#### **Supplementary Figures and Tables**

**FIGURE S1. Predicted structural features of** *M. sedula* **MCE.** A) Multiple amino acid sequence alignment for MCE from *M. sedula*, *P. shermanii*, *T. tengcongensis*, and hypothetical protein of *Bacillus halodurans* C-125 (PDB: 3OA4). The conserved amino acid residues are shaded black, similar amino acids are boxed, and predicted residues for divalent cation binding are indicated by arrows. B) Predicted structure of *M. sedula* MMCE monomer, based on hypothetical protein BH1468 (PDB: <u>3OA4</u>) from *Bacillus halodurans* C-125, using the ModWeb online server (1, 2). C) The predicted metal binding site of *M. sedula* MCE, identified by comparison with that of *P. shermanii* and *T. tengcongensis* MCEs, metal binding residues were predicted to be H<sup>8</sup>, E<sup>57</sup>, H<sup>84</sup>, and E<sup>134</sup>.

Figure S2. Alignment of amino acid sequences of MCM- $\alpha$  from archaea and bacteria, and other coenzyme  $B_{12}$ -dependent enzymes. The enzymes shown are as follows: MCM- $\alpha$  of *M*. sedula DSM 5348 (MCMa Mse), MCM-a of M. cuprina Ar-4 (MCMa Mcu), MCM-a of S. solfataricus P2 (MCMα Sso), MCM-α of S. tokodaii str. 7 (MCMα Sto), MCM-α of S. acidocaldarius DSM 639 (MCMβ Sac), MCM-α of S. islandicus M.14.25 (MCMα Sis), MCM-α of A. hospitalis W1 (MCMa Aho), MCM-a of V. moutnovskia 768-28 (MCMa Vmo), MCM-a of V. distributa DSM 14429 (MCMa\_Vdi), MCM-a of A. saccharovorans 345-15 (MCMa\_Asa), MCM-a of T. sibiricus MM 739 (MCMa Tsi), MCM-a of T. barophilus MP (MCMa Tba), MCM-a of P. furiosus DSM 3638 (MCMa Pfu), MCM-a of P. sp. NA2 (MCMa Psp), MCM-a of P. horikoshii OT3 (MCMα Pho), MCM-α of T. gammatolerans EJ3 (MCMα Tga), MCM-α of P. abyssi GE5 (MCMα\_Pab), MCM-α of T. onnurineus NA1(MCMα\_Ton), MCM-α of C. sp. Y-400-fl (MCMα Csp), MCM-α of C. aurantiacus J-10-fl (MCMα Cau), MCM-α of C. aggregans DSM 9485 (MCMα Cag), N-terminal of MCM-α of H. sapiens (MCMα Hsa), N-terminal of MCM-α of M. musculus (MCMa Mmu), N-terminal of MCM-a of P. shermanii (MCMa Psh), a-subunit of isobutyryl-CoA mutase of S. cinnamonensis (ICMa\_Sci), a-subunit of glutamate mutase of C. tetanomorphum (GLMa Cte).

**Figure S3. A)** Alignment of amino acid sequences of MCM-β from archaea and bacteria, and other coenzyme B<sub>12</sub>-dependent enzymes. The enzymes shown are listed as follows: MCM-β of *M. sedula* DSM 5348 (MCMβ\_Mse), MCM-β of *A. pernix* K1 (MCMβ\_Ape), *V. moutnovskia* 768-28 (MCMβ\_Vmo), MCM-β of *A. saccharovorans* 345-15 (MCMβ\_Asa), MCM-β of *T. sibiricus* MM 739 (MCMβ\_Tsi), MCM-β of *C. sp.* Y-400-fl (MCMβ\_Csp), C-terminal of MCM-α of *H. sapiens* (MCMα\_Hsa), C-terminal of MCM-α of *M. musculus* (MCMα\_Mmu), Cterminal of MCM-α of *P. shermanii* (MCMα\_Psh), β-subunit of isobutyryl-CoA mutase of *S. cinnamonensis* (ICM β\_Sci), β-subunit of glutamate mutase of *C. tetanomorphum* (GLMβ\_Cte). The conserved amino acids are shaded black, and similar amino acids are boxed. The fingerprint "DXHXXG-SXL-GG" (where X is any amino acid) is indicated by an arrow. The residues H<sup>21</sup>-D<sup>19</sup>-K<sup>15</sup> for the hydrogen-bonding network for coenzyme B<sub>12</sub> binding was indicated by asterisk. **B)** Three dimensional model prediction for MCM-α (**B**) and MCM-β (**C**). The three dimensional model of MCM-α and MCM-β were based, respectively, on MCM (PDB: 2XIJ, *Homo sapiens*) and MCM-β (PDB: 2YXB, *Aeropyrum Pernix*), using the ModWeb online server.

Figure S4. Relationship of 3-hydroxypropionate/4-hydroxybutyrate cycle with the metabolism of branched amino acids (valine, leucine, isoleucine, methionine) and propanoate to central carbon metabolism. Enzymes E1: ACC; E2: MCR; E3: MSR; E4: HPCS; E5: HPCD; E6: ACR; E7: MCE; E8: MCM; E9: SSR; E10: HBCS; E11: HBCD; E12: CCH; E13: ACK; E14: acetate kinase; E15: acetate-CoA ligase; E16: branched-chain-amino-acid transaminase; E17: 3-methyl-2-oxobutanoate dehydrogenase; E18: acyl-CoA dehydrogenase; E19: enoyl-CoA hydratase; E20: 3-hydroxyisobutyryl-CoA hydrolase; E21: 3-hydroxyisobutyrate dehydrogenase; E22: methylmalonate-semialdehyde dehydrogenase; E23: 3-hydroxyacyl-CoA dehydrogenase; E24: acetyl-CoA C-acyltransferase.

## SUPPLEMENTARY TABLES AND FIGURES

TAB	TABLE S1. Primer sequences used for cloning <i>M. sedula</i> MCE (Msed_0639)         and MCM (Msed_0638, Msed_2055)												
Gene Orientation Sequence													
тсе	Forward	5'-GACGACGACAAGATGAAGGGCAACAGTAAAGAAAG-3'											
	Reverse	5'-GAGGAGAAGCCCGGTTAAACAACTTCCACTTTTG-3'											
тст-а	Forward	5'-CCCATTATACCTATTCTCTTCACTTTGCTCTCCTCTGCG-3'											
	Reverse	5'-TGCTCAATTGAGCGATTTTTTCATCCAAGGTCATCCTGG-3'											
тст-В	Forward	5'-GATGGACTGGTGGTGTCGGCTTACTTTGGTGTTAATATGC-3'											
	Reverse	5'-GCATATTAACACCAAAGTAAGCCGACACCACCAGTCCATC-3'											

						le	dentified	l in geno	ome (Y/N	)				
		ACC <sup>1</sup>	MCR <sup>1</sup>	MSR <sup>1</sup>	HPCS <sup>1</sup>	HPCD <sup>1</sup>	<b>ACR</b> <sup>1</sup>	MCE <sup>1</sup>	MCM <sup>1</sup>	SSR <sup>1</sup>	HBCS <sup>1</sup>	HBCD <sup>1</sup>	<b>CCH</b> <sup>1</sup>	<b>ACK</b> <sup>1</sup>
Sulfolobaceae	Metallosphaera sedula DSM	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A <sup>2</sup>	Y	Y	Y
	Metallosphaera cuprina Ar-4	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Acidianus hospitalis W1	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus tokodaii str. 7	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus acidocaldarius DSM	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus Y.G.57.14	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus Y.N.15.51	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus L.S.2.15	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus L.D.8.5	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus M.16.4	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus solfataricus P2	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
	Sulfolobus islandicus M.14.25	Y	Y	Y	Y	Y	Y	Y	Y	Y	N/A	Y	Y	Y
Thermoproteales	Vulcanisaeta moutnovskia 768-28	Ν	N	N	Y	N	Y	N	Y	Ν	N/A	N	Y	Y
	Vulcanisaeta distributa DSM	N	N	N	Y	Y	Y	Y	Y	Ν	N/A	N	Y	Y
Acidilobales	Acidilobus saccharovorans 345-	N	N	N	Y	Y	Y	N	Y	Ν	N/A	N	Y	Y
Desulfurococcales	Aeropyrum pernix K1	Ν	N	N	Ν	Y	Ν	N	Y	Ν	N/A	N	Y	Y
	Ignicoccus hospitalis KIN4/I	N	Y	N	Ν	Ν	Ν	N	Ν	Ν	N/A	Y	Y	Y
Euryarchaeotes	Thermococcus sibiricus MM 739	Ν	N	N	Ν	N	Ν	Y	Y	Ν	N/A	N	N	N
(Thermococcales)	Thermococcus barophilus MP	Ν	N	N	Ν	N	N	Y	Y	Ν	N/A	Ν	Ν	Ν
	Pyrococcus furiosus DSM 3638	Ν	N	N	Ν	N	Ν	Y	Y	Ν	N/A	N	N	Ν
	Pyrococcus sp. NA2	Ν	Y	Ν	Ν	N	Ν	Y	Y	Ν	N/A	Ν	N	Ν
	Pyrococcus horikoshii OT3	Ν	N	Ν	Ν	Ν	Ν	Y	Y	Ν	N/A	Ν	Ν	Ν

# TABLE S2. Enzymes of 3-hydroxypropionate/4-hydroxybutyrate cycle

	Thermococcus gammatolerans		N	Ν	Y	Ν	Ν	Y	Y	Ν	N/A	Ν	N	Ν
	Pyrococcus abyssi GE5	N	N	Ν	N	Ν	N	Y	Y	Ν	N/A	Ν	Ν	Ν
	Thermococcus onnurineus NA1	N	N	Ν	Ν	Ν	Ν	Y	Y	Ν	N/A	Ν	N	N
Chloroflexales	Chloroflexus sp. Y-400-fl	Y	Y	Ν	N	Ν	N	Y	Y	Ν	N/A	Ν	Ν	Ν
	Chloroflexus aurantiacus J-10-fl	Y	Y	Ν	N	Ν	Ν	Y	Y	N	N/A	N	N	N
	Chloroflexus aggregans DSM	Y	Y	Ν	N	Ν	N	Y	Y	Ν	N/A	Ν	Ν	Ν
<sup>1</sup> ACC(Msed_0147	<sup>1</sup> ACC(Msed_0147, 0148, 1375), MCR(Msed_0709), MSR(Msed_1993), HPCS(Msed_1456), HPCD(Msed_2001), ACR(Msed_1426), MCE(Msed_0639),													
MCM(Msed_0638, Msed_2055), SSR(Msed_1424), HBCS, HBCD(Msed_1321), CCH(Msed_0399), ACK(Msed_0656).														
<sup>2</sup> N/A: No information is available.														

	TABLE S3. Compar	isons of putativ	/e gene	e clusters	s containin	g MCE, MCN	/l in m	icrobial genomes	
	Organism				Genetic	constitutio	n		PF <sup>1</sup>
Sulfolobaceae	Metallosphaera sedula DSM 5348	0637	0638	- 0639	- 0640	0641		2054 2055 2056 2057	AB <sup>2</sup>
	Metallosphaera cuprina Ar-4	1515	1516	- 1517	1518	1519		0235 0234 0233	
	Acidianus hospitalis W1	2215	2216	- 2217	- 2218	2219			
	Sulfolobus tokodaii str. 7	0551	0552	- 0554 -	- 0555 0	556		2096 2097 2098	
	Sulfolobus acidocaldarius DSM 639	0925	0924	0923	- 0922	0921		0062 0061 0060	
	Sulfolobus islandicus	0218	0219	0220	- 0221	0222			
	Sulfolobus islandicus Y.N.15.51	2821	2822	2823	- 2824	2825			
	Sulfolobus islandicus L.S.2.15	0245	0246	0247	- 0248	0249			
	Sulfolobus islandicus L.D.8.5	0219	0220	- 0221	- 0222	0223			
	Sulfolobus islandicus M.16.4	0233	0234	0235	- 0236	0237			
	Sulfolobus solfataricus P2	2423	2424	2425	2426	2427		2267 2266 2265 2264	
	Sulfolobus islandicus M.14.25	0214	0215)	0216	- 0217	0218			
Thermoproteales	Vulcanisaeta moutnovskia 768-28	<mark>0924</mark>	0925	0926	0927				B <sup>2</sup>
	Vulcanisaeta distributa DSM 14429	0036	0037	0038	0039	0040			
Acidilobales	Acidilobus saccharovorans 345-15	1077	10	1079					

Desulfurococcales	Aeropyrum pernix K1	1687 1686 1683
Euryarchaeotes	Thermococcus sibiricus MM 739	
(Thermococcales)	Thermococcus barophilus MP	
	Pyrococcus furiosus DSM 3638	
	Pyrococcus sp. NA20788	
	Pyrococcus horikoshii OT3	
	Thermococcus gammatolerans EJ3	
	Pyrococcus abyssi GE5	
	Thermococcus onnurineus NA1	
Chloroflexales	Chloroflexus sp. Y-400-fl	1995 2705 2706 3283 0049 0048 BC <sup>2</sup>
	Chloroflexus aurantiacus J-10-fl	
	Chloroflexus aggregans DSM 9485	2545 1348 1349 0586 0587
	> 🗪	
Phosphoribosyltr	ansferase Methylmalonyl-CoA e	pimerase Methylmalonyl-CoA mutase ZPR1-related zinc catalytic subunit Einger protein Signer Pro
Hypothetical	protein Methylmalonyl-C decarboxylase	oA Glucose-6-phosphate isomerase Ribosomal protein Amino acid transporter LAO/AO transport system ATPase
<sup>1</sup> PF: propose	ed function;	
<sup>2</sup> A: Autotroph	nic carbon fixation through 3	-hydroxypropionate/4-hydroxybutyrate cycle; B: Metabolism of branched amino acids (valine, isoleucine,
methionine) a	and propanoate. C: Autotrop	phic carbon fixation through 3-Hydroxypropionate bicycle.

	Organism	MCE (Msec	L_0639)	MCM-a (Mse	ed_0638)	MCM-β (Ms	ed_2055)					
		Gene	Identity	Gene	Identity	Gene	Identity					
		symbol	(%)	symbol	(%)	symbol	(%)					
Sulfolobaceae	Metallosphaera sedula DSM 5348	Msed_0639	100	Msed_0638	100	Msed_2055	100					
	Metallosphaera cuprina Ar-4	Mcup_1517	91	Mcup_1516	93	Mcup_0235	86					
	Acidianus hospitalis W1	Ahos_2217	67	Ahos_2216	83	Ahos_0509	78					
	Sulfolobus tokodaii str. 7	ST0554	74	ST0552	82	ST2096	76					
	Sulfolobus acidocaldarius DSM 639	Saci_0923	64	Saci_0924	79	Saci_0062	74					
	Sulfolobus islandicus Y.G.57.14	YG5714_0220	66	YG5714_0219	79	YG5714_0078	76					
	Sulfolobus islandicus Y.N.15.51	YN1551_2823	66	YN1551_2822	79	YN1551_0076	76					
	Sulfolobus islandicus L.S.2.15	LS215_0247	65	LS215_0246	79	LS215_0076	76					
	Sulfolobus islandicus L.D.8.5	LD85_0221	66	LD85_0220	78	LD85_0076	76					
	Sulfolobus islandicus M.16.4	M164_0235	66	M164_0234	79	M164_0076	76					
	Sulfolobus solfataricus P2	SSO2425	64	SSO2424	78	SSO2266	79					
	Sulfolobus islandicus M.14.25	M1425_0216	65	M1425_0215	78	M1425_0076	76					
Thermoproteales	Vulcanisaeta moutnovskia 768-28	VMUT_0926	43	VMUT_0924	61	VMUT_0925	63					
	Vulcanisaeta distributa DSM 14429	Vdis_0039	42	Vdis_0037	61	Vdis_0038	59					
Acidilobales	Acidilobus saccharovorans 345-15	N/A	N/A	ASAC_1077	57	ASAC_1078	61					
Desulfurococcales	Aeropyrum pernix K1	N/A	N/A	APE_1687	57	APE_1686	63					
	Ignicoccus hospitalis KIN4/I	N/A	N/A	N/A	N/A	N/A	N/A					
Euryarchaeotes	Thermococcus sibiricus MM 739	TSIB_1401	43	TSIB_0812	61	TSIB_1402	59					
(Thormospecies)	Thermococcus barophilus MP	TERMP_1057	45	TERMP_1292	61	TERMP_1059	58					
(Thermococcales)	Pyrococcus furiosus DSM 3638	PF1948	46	PF1477	62	PF1946	60					
	Pyrococcus sp. NA2	PNA2_0788	48	PNA2_1880	62	PNA2_0709	61					

## TABLE S4. Methylmalonyl-CoA epimerase and methylmalonyl-CoA mutase homologs

	Pyrococcus horikoshii OT3	PH0272	48	PH1306	61	PH0275	61
	Thermococcus gammatolerans EJ3	TGAM_1929	46	TGAM_1685	61	TGAM_1931	55
	Pyrococcus abyssi GE5	PAB2438	48	PAB1800	62	PABmcmA2	61
	Thermococcus onnurineus NA1	TON_1074	45	TON_1110	61	TON_1076	63
Chloroflexales	Chloroflexus sp. Y-400-fl	Chy400_3283	39	Chy400_1995	53	Chy400_0048	56
	Chloroflexus aurantiacus J-10-fl	Caur_3037	39	Caur_1844	53	Caur_0042	56
	Chloroflexus aggregans DSM 9485	Cagg_0981	41	Cagg_2545	52	Cagg_0587	56

TABLE S5.	TABLE S5. Transcription analysis of gene cluster of MCE (Msed_0639), MCM (Msed_0638, Msed_2055) for <i>M. sedula</i> under													
	autotrophic (AC) and heterotrop	ohic (HT) cond	itions.											
	Appotation	Transcription	Transcription	Fold change <sup>3</sup>	Significance <sup>4</sup>									
	Annotation	level AC <sup>1</sup>	level HC <sup>2</sup>	Fold change	$(-\log_{10} P \text{ value})$									
Msed_0637	Phosphoribosyltransferase	-0.31	0.24	0.68	1.58									
Msed_0638	Methylmalonyl-CoA mutase-catalytic subunit (α)	4.36	1.21	8.91	15.48									
Msed_0639	Methylmalonyl-CoA epimerase	3.16	1.00	4.47	6.54									
Msed_0640	Heat shock protein Hsp20	2.74	0.88	3.63	7.13									
Msed_0641	ZPR1-related zinc finger protein	0.67	1.01	0.79	0.71									
Msed_2054	Hypothetical protein	-0.26	1.37	0.32	5.26									
Msed_2055	Methylmalonyl-CoA mutase-coenzyme $B_{12}$ binding subunit ( $\beta$ )	3.14	1.52	3.08	3.97									
Msed_2056	LAO/AO transport system ATPase	1.83	-0.77	6.05	9.58									
Msed_2057	Hypothetical protein	-0.05	-1.88	3.57	5.64									
<sup>1</sup> Lea: <sup>2</sup> Lea: <sup>3</sup> Fold <sup>4</sup> Bon	<sup>1</sup> Least-squares mean (Ism) of normalized log2-transformed transcription levels; AC: Autotrophic condition <sup>2</sup> Least-squares mean (Ism) of normalized log2-transformed transcription levels; HC: Heterotrophic condition <sup>3</sup> Fold change = 2 <sup>(AC-HC)</sup> <sup>4</sup> Bonferroni correction for this data set was 5.4													



**FIGURE S1. Predicted structural features of** *M. sedula* **MCE.** A) Multiple amino acid sequence alignment for MCE from *M. sedula, P. shermanii, T. tengcongensis*, and hypothetical protein of *Bacillus halodurans* C-125 (PDB: 3OA4). The conserved amino acid residues are shaded black, similar amino acids are boxed, and predicted residues for divalent cation binding are indicated by arrows. B) Predicted structure of *M. sedula* MMCE monomer, based on hypothetical protein BH1468 (PDB: <u>3OA4</u>) from *Bacillus halodurans* C-125, using the ModWeb online server (1, 2). C) The predicted metal binding site of *M. sedula* MCE, identified by comparison with that of *P. shermanii* and *T. tengcongensis* MCEs, metal binding residues were predicted to be H<sup>8</sup>, E<sup>57</sup>, H<sup>84</sup>, and E<sup>134</sup>.

		α1	η1	β1 β2	η2			β3	α2	β4	α3	η3	α4 
	30	40 5	a 1111	- TT -	AAA	80 90	100	110	120	130	140	150 10	60 170 180
MCMa Hsa	LIOORLLHO	OOPLHPEWAALARN	OlkgknpEdli	WHTPEGISIK	PLYSKRD	THD LPEELPGVRPP	TRGPYPT ((YTP)	R PWT I RQYAG	FSTVERSNRFTI	KD NIKA GOOGUSV	AFULARHRGY	DSDITPRVRGDVG	AGVAIDT. VEDTKI LEDGIELE
MCMa_Mse	NVTPERVKE	WE SKYLOPWISKRK	ERENEPTTPSC	IBIKTLYTPL	<b>DL</b>	DYEERIGPPGEYPY	TRGIYPINYRG	RIWTIRQYAG	FGSAEDTRARFS	RKLLEACOTGEST	AFULPTOLGL	DPDITELAYTEVG	VVGVSMPH.WREMDIVTNQIPLN
MCMa_Mcu	NVTQERVNE	WEREYLNPWLAKER	ERKVEPTTPSC	IEVKSLYTPL	DL	DYEERVGPPGEYPF	TRGIYPIIMYRG	RIWTIRQYAG	FGSAEDTRIRFI	KKLLEAGOTGLST	AFULPROLGL	DPDNDLAYTEVG	VVGVSMPH.WREMDLVTIGIPLI
MCMa_Sso	NDVEDRIKE	WEEKVY 55WVKKRG	ERKKEPKTPSC	IHIKPVYTPL	DV	SVARETGPPGEYPF	TRGITPHNIRG	RIWTIRQIAG	POSAEETRS RFI	RELIGNED	A FULP CLGL	DPDHELAYTEIG DPDHTLAFTEVC	VVGVSMPH.WKEMDIVKSGIPLD
MCMa_Sto	DELLBESE	WEBEVLEPWISKEP	REFUTE TAPSO	TLVEBLYTPL	DQ	DYLSKLGPPGEYPY	TRGIYPHMYRG	RLWTIRQYAG	YGSAEDTNYRFI	RKLLEAGOTGISM	AFULPHOLGL	DPDHKLAFTEVG	VVEVSLPH.WKEMDLVKSDIPLO
MCMa_Sis	NDIEDRIKE	WEETVYLSWVRKRG	ERKKEFKTFSG	IHIKPVYTPL	DV	NYMERLGLPGEYPF	TRGIYPINYRG	RIWTIRQYAG	FGSAEETISRFI	RKLLEAGOTGISM	AFULPROLGL	DPDHELAYTEVG	VVGVSMPH.WREMDMVKSGIPLD
MCMa_Aho	NDIDERIKE	WINLYTS.WIAKRK	ERRORFITFSC	IEVKPLYTPL	DL	NYVDRIGPPGMYPP	TRGIYPHMYRG	RIWTIRQYAG	FGSAEDTRLRFI	RKLLEAGOTGUS	AFULPROLGL	DPDQELAPTEVG	VVGVSMPH.WREMDLVMNQIPMD
MCMa_Vmo	DKIKEKYDE	WVREFLLFTLKKVP	EWR.KPITSPO	VEIKPLYTPL	DVKD	BYLDELGPPGEYPL	TRGITPSMIRS	RIWTPREISG	POSPEDICKRI	KPLISOCOTONSV	AFULPHOLGL	DPDHELAYPEVG DPDHELAYPEVG	KVEVSVPE.VVSNSLLPDDIDIS
MCMa Asa	KKISDKASE	WERTTLOOWLORLE	EROOBFTTLSL	IPIKEVYTPA	DIP	DYMERLGLPGEYPF	TRGINATMYRA	RLWTHRMFSG	YGSPEDTRERLI	KF LIEHGETGISI	AFMYPALVGI	DPDDPMAEGEVG	IVEVSVPT. IVDMEVVPDGIDMG
MCMa_Tsi	EEIKKTEEE	WHERTVEPPIAKEP	ERKEKFMTDDG	FEIKRTYTFA	DL.E	DYLERLNPPGQYPF	TRGVYATMYRG	RLWTHRQYAG	FGTAEESNKRYI	KY LLEQ <b>G</b> QTG <b>L</b> SV	AFULPACIGY	DSDHPMAEGEVGI	KVGVAIDS.LKDMEILPDGIPLD
MCMa_1ba	DEIRKAEQE	WEENVVKPLIAKRP	ERKEKFMTDDG	FEIKRVYTFA	DLGEDW	DYMERLGPPGQYPF	TRGVYATMYRG	RFWTMRQYAG	YATAEESNKRYI	KYLLEOCOTGUSV	AFELPROLGY	DSDHPMAEGEVGI	KVGVAIDS.LWDMEILPDGIPLD
MCMa_Psp	AKIREEEKF	WEETTVKKFLEKAP	ERKEKFMTDDG	PEIKRIYTPA	DLGEDW	NYMERLGPPGEYPF	TRGVYATNYRG	RIWTHROYAG	YATABESRERT	KYLLSOCOTG SV	AFULPHOLGY	DSDHPLAEGEVGI	KVEVALDS.LWDMELLPDGIPLD
MCMa_Pho	AKIREEEKF	WEETTVKKFIEKRP	ERKEKFMTDDG	FEIKRLYTPA	D LGE D W	DYLERLGPPGEYPF	TRGVYATMYRG	RFWTMRQYAG	YATAEESNKRYI	KY LLEOGOTGE SV	AFULPACLGY	DSDHPMAEGEVGI	KVGVAIDS. LWDMRILPDGIPLD
MCMa_Tga	KK I KEEEK	WEETTVEEFLEKAP	ERKERFMTDDG	FEIKRIYTFA	DLGE	DYLERLGPPGEYPF	TRGVYATMYRG	RIWTKRQYAG	YATAEESNKRYI	KYLLSQ <b>G</b> QTG <b>L</b> SV	AFULPACLGY	DSDHPLAEGEVGI	KVGVAIDS.LWDMRILPDGIPLD
MCMa_Pab	KK I REEEKF	WEETTVEEPLEKAP	ERKERPMTDDG	PEIKRVYTPA	DLGEDW	DYMERLGPPGEYPF	TRGVYATMYRG	RIWTHRQYAG	YATA EESNIKRYI	KYLLSOCOTOUSV	AFELPROLGY	DSDHPLAEGEVGI	KVGVAIDS.LWDMEILPDGIPLD
MCMa Csp	RAIKQABBE	WEEKVVKPLIAKRP	ERKEKPMTDDG	PELKRVYTPA	DLTEDGETLTD	HFLENIAYPGOYPF	TRGIHFTGYRG	KLWTHRMFAG	FGSAEETNARFI	KY LLEOGOTG SI	APMAPPUTYGE	DTDHPLVBGBVG	KCGVAVISS LADMET LLAD VPLD
MCMa_Cau	BOLAAAHEC	WEOOCLWFALRRTF	ERSGPFMTTSS	APIERLYTPL	DLTRDGETLTD	HFLENIAYPGQYPF	TRGIHPTGYRG	K LWT: RMFAG	FGSAEETNARFI	KY LLEOGOTGESI	AFOMPALYGR	DTDHFLVEGEFGI	CCVAVSS. LADMEILLAD LPLD
MCMa_Cag	BOLHAAQQ	WEQQCLWPTLKRTP	ERPGPPMTTSS	APVERLYTPL	DLATHGQSLTE	HFLHNIGYPGQYPF	TRGIHPTGYRG	KLWTHRMFAG	FGSAEETNARFI	KF LLEQCOTGESI	AFOMPALYGR	DTDHPLVEGEFGI	KCGVAVSS.LADMEILLDGLPLD
MCMa_Mmu	RWERLLH	QQPLHPEWAVLARK	QLEGENPEDLI	WHTPEGISIK	PLYSRAD	TLDLPEELPGVKPF	TRGPYPTMYTY	RPWTIRQYAG	PSTVEBSREPT	KDNIKAROOGUSV	AFULANHRGY	DSDITFRVRGDVG	WAGVAIDT. VEDTKILFDGIPLE
ICMa Sci	LPRPDSVDI	GIIAPVPADAAQRPE	ELAAKAGTEEA	WETAEQIPVG		DRDWEDTINGIFFF		RTWTIROFAG	FGNAEOTNERYI	KNILANGGGGISV	APMAPHINGE	DSDDPRSLGRVG	HCGVAIDS A ADMEVIERD TPLO
GI Ma_Cte	MELKNEP	WT DEEP PROREEVL	KOWPTGREVDI	QEAVDYLE			ADKLVRAKEAG	ITLAOPRAGY	ALLDEHINLLRY	LODEGGADLEPS	TIDAYTRONE	YEECEIGIKESE	RAGRSLLIGFFGVIHGVRGCRKV
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MCMa llas	VMCUCMTMU	200	219 RECOVER STR	220	230		260 Rokressor	270		250			
MCMa Mse	KVSTSMTIN	TANELLISMYVATAE	RARGVERERIT	TTONDILKEN	TARENTTIPPE	PSMRVATDIFEITA	KNTPKWHPTST	SCYNTREAGA	DEVLEVARTIN	DGLEISRIGLQAG	G. LTIDEFAPE.	LSPPRSCVTNLPI	REVEKTEA ARRAWARDIEKREDEK
MCMa Mcu	KVSTSMTIN	TAKE LLSMY AAVA H	ESRGVSLTEID	TVONDILKEY	TARENTITPPE	SMRYAIDIIEYSYI	KHIPKWHPISI	SCYHIREAGA	DULEVAFTL	DGIEYVRETLER	G. IFVDDFAPT	LSFFFAGYTNLFI	EEVEKFRA ARRMWAE IN RDEFN AK
MCMa_Sso	KVTTSMTIN	TAKELLSMLIATSE	ESRNINK SVLD	TVQNDILKEY	TARENFIYPPS	PSMRYAIDIIEYSAI	K Y LP K WHP I S I	SCYHIREAGA	DEVLEVAFT LE	DGMEYVRRTMER	G. INVDEFAPH	LSFFFAArsDIFI	EEVAKFRA ARRMWAR IMKEVFU AK
MCMa_Sto	KVTTSMTIN	A TALE LLSMY VATAE	BARGIDKKVLD	TVQNDILKEY	IAR ENFLYPPE	PSMRYAIDLIEYSAI	KHIPKWYPISI	SHYHIREAGA	DHILEVAFT LH	DGIEYVRETMER	G. IPVDEFAPK	LSFFFAGYTNIFI	EEVA KPRA ARRMWAR IM KEMPG AK
MCMa_Sis	KVSTSMTIN	TANELLSMITATTE	RSRNINKHVID	TVONDILKEY	TARENFITPPS	PSMRYAIDIIEYSAI	KYLPKWHPISI	SAYHIREAGA	DAVLE VAFT LA	DGIEIVRATIER	G. ISVDDFAPK	LSPEPAATTALEI	EEVEKPEA ARRAWARTOKEMPU AK
MCMa_Aho	KVTTSMTIN	A TAME LMSMY IATA P	ESRGIDKKVLD	TVONDILKEY	TARENFLYPPE	PSLRYAIDLIEYSYI	KHIPKWHPISI	SCYHIREAGA	DVLEVAFTLE	DGIEYVRKTLER	G. INVDDFAPT	LSFFFAGYTNIFI	EEVEKPRAARRMWAE IM KEEFFITAK
MCMa_Vmo	RITTSFTIN	ATAABILSMYITVAB	ESRGIDKAVLD	TIQNDILKEN	TARNLYIYPPI	HSMRYTTDIIAYTSI	KHLPKWHPISI	SCYHFREAGA	TOVOE LAFT LO	DAIEYTNWVINRU	WRISVDDPAPG	LSFFFAATTNLFI	EEISKFRAARRLYARIMKERFGAR
MCMa_va/	KITTSFTIN	A TARELLSMY ITVAE	ESRGIDKAVLD REOGVEV SOLG	TIONDILKER	MAGESVVPPP	PAVKUANDITRWSVI	KULPKWHPISI	SCYNTREAGA	THVOR LAFT LA	DAIEYTNWVINRU	WENTVDDPAPG.	LSFFFAATTNLFI	EEVMKFRAARRLYARIMKERFGVK PPTHKPDAADDMWARTMDDRPDASK
MCMa_Tsi	KVSTSMTIN	TAANLLAMYILVG	HOGVFODOLR	TVONDVLKEY	IARGTYIFPPC	PSMRLTTDIIMYCAI	EHVPKWISISI	SGYHIREAGA	NOVOE VAPT LO	DGIEYVKAVIAR	G. ND VDKFAPR	LSFFFIAHINFLI	EEISKFRAARRLWARIMKERFIJAK
MCMa_Tba	KVSTSMTIN	STAAN LLAMY I LVA	EFQGVPQHVLR	TVQNDILKEY	IARGTYIFPPG	PSMRLTTDIIMYCAI	BHVPKWNPISI	SCYHIREAGA	MOVOEVAPT LO	DGIEYVKAVIER(	G. ND VDKPAPR	LSFFFNAHNNFLI	EEIAKFRAARRLWARIMKERFGAK
MCMa_Ptu MCMa_Psp	KVSTSMTIN	A TAAN LLAMY I LVA P	BEOGVEORVIR	TVONDILKEY	IARGTYIF PPC	PSMRLTTDIIMYCAI	ENVPENNPISI	SCYHIREAGA	TEVOEVAFTLE	DGIEYVKAVIER	G. ND VDKFAPR	LSFFFAAHINFLI	EEIAKFRAARRLWAYIMKEWFUAK
MCMa_Pho	KVSTSMTIN	TAAH LLAMY I LVAP	EFOGIPOEKIR	TVONDILKEY	TARGTYIPPPC	PSMRLTTDIIMYCAI	ENIPEWNSISI	SEYHIREAGA	UNVORVART IN	DGIEYVKAVIER	G. NEVDEPAPE	LS FFF TAHTNE LI	E E E K F BA A B B LW AY IN KEW FU AK
MCMa_Tga	KVSTSMTIN	ATAANLLAMYILVAR	EEQGVPQEKLR	TVONDILKEY	IARGTYIFPPO	PSMRLTTDIIMYCAI	ENVPKWNPISI	SCYHIREAGA	VOE VAFT L	DGIEYVKAVIER	G. ND VDEPAPE	LSFFFAAHINFLI	EEISKFRAARRLWAY IM KEMPU AK
MCMa_Pab	KVSTSMTIN	A TAAN LLAMY I LVA H	BEQGVPOHVLR	TVQNDILKEY	TARGTYIFPPC	PSMRLTTDIIMYCAI	ENVPKWNPISI	SCYHIREAGA	MEVOEVAFT LE	DGIEYVKAVIER	G. HD VDKFAPR	LSFFFAAHINFLI	EEIAKFRAARRLWAYIMKEMF11 AK
MCMa_Csp	AVSTSMTIN OVSTSMTIN	TAAN LLAMY I LVA B	ELOGVEP EQLE	TVQNDILKEY	LARGTYLF PPC	PSMRLTTDIIMYCAI	BHVPKWNPISI BHVDOWNPISI	SOTHIREAGA	THUCE VAFT LO	DGIEYVKAVIER(	G. ND VDEFAGE	LSFFFIAHINFL	EEIMKYNA ARRLWAYIN KEWPUAK
MCMa_Cau	QVSTSMTIN	PARIMANYLVVA	EFRGIPWSOLR	TIONDILKEY	IAQUEYIFPPE	PSMRLVVDTIEFAAI	RHVPQWNPISV	SCYHIREAGS	TOVOE LAFT 1	DGFAYVEAALER	G. LD IDEFAPE	LSFFFIAHIDFFI	EEINKYNA ARRIWARAM RERYGAK
MCMa_Cag	QVSTSMTIN	PAAMIWANY LVVA	EFRGIPWSKLR	TIQNDILKEY	IAQUETIFPFE	PSMRLVVDTIEFATI	RHVPQWNPISV	SCYHIREAGS	TAVOE LAFT LA	DGFAYVEAALER	G. LD IDEFAPR	ISFFFIAHNDFFI	EEINKYNA ARRIWARAM RERYGAK
MCMa_Mmu	KMSVSMTMN	3 AVIPVLATFIVTGE	EEQGVPREKLT	TIQNDILKEN	MVRNTYIFPPE	PSMKIIADIFQYTA	QHMPK PIISISI NUMPK PIISISI	SEY HMOEAGA	DAILE LAYT IN	DGLEYCRIGLOA	G. LT I DEFAPR	LSFFWGIGMNFY	MEINKMURAGRRLWAHLIEKMPOPK
ICMa Sci	DVTTSMTT	PAUP VPCMY LVAA	REGGVICP EQUA	TLOTDIFKEY	LAOKEWLFOPE	PHLRLIGDLMBHCAI	RDIPAYEPLSV	SCYHIREAGA	TAAORLAYTIN	DGVDYIRAGESV	S. LIVDOFAPR	LSFFRGIGNEF	RETEKPENA ARKLWARLYHOPG. PK RETEKPENA ARRTWARWI, RDRVIG SM
GLMa Cte	LESVNLPLQ	RHGTPDSRLLAEII	LEAGGWT SNEG	GISYNIPYAH	SVPIDECLEDW	YCDRLVGFYEEOGT	VHINREFFGPL	TGT LVPPSMS	NUSITEALLA	AEQGVENITVGY	G	ECGNML	ODIALEC LEEQT NEYLKAYG Y
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MCMa_Hsa	GVNKYQLE KEDAVEVLAID	11TSVR11RQIEKLKKIKSS	DOALABHCLABALGL	TVKSARIARNTQIIIQE E	SGIPEVAD	PWGGSYMMECLTNDVYDAALKLINEIEEMG.	
MCMa_Mse	GVNMSYEPDWIGTTEVPRV	<b>HPEIRERVLTRLKKYRSE</b>	DQMKVRDSLMBAVAL	SEKAAKIAIRVQQIVAYE	SGSTETVD	PLAGSYYVBWLTDEIEERAWKIIERVEGMG.	
MCMa_Mcu	GVNMSYEP DWIGTTEVFRV	RFEVRERVISRLKNYRSE	DEMKVRDSIMBAVAL	SEKAAKIAIRVQQIVAYE	SGSTETVD	PLAGSYYVEWLTDEIEERAWKIIERVEGMG.	
MCMa_Sso	GVNMYYEP EWIGTTEIPRV	HPEVRERVI SRLKKYKQE	DEMKLRESLINDALAL	TEKAAKIAIRVQQIIAmE	SGAADVVD	PLGGSYYIBWLTDEIEERAWKIID@VEKMG.	GMIKAIEnGYPQAQI
	GVNRFYEP DWIGTTEVPRV	TPEVRIRVLERLKKYRSE	DEIKWRDSLINBALAL	SEKAAKIAIRVQQIIAYE	SGAADTID	PLAGSYYIDALTDEIEEKAWKIIEKIESMG.	
MCMa_Sis	GVNRITEP DWIGTTEVPRV	HPLYRDRILORLARYKKE	DITSKVEGSLSBALGL	STERAARIAIRV QQVIAH E	SGATDTID	PIAGSYYVIWLTDEIEEHAWKILYDIERMG.	GMMKAIEVEYPQAQI
MCMa Abo	GUNRAVEC DETGTTETERV	MPRAKERAL SKIKKIKOR	DUTKSKD CLEVELT AL	STERAARIAIRV QQIIAIIE:	SGAADIVD.	PLOGSYTIM LTDEIEERAWKIIDQVERMG.	GRIKALENGYPQAQI
MCMa Vmo	GUNWER PETTICE	TPUCDEDCT KDVDD1/DDN	DEPARTES INTELLE	TERSORIALE ALEVOOUTAVE	SGAT BTVD.	PLAGSIIISWLTDEIEERAWKVIDHIEKMG.	GUT KAURAURA
MCMa_Vdi	GUNNERS PRETATELARY	DPUSDPDCT KDVDPUDPS	DE PARPES LITINAT. AL	TERSTRIALEVOOVIAVE	SGVIDSID.	PLOGSIIIIMATUTIEEEVONIIDITUKIG.	CUT KAVEIGIPORAL
MCMa_Asa	GUNIFTENE VEDVEKVPLLEFD	OCELEKKOKORIAOVRSM	DOORWSBALDBPPPV	SEPAAKTALETOOTTAVE	CV2 DAID.	PLOGSTITEMETDITEBES WIRTIDITER.	GWTR AVELOTPORET
MCMa_Tsi	GVNEFIVDEPLDVEILKV	DPSIRDKOI ERLKKLRSE	DITKKVEBALITEALSL	TEKSVRIALRT QQIIAY R	SGVUDTID	PLOGSYYIEWLTDHIEREAMKYIEKIESMG	GNNKAIREGYTOKEI
MCMa_Tba	GVNRFVVDEFIEVEILKV	DPSIRDKOIERLRK LRSE	DIKKVEBALDBALSL	TEKSVRIALRT QQIIAY E	SGVVDTID	PLOGATYIDWLTDHIEEEAMKYIEKIERMG	GMMRAIERGYIOKEI
MCMa_Pfu	GVNRFVTDEPIEVEILKV	DPSIREKOIERLKKLRSE	DITKKVEBALDBALSL	TEKSVRIALRT QQIIAY R	SGVUDTVD	PLOGAYYIDWLTDHIPERALKYIBEIEEMG	GMMBALERGYVOKEL
MCMa_Psp	GVNAFVTDEFIEVEILKV	DPSIREKQIERLKKLRSE	DURKVQEALDBALSL	TEKSVRIALRT QQIIAY	SGVVDTVD	PLGGAYYIEWLTDHIYEEALKYIEKIQKMG	GMMRAIER YVOREI
MCMa_Tap	GVNRFQTDEFIEVEILKV	DPSIREKQIERLKKLRSE	DSKKVERALDBALSL	TEKSVRIALRT QQIIAY E	SGVVDTVD	PLGGAYYIEWLTDHIYEEALKYIERIQRMG.	GMMRAIERGYIQKEI
MCMa_Pab	GVNRFVTDEPIEVEILKV	DPSIRDKQIERLKKLRSE	DITKKVEEALDEALSL	TEKSVRIALRT QQIIAY E	SGV[VD]TVD:	PLGGAYYIEWLTDHIPEEALKYIERIQKMG.	GMMRAIERGYVQKEI
MCMa_Tab	GVNAFVSDEFIEVEILKV	DPSIREKQIARLKKLRSE	DIKKVOETLDBALSL	TEKSVRIALRT QQII AY E	SGV VD TVD:	PLGGAYYI 🖸 🛛 LTDHIYEEALKYI BKI QKMG.	GMMRAIERGYIQREI
MCMa_Csp	GVNEFIVDEFLDVEILKV	DPSIREKQIERLKKLRSE	DURKVEBALDBALSL	TEKSVRIALRT QQIIAY E	SGV VD TID:	PLGGAYYI 🖸 🛚 🛛 LTDH IYEEA LKYI BRI QRMG.	GMMRAIERGYIQREI
MCMa Cau	GVNAFQDDBFLTIFILQM	DPEGEKRHLERLNRVRRE	DOALVARRIANALAL	SEKAVTIALRTQQIIAYE	SGVANTVD	PLGGSYFVDALTDRMEREAQQIFDAINAQG.	GVIAAIRnGYYHREI
MCMa Caa	GVNAFODDEPLTIPILON	DPEGEKRHLERLNRVRRE	DOALVARRIADALAL	SEKAVTIALRT QQIIAY E	SGVANTVD	PLGGSYFVEALTDRMEREAQQIFDAINAQG.	GVIAAIRnGYYHREI
MCMa Mmu	GUNAFOADEPLEIPILON	THE GERRENT BELLARVERED	DODLVARRIADALAL	SEKAVTIALRT QQIIAYE	SGVANTVD	PLOGSYFVDALTDRMEREAQQIFDAINAQG.	GVIAAIRMCYPHREI
MCMa Psh	GUNRIQLE REDSVEVIAID	ITSVERIOI BELERIKSSE	DOALABOCISINALGI	TVRSARIARNT QITT QE E	SGIPKVAD	PWGGSYMMOSSLTND VYEAALKILIYEVEEMIG.	GKAKAVAEGIPKLRI
ICMa Sci	GVNRIRLE HEFFLDVLRVD	CURVED BOUNDIACOVOD	DESCRIPTION OF THE	STDFSARIARNTQLFLQOE	SGTT RVID.	PWSGSAYVBELTWOLLARKAWGHLIQEVERVG.	GRAKALEKGIPKNRI
GI Ma Cte	AGENMEUR DULGCURY	TERGNUDETERTKNVNDE	LA PRAKE P CRIMAT GT	TKRANA SCIKATKNA Lu	LOVANVAD.	PLOGS WIINGLIDKIERDAEKIFEQIKERGE	RACEDGORFIGFITSGILRGIEDGWFTGEI
OLING_OIE	HOMPH TR	DECH TELEBORN INKE	Burning a DK DKI OT	INDIANOSIKAIKAADA .	, п цво <u>о</u> .	MULLES VETEL BURNT TWEET VETER VETER TRE	

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	470*	480	490	- *		500		51%		520		530		54	o.		55	P.	561	P.	570		580
MCMa_Hsa	EECAAR	RQARIDSG	SEVIVGVN	KYQLE	R	EDAVE	V LA I D	NTSVR	HRQI	EKTKK	IKSS	DQALA	EHCL	ALTE	CAASG	DG	. HILS	а ња 🛛 в з	SRARO	TVGEI	TDALK	«VpGEн	(KAND RI
MCMa_Mse	AESAYR	LOKKIEEG	EMIRVGVN	KSYEP	D	WIGTTH	EVPRV	HPEIR	ERVL	TRLKK	YRSE	DONKV	RDSLA	TA LRE	AAENP	SVILPP		. YVLD3	IKRGO	TVGEI	SSTLR	B I WG B Y	KEPIII
	AESSYR	LOKKVEEG	DMIRVGVN	MSYEP	D	WIGTTI	EVERV	RPEVR	ERVI	SRLKN	YRSE	DEMKV	RDSIN	IS LRR	AAESP	STHLFP		. YVLD3	IKKGO	TVGEI	SGTLR	BINGEY	KEPIII
	AESAIN	TORRIEEG	DLGKVGVN	RITEP	<b>E</b>	WIGTTI	RIFRV	TPEVR	BRVI	BDIKK	TROB	DERKI	RESLA	NLRE	IAEKE	IEIILFF		YMID3	IRAG	TVGET	SGVLR	DINGEY	KEPSI
MCMg_Sco	ABSAIN	TOKRIESG	DICKVGVN	NUT		WIGTT	BVPRV	TPEVR	DDTL	ODIAN	TRSE	DELKW	RUSLI	DIRE	AAEKE	TEILPP		. YILHS	IKAG	TVGEI	SGTLR	BINGEY	REPSI
MCMa_Sis	ABSSIN	TOKETEGE	DLORVGVN	WVVPP		WIGTTI		TELVE	PDUT	GRINK	VROP		BOSLO	NIDE	AADKE			. YILDS	TRSG	TVGEV	SSVLR	LWGEY	KEPSL
MCMa Aho	ARSSYR	LOKRIERG	DITENCOVN	PAVES	B	WIGTT	BTPRV	TPAVE	BBVT	SRIKO	VKEN	DUTK	KDSTA	K L DEC	AARG			vyl.na	TEAG	TTGET	SSVER	UNGRY	KEPSI
MCMa_Vmo	AESAYR	YOKMVERG	BIAVIGVN	FRE		RELHIN	FRE	DPVSR	BRSI	KRVRE	UREN	DEEAW	REALD	TRIBE	AADBRI	RUVER		VILUS	URAR	TTGEN	SSVIR	VIGEV	KPPST
MCMa_ <i>Vdi</i>	AESAYC	YORMVEEG	KIAVIGVN	KFRE.	E	EELHII	BLHRV	DFVSR	ERSI	KRVRE	VRES	DREAW	BRAL	ELRE	VADRE	DENVER		YILHS	VKAR	TVGEI	SGVLR	VRGEY	KPPSI
MCMa_Asa	ADAAYK	FOKDVEEG	RRFIVGVN	IFTEN	EVED	VREVPI	LLEFD	QOEIE	KKQK	QRIAQ	VRSM	DQQR 10	SRALI	ELRE	AAEK.	BHINP		YILHS	VKAY	TLGEI	KUTLK	VYGVY	VEPPI
MCMa_Tsi	ADSAYK	YQKEVEER	RIIVGVN	EFIV.	D	EPLDVI	BILKV	DFSIR	DKQI	ERLKK	LRSE	DURKV	EEAL	ELRE	AAESE	DHILMP		YIIES	HKHL	TLGEV	TDVLR	ZVWGEY	RAPLI
MCMa_Dfu	ADSAYK	YQKEVEEG	RRIVGVN	κ <b>F</b> VV.	D	EFIEVE	e I LKV	DPSIR	DKQI	ERLRK	LRSE	DINKKV	E B A LI	KLRh	AAEKE	D VII LM P		. YIIES	HRHL	TLGEV	TOVLR	B V WG B Y	RAPLI
MCMa_Pap	AEAAYK	YQKEIEEG	<b>RIIVGVN</b>	RFVT.	D	EFIEVE	BINKV	DPSIR	EKQI	ERLKK	LRSE	<b>D</b> DRKKV	E E A  L I	KLRİKİ	AAEKE	DEITLMP		. YIIES	HKHL	TLQEV	ήτο VLR	e I m G E Y	RAPLI
MCMa_Psp	AEAAYK	YQKEIEEG	KRIIVGVN	AFVT.	D	EPIEVI	BILKV	DPSIR	EKQI	ERLKK	LRSE	арикку	QEALI	KLRM	AAEKE	DEILNP		. YIIE?	HRHL	TLQEV	TOVLR	Z I WGEY	RAPLI
MCMa <sup>T</sup> ga	ADAAYK	YQKEIEEG	KRIIVGVN	KFQT.	D	EPIEVI	EILKV	DFSIR	EKQI	ERLKK	LRSE	9D S KK V	EBALI	KLRI	AAETE	DENTR		. YIIE?	HRHL	TLGEV	TDVLR	B V W G B Y	RAPLI
MCMa Pab	AEAAYK	YOKEIEEG	KRIIVGVN	KFVT.	D	EPIEVI	BILKV	DPSIR	DKQI	ERLKK	LRSE	арикку	BEALI	KLRI	AAEKE	DENTR		YIIE3	HRHL	TLQEV	TDVLR	BINGEY	RAPLI
MCMa_Ton	ABAAYK	TOKETEEG	RRIIVGVN	APVS.	D	EPIEVE	BILKV	DPSIR	EKQL	ARLKK	LRSE	SDITKK V		OK LRII	AAEKE	DVIILMP		YILE?	HKHL	TLOBY	TDVLR	E VNG EY	RAPLI
MCMa_Csp	ABSAIN	YOOR TRRG	TRIIVGVN	B PODD		EPLDVI	BITTON	DPSIR	PDOL	PDIND			APP TO	RIB	A A B A B	DENTLIP		TTTER	THRH L	TLGEV	C D V L R	SVAGE1	RAPLI
MCMa_Cau	ADAATA	YOOPTDRO	PRIIVGVN				TTOP	DEBGE	TDOL	PDIND	DDDD		APPL	TELR.	2 2 2 0 00	TRACE		a TIDO	WEAL OF	TLORN	CDVLR		Dongu
MCMa_Cag	ADAAYB	YOOFIDKG	BRIIVGVN	AFOAD		EPLEIN	PILON	DPEGE	FRHL	ERLNR	URRE		ABBI		3 3 3 0 0	TUMME		aTLuc	UBAV	TLGEN	CDVLR	VPGVV	DODTY
MCMa_Mmu	EECAAR	ROARIDSG	SEVIVGVN	FYOLE	K	EDSVET	LAID	ITSVR	EKOL	EKLKK	IKSS	DOALA	BOCL	ALTO	CAASG	DG	HIL	LAVDS	ABAB	TVGEI	TDALK	VEGER	KANDR
MCMa_Psh	EEAAAB	TOARIDSG	BOPLIGVN	EYELE	н	EPPLDY	LEVD	USTVL	ABOK	AKLVK	LRAE	DPEKU	KAAL	KITW	AAANP	DERDPE	BILLI	LCIDS	GRAM	TVGEN	SDALE	VFGBY	TAOLE
ICMa_Sci	AESAFC	YORS LEKG	DKRVVGVN	CLEGS		VIGDLE	BILRY	SHEVE	REOV	RELAG	RKGR	DDARV	RASL	AML.	AAARD	SIMIA		PHLES	VRAE	TLGEI	CGVLR	BRGVY	VEPPGI
GLMa_Cte	VKAFET	GVMDIPFG	PSEYNAGE	MPVR		DHL	3 CVRY	LEFGN	VPPT	EELKN	YNRE	LAERA	KPEGE	EVSP	QMVID	DIFAVG		🗋	K G1	LIGRE	ENK		

Figure S2. Alignment of amino acid sequences of MCM- $\alpha$  from archaea and bacteria and other coenzyme B<sub>12</sub>-dependent enzymes. The enzymes shown are as follows: MCM- $\alpha$  of *M. sedula* DSM 5348 (MCM $\alpha$ \_*Mse*), MCM- $\alpha$  of *M. cuprina* Ar-4 (MCM $\alpha$ \_*Mcu*), MCM- $\alpha$  of *S. solfataricus* P2 (MCM $\alpha$ \_*Sso*), MCM- $\alpha$  of *S. tokodaii* str. 7 (MCM $\alpha$ \_*Sto*), MCM- $\alpha$  of *S. acidocaldarius* DSM 639 (MCM $\beta$ \_*Sac*), MCM- $\alpha$  of *S. islandicus* M.14.25 (MCM $\alpha$ \_*Sis*), MCM- $\alpha$  of *A. hospitalis* W1 (MCM $\alpha$ \_*Aho*), MCM- $\alpha$  of *V. moutnovskia* 768-28 (MCM $\alpha$ \_*Vmo*), MCM- $\alpha$  of *V. distributa* DSM 14429 (MCM $\alpha$ \_*Vdi*), MCM- $\alpha$  of *A. saccharovorans* 345-15 (MCMa\_Asa), MCM- $\alpha$  of *T. sibiricus* MM 739 (MCMa\_Tsi), MCM- $\alpha$  of *T. barophilus* MP (MCMa\_Tba), MCM- $\alpha$  of *P. furiosus* DSM 3638 (MCMa\_*Pfu*), MCM- $\alpha$  of *P. sp.* NA2 (MCMa\_*Psp*), MCM- $\alpha$  of *P. horikoshii* OT3 (MCMa\_*Pho*), MCM- $\alpha$  of *T. gammatolerans* EJ3 (MCMa\_*Tga*), MCM- $\alpha$  of *P. abyssi* GE5 (MCMa\_*Pab*), MCM- $\alpha$  of *T. onnurineus* NA1(MCMa\_*Ton*), MCM- $\alpha$  of *C. sp.* Y-400-fl (MCMa\_*Csp*), MCM- $\alpha$  of *C. aurantiacus* J-10-fl (MCMa\_*Cau*), MCM- $\alpha$  of *C. aggregans* DSM 9485 (MCMa\_*Cag*), N-terminal of MCM- $\alpha$  of *H. sapiens* (MCMa\_*Hsa*), N-terminal of MCM- $\alpha$  of *M. musculus* (MCMa\_*Mmu*), N-terminal of MCM- $\alpha$  of *P. shermanii* (MCMa\_*Psh*),  $\alpha$ -subunit of isobutyryl-CoA mutase of *S. cinnamonensis* (ICMa\_*Sci*),  $\alpha$ -subunit of glutamate mutase of *C. tetanomorphum* (GLMa\_*Cte*).





**Figure S3. A)** Alignment of amino acid sequences of MCM-β from archaea and bacteria, and other coenzyme B<sub>12</sub>-dependent enzymes. The enzymes shown are listed as follows: MCM-β of *M. sedula* DSM 5348 (MCMβ\_*Mse*), MCM-β of *A. pernix* K1 (MCMβ\_*Ape*), *V. moutnovskia* 768-28 (MCMβ\_*Vmo*), MCM-β of *A. saccharovorans* 345-15 (MCMβ\_*Asa*), MCM-β of *T. sibiricus* MM 739 (MCMβ\_*Tsi*), MCM-β of *C. sp.* Y-400-fl (MCMβ\_*Csp*), C-terminal of MCM-α of *H. sapiens* (MCMα\_*Hsa*), C-terminal of MCM-α of *M. musculus* (MCMα\_*Mmu*), C-terminal of MCM-α of *P. shermanii* (MCMα\_*Psh*), β-subunit of isobutyryl-CoA mutase of *S. cinnamonensis* (ICM β\_*Sci*), β-subunit of glutamate mutase of *C. tetanomorphum* (GLMβ\_*Cte*). The conserved amino acids are shaded black, and similar amino acids are boxed. The fingerprint "DXHXXG-SXL-GG" (where X is any amino acid) is indicated by an arrow. The residues  $H^{21}$ -D<sup>19</sup>-K<sup>15</sup> for the hydrogen-bonding network for coenzyme B<sub>12</sub> binding was indicated by asterisk. **B) Three dimensional model prediction for MCM-α (B) and MCM-β (C).** The three dimensional model of MCM-α and MCM-β were based, respectively, on MCM (PDB: <u>2XIJ</u>, *Homo sapiens*) and MCM-β (PDB: <u>2YXB</u>, *Aeropyrum Pernix*), using the ModWeb online server.



Figure S4. Relationship of 3-hydroxypropionate/4-hydroxybutyrate cycle with the metabolism of branched amino acids (valine, leucine, isoleucine, methionine) and propanoate to central carbon metabolism. Enzymes E1: ACC; E2: MCR; E3: MSR; E4: HPCS; E5: HPCD; E6: ACR; E7: MCE; E8: MCM; E9: SSR; E10: HBCS; E11: HBCD; E12: CCH; E13: ACK; E14: acetate kinase; E15: acetate-CoA ligase; E16: branched-chain-amino-acid transaminase; E17: 3-methyl-2-oxobutanoate dehydrogenase; E18: acyl-CoA dehydrogenase; E19: enoyl-CoA hydratase; E20: 3-hydroxyisobutyryl-CoA hydrolase; E21: 3-hydroxyisobutyrate dehydrogenase; E22: methylmalonate-semialdehyde dehydrogenase; E23: 3-hydroxyacyl-CoA dehydrogenase; E24: acetyl-CoA C-acyltransferase.

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