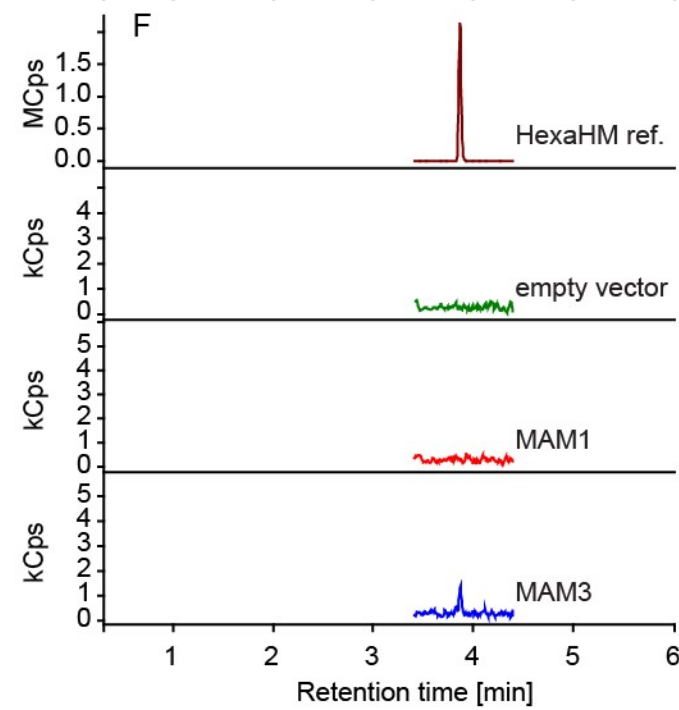
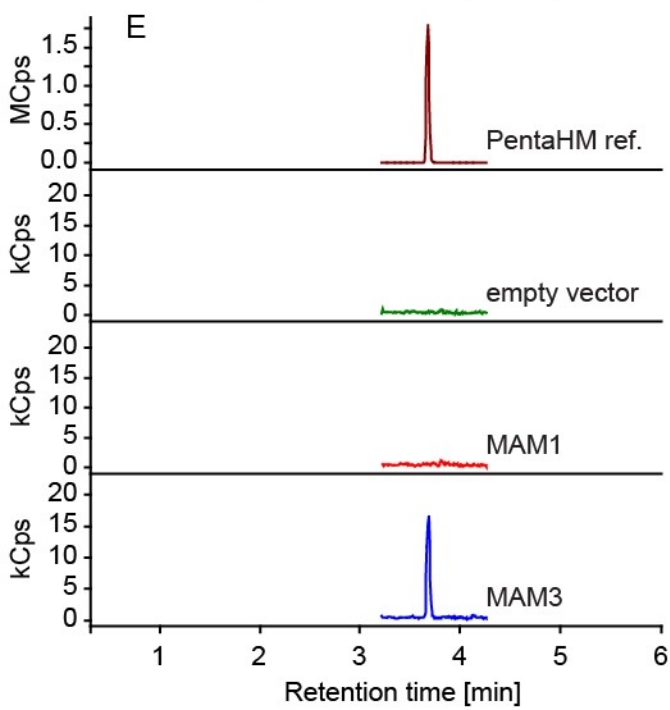
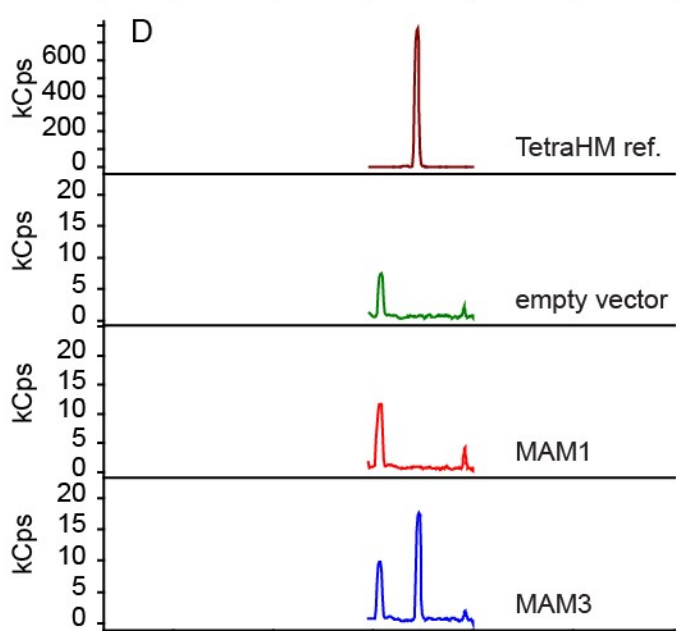
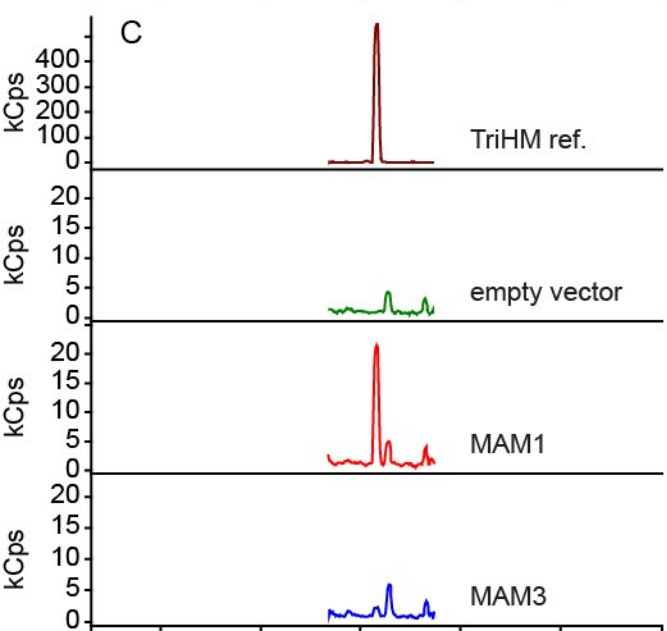
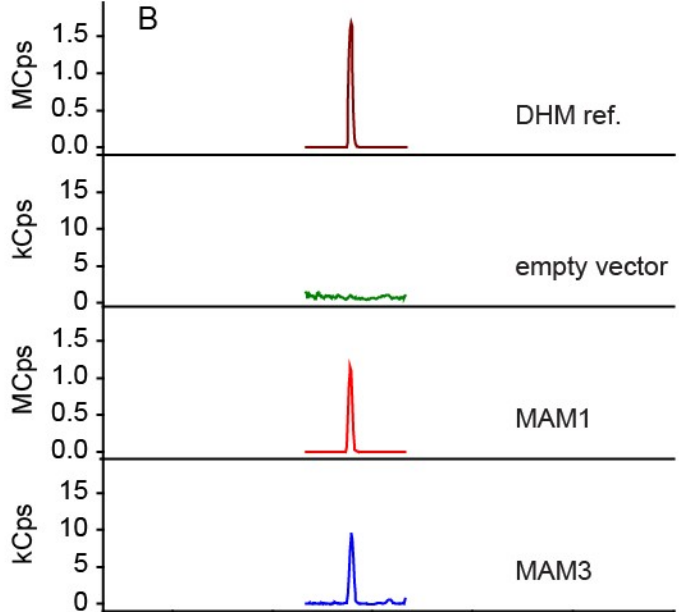
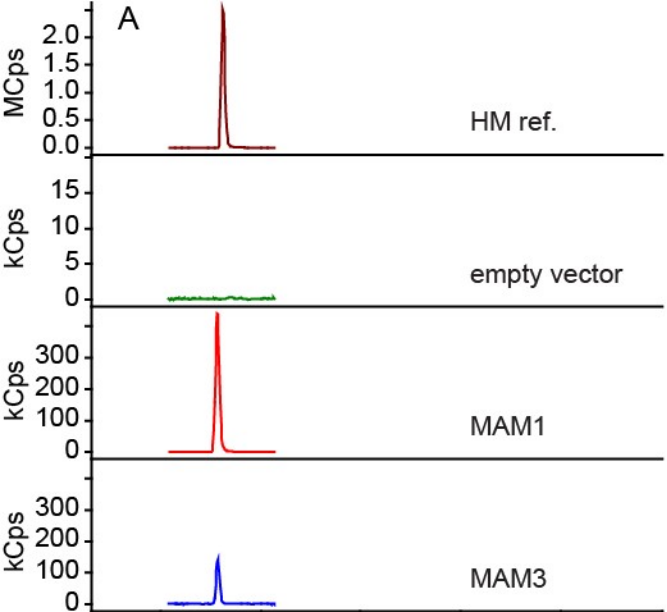
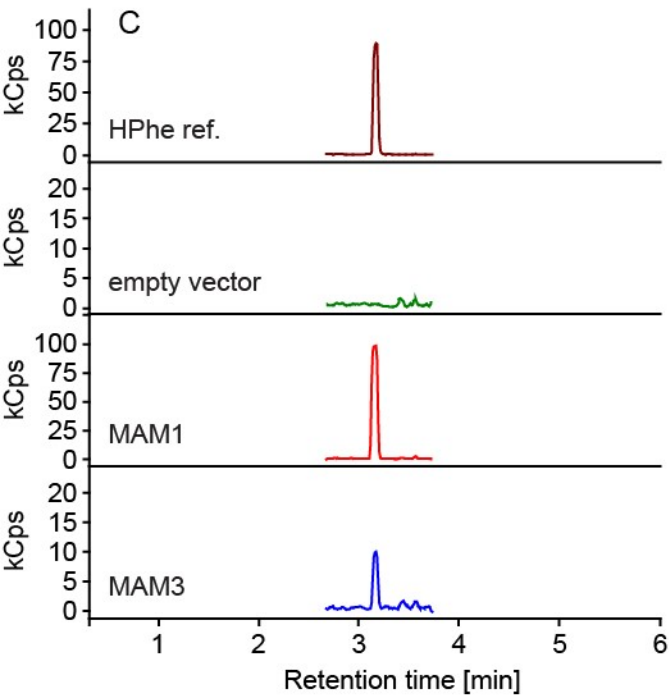
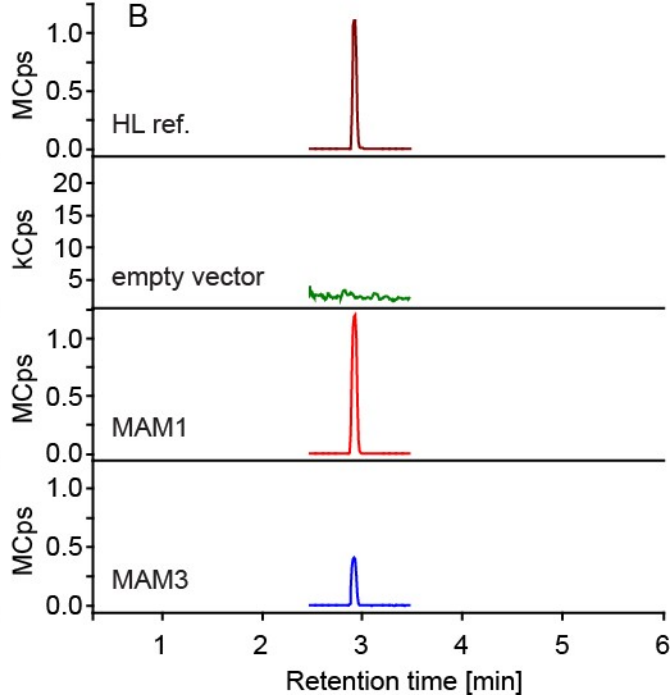
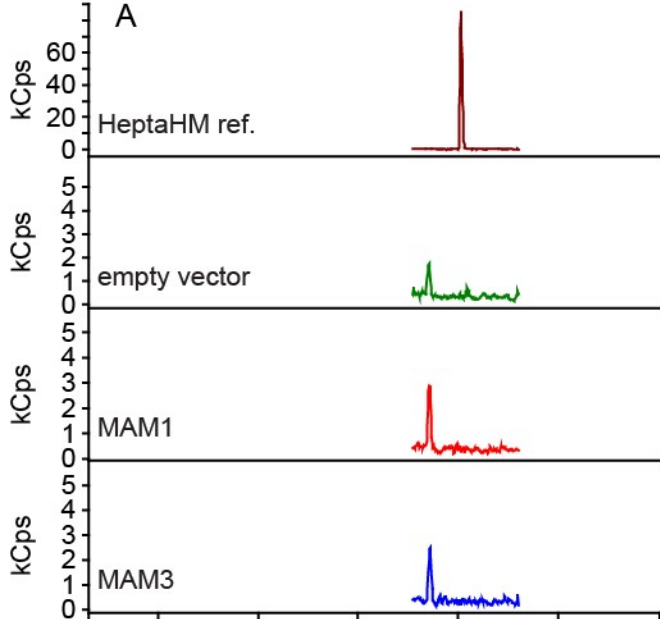
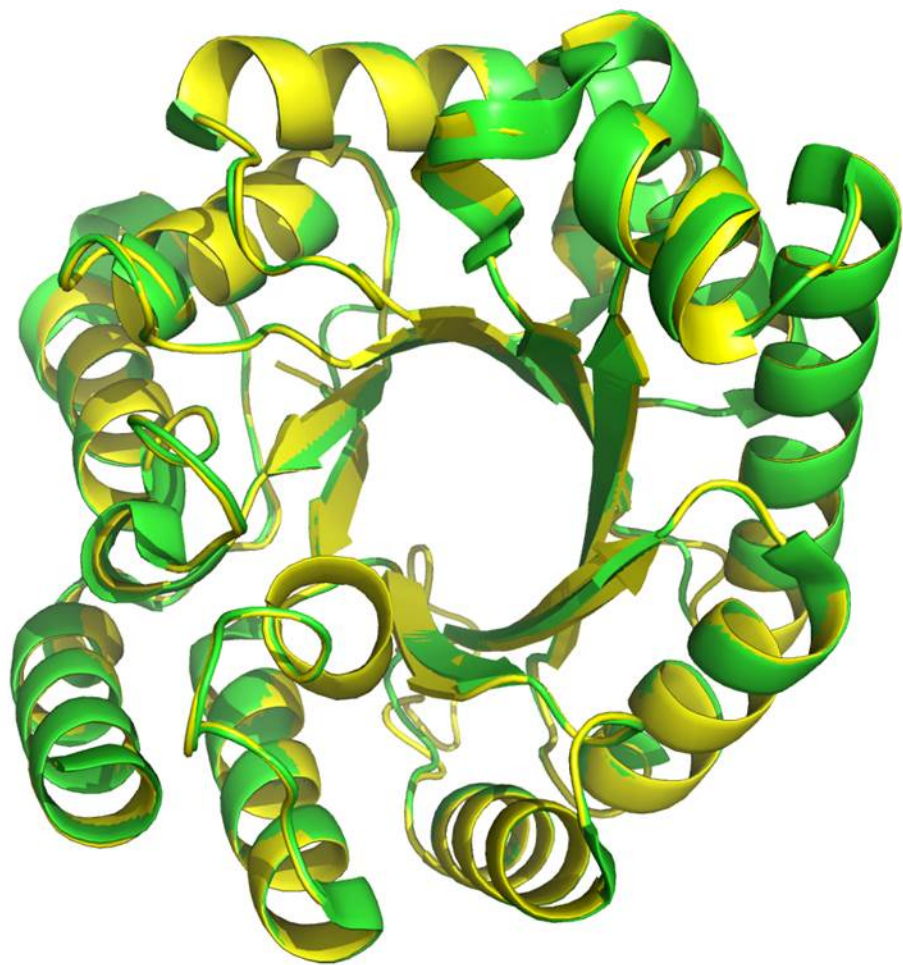


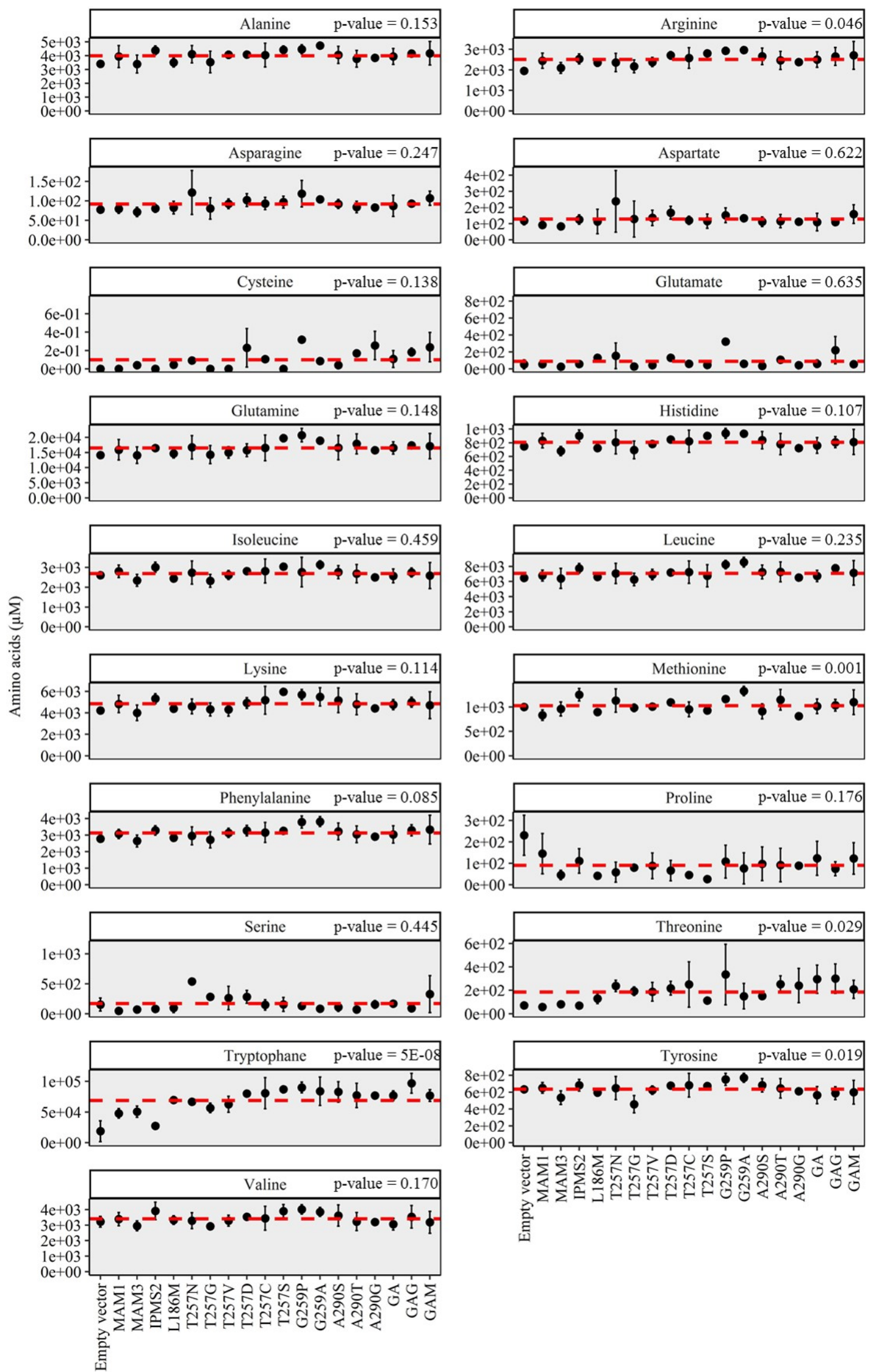
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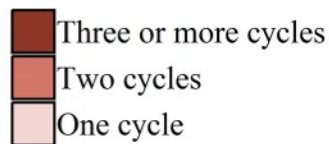
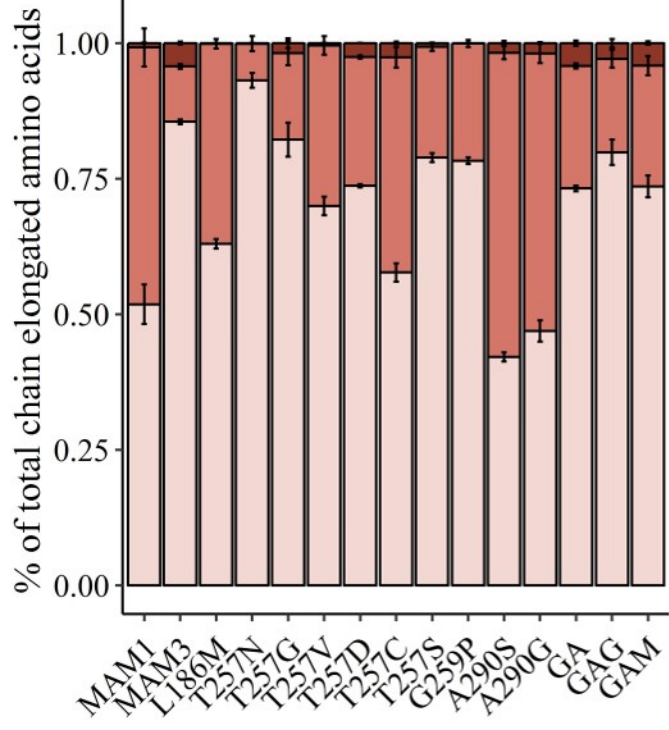
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AMAM1	1		100.00	99.41	95.45	92.11	92.11	91.32	85.85	86.05	82.09	87.82	85.32	75.55	79.49	79.53	79.96	79.61	79.84	79.65	73.59	79.06	75.73	77.60	77.80	77.21	77.80	79.02	77.76	75.49	76.67	73.92	75.98	69.85	77.56	77.56	76.97	77.17	76.97	79.33	75.59	77.17	75.83	72.05	71.65	70.67	71.71	72.62	72.82	65.94	60.89	60.95	60.75	76.32	75.93	76.22	45.31	44.70
AtMAM1	2	0		99.41	95.45	92.11	92.11	91.32	85.85	86.05	82.09	87.82	85.32	75.55	79.49	79.53	79.96	79.61	79.84	79.65	73.59	79.06	75.73	77.60	77.80	77.21	77.80	79.02	77.76	75.49	76.67	73.92	75.98	69.85	77.56	77.56	76.97	77.17	76.97	79.33	75.59	77.17	75.83	72.05	71.65	70.67	71.71	72.62	72.82	65.94	60.89	60.95	60.75	76.32	75.93	76.22	45.31	44.70
AtsMAM1	3	3	3		95.26	91.91	91.91	91.12	86.05	86.05	81.89	87.82	85.32	75.55	79.49	79.53	80.15	79.61	80.04	79.84	73.77	79.26	75.73	78.00	78.19	77.60	78.19	79.02	78.15	75.69	76.86	74.12	76.17	70.22	77.76	77.76	77.17	77.36	77.17	79.53	75.79	77.36	75.83	72.24	71.85	70.87	72.10	72.62	72.82	65.94	60.89	60.95	60.75	76.52	76.13	76.41	45.31	44.70
AMAM2	4	23	23	24		93.69	93.69	92.90	87.03	87.23	82.87	88.41	86.69	76.65	80.66	80.12	81.09	79.41	79.26	79.06	73.22	78.47	74.95	78.59	78.78	78.19	78.78	80.00	78.74	75.10	76.47	73.92	75.59	69.85	75.79	75.98	75.20	74.61	74.41	77.56	74.41	75.79	74.66	71.06	70.67	70.47	71.51	71.46	71.65	65.35	61.28	61.54	61.34	75.34	74.95	75.24	44.69	43.93
AIIMAM2	5	40	40	41	32		99.21	96.84	88.80	88.61	84.84	90.37	88.45	77.57	81.45	81.73	82.06	80.63	78.91	78.71	72.73	77.73	74.41	78.04	78.24	77.65	78.24	80.43	77.80	74.76	76.52	73.78	75.44	69.54	76.62	76.82	76.03	75.64	75.44	78.19	73.48	75.05	74.31	69.94	69.16	68.96	70.59	71.51	71.71	65.03	60.97	61.22	61.02	75.39	75.00	75.68	45.00	44.55
AlpMAMa	6	40	40	41	32	4		96.84	89.00	88.80	85.04	90.37	88.65	77.76	81.64	81.93	82.24	80.23	79.10	78.91	72.91	77.93	74.61	78.04	78.24	77.65	78.24	80.43	77.80	74.56	76.32	73.58	75.24	69.54	76.62	76.82	76.03	75.64	75.44	78.39	73.48	75.05	74.31	69.94	69.16	68.96	70.78	71.51	71.71	65.03	60.97	61.42	61.22	75.00	74.61	75.49	45.16	44.70
AcMAMa	7	44	44	45	36	16	16		88.02	87.82	83.86	89.39	87.87	76.84	80.66	80.75	81.31	79.84	78.12	77.93	71.82	76.76	74.22	77.45	77.65	77.06	77.65	80.23	77.41	74.56	75.93	73.19	75.44	69.54	75.83	76.03	75.25	74.85	74.66	77.60	73.08	74.66	74.12	69.55	68.76	68.57	70.59	71.32	71.51	64.83	61.17	60.83	60.63	74.22	73.83	74.90	44.69	44.24
CsMAM2.1	8	72	72	71	66	57	56	61		97.42	92.06	93.45	92.13	77.39	81.45	80.94	80.93	78.54	78.52	78.32	72.18	77.15	73.63	76.67	76.86	76.27	76.86	76.91	77.67	73.39	75.34	71.82	74.07	69.17	75.25	75.44	75.64	75.83	76.03	76.62	72.69	73.92	72.94	69.17	68.38	68.18	70.61	71.07	71.26	64.82	59.88	60.79	60.79	73.87	73.28	74.07	45.62	44.55
CsMAM2.2	9	71	71	71	65	58	57	62	13		92.86	93.85	92.91	77.39	81.45	80.94	80.75	78.74	79.10	78.91	73.09	77.73	73.63	77.45	77.65	77.06	77.65	77.69	78.46	73.39	75.54	72.21	74.66	69.54	74.85	75.05	75.64	76.03	76.23	77.41	72.89	74.12	73.53	69.17	68.38	68.18	70.41	71.65	71.84	65.42	60.67	61.39	61.39	74.07	73.48	74.46	45.62	44.55
CsMAM1	10	91	91	92	87	77	76	82	40	36		89.09	87.99	73.53	77.34	77.01	77.20	78.31	75.64	75.44	69.29	74.07	75.56	73.14	73.33	72.75	73.33	72.99	73.91	70.45	72.02	68.88	72.02	66.79	72.10	72.30	72.69	73.08	73.28	74.26	69.74	70.78	70.00	66.60	65.81	66.00	67.86	70.75	70.75	65.11	59.96	60.20	60.20	69.74	69.16	70.57	44.20	43.73
BdMAM1	11	62	62	62	59	49	49	54	33	31	55		92.32	78.12	82.23	82.51	81.87	80.31	80.27	80.08	73.82	78.91	75.20	78.82	79.02	78.43	79.02	78.86	79.05	74.17	76.32	73.19	75.24	70.09	75.83	76.03	76.62	76.42	76.23	78.59	73.87	74.90	74.12	69.96	69.17	68.77	71.20	72.43	72.62	66.21	61.84	61.98	61.78	75.05	74.26	74.66	45.78	45.17
CrMAM2	12	75	75	75	68	59	58	62	40	36	61	39		76.56	80.54	79.84	79.70	78.47	78.40	78.21	72.10	76.85	73.35	76.37	76.56	75.98	76.56	76.61	77.95	72.51	74.46	72.32	73.98	69.29	75.15	75.34	75.73	75.34	75.34	77.10	72.02	72.99	72.66	69.09	68.31	68.11	70.53	70.66	70.85	64.44	59.92	60.43	60.24	72.21	71.62	72.82	45.48	44.57
BooMAM2	13	133	133	133	127	122	121	126	123	123	144	119	128		93.15	87.22	87.82	75.46	75.41	75.23	74.95	75.41	71.01	72.79	72.98	72.43	73.35	72.66	72.56	69.72	70.83	67.71	70.28	69.33	72.19	72.38	73.11	72.19	72.01	73.11	70.53	71.32	71.14	64.94	64.21	63.84	65.19	68.49	68.67	62.92	57.95	58.04	57.86	68.50	68.13	69.53	43.60	42.88
BnMAM2	14	105	105	105	99	95	94	99	95	95	116	91	100	37		91.73	84.89	79.18	79.34	79.14	73.14	79.34	74.66	76.56	76.76	76.17	77.15	76.41	76.32	73.29	74.46	71.15	73.59	68.37	75.93	76.13	77.10	75.93	75.73	76.91	74.17	75.00	74.80	68.24	67.45	67.06	68.69	72.20	72.39	66.67	61.24	61.49	61.30	71.98	71.60	73.06	45.16	44.39
RsMAM2	15	104	104	104	101	93	92	98	97	97	117	89	103	69	42		84.40	79.22	79.96	79.76	73.31	79.96	75.05	76.77	76.97	76.38	77.17	76.62	76.68	73.67	74.85	72.30	73.97	68.88	76.13	76.33	77.32	75.94	75.74	76.53	74.36	75.59	75.00	68.32	67.52	66.93	68.77	71.65	71.84	65.74	60.67	61.90	61.71	71.96	71.57	73.83	45.31	45.17
EsMAM2	16	107	107	106	101	96	95	100	102	103	122	97	109	66	81	83		80.41	79.44	79.25	77.88	79.25	74.39	76.59	76.78	76.22	76.97	76.45	75.80	72.52	73.64	70.65	72.90	70.02	75.23	75.42	75.23	74.67	74.48	75.98	72.05	72.66	72.47	67.60	66.85	66.85	68.22	69.81	70.00	62.92	58.07	59.10	59.10	71.46	70.90	72.86	44.29	43.86
EsMAM1	17	104	104	104	105	99	101	103	109	108	108	100	110	134	107	106	105		77.19	77.00	70.96	76.41	75.94	75.73	75.93	75.34	75.93	75.20	75.00	71.29	72.85	70.12	73.53	66.91	74.71	74.90	74.51	73.73	73.53	75.69	72.55	73.19	74.12	69.88	69.09	68.50	68.76	75.64	75.84	68.88	63.29	65.19	64.99	71.62	71.04	73.83	44.53	44.86
BooMAM1.1	18	103	103	102	106	108	107	112	110	107	124	101	111	134	106	102	110	117		99.80	90.61	92.28	87.52	76.27	76.47	75.88	76.67	75.69	74.71	71.76	73.53	70.39	72.96	67.58	76.08	76.27	76.67	76.08	76.27	77.06	73.92	74.95	74.95	70.45	69.86	69.08	68.75	70.02	70.21	63.01	57.06	58.43	58.43	72.21	71.62	72.90	45.00	45.02
BnMAM1.1	19	104	104	103	107	109	108	113	111	108	125	102	112	135	107	103	111	118	1		90.42	92.08	87.33	76.08	76.27	75.69	76.47	75.49	74.51	71.57	73.33	70.39	72.76	67.40	76.08	76.27	76.47	75.88	76.08	76.86	73.73	74.76	74.76	70.45	69.86	69.08	68.75	70.02	70.21	63.01	57.06	58.43	58.43	72.02	71.43	72.71	45.00	45.02
BrMAM1.1	20	145	145	144	147	150	149	155	153	148	168	144	154	138	148	146	121	160	51	52		86.37	80.85	70.07	70.26	69.71	70.44	69.53	68.80	66.42	67.88	64.96	66.91	66.36	69.89	70.07	70.44	69.71	69.89	70.44	67.70	68.67	68.67	65.03	64.48	63.75	63.45	64.98	65.16	58.11	52.89	53.83	54.01	66.30	65.76	67.70	42.48	42.21
BJPMS1	21	107	107	106	110	114	113	119	117	114	132	108	119	134	106	102	111	121	39	40	74		86.34	76.27	76.47	75.88	76.67	75.69	75.49	71.96	73.53	70.20	72.76	67.58	75.49	75.69	76.27	75.29	75.49	76.27	74.12	75.34	75.15	70.84	70.25	69.28	68.75	69.83	70.02	62.43	56.87	57.84	57.65	71.62	71.23	73.49	45.16	44.70
EvMAM	22	124	124	124	128	131	130	132	135	135	120	127	137	158	130	127	137	121	63	64	104	69		73.37	73.																																	

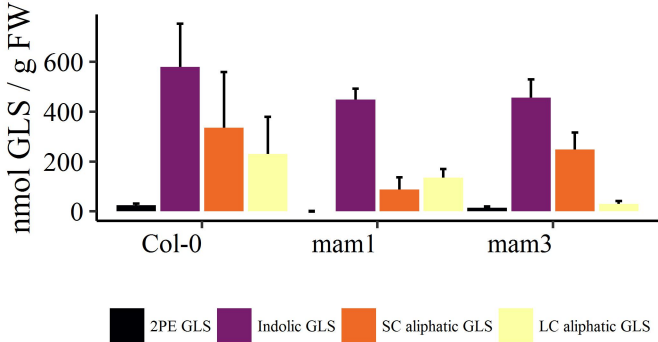
















## Supplementary Figure legends

**Supplementary Figure S1.** Alignment of 57 MAM and 2 IPMS full protein sequences. According to *A. thaliana* MAM1 numbering, only Leu186, Thr257, Ile258, Gly259 and Ala290 residues are shown.

**Supplementary Figure S2.** Matrix from the alignment of MAM and IPMS enzyme sequences. Upper part indicates sequence similarity in percentage and the lower part shows differences between the protein sequences. Two MAM sequences have been removed from the matrix, as the comparison indicated low sequence similarity due to poor quality of the sequence data.

**Supplementary Figure S3.** LC-MS traces of homomethionine (HM), dihomomethionine (DHM), trihomomethionine (TriHM), tetrahomomethionine (TetraHM), pentahomomethionine (PentaHM) and hexahomomethionine (HexaHM). A representative sample of MAM1 and MAM3 containing strains as well as an empty vector control are shown. For each compound, the pure sample is shown in the top panel.

**Supplementary Figure S4.** LC-MS traces of heptahomomethionine (HeptaHM), homoleucine (HL) and homophenylalanine (HPhe). A representative sample of MAM1 and MAM3 containing strains as well as an empty vector control are shown. For each compound, the pure sample is shown in the top panel.

**Supplementary Figure S5.** Homology model of MAM1 from *A. thaliana*. (yellow) superimposed on the crystal structure of *N. meningitidis* IPMS (green). Only the  $(\beta/\alpha)_8$  catalytic barrel is shown. The RMSD value is 0.26 Å.

**Supplementary Figure S6.** Protein amino acids monitored in this study. Each graph shows levels of one amino acid in the media of *E. coli* strains expressing MAM variants and an empty vector control. The mean of all cultures is indicated by the red line. ANOVA was used to investigate changes in the individual amino acids between the cultures. p-values are shown in upper right corner of each graph. Data represents average and standard deviation of three biological replicates each grown in three technical replicates.

**Supplementary Figure S7.** Produced chain elongated amino acids were grouped according to how many methylene groups were added to the methionine, phenylalanine or leucine structures (one, two or three and above). Bars represents the percentage of each group of products relative to the total production within each culture. Data represents average and standard deviation of three biological replicates each grown in three technical replicates.

**Supplementary Figure S8.** Glucosinolate analysis in *A. thaliana* ecotype Col-0 and knockout mutants mam1 and mam3. Glucosinolates (GLS) were grouped into aromatic (2PE) GLSs, indole GLSs and short chain (SC – one to three elongation rounds) and long chain (LC – four elongation rounds and above) aliphatic GLSs. Data represents average and standard deviation of 3-7 biological replicates.

**Supplementary Figure S9.** Protein levels in *E. coli* strains expressing the chain elongation pathway genes, A) *BCAT4*, B) *MAM1*, C) *LSU1*, D) *MAM3*, E) *SSU3*, F) *IPMS2* and G) *IPMDH1* and H) *E. coli* housekeeping gene *ICD*. A-G are normalized the *ICD*, while the *ICD* is not normalized. Different colours indicate individual peptides within each protein. Data represents average and standard deviation of three biological replicates.

## Supplementary Tables

**Supplementary Table S1.** List of primers used in this study. Lower case letters denotes the USER tail used for cloning. Uracils are marked in blue. Mutated nucleotides are marked in red.

Name	Sequence	Description
MAM1_fwd	ggcttaa <u>u</u> ATGCATCACCACCACCATCACAACACTATGTGCGTGTATTC	<i>MAM1</i> forward primer
BCAT4_rev	ggttta <u>u</u> TCAGCCCTGGCGGTC AAT	<i>BCAT4</i> reverse primer
MAM3_fwd	ggcttaa <u>u</u> ATGCATCACCACCACCATCACGCTGAGTCCAAAAAGGTGGC	<i>MAM3</i> forward primer
MAM3_rev	acaaaatta <u>u</u> TTCTAGAGGGGTTATACAACAGCGGAAATC	<i>MAM3</i> reverse primer
IPMS2_fwd	ggcttaa <u>u</u> ATGCATCACCACCACCATCACATGGAGTCTTCGATTCTCA	<i>IPMS2</i> forward primer
IPMS2_rev	acaaaatta <u>u</u> TTCTAGAGGGGTCAGGCAGGGACTTCGTTG	<i>IPMS2</i> reverse primer
L186_fwd	acatctactag <u>u</u> GACATTCACATGAAATATAAG	Fusion primer for <i>L186</i> -mutant
L186M_rev	actagtagatg <u>u</u> GAATAC <b>CAT</b> TATCCTTGGCCTC	Fusion primer for <i>L186M</i> -mutant
T257/G259_fwd	acgtaggg <u>u</u> CAACATGCCACATGAATACGG	Fusion primer for <i>T257</i> -mutant
T257N_rev	atccctaccg <u>u</u> ATCACCGAT <b>GTT</b> CACCACCGTAA	Fusion primer for <i>T257N</i> -mutant
T257G_rev	atccctaccg <u>u</u> ATCACCGAT <b>GCC</b> CACCACCGTAA	Fusion primer for <i>T257G</i> -mutant
T257V_rev	atccctaccg <u>u</u> ATCACCGAT <b>GAC</b> CACCACCGTAA	Fusion primer for <i>T257V</i> -mutant
T257D_rev	atccctaccg <u>u</u> ATCACCGAT <b>GTC</b> CACCACCGTAA	Fusion primer for <i>T257D</i> -mutant
T257C_rev	atccctaccg <u>u</u> ATCACCGAT <b>GCA</b> CACCACCGTAA	Fusion primer for <i>T257C</i> -mutant
T257S_rev	atccctaccg <u>u</u> ATCACCGAT <b>GCT</b> CACCACCGTAA	Fusion primer for <i>T257S</i> -mutant
G259P_rev	atccctaccg <u>u</u> ATC <b>TGG</b> GATGGTCACCACCGTAA	Fusion primer for <i>G259P</i> -mutant
G259A_rev	atccctaccg <u>u</u> ATC <b>GGC</b> GATGGTCACCACCGTAA	Fusion primer for <i>G259A</i> -mutant
A290S_fwd	acgatggtg <u>u</u> <b>CAGC</b> GTTCATTGTCACAACGAC	Fusion primer for <i>A290S</i> -mutant
A290T_fwd	acgatggtg <u>u</u> <b>CACC</b> GTTCATTGTCACAACGAC	Fusion primer for <i>A290T</i> -mutant
A290G_fwd	acgatggtg <u>u</u> <b>CGGC</b> GTTCATTGTCACAACGAC	Fusion primer for <i>A290G</i> -mutant
A290_rev	acgacaacatc <u>u</u> CAATTCCAGGGGTGTTTGCTTTG	Fusion primer for <i>A290</i> -mutant
GA_rev	atccctaccg <u>u</u> ATC <b>GGC</b> GAT <b>GCC</b> CACCACCGTAA	Fusion primer for <i>T257G/G259A</i> -mutant

**Supplementary Table S2.** Transitions and response factors used to quantify levels of chain elongated amino acids. Response factors of methionine- and leucine-derived products were reported in (20).

Amino acid	Q1	Q3	CE	Internal standard	Q1	Q3	Response factor
<b>HPhe</b>	180.1	91.1 <sup>Qt</sup>	-22	13C,15N-Phe	176.2	129.2	1.61
	180.1	134.1	-8				
	180.1	117.1	-13				
<b>HM</b>	164.2	70.3 <sup>Qt</sup>	-16	13C,15N-Val	124.1	77.2	0.35
<b>DHM</b>	178.2	84.2 <sup>Qt</sup>	-14	13C,15N-Phe	176.2	129.2	1.05
	178.2	132.1	-10				
<b>TriHM</b>	192.2	98.2 <sup>Qt</sup>	-14	13C,15N-Phe	176.2	129.2	1.25
	192.2	146.1	-9				
<b>TetraHM</b>	206.2	112.2 <sup>Qt</sup>	-13	13C,15N-Phe	176.2	129.2	0.91
	206.2	160.1	-10				
<b>PentaHM</b>	220.3	126.2 <sup>Qt</sup>	-16	13C,15N-Phe	176.2	129.2	0.41
	220.3	174.1	-10				
<b>HexaHM</b>	234.4	140.2 <sup>Qt</sup>	-16	13C,15N-Phe	176.2	129.2	0.36
	234.4	188.1	-11				
<b>HeptaHM</b>	248.2	188.1 <sup>Qt</sup>	-10	13C,15N-Phe	176.2	129.2	n.d.
	148.2	154.1	-16				
<b>HL</b>	146.2	100.1	10	13C,15N-Phe	176.2	129.2	0.88
<b>DHL</b>	160.2	114.1	-10	13C,15N-Phe	176.2	129.2	1.00*
<b>TriHL</b>	174.2	128.1	-10	13C,15N-Phe	176.2	129.2	1.00*

\*Response factors for DHL and TriHL were assumed to be 1.00. CE = collision energy. Q = quadrupole. Qt = quantifier transition

**Supplemental Table S3:** Transitions used for Selected Reaction Monitoring (SRM) for targeted proteomics on peptides of methionine chain elongation pathway proteins. Retention times and parent ion to fragment ion transitions are given. All peptides were selected in Q1 as the double-charged ions  $[M+H]^{2+}$  and fragment ions in Q3 as single-charged ions  $[M+H]^+$ . Collision energies (CE) for natural non-labelled (light) and isotopically labelled (heavy) peptides were identical.

Protein name	AGI code	Peptide	RT	Light peptide		Heavy peptide		CE
				Q1 $[M+H]^{2+}$	Q3 $[M+H]^+$	Q1 $[M+H]^{2+}$	Q3 $[M+H]^+$	
BCAT4	At3g19710	TGEETLAAK	1.60	460.25	761.42	464.25	769.42	-13
			1.60	460.25	818.44	464.25	826.44	-15
			1.60	460.25	632.38	464.25	640.38	-14
		LYETLSDIQTGR*	8.30	698.36	776.4	703.36	786.4	-19
			8.30	698.36	990.53	703.36	1000.53	-26
			8.30	698.36	1119.57	703.36	1129.57	-23
		SITNYCPVWIPLAEAK	18.70	931.49	927.54	935.49	935.54	-3
			18.70	931.49	1123.67	935.49	1131.67	-29
			18.70	931.49	628.38	935.49	636.38	-41
		GNVVSTPTIAGTILPGVTR	16.50	927.03	529.32	932.03	539.32	-29
			16.50	927.03	642.4	932.03	652.4	-28
			16.50	927.03	642.4	932.03	652.4	-28
MAM1	At5g23010	SLGFNDIQFGCEDGGR*	13.60	886.39	897.36	891.39	907.36	-31
			13.60	886.39	1025.42	891.39	1035.42	-33
			13.60	886.39	404.2	891.39	414.2	-41
		DGEQSPGGS LTPPQK	2.50	749.37	981.55	753.37	989.55	-23
			2.50	749.37	1068.58	753.37	1076.58	-25
			2.50	749.37	469.29	753.37	477.29	-30
		STYEILSPEDIGIVK	17.00	832.45	957.54	836.45	965.54	-22
			17.00	832.45	870.51	836.45	878.51	-25
			17.00	832.45	1070.62	836.45	1078.62	-24
		SGNASLEEVVMALK	17.50	724.38	918.51	728.38	1126.63	-24
			17.50	724.38	1118.63	728.38	1039.59	-24
			17.50	724.38	1031.59	728.38	926.51	-23
MAM3	At5g23020	GESLMDGVYTK	6.70	600.29	813.4	604.29	821.4	-19
			6.70	600.29	1013.51	604.29	1021.51	-16
			6.70	600.29	682.35	604.29	690.35	-19
		ALVVNGAEISSEK	5.70	658.86	934.46	662.86	942.46	-20
			5.70	658.86	1033.53	662.86	1041.53	-20
			5.70	658.86	820.42	662.86	828.42	-21
		SGNAPLEEVVMALK	18.70	729.39	1128.65	733.39	1136.65	-21
			18.70	729.39	918.51	733.39	926.51	-25
			18.70	729.39	588.4	733.39	596.4	-23
		STYEILSPEDVGIVK*	15.50	825.44	943.52	829.44	951.52	-23
			15.50	825.44	856.49	829.44	864.49	-23
			15.50	825.44	1056.61	829.44	1064.61	-25
DGEQSPGAALTPPQK	3.40	748.38	469.29	752.38	477.29	-32		
	3.40	748.38	372.24	752.38	380.24	-41		

			3.40	748.38	979.57	752.38	987.57	-24
IPMS2	At1g74040	GTYEIMSPPEEIGLER*	15.40	889.94	1102.53	894.94	1112.53	-28
			15.40	889.94	942.5	894.94	952.5	-32
IPMI-LSU1	At4g13430	FILDGEMPSYLQAK*	16.90	806.42	806.45	810.42	814.45	-26
			16.90	806.42	937.5	810.42	945.5	-24
			16.90	806.42	1123.56	810.42	1131.56	-24
		VWMDVYALPVPAGGK	18.50	830.44	682.4	834.44	690.4	-21
			18.50	830.44	486.28	834.44	494.28	-37
			18.50	830.44	261.17	834.44	269.17	-49
IPMI-SSU3	At3g58990	LGSFALNGLPK	12.60	558.83	712.45	562.83	720.45	-19
			12.60	558.83	1003.57	562.83	1011.57	-18
			12.60	558.83	641.41	562.83	649.41	-17
		EDGSLLINHTTR	3.90	721.87	854.49	726.87	864.49	-29
			3.90	721.87	967.58	726.87	977.58	-29
			3.90	721.87	741.41	726.87	751.41	-28
		NCVATGEIFPLESEVR*	15.10	910.95	829.45	915.95	839.45	-30
			15.10	910.95	976.52	915.95	986.52	-30
			15.10	910.95	490.27	915.95	500.27	-37
IPMDH1	At5g14200	LSDAILLGAIGGYK*	17.00	695.91	891.54	699.91	899.54	-19
			17.00	695.91	778.46	699.91	786.46	-20
			17.00	695.91	1004.63	699.91	1012.63	-22
		AGSLEGLEFDFK	14.20	656.83	855.44	660.83	863.44	-20
			14.20	656.83	984.48	660.83	992.48	-18
			14.20	656.83	685.33	660.83	693.33	-17
		IEDAVVDALNK	6.05	593.83	944.52	597.83	952.52	-17
			6.05	593.83	659.39	597.83	667.39	-17
			6.05	593.83	758.45	597.83	766.45	-17
ICD	JW1122	GPLTTPVGGGIR*	6.37	562.83	655.40	567.83	665.40	-20
			6.37	562.83	857.49	567.83	867.49	-21
			6.37	562.83	756.44	567.83	766.44	-19

\*= peptides represented in Figure 8.



**Supplemental Table S4:** Pairwise t-test of the methionine levels from media of *E. coli* strains expression the chain elongation pathway with 18 different MAM variants and an empty vector control. p-values shown.

	Empty vector	MAM1	MAM3	IPMS2	L186M	T257N	T257G	T257V	T257D	T257C	T257S	G259P	G259A	A290S	A290T	A290G	GA	GAG
MAM1	0.1316	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
MAM3	0.7101	0.2507	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
IPMS2	0.0254	0.0004	0.5510	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L186M	0.3535	0.0103	0.5755	0.0023	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T257N	0.2301	0.0088	0.1192	0.2755	0.0372	-	-	-	-	-	-	-	-	-	-	-	-	-
T257G	0.8806	0.1727	0.8245	0.0178	0.4355	0.1784	-	-	-	-	-	-	-	-	-	-	-	-
T257V	0.9379	0.1136	0.6532	0.0305	0.3152	0.2609	0.8196	-	-	-	-	-	-	-	-	-	-	-
T257D	0.3792	0.0199	0.2139	0.1591	0.0752	0.7432	0.3045	0.4223	-	-	-	-	-	-	-	-	-	-
T257C	0.6634	0.2773	0.9491	0.0087	0.6195	0.1055	0.7753	0.6080	0.1920	-	-	-	-	-	-	-	-	-
T257S	0.5230	0.3757	0.7885	0.0051	0.7698	0.0700	0.6245	0.4740	0.1332	0.8379	-	-	-	-	-	-	-	-
G259P	0.1362	0.0040	0.0655	0.4266	0.0185	0.7637	0.1024	0.1569	0.5307	0.0572	0.0366	-	-	-	-	-	-	-
G259A	0.0043	4.9e-05	0.0016	0.4823	0.0003	0.0773	0.0029	0.0053	0.0383	0.0013	0.0007	0.1385	-	-	-	-	-	-
A290S	0.4230	0.4693	0.6657	0.0033	0.8977	0.0494	0.5140	0.3799	0.0974	0.7125	0.8695	0.0251	0.0005	-	-	-	-	-
A290T	0.1735	0.0057	0.0862	0.3536	0.0254	0.8680	0.1323	0.1985	0.6218	0.0758	0.0492	0.8930	0.1075	0.0342	-	-	-	-
A290G	0.0920	0.8519	0.1836	0.0002	0.4347	0.0054	0.1229	0.0786	0.0126	0.2048	0.2851	0.0024	2.8e-05	0.3639	0.0035	-	-	-
GA	0.8826	0.0993	0.6039	0.0357	0.2834	0.2909	0.7659	0.9444	0.4632	0.5604	0.4326	0.1776	0.0064	0.3438	0.2232	0.0681	-	-
GAG	0.7299	0.0666	0.4745	0.0552	0.2058	0.3888	0.6206	0.7891	0.5911	0.4364	0.3272	0.2475	0.0106	0.2541	0.3053	0.0446	0.8432	-
GAM	0.3673	0.0189	0.2059	0.1656	0.0718	0.7602	0.2943	0.4096	0.9821	0.1847	0.1278	0.5454	0.0403	0.0931	0.6377	0.0119	0.4498	0.5758