HG3	12	69
3.898	HB	2	59	7.743	HN	7	64	7.958	HN	12	69
1.067	HG2	2	59	118.575	N	7	64	118.439	N	12	69
7.782	HN	2	59	44.242	CA	8	65	53.836	CA	13	70
115.017	N	2	59	3.722	HA2	8	65	4.552	HA	13	70
61.964	CA	3	60	3.618	HA3	8	65	3.069	HB2	13	70
31.169	CB	3	60	8.070	HN	8	65	2.942	HB3	13	70
26.504	CG	3	60	105.374	N	8	65	7.486	HD2	13	70
4.271	HA	3	60	51.931	CA	9	66	7.782	HE2	13	70
2.022	HB	3	60	4.511	HA	9	66	8.209	HN	13	70
2.022	HB2	3	60	2.346	HB2	9	66	117.282	N	13	70
3.647	HD2	3	60	2.327	HB3	9	66	54.726	CA	14	71
1.824	HG2	3	60	8.080	HN	9	66	29.858	CB	14	71
1.772	HG3	3	60	117.490	N	9	66	33.526	CG	14	71
52.010	CA	4	61	56.678	CA	10	67	4.196	HA	14	71
37.764	CB	4	61	38.149	CB	10	67	1.877	HB2	14	71
4.446	HA	4	61	132.236	CD1	10	67	1.753	HB3	14	71
2.686	HB2	4	61	117.122	CE1	10	67	7.283	HE21	14	71
2.660	HB3	4	61	4.297	HA	10	67	6.830	HE22	14	71
8.106	HN	4	61	2.928	HB2	10	67	2.098	HG2	14	71
116.069	N	4	61	2.690	HB3	10	67	8.111	HN	14	71
53.583	CA	5	62	6.970	HD	10	67	118.876	N	14	71
42.827	CB	5	62	6.971	HD1	10	67	109.292	NE2	14	71
25.313	CD1	5	62	6.970	HD2	10	67	54.379	CA	15	72
23.651	CD2	5	62	6.610	HE1	10	67	31.162	CB	15	72
26.175	CG	5	62	6.611	HE2	10	67	27.192	CG	15	72
4.216	HA	5	62	7.918	HN	10	67	4.160	HA	15	72
1.419	HB2	5	62	117.456	N	10	67	1.515	HB2	15	72
0.834	HD1	5	62	54.296	CA	11	68	1.667	HB3	15	72
0.792	HD2	5	62	29.858	CB	11	68	3.075	HD2	15	72
1.548	HG	5	62	4.160	HA	11	68	1.523	HG2	15	72
7.618	HN	5	62	1.875	HB2	11	68	1.448	HG3	15	72
117.898	N	5	62	1.751	HB3	11	68	8.130	HN	15	72
53.336	CA	6	63	7.295	HE21	11	68	119.157	N	15	72
42.434	CB	6	63	6.829	HE22	11	68				
25.124	CD1	6	63	2.131	HG2	11	68				
23.621	CD2	6	63	2.085	HG3	11	68				
26.175	CG	6	63	7.911	HN	11	68				
4.250	HA	6	63	116.973	N	11	68				
1.449	HB2	6	63	109.433	NE2	11	68				
0.839	HD1	6	63								
0.789	HD2	6	63								
1.563	HG	6	63								
7.832	HN	6	63								

#res2 corresponds to the numbering of the full-length isoform 1.

E) Isoform 1d

$\delta$ , ppm	Atom	#res	#res 2
54.248	CA	1	73
33.731	CB	1	73
4.262	HA	1	73
1.746	HB1	1	73
1.863	HB2	1	73
8.060	HN	1	73
122.890	N	1	73
53.897	CA	2	74
33.350	CB	2	74
28.597	CD	2	74
41.005	CE	2	74
24.229	CG	2	74
4.201	HA	2	74
1.580	HB1	2	74
1.455	HB2	2	74
1.469	HD#	2	74
2.708	HE#	2	74
2.694	HE1	2	74
1.249	HG#	2	74
1.251	HG1	2	74
7.966	HN	2	74
117.885	N	2	74
51.883	CA	3	75
4.476	HA	3	75
2.370	HB1	3	75
7.369	HD21	3	75
6.902	HD22	3	75
7.999	HN	3	75
116.919	N	3	75
56.517	CA	4	76
38.393	CB	4	76
132.263	CD1	4	76
117.003	CE1	4	76
4.313	HA	4	76
2.881	HB1	4	76
2.680	HB2	4	76
6.958	HD1	4	76
6.598	HE1	4	76
7.836	HN	4	76
116.665	N	4	76
53.625	CA	5	77
42.524	CB	5	77
23.698	CD1	5	77
25.225	CD2	5	77
26.236	CG	5	77
4.218	HA	5	77
1.423	HB1	5	77
1.474	HB2	5	77
0.804	HD1	5	77
0.851	HD2	5	77
1.542	HG	5	77
7.967	HN	5	77
117.885	N	5	77

$\delta$ , ppm	Atom	#res	#res 2
54.232	CA	6	78
29.561	CB	6	78
32.230	CG	6	78
4.220	HA	6	78
1.870	HB1	6	78
1.729	HB2	6	78
2.217	HG1	6	78
7.884	HN	6	78
117.184	N	6	78
53.684	CA	7	79
29.483	CB	7	79
32.202	CG	7	79
4.283	HA	7	79
1.849	HB1	7	79
1.707	HB2	7	79
2.176	HG1	7	79
7.860	HN	7	79
117.836	N	7	79
1.931	HB	8	80
59.736	CA	8	80
32.660	CB	8	80
21.277	CG	8	80
4.157	HA	8	80
1.931	HB	8	80
0.804	HG#	8	80
7.839	HN	8	80
115.881	N	8	80
57.291	CA	9	81
27.981	CB	9	81
4.372	HA	9	81
2.738	HB1	9	81
2.651	HB2	9	81
2.289	HG	9	81
8.147	HN	9	81
119.685	N	9	81
53.103	CA	10	82
29.562	CB	10	82
32.211	CG	10	82
4.215	HA	10	82
1.831	HB1	10	82
1.672	HB2	10	82
2.182	HG1	10	82
7.996	HN	10	82
118.837	N	10	82
51.753	CA	11	83
4.476	HA	11	83
2.325	HB1	11	83
2.314	HB2	11	83
7.329	HD21	11	83
6.897	HD22	11	83
8.022	HN	11	83
117.331	N	11	83

$\delta$ , ppm	Atom	#res	#res 2
55.899	CA	12	84
39.213	CB	12	84
131.260	CD1	12	84
130.134	CE1	12	84
128.285	CZ	12	84
4.474	HA	12	84
2.977	HB1	12	84
2.753	HB2	12	84
7.158	HD1	12	84
7.164	HE1	12	84
7.944	HN	12	84
7.116	HZ	12	84
115.608	N	12	84
59.334	CA	13	85
38.607	CB	13	85
17.375	CD1	13	85
26.298	CG1	13	85
13.124	CG2	13	85
4.096	HA	13	85
1.664	HB	13	85
0.705	HD1#	13	85
1.314	HG11	13	85
0.987	HG12	13	85
0.746	HG2#	13	85
7.834	HN	13	85
115.881	N	13	85
55.903	CA	14	86
38.805	CB	14	86
132.263	CD1	14	86
117.003	CE1	14	86
4.531	HA	14	86
2.820	HB1	14	86
2.681	HB2	14	86
6.951	HD1	14	86
6.582	HE1	14	86
7.860	HN	14	86
119.889	N	14	86
58.001	CA	15	87
69.053	CB	15	87
21.073	CG2	15	87
4.422	HA	15	87
3.874	HB	15	87
1.045	HG2#	15	87
7.941	HN	15	87
116.823	N	15	87
61.459	CA	16	88
31.400	CB	16	88
49.237	CD	16	88
26.544	CG	16	88
4.198	HA	16	88
1.985	HB#	16	88
3.561	HD1	16	88
3.517	HD2	16	88
1.787	HG1	16	88
1.744	HG2	16	88

#res2 corresponds to the numbering of the full-length isoform 1.

F) Isoform 3

$\delta$ , ppm	Atom	#res	$\delta$ , ppm	Atom	#res	$\delta$ , ppm	Atom	#res	$\delta$ , ppm	Atom	#res
33.341	CB	1	53.444	CA	9	30.943	CB	16	51.538	CA	20
4.307	HA	1	42.395	CB	9	49.143	CD	16	19.399	CB	20
1.954	HB2	1	25.243	CD1	9	26.721	CG	16	4.149	HA	20
1.898	HB3	1	23.876	CD2	9	2.134	HB2	16	1.247	HB	20
7.802	HN	1	26.305	CG	9	1.827	HB3	16	7.947	HN	20
118.921	N	1	4.255	HA	9	3.686	HD2	16	122.657	N	20
54.636	CA	2	1.434	HB2	9	3.587	HD3	16	53.786	CA	21
33.494	CB	2	1.492	HB3	9	1.894	HG2	16	42.381	CB	21
28.868	CD	2	0.840	HD1	9	56.069	CA	16	23.485	CD2	21
24.373	CG	2	0.787	HD2	9	26.719	CB	16	26.205	CG	21
4.311	HA	2	1.585	HG	9	33.906	CG	16	4.204	HA	21
1.647	HB2	2	8.079	HN	9	3.978	HA	16	1.512	HB2	21
1.511	HB3	2	119.986	N	9	1.907	HB2	16	1.450	HB3	21
1.510	HD2	2	60.258	CA	10	1.826	HB3	16	0.812	HD1	21
1.292	HG2	2	32.379	CB	10	2.080	HG2	16	0.780	HD2	21
1.331	HG3	2	20.538	CG1	10	2.128	HG3	16	1.675	HG	21
8.568	HN	2	4.090	HA	10	7.835	HN	16	7.826	HN	21
122.313	N	2	1.894	HB	10	117.310	N	16	116.404	N	21
53.042	CA	3	0.747	HG1	10	54.618	CA	17	57.843	CA	22
41.910	CB	3	7.677	HN	10	42.381	CB	17	63.501	CB	22
24.795	CD1	3	115.860	N	10	25.243	CD1	17	4.191	HA	22
23.887	CD2	3	60.246	CA	11	23.475	CD2	17	3.632	HB2	22
26.305	CG	3	32.585	CB	11	26.305	CG	17	3.567	HB3	22
4.365	HA	3	21.322	CG1	11	4.102	HA	17	7.727	HN	22
1.450	HB3	3	4.034	HA	11	1.511	HB2	17	112.651	N	22
0.854	HD1	3	1.893	HB	11	0.839	HD1	17	54.014	CA	23
0.810	HD2	3	0.727	HG1	11	0.784	HD2	17	29.023	CB	23
1.587	HG	3	7.651	HN	11	1.591	HG	17	4.499	HA	23
8.170	HN	3	117.668	N	11	7.762	HN	17	3.040	HB2	23
120.604	N	3	56.129	CA	12	118.462	N	17	2.878	HB3	23
57.244	CA	4	39.459	CB	12	54.604	CA	18	7.273	HD2	23
63.915	CB	4	4.567	HA	12	41.910	CB	18	7.911	HN	23
4.236	HA	4	3.011	HB2	12	25.243	CD1	18	116.331	N	23
3.590	HB2	4	2.777	HB3	12	23.504	CD2	18	56.255	CA	24
3.524	HB3	4	7.949	HN	12	26.182	CG	18	38.798	CB	24
7.907	HN	4	117.885	N	12	4.133	HA	18	4.468	HA	24
113.190	N	4	56.843	CA	13	1.594	HB2	18	2.858	HB2	24
44.305	CA	5	63.914	CB	13	1.440	HB3	18	2.684	HB3	24
3.761	HA2	5	4.364	HA	13	0.837	HD1	18	6.959	HD1	24
3.685	HA3	5	3.610	HB2	13	0.777	HD2	18	6.586	HD2	24
8.114	HN	5	3.569	HB3	13	1.663	HG	18	9.129	HH	24
107.450	N	5	8.115	HN	13	7.915	HN	18	7.841	HN	24
50.353	CA	6	112.976	N	13	118.294	N	18	117.310	N	24
20.350	CB	6	54.599	CA	14	61.454	CA	19	58.960	CA	25
4.278	HA	6	41.901	CB	14	32.119	CB	19	69.139	CB	25
1.182	HB	6	24.753	CD1	14	21.314	CG1	19	21.488	CG	25
7.995	HN	6	23.898	CD2	14	20.922	CG2	19	4.341	HA	25
120.317	N	6	26.282	CG	14	3.896	HA	19	3.805	HB	25
52.014	CA	7	4.136	HA	14	1.972	HB	19	1.102	HG	25
39.026	CB	7	1.526	HB2	14	0.808	HG1	19	8.177	HN	25
4.516	HA	7	0.879	HD1	14	0.851	HG2	19	118.116	N	25
2.549	HB1	7	0.841	HD2	14	7.695	HN	19	4.196	HA	26
2.438	HB2	7	1.618	HG	14	115.385	N	19	2.131	HB2	26
8.211	HN	7	8.255	HN	14				1.827	HB3	26
116.762	N	7	122.056	N	14				3.689	HD2	26
57.221	CA	8	54.975	CA	15				1.893	HG2	26
28.249	CB	8	42.374	CB	15						
4.335	HA	8	26.305	CG	15						
2.729	HB2	8	4.077	HA	15						
7.886	HN	8	1.508	HB2	15						
115.322	N	8	1.454	HB3	15						
			0.844	HD1	15						
			0.808	HD2	15						
			1.583	HG	15						
			7.948	HN	15						
			119.248	N	15						

G) Isoform 2a

$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2
59.991	CA	1	19	51.719	CA	7	25	57.037	CA	13	31
32.416	CB	1	19	4.588	HA	7	25	28.125	CB	13	31
20.343	CG1	1	19	2.703	HB2	7	25	4.418	HA	13	31
4.071	HA	1	19	8.499	HN	7	25	2.733	HB2	13	31
1.872	HB	1	19	120.306	N	7	25	7.855	HN	13	31
0.774	HG1	1	19	59.012	CA	8	26	117.182	N	13	31
7.854	HN	1	19	39.153	CB	8	26	52.561	CA	14	32
120.273	N	1	19	13.225	CD1	8	26	4.508	HA	14	32
50.369	CA	2	20	26.347	CG1	8	26	7.403	HD21	14	32
20.141	CB	2	20	4.137	HA	8	26	6.978	HD22	14	32
4.194	HA	2	20	1.660	HB	8	26	8.212	HN	14	32
1.112	HB	2	20	0.771	HD1	8	26	119.469	N	14	32
7.979	HN	2	20	1.368	HG12	8	26	54.532	CA	15	33
122.824	N	2	20	1.023	HG13	8	26	33.218	CB	15	33
55.810	CA	3	21	7.646	HN	8	26	24.219	CG	15	33
39.308	CB	3	21	115.670	N	8	26	4.289	HA	15	33
131.333	CD1	3	21	52.106	CA	9	27	1.689	HB2	15	33
130.138	CE1	3	21	41.081	CB	9	27	1.496	HB3	15	33
128.403	CZ	3	21	4.525	HA	9	27	1.297	HG2	15	33
4.493	HA	3	21	2.846	HB2	9	27	7.977	HN	15	33
2.995	HB2	3	21	7.361	HD21	9	27	117.974	N	15	33
2.766	HB3	3	21	6.904	HD22	9	27	7.859	HN	16	34
7.193	HD1	3	21	8.112	HN	9	27	60.513	CA	16	34
7.193	HE1	3	21	119.815	N	9	27	68.633	CB	16	34
7.870	HN	3	21	51.748	CA	10	28	21.954	CG	16	34
7.143	HZ	3	21	4.534	HA	10	28	4.215	HA	16	34
115.333	N	3	21	2.640	HB2	10	28	3.973	HB	16	34
57.240	CA	4	22	8.119	HN	10	28	1.011	HG2	16	34
63.658	CB	4	22	117.499	N	10	28	7.858	HN	16	34
4.240	HA	4	22	59.345	CA	11	29	111.675	N	16	34
3.587	HB2	4	22	38.499	CB	11	29	59.960	CA	17	35
3.537	HB3	4	22	17.456	CD1	11	29	32.422	CB	17	35
7.996	HN	4	22	26.959	CG1	11	29	20.154	CG1	17	35
113.147	N	4	22	4.181	HA	11	29	4.159	HA	17	35
53.793	CA	5	23	1.759	HB	11	29	2.007	HB	17	35
28.872	CB	5	23	0.786	HD1	11	29	0.834	HG1	17	35
119.112	CD2	5	23	1.412	HG12	11	29	7.653	HN	17	35
4.614	HA	5	23	1.053	HG13	11	29	115.654	N	17	35
2.966	HB2	5	23	7.675	HN	11	29	60.225	CA	18	36
3.123	HB3	5	23	115.641	N	11	29	28.111	CB	18	36
7.318	HD2	5	23	60.513	CA	12	30	4.266	HA	18	36
8.219	HN	5	23	68.713	CB	12	30	2.773	HB2	18	36
117.353	N	5	23	21.835	CG	12	30	2.668	HB3	18	36
57.037	CA	6	24	4.218	HA	12	30	7.932	HN	18	36
28.420	CB	6	24	3.950	HB	12	30	118.515	N	18	36
4.406	HA	6	24	1.006	HG2	12	30				
2.723	HB2	6	24	7.776	HN	12	30				
8.058	HN	6	24	113.973	N	12	30				
116.333	N	6	24								

#res2 corresponds to the numbering of the full-length isoform 2.

## H) Isoform 2b

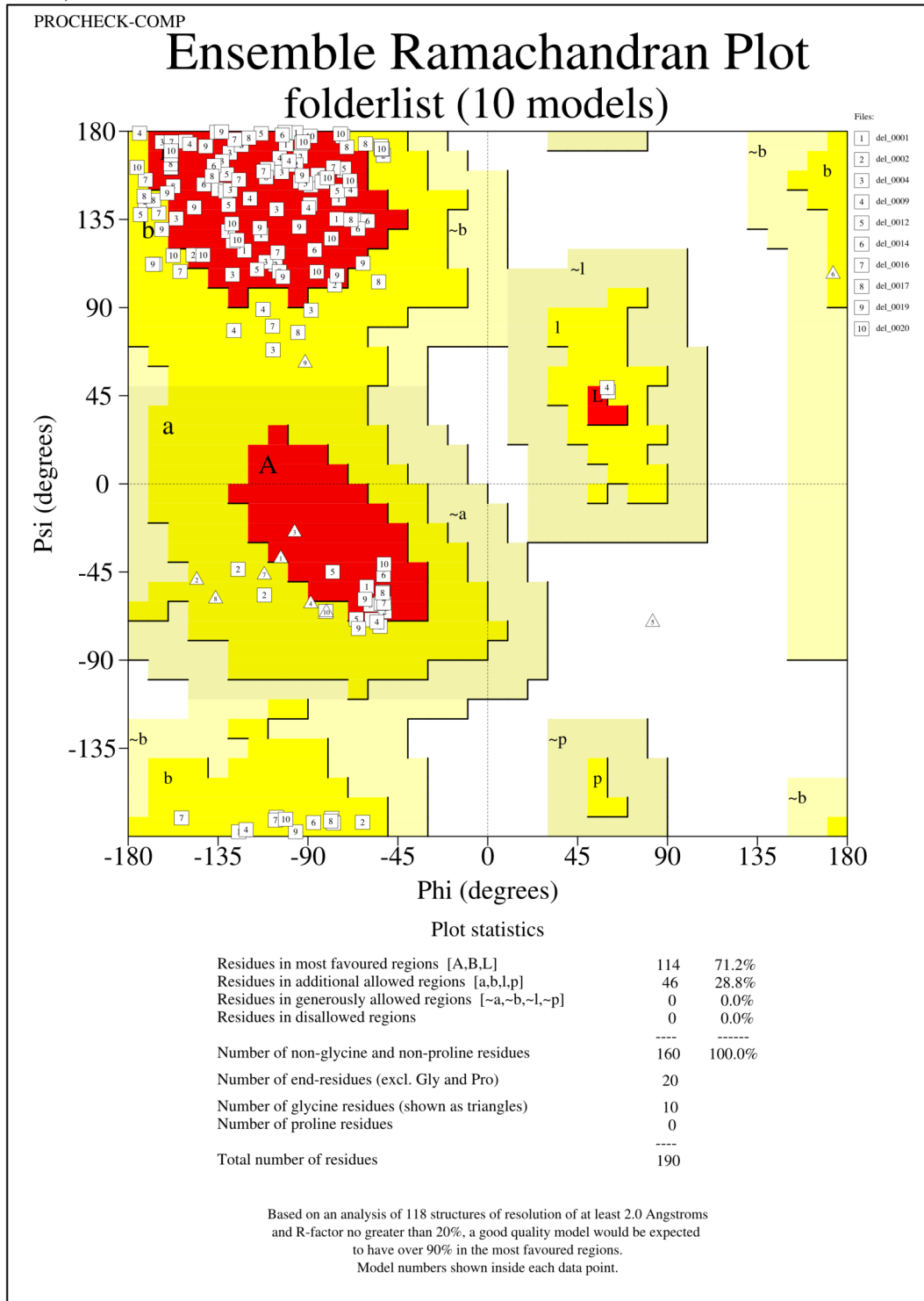
$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2	$\delta$ , ppm	Atom	#res	#res 2
42.623	CB	1	37	58.940	CA	8	44	2.765	HB3	13	49
4.541	HA	1	37	38.418	CB	8	44	58.940	CA	13	49
3.072	HB2	1	37	12.968	CD1	8	44	38.418	CB	13	49
2.825	HB3	1	37	26.234	CG1	8	44	12.856	CD1	13	49
8.225	HN	1	37	17.173	CG2	8	44	26.034	CG1	13	49
121.798	N	1	37	4.131	HA	8	44	17.121	CG2	13	49
50.166	CA	2	38	1.695	HB	8	44	4.118	HA	13	49
19.920	CB	2	38	0.780	HD1	8	44	1.681	HB	13	49
4.323	HA	2	38	1.428	HG12	8	44	0.761	HD1	13	49
1.210	HB	2	38	1.057	HG13	8	44	1.330	HG12	13	49
8.122	HN	2	38	0.815	HG2	8	44	1.000	HG13	13	49
121.648	N	2	38	7.859	HN	8	44	0.723	HG2	13	49
56.824	CA	3	39	116.752	N	8	44	7.860	HN	13	49
63.464	CB	3	39	43.781	CA	9	45	115.900	N	13	49
4.281	HA	3	39	3.770	HA2	9	45	55.632	CA	14	50
3.626	HB2	3	39	3.668	HA3	9	45	38.592	CB	14	50
3.550	HB3	3	39	8.133	HN	9	45	132.012	CD2	14	50
7.996	HN	3	39	109.009	N	9	45	116.628	CE2	14	50
112.434	N	3	39	53.503	CA	10	46	4.544	HA	14	50
54.062	CA	4	40	29.669	CB	10	46	2.830	HB2	14	50
28.812	CB	4	40	4.276	HA	10	46	2.698	HB3	14	50
31.838	CG	4	40	1.828	HB2	10	46	6.961	HD1	14	50
4.223	HA	4	40	1.671	HB3	10	46	6.963	HD2	14	50
1.927	HB2	4	40	2.186	HG1	10	46	6.592	HE2	14	50
1.751	HB3	4	40	2.185	HG2	10	46	7.887	HN	14	50
2.233	HG2	4	40	7.936	HN	10	46	119.972	N	14	50
2.234	HG3	4	40	116.836	N	10	46	57.676	CA	15	51
8.041	HN	4	40	51.508	CA	11	47	68.711	CB	15	51
118.622	N	4	40	39.096	CB	11	47	20.797	CG2	15	51
51.832	CA	5	41	4.511	HA	11	47	4.435	HA	15	51
4.475	HA	5	41	2.337	HB2	11	47	3.887	HB	15	51
8.104	HN	5	41	2.186	HB3	11	47	1.055	HG2	15	51
116.724	N	5	41	7.345	HD21	11	47	7.958	HN	15	51
44.093	CA	6	42	6.913	HD22	11	47	116.655	N	15	51
3.757	HA2	6	42	8.129	HN	11	47	61.259	CA	16	52
3.628	HA3	6	42	117.942	N	11	47	31.073	CB	16	52
8.038	HN	6	42	55.644	CA	12	48	48.987	CD	16	52
105.697	N	6	42	38.947	CB	12	48	26.227	CG	16	52
54.013	CA	7	43	131.014	CD1	12	48	4.206	HA	16	52
33.014	CB	7	43	129.854	CE1	12	48	1.992	HB2	16	52
28.397	CD	7	43	128.018	CZ	12	48	1.782	HB3	16	52
40.496	CE	7	43	4.488	HA	12	48	3.571	HD2	16	52
23.962	CG	7	43	2.984	HB2	12	48	3.522	HD3	16	52
4.298	HA	7	43	2.766	HB3	12	48	1.806	HG2	16	52
1.612	HB2	7	43	7.173	HD1	12	48	1.748	HG3	16	52
1.532	HB3	7	43	7.173	HD2	12	48				
1.502	HD2	7	43	7.173	HE1	12	48				
1.534	HD3	7	43	7.950	HN	12	48				
2.739	HE2	7	43	7.134	HZ	12	48				
2.739	HE3	7	43	115.608	N	12	48				
1.298	HG2	7	43								
1.250	HG3	7	43								
7.809	HN	7	43								
116.968	N	7	43								
7.812	NH	7	43								

#res2 corresponds to the numbering of the full-length isoform 2.

Annex D - Ramachandran plots for A) MEG 2.1 iso1a, B) MEG 2.1 iso1b, C) MEG 2.1 iso 1f, D) MEG 2.1 iso1g, E) MEG 2.1 iso 2a and F) MEG 2.1 iso 2b. The repartition of the angles in function of the favored, allowed, or disallowed regions is indicated under each plot.

### Validation of the reconstructed structures (best 10 models)

A) Isoform 1a

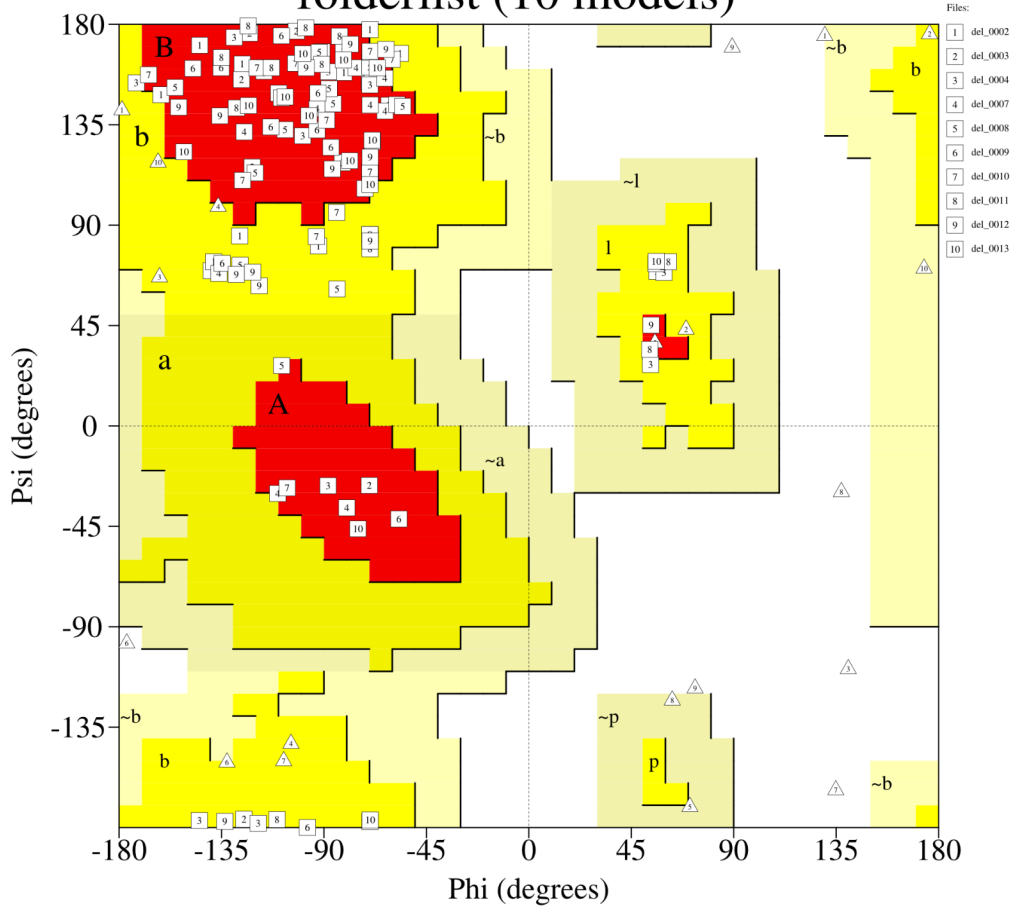


B) Isoform 1b

PROCHECK-COMP

# Ensemble Ramachandran Plot

## folderlist (10 models)



- Files:
- 1 del\_0002
  - 2 del\_0003
  - 3 del\_0004
  - 4 del\_0007
  - 5 del\_0008
  - 6 del\_0009
  - 7 del\_0010
  - 8 del\_0011
  - 9 del\_0012
  - 10 del\_0013

Plot statistics

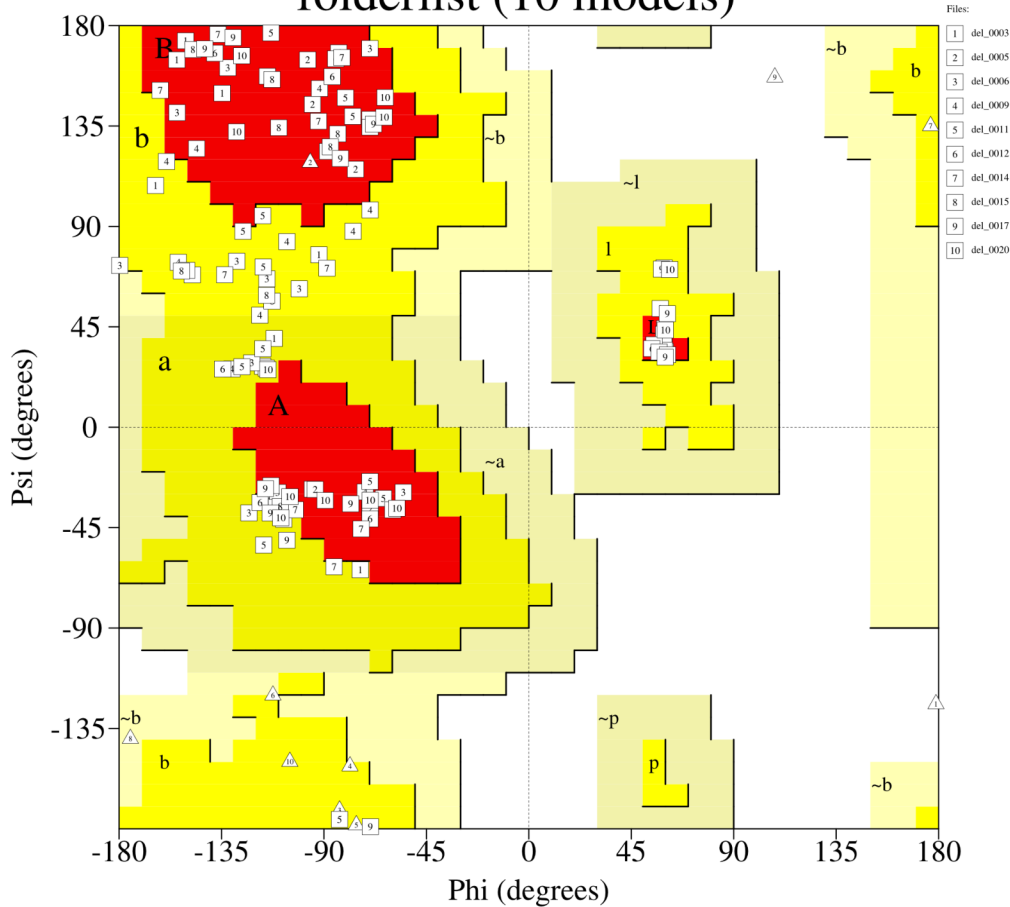
Residues in most favoured regions [A,B,L]	79	71.8%
Residues in additional allowed regions [a,b,l,p]	31	28.2%
Residues in generously allowed regions [-a,-b,-l,-p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	110	100.0%
Number of end-residues (excl. Gly and Pro)	10	
Number of glycine residues (shown as triangles)	30	
Number of proline residues	20	
-----		
Total number of residues	170	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.  
Model numbers shown inside each data point.

C) Isoform 1f

PROCHECK-COMP

# Ensemble Ramachandran Plot folderlist (10 models)



Files:

1	del_0003
2	del_0005
3	del_0006
4	del_0009
5	del_0011
6	del_0012
7	del_0014
8	del_0015
9	del_0017
10	del_0020

Plot statistics

Residues in most favoured regions [A,B,L]	62	56.4%
Residues in additional allowed regions [a,b,l,p]	48	43.6%
Residues in generously allowed regions [-a,-b,-l,-p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	110	100.0%
Number of end-residues (excl. Gly and Pro)	20	
Number of glycine residues (shown as triangles)	10	
Number of proline residues	10	
-----		
Total number of residues	150	

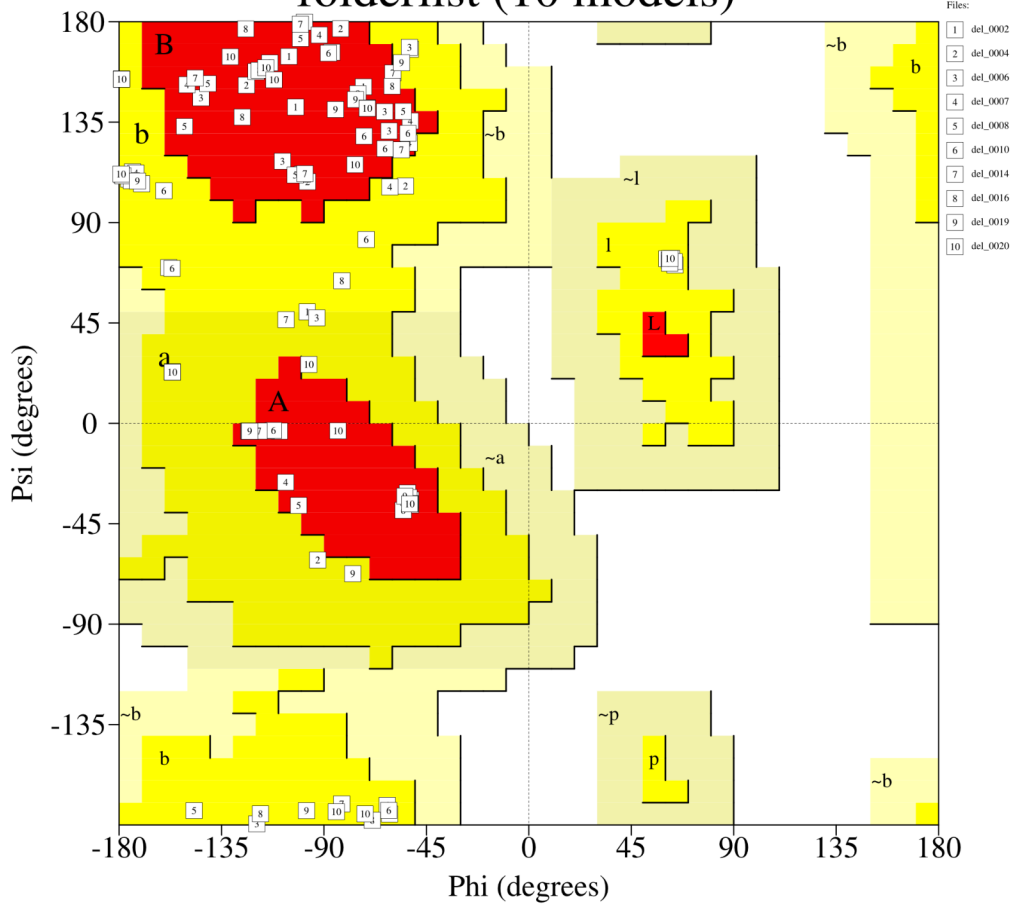
Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.  
Model numbers shown inside each data point.



D) Isoform 1g

PROCHECK-COMP

# Ensemble Ramachandran Plot folderlist (10 models)



Plot statistics

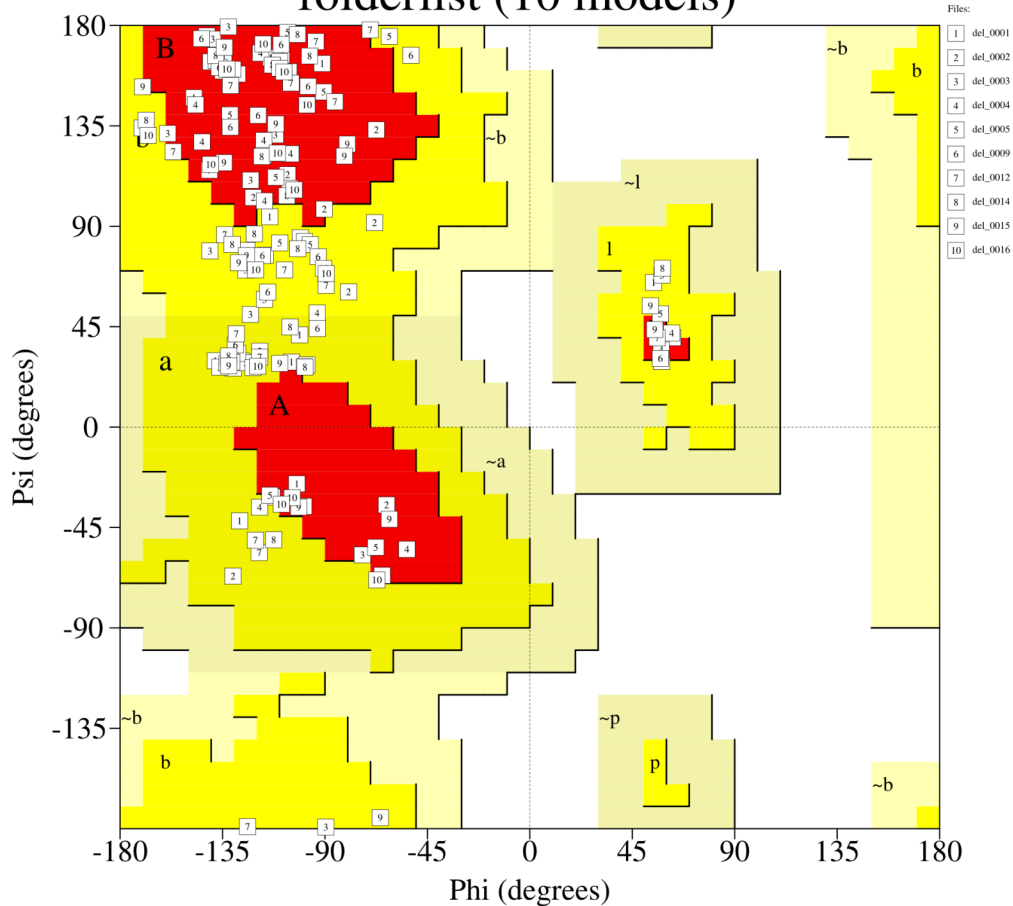
Residues in most favoured regions [A,B,L]	75	53.6%
Residues in additional allowed regions [a,b,l,p]	65	46.4%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	140	100.0%
Number of end-residues (excl. Gly and Pro)	10	
Number of glycine residues (shown as triangles)	0	
Number of proline residues	10	
-----		
Total number of residues	160	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.  
Model numbers shown inside each data point.

E) Isoform 2a

PROCHECK-COMP

# Ensemble Ramachandran Plot folderlist (10 models)



- Files:
- 1 del\_0001
  - 2 del\_0002
  - 3 del\_0003
  - 4 del\_0004
  - 5 del\_0005
  - 6 del\_0009
  - 7 del\_0012
  - 8 del\_0014
  - 9 del\_0015
  - 10 del\_0016

Plot statistics

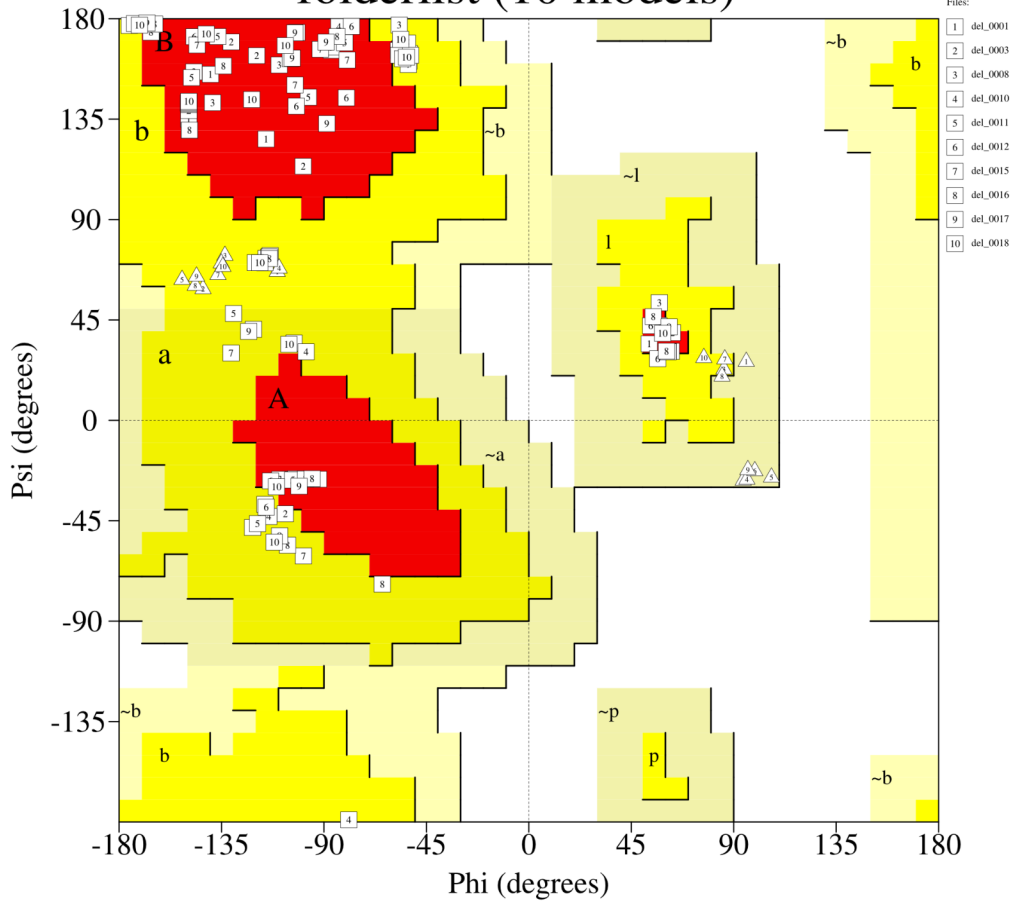
Residues in most favoured regions [A,B,L]	84	52.5%
Residues in additional allowed regions [a,b,l,p]	76	47.5%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	160	100.0%
Number of end-residues (excl. Gly and Pro)	20	
Number of glycine residues (shown as triangles)	0	
Number of proline residues	0	
-----		
Total number of residues	180	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.  
Model numbers shown inside each data point.

F) Isoform 2b

PROCHECK-COMP

# Ensemble Ramachandran Plot folderlist (10 models)



- Files:
- 1 del\_0001
  - 2 del\_0003
  - 3 del\_0008
  - 4 del\_0010
  - 5 del\_0011
  - 6 del\_0012
  - 7 del\_0015
  - 8 del\_0016
  - 9 del\_0017
  - 10 del\_0018

Plot statistics

Residues in most favoured regions [A,B,L]	71	59.2%
Residues in additional allowed regions [a,b,l,p]	49	40.8%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	120	100.0%
Number of end-residues (excl. Gly and Pro)	10	
Number of glycine residues (shown as triangles)	20	
Number of proline residues	10	
-----		
Total number of residues	160	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.  
Model numbers shown inside each data point.