








Figure S01 – S08: Metabolic maps

Legend

In each of the 21 maps that follow, enzymatic reactions are shown along with indications of the presence or absence of the associated enzymes in *Rippkaea* PCC 8802, in the Rhopalodian endosymbionts, and in the nitroplast of *Braarudosphaera bigelowii* (UCYN-A). The specific genes encoding the relevant proteins are given in Supplemental Table S2, along with the names and symbols of the proteins.

The drawings of the maps are derived -- but highly simplified -- from KEGG metabolic maps [Kanehisa et al, 2021]. Most reactions not present in *Rippkaea* PCC 8802 have been eliminated. Rarely, reactions indicated by appropriate literature to be pertinent have been added.

The presence or absence of enzymes are indicated in the following ways

	Present in <i>Rippkaea</i> PCC 8002, Rhopalodian endosymbionts, and UCYN-A
	* Present in some but not all Rhopalodian endosymbionts
	Present in Rhopalodian endosymbionts but not <i>Rippkaea</i> PCC 8002
	Absent in Rhopalodian endosymbionts
	Absent in UCYN-A
	Absent in <i>Rippkaea</i> PCC 8002 and all endosymbionts
	Complicated... see comment in Supplemental Table S2 (appropriate tab)

As an additional cue, enzymes present in *Rippkaea* PCC 8002 and the Rhopalodian endosymbionts have names in black font, those absent in the endosymbionts have names in red font, and those present only in the Rhopalodian endosymbionts have names in blue font. Those absent in all considered genomes have names in gray font. The EC numbers in the boxes can serve to identify the enzymes in Supplemental Table S2 (appropriate tab).

Outside pathways that contribute substrates to the pathway under consideration are outlined in pink if the complete pathway is absent in UCYN-A.

See Supplemental Table S1 for the source of genomes and appropriate tabs in Supplemental Table S2 for details about genes and abbreviations in the mapped pathways.

Figure S01: Glycogen metabolism
(derived from KEGG pathway map 00500)

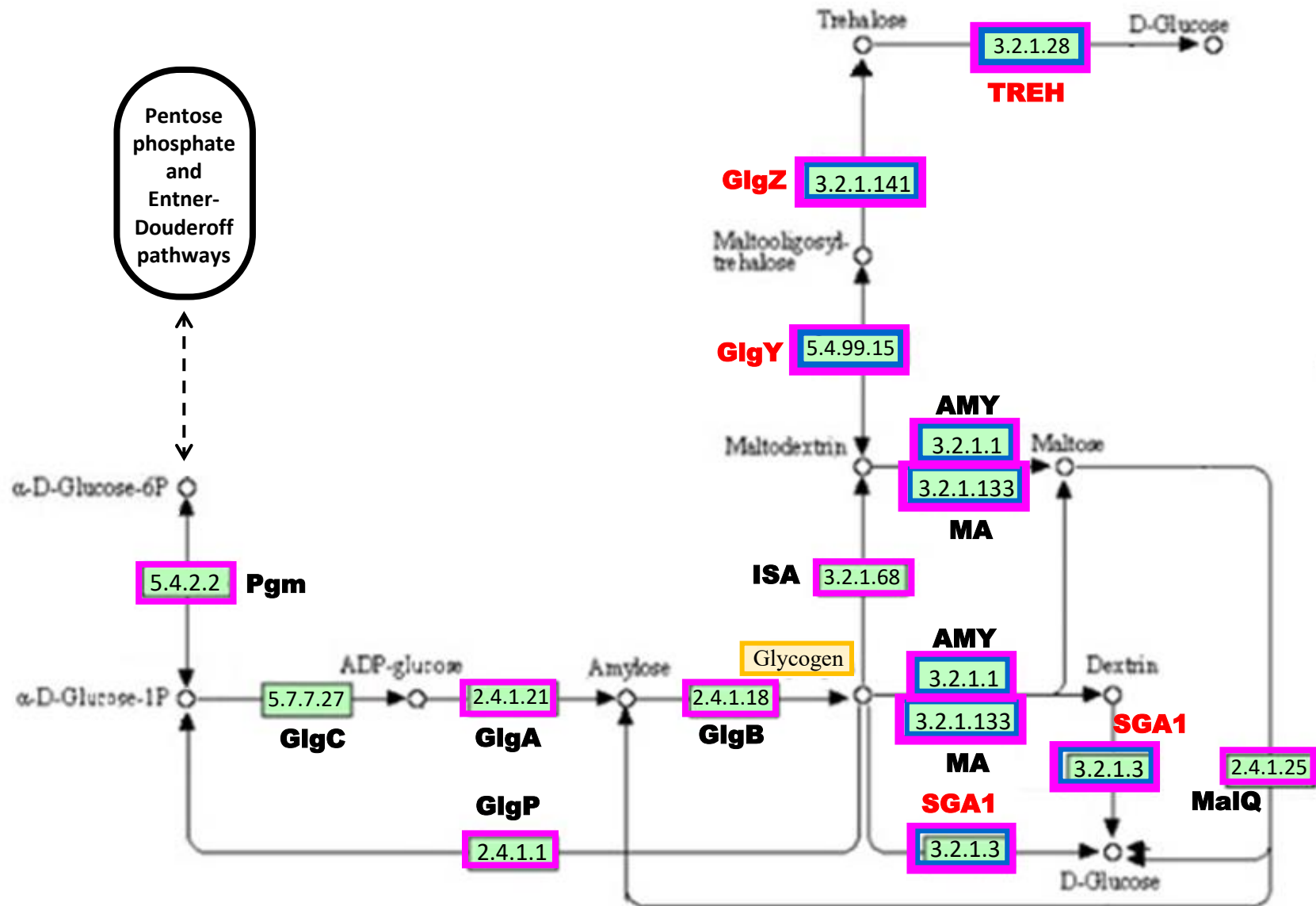


Figure S02: Glycolysis
(derived from KEGG pathway map 00010)

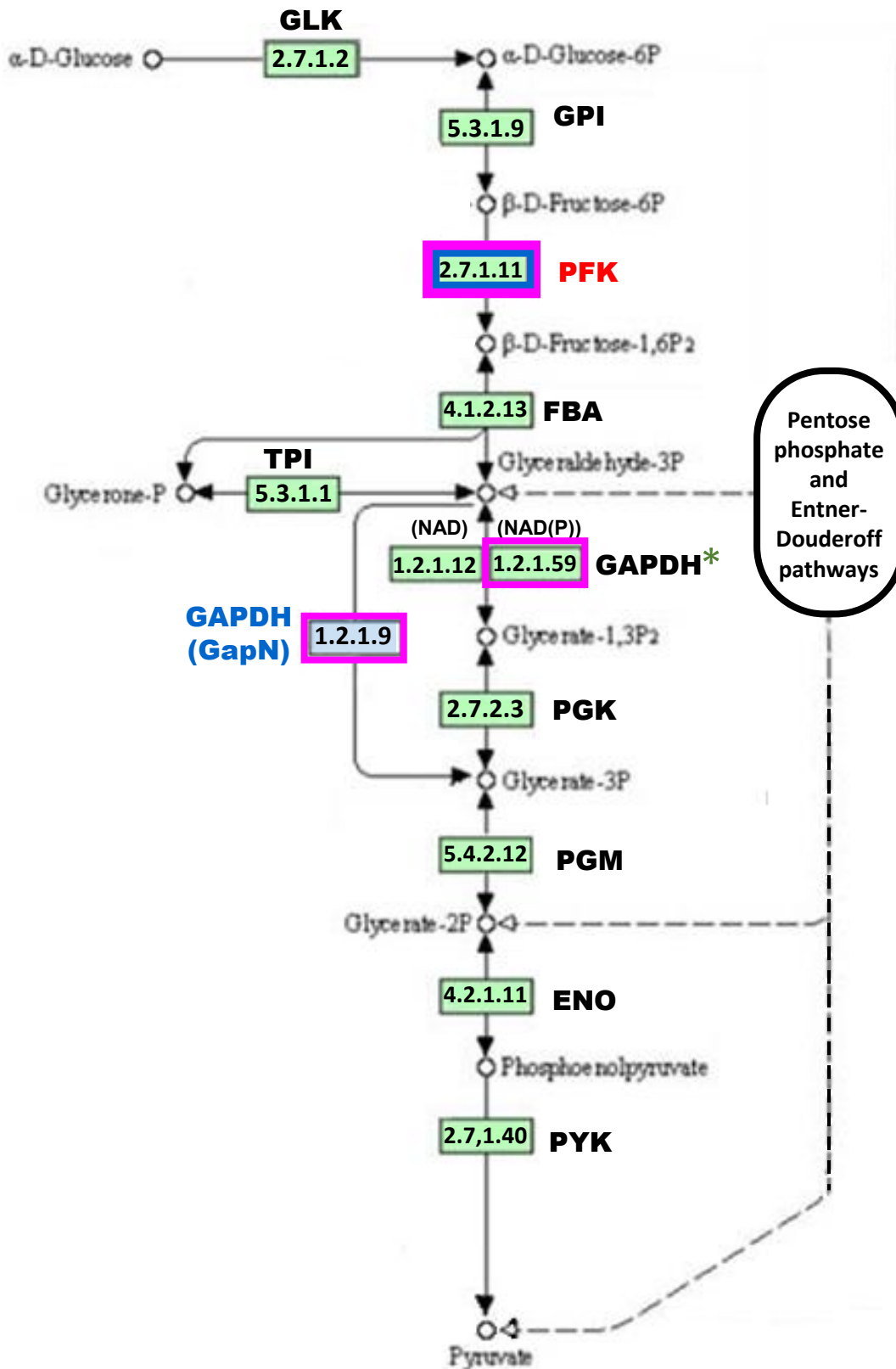


Figure S03: Pentose Phosphate and Entner-Doudoroff Pathways

(derived from KEGG pathway map 00030)

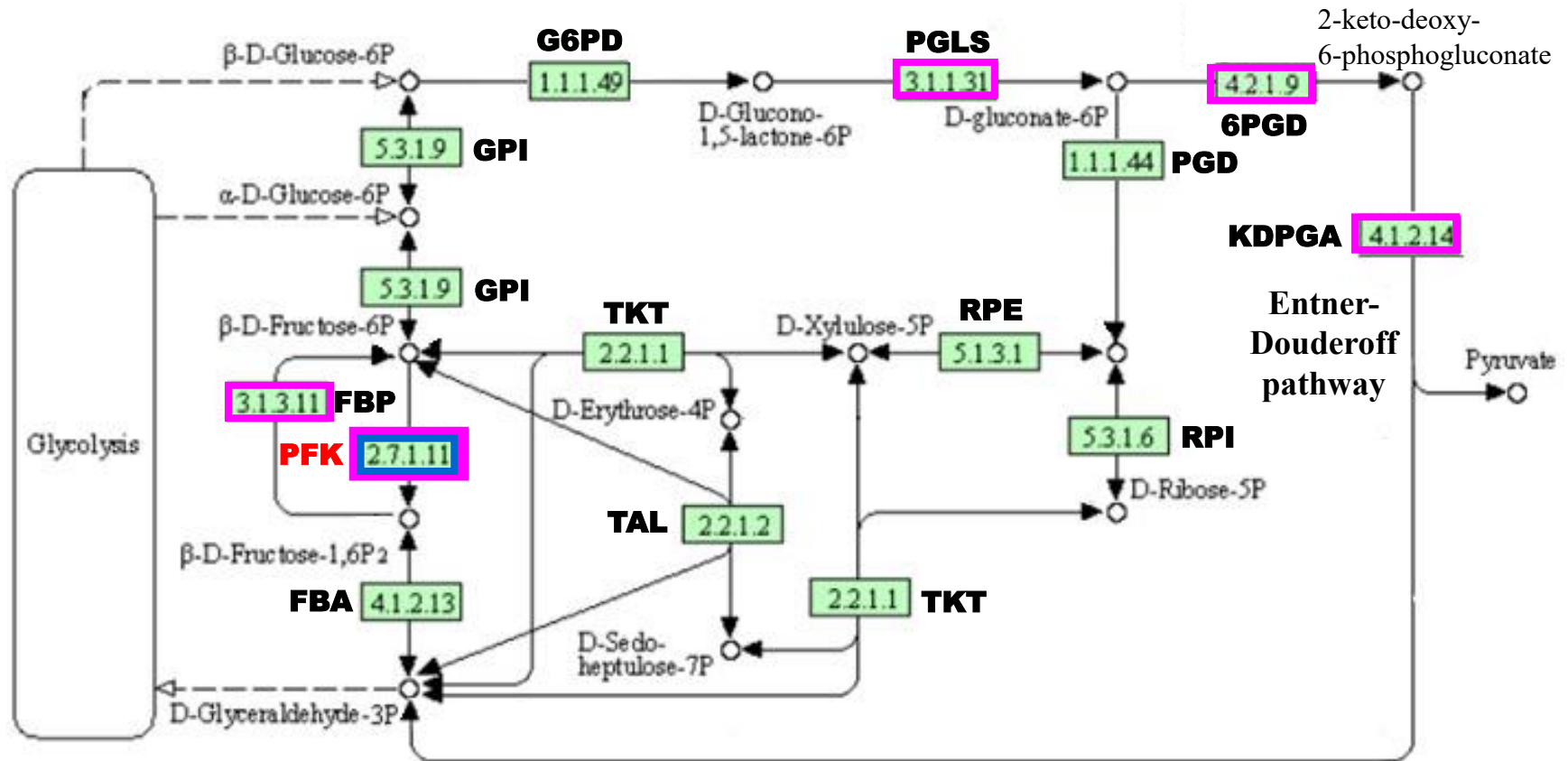


Figure S04: Tricarboxylic acid cycle
(derived from KEGG pathway map 00020)

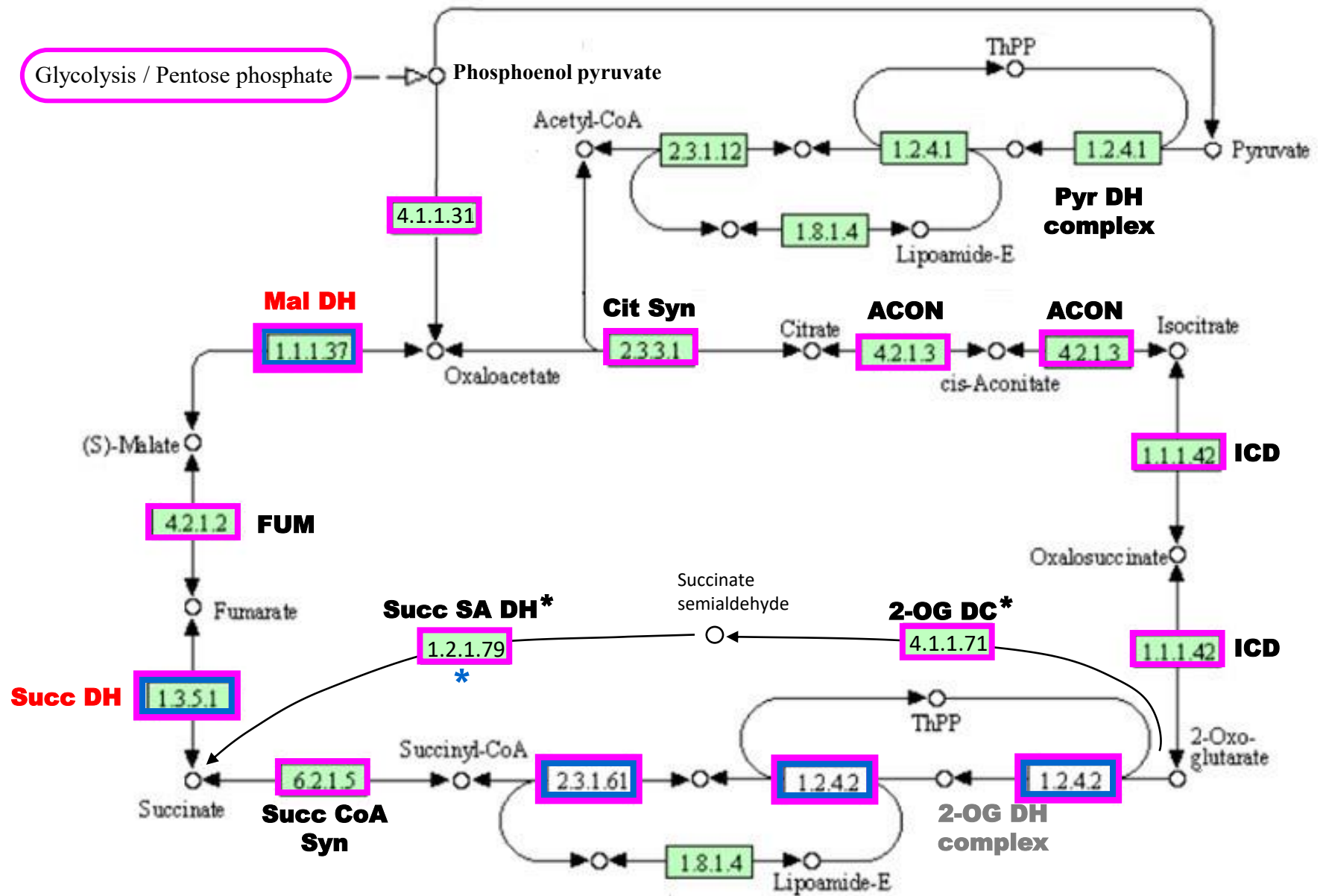


Figure S05: Biotin biosynthesis
(derived from KEGG pathway map 00780)

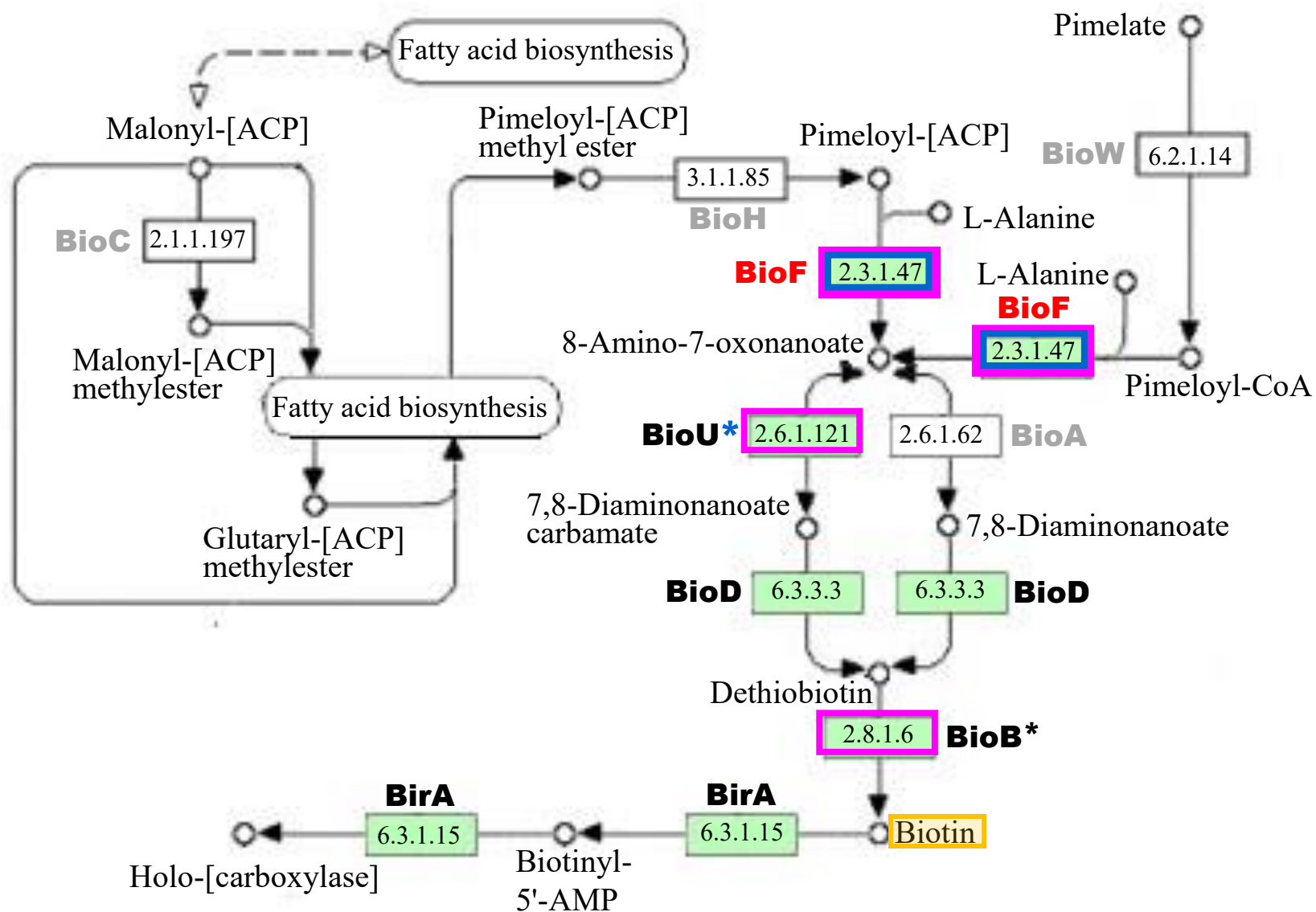
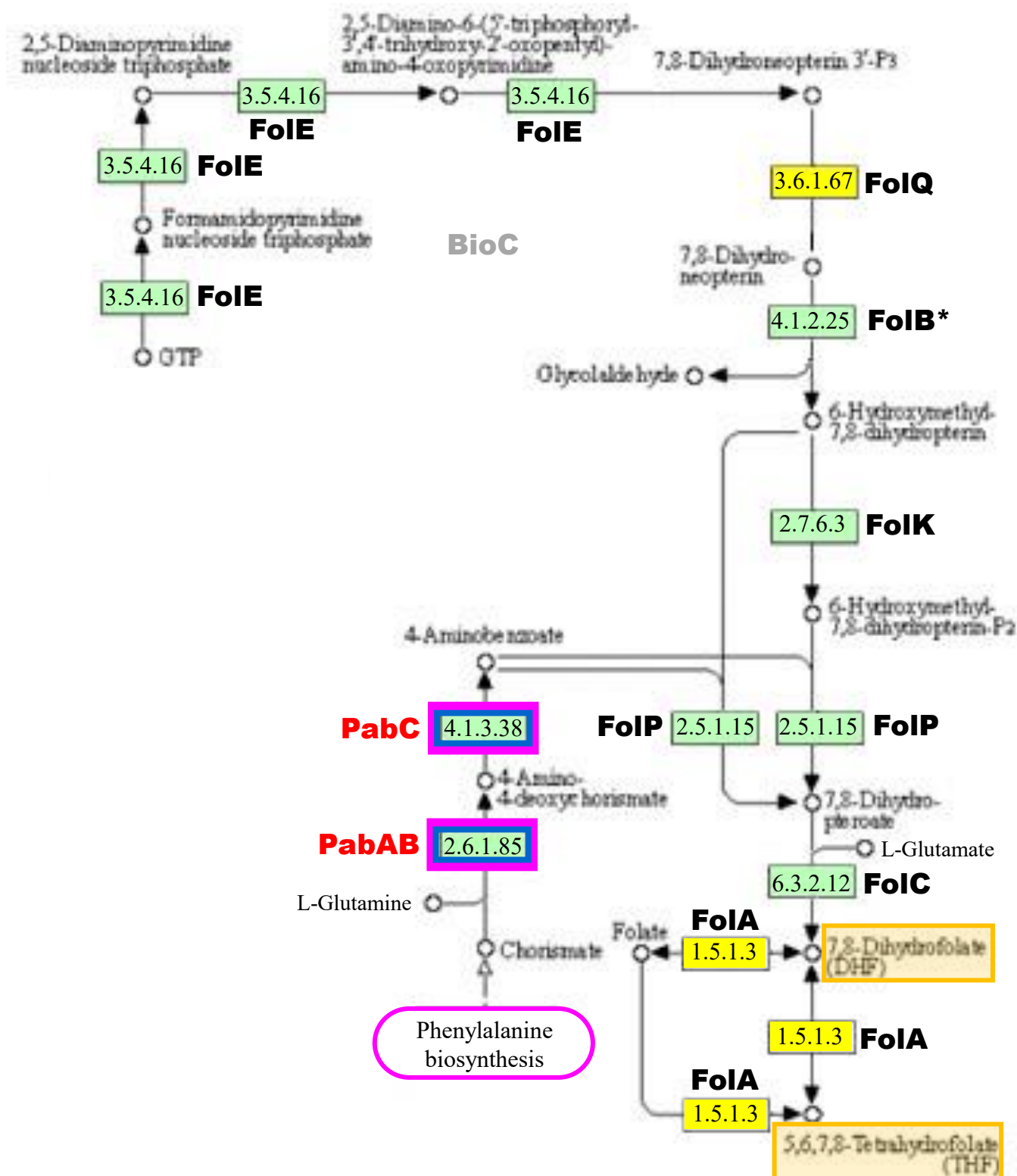


Figure S06: Folate and derivatives biosynthesis
(derived from KEGG pathway map 00790)



(derived from KEGG pathway map 00770)

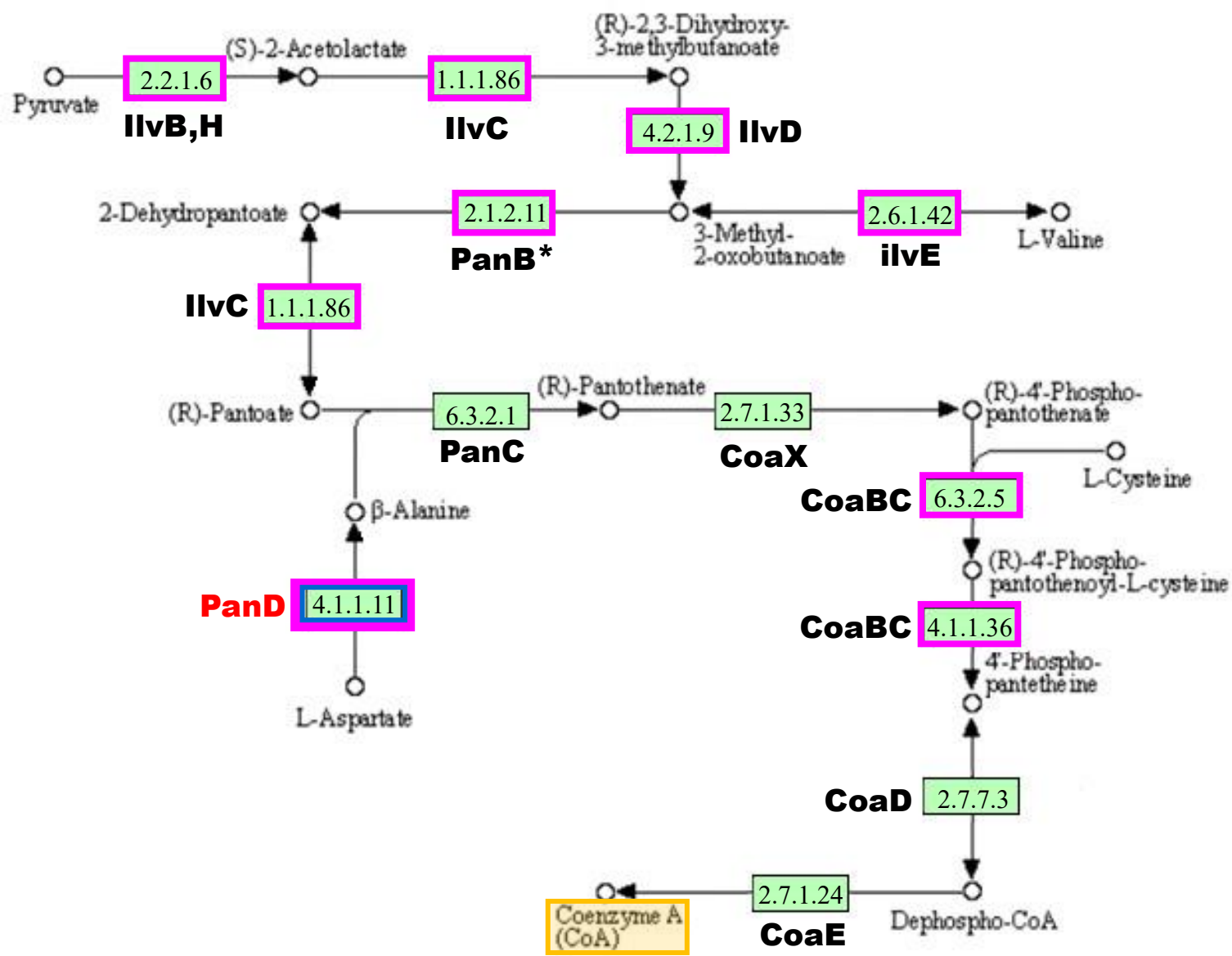
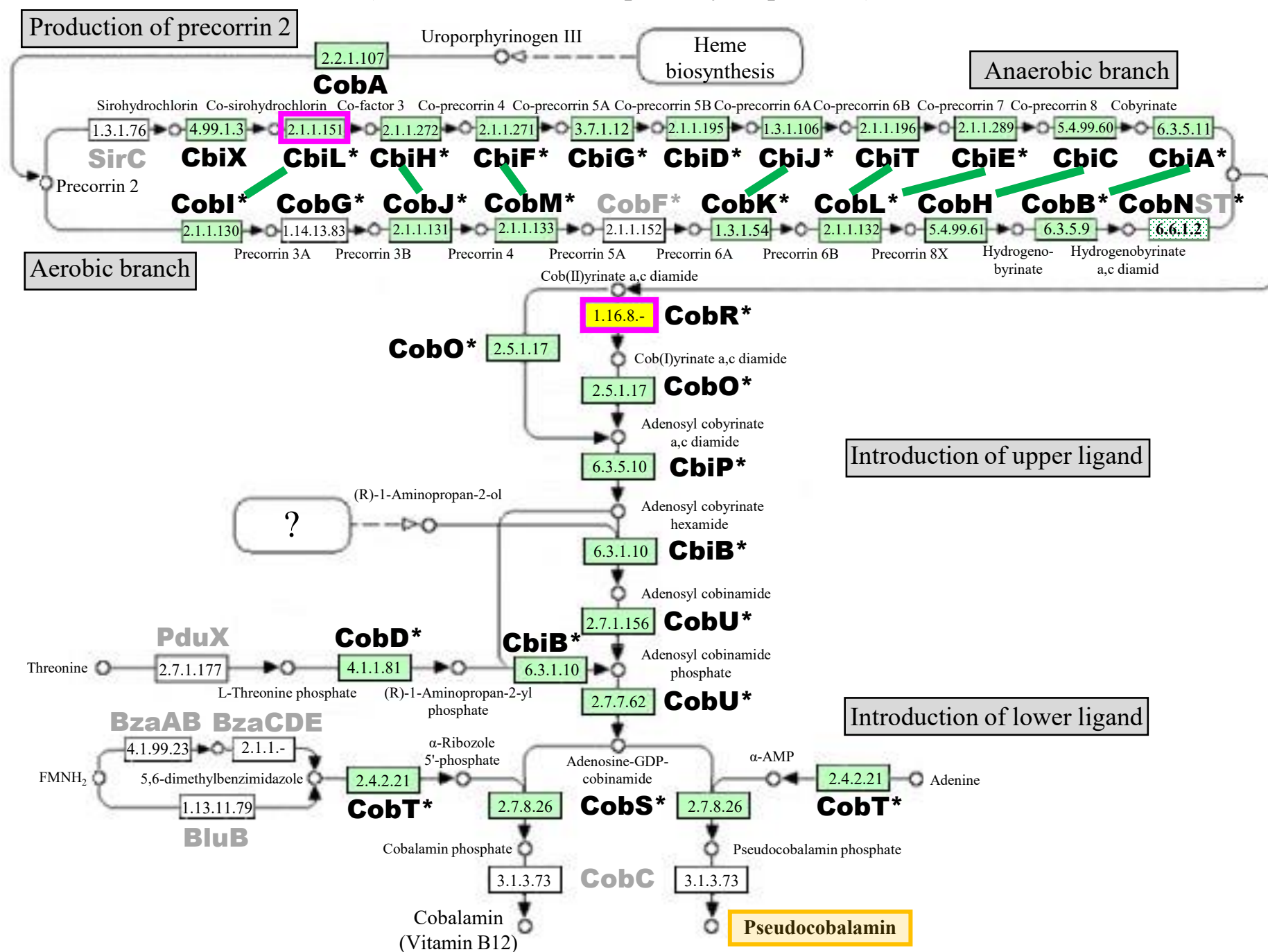


Figure S08: Pseudocobalamin biosynthesis
(derived from KEGG pathway map 00860)



Supplemental Fig. S09: Alignment of Small Chlorophyll- α binding-like proteins*

Symbol	Organism / Protein
<u>Free-living cyanobacterial relatives of Rhopalodian endosymbionts</u>	
C51142	Crocospaera (Cyanotheca) ATCC 51142 ScpA' (Cce_2568), ScpB (Cce_1543), ScpD (), ScpE (Cce_4826)
R8802	Rippkaca (Cyanotheca) PCC 8802 ScpA' (Cyan8802-0327), ScoE (Cyan8802-0691)
S6803	Synechocystis (Kazusa) PCC 6803 ScpA' (Slr0839), ScpB (Ssl1633), ScpC (Ssl2542), ScpD (Ssr2595), ScpE (Ssr1789)
<u>Endosymbionts with nearly intact chlorophyll biosynthesis pathways</u>	
EpSB	Endosymbiont from Epithemia pelagica ScpA' (OXU93-06980)
EcSB	Endosymbiont from Epithemia clementina ScpA' (chromosome from 104894 to 103860), ScpB (P3F56-03335)
RgSB	Endosymbiont from Rhopalodia gibberula ScpA' (RgRSB-0066)
UCYN-A	Endosymbiont from Braarudosphaera bigelowii ScpA' (UcynA-06750), ScpE (UcynA-03290)
<u>Endosymbionts without nearly intact chlorophyll biosynthesis pathways</u>	
RaSB	Endosymbiont from Rhopalodia gibba 17Bon1 ScpA' (JJP05-05120), ScpE (JJP05-08540)
EaSB	Endosymbiont from Epithemia adnate Bon 19 ScpA' (KPI85-04805)
EtSB	Endosymbiont from Epithemia turgida ScpA' (EtSB-0121)

* Residues in alignment highlighted in green match residues identified by Funk & Vermaas (1999). [Biochem \(1999\) 28:9937-9404](#) conserved amongst all SCP proteins.

Supplemental Fig. S09: ScpA-E alignment (continued)

ScpA' (Slr0839)	1	-----	-----	-----	MDSL	NDPPCTFETV	PHPKKN-MKM
ScpA' (R8802)	1	-----	-----	-----	TKSL	QEPPCTFNQV	IHPKEN-MKM
ScpA' (C51142)	1	AGITNFLRVP	ALNTHPLFIN	ALADLVTHSL	QASPVTFCV	THPKEN-MKM	
ScpA' (RgSB)	1	-----	-----	-----	TKSL	QEPPCTFDTV	IRPNRN-LKS
ScpA' (EcSB)	1	-----	-----	-----	TKSL	QEPPCTFDSV	IRPRKN-LKI
ScpA' (EtSB)	1	-----	-----	-----	TKSL	KEPPCTFDTV	IRLKKI--KI
ScpA' (EaSB)	1	-----	-----	-----	TKSL	KEPPCTFDTV	IRLKKI--KI
ScpA' (RaSB)	1	-----	-----	-----	TKSL	EEPPCTFDTV	IRPKKTPQNI
ScpA' (EpSB)	1	-----	-----	-----	TKSL	QESPYTFDKV	IRPKEN-RII
ScpA' (UCYNA)	1	-----	-----	-----	IHSL	EKPPVTFKCI	THPREN-II I
ScpB (C51142)	1	-----	-----	-----	-----	MKSN	NQNEG-----
ScpB (EcSB)	1	-----	-----	-----	-----	MTNS	KQYER-----
ScpB (Ssl1633)	1	-----	-----	-----	-----	MNNE	NS-----
ScpE (C51142)	1	-----	-----	-----	-----	MSEPSTQPT	ETPNLE----
ScpE (R8802)	1	-----	-----	-----	-----	MADSQSQPT	ESPKLE----
ScpE (Ssr1789)	1	-----	-----	-----	-----	MSE-ELQPN	QTPVQE----
ScpE (RaSB)	1	-----	-----	-----	-----	MPDSQFQPT	KTPKLR----
ScpE (UCYNA)	1	-----	-----	-----	-----	MNTNT	DKRAFD-----
ScpD (Ssr2595)	1	-----	-----	-----	-----	MTSRGFRLD	QDNRLNNFAI
ScpD (C51142)	1	-----	-----	-----	-----	MTSRSYVTE	EQGRLNNYAI
ScpC (Ssl2542)	1	-----	-----	-----	-----	MTTRGFRLD	QDNRLNNFAI

ScpA' (Slr0839)	24	YPQ---ERW	EWGLTTAAEV	WNGRLAMLGF	I-ALLVELIS	GQGPLHFVGL	L
ScpA' (R8802)	24	YPQ---ERW	QWGLTTAAEV	WNGRLAMVGF	I-ALLIELIS	GHGPLHFVGL	L
ScpA' (C51142)	50	YPQ---ERW	QWGMTTAAEV	WNGRLAMIGF	L-ALLIELIT	GYGPLHYVGL	L
ScpA' (RgSB)	24	CTQ---KHY	-----ILKL	FKKLISNIGK	L-LKKQELKI	FIEFLR----	-
ScpA' (EcSB)	24	YPQ---E--	-----	-----	-----	-----	-
ScpA' (EtSB)	23	CP-----	-----	-----	-----	-----	-
ScpA' (EaSB)	23	CP-----	-----	-----	-----	-----	-
ScpA' (RaSB)	25	TY-----	-----	-----	-----	-----	-
ScpA' (EpSB)	24	CSQ---EYW	RRSITTTIEV	WNTRLAIIGF	I-ALLFELIS	GHGLLHLAGL	L
ScpA' (UCYNA)	24	YPK---KSW	QWGITSTA EV	WNGRLAMLGF	V-ALLVELIS	GHGILHYLGI	I
ScpB (C51142)	10	-----	KFGFTGYAEN	WNGRLAMIGF	ISALIVELVT	GQGVLFHWGL	L
ScpB (EcSB)	10	-----	KFGFTAYAET	LNGRLAMIGF	LAVLITELVT	VQEVLFHWGL	L
ScpB (Ssl1633)	7	-----	KFGFTAFAEN	WNGRLAMIGF	SSALILELVS	GQGVLFHFFGI	L
ScpE (C51142)	16	EP-----	KFGFNDYAER	LNGRAAMVGF	LLILVIEYLT	GQGLLSWLGL	Q
ScpE (R8802)	16	DP-----	KFGFNDYAER	LNGRAAMVGF	VLTLVIEYLT	GQGLLSWLGL	H
ScpE (Ssr1789)	15	DP-----	KFGFNNTAEK	LNGRAAMVGF	LLILVIEYFT	NQGVLAWLGL	R
ScpE (RaSB)	16	EP-----	KFGFNEYTKH	LNVRTAIIGF	VPSLLIEYLT	GQGLLNSLG-	-
ScpE (UCYNA)	12	EP-----	KFGFTEYAER	LNGRAAMIGI	MSIFIIEYIS	GQGIFHWLGL	-
ScpD (Ssr2595)	20	EPPVYVDSSV	QAGWTEYA EK	MNGRFAMIGF	VSLAMEVIT	GHGIVGWLLS	L
ScpD (C51142)	20	EPKMYVDQKK	QFGFNKYA EK	LNGRLAMIGF	ISLLAFESLT	GQGLVTWLTN	L
ScpC (Ssl2542)	20	EPEVYVDSSV	QAGWTKYA EK	MNGRFAMIGF	ASLLIMEVVT	GHGVIGWLNS	L

Supplemental Fig. S10: Alignment of maltose transporter-like proteins

Symbol	Organism / Protein	Conserved residues
Heterotrophic bacteria		
MalY-CauCr ^a	Caulobacter crescentus (vibrioides) CB15 / Cc2283 (Q9A612)	126
MalT-LacRe ^b	Lactobacillus reuteri TD1 / KEK15710	126
MalT-SheOn ^c	Shewanella oneidensis / WP_011072433	126
Free-living cyanobacterial relative of Rhopalodian endosymbionts		
C51142	Crocospaera (Cyanotheca) ATCC 51142 / Cce_4761	93 (74%)
Rhopalodian endosymbionts with MalT-like proteins		
EpSB	Endosymbiont from Epithemia pelagica / OXU93-05180	91 (72%)
EcSB	Endosymbiont from Epithemia clementina / P3F56-03655	89 (71%)
RgSB	Endosymbiont from Rhopalodia gibberula / RGRSB-0706	91 (72%)
RaSB	Endosymbiont from Rhopalodia gibba / JJP05-08305	89 (71%)

^a Described by Lohmiller et al (2008). [Microbiol 154:1748-1754](#).

^b Described by Zhao & Gänzle (2018). [Int J Food Microbiol 272:12-21](#).

^c Described by Rodionov et al (2010). [BMC Genom 11:494](#).

MalT-LacRe	1	-----	-----	---MSQEKST	G-----AG	LPTLSKSTIW
MalT-SheOn	1	-----M	SADHTVTQLD	S-FSATTHSH	ATHS-----V	QPELNFWQIF
MalY-CauCr	1	MHFTLRVASA	RAQMPPAKRD	EKFCEPAGST	GGRSGGGSMA	RQRLSFLQIW
RgSb	1	-----	-----	-----MEKKF	-----K	KKVRNFWQLW
RaSb	1	-----	-----	-----MTEKKI	-----T	KKVQNFQWLW
EcSB	1	-----	-----	-----MT	-----E	KKIRNFWQLW
EpSB	1	-----	---MIKVKSS	QKISYDENKI	-----N	KQVQSFQWLW
C51142	1	-----	-----	---MMTTEKK	-----P	NRTRNFFELW
consensus	1					. : :

MalT-LacRe	21	MINFGFLGVQ	TAFTLQSSQM	SRIFQTIGAD	PNNLGWFFIL	PPLAGLIVQP
MalT-SheOn	36	NMCFGFLGIQ	FGFALQNANV	SRIFQTLGAS	IDEIPILWIA	APLTGLLVQP
MalY-CauCr	51	NMCFGFFGIQ	IGFGLQNANT	SRIFQSLGVD	VNHLAILWIA	APATGLLVQP
RgSb	17	NMNVGFFGVQ	YGWALQMANT	SAIYEYLGAD	PEQIPTLWLA	APLSGLIAQP
RaSb	18	NMNVGFCGIQ	YGWALQMANT	SAIYEYLGAD	PEQIPMLWLA	APLSGLIAQP
EcSB	14	NMNVGFFGIQ	YGWALQMANT	SAIYEYLGAE	PEQIPMLWLA	APLSGLIAQP
EpSB	29	NMNVGLFGIQ	YGWALQMANT	SAIYEYLGAD	PEQLPMLWLA	APLSGLIAQP
C51142	19	NMSFGFFGIQ	YGWALQMANT	SAIYEYLGAN	PEQIPLLWLA	APVSGLIAQP
consensus	51	: .*: **: *	: : ** : :	* *:: :*..	: : : : :	. * :***: **

MalT-LacRe	71	IIGYYSRDTW	APKLGRRRLP	YLLLGMIIVAV	IVMILLPNSG	SFGFGYGSLA
MalT-SheOn	86	IIGYLSDNWT	G--CLGRRRP	YFLIGAILTT	LAIFVMPHS-	-----P
MalY-CauCr	101	IIGHFSDKTW	G--RFGRRRP	YFFWGAILTT	LALLVMPNS-	-----P
RgSb	67	IIGYMSDHTW	G--PLGRRRP	YFLLGAVISS	IALILMPNS-	-----S
RaSb	68	IIGYMSDRTW	G--PLGRRRP	YFLLGAILSS	IALILMPNS-	-----S
EcSB	64	IIGYMSDRTW	G--PLGRRRP	YFLLGAIFSS	IALILMPNS-	-----S
EpSB	79	IIGYMSDRTW	G--PLGRRRP	YFLLGAILSS	IVLVLPNS-	-----S
C51142	69	IIGYMSDRTW	G--PLGRRRP	YFLVGAILSS	IALVLMPNS-	-----S
consensus	101	***: **. **	. *** *	*:: * : :	: : : : : *	.

Supplemental Fig. S10: Alignment of MalT-like proteins (continued)

MalT-LacRe	121	ALWFGAITVA	LLDLSSNVAM	QPFKMMVGDM	VNDDQKSYAY	GIQSFLSNTG
MalT-SheOn	124	TLWIAAGMLW	IMDASINIAM	EPFRAFVGDN	LPPSQRTQGY	AMQSFFFIGIG
MalY-CauCr	139	TLWVAAAALW	IMDASINITM	EPFRAFVGDN	LPDEQRATGY	AMQSFFFIGLG
RgSb	105	SLWMAAGLLW	ILDTSINISM	EPFRAFITDL	LPQKQHTRGF	SMQSFFFIGAG
RaSb	106	SLWMSAGLLW	LLDTSVNISM	EPFRAFIVDL	LPQKQHTRGF	SMQSFFFIGAG
EcSB	102	SLWMAAGLLW	ILDTSVNISM	EPFRAFIADL	LPQKQHTRGF	SMQGFFIGAG
EpSB	117	SLLMAAGLLW	ILDTSVNISM	EPFRAFITDL	LPQKQHIIGF	SMQSFFFIGAG
C51142	107	TLWMAAGLLW	ILDTSVNISM	EPFRAFIADL	LPEKQHTQGF	SMQTFFFIGFG
consensus	151	:*..* :	::* * *::*	::*: :: *	: .*: .: .:* *: . *	
MalT-LacRe	171	AVLAAVFPFI	LTAWFGVRNT	AK-RGVVPDS	VIIAFYVGAA	LLVVTSLFTV
MalT-SheOn	174	AVVASALPYI	LSNFFNVANT	AP-AGEIADS	VRYAFYFGGT	VLFLAVTWTV
MalY-CauCr	189	AVFASALPWM	LTNWFVDVANT	AP-AGQVPDS	VRIAFYTGGA	GLLLAVLWTV
RgSb	155	AVMASLSPWI	LTHLFHVGDR	R--DLGVPPS	VKLSFYIGAV	VFLGTVIWTV
RaSb	156	AVMASLSPWI	LTHLFHVGDR	R--EPGVPPS	VKLSFYIGAV	VFLGTVVWTV
EcSB	152	AVTASLFPWI	LTHLFHVDDR	K--ELGVPPS	VKSSFYIGAA	VFLGTVIWTV
EpSB	167	AVIASLSPWI	LTHIFHMDDT	K--KVGIPFS	VKSSFYIGAA	IFLGTVIWTV
C51142	157	AVVASVSPWI	LTHVFGLSNT	TNAEGVPFT	VKVSFYIGAA	VFLFTVLWTV
consensus	201	** *: *::	*: * : :	:: : *	:** *..	:: : : **
MalT-LacRe	220	FRVHEYDPAT	YAKYHGISED	DNKEGGNW--	-----	-----
MalT-SheOn	223	ISTKEYSPPEE	LAAFHAKTKT	DVEEQCKRSR	THKDYQFASF	VWMG---LGA
MalY-CauCr	238	FTTREYSPEQ	LTAF-EKAER	EIAGLGLHEE	PEPSVNAYIA	LGVGGVLLGA
RgSb	203	VTTSETPPKN	LEKIRNAQKS	KSILDKST--	-----	-----
RaSb	204	VTTSETPPKN	LEKIQNAQES	KSTLNKVT--	-----	-----
EcSB	200	VTTSETPPKN	LEKIRNAQKS	KSALDKVT--	-----	-----
EpSB	215	VTTSETPPRN	LEKIKNFQEG	KSTLDKVT--	-----	-----
C51142	207	FTTEEKPPQN	LKAMQQANES	KDAGDKLG--	-----	-----
consensus	251	. . * *	:	.		
MalT-LacRe	247	-----	-----	-----	-----	-----
MalT-SheOn	270	LLTFTVWAQD	LDKQLYILSI	GIFAFGPLQL	YCALRLSQSQ	PSQRAQLGMV
MalY-CauCr	287	ALALIVWGAG	LEKELYVLG	LLFAFG-LAG	VAGARFKRIG	RTDNGFS---
RgSb	230	-----	-----	-----	-----	-----
RaSb	231	-----	-----	-----	-----	-----
EcSB	227	-----	-----	-----	-----	-----
EpSB	242	-----	-----	-----	-----	-----
C51142	234	-----	-----	-----	-----	-----
consensus	301					
MalT-LacRe	248	---FTLLKHA	PKAFWTVTLV	QFFCWFAFQY	LWTYSAGAI	KNVWNTVDAT
MalT-SheOn	320	FNVVDDL FHM	PKAMHQLAIV	QFFSWFALFA	MWIYTTSAVT	SYHFGSSDVL
MalY-CauCr	333	-EVLADVFRM	PKTMRQLAVV	QFFSWFGLFA	MWIYTTPAVA	TVHFGAVDAS
RgSb	231	-EILWLIKAM	PTTMKQLAVV	QFFTWLGI FC	VFLYFPPAVA	HHIFGAVQEH
RaSb	232	-EIFWLIKAM	PTTMKQLAVV	QFFTWLGI FC	VFLYFPPSVA	HHIFGAVQEN
EcSB	228	-EIFWLIKAM	PTTMKQLAVV	QFFTWLGI FC	VFLYFPPAVA	HNIFGAVREN
EpSB	243	-EIVLLIKAM	PTTMKQLAVV	QFFTWLGI FC	VFLYFPPAIA	HHVFGAVRGD
C51142	235	-EILNLIKAT	PKTMKQLAVV	QFFTWLGVFC	MFLYFPPAVA	HNIFGAVEEN
consensus	351	. :	*::: :::*	*** *::..	:: * . :::	:::

Supplemental Fig. S10: Alignment of MalT-like proteins (continued)

MalT-LacRe	295	SAGYQAAGNW	YGVLSAVQSI	AAVIWSYVLA	KVPNKY-HKL	GYGGSLLLGA
MalT-SheOn	370	SQAYNDGADW	VGVLFAASYNG	FSAIAALFIP	LLAKRIGIKL	THTFNMFCGG
MalY-CauCr	382	SKAYNEGADW	VGVLFAVYNG	VAALAALVIP	LMVKVTSRRV	SHAVCLGLGA
RgSb	280	SQLYTDGIEW	AGICIAVYNG	VCFIFSWLLP	KLTEIINHKI	AHSLCLICGG
RaSb	281	SQLYTDGIEW	AGICIAVYNG	ICFIFSLLLP	KLTEIINHKI	AHSLCLICGG
EcSB	277	SQLYTDGIEW	AGICIAVYNG	VCLIFSWLLP	KLTEIINHKI	AHSLCLICGG
EpSB	292	SQVYKDGIEW	AGICIAVYNG	VCIIFSWLLP	TLTEIINHKI	AHSLCLICGG
C51142	284	SALYTEGIEW	AGICIAVYNG	VCFLFSWILP	NLTARLGRKM	THSLCLICGG
consensus	401	* * . :*	*: * .	. : : .:	:	:: : : *
MalT-LacRe	344	LGFISSVFFVH	DQWTLIVSYT	LVGIAWAAMN	TYPLTIVTNA	LTGKHMGTYL
MalT-SheOn	420	FGLISFYFIK	DPNLLWLAMI	GVGIAWASIL	SIPYAILSGT	LPPKKMGVYM
MalY-CauCr	432	LGLLSFLVIR	DPGLLWIGMV	GVGFAWSSIL	STPYSILAGA	LPARKMGVYM
RgSb	330	IGLISLVFVD	HPLWVLWPMV	GFGIAWSSIL	AIPYSILSRT	LTSQNTGLYM
RaSb	331	VGLISLVFVE	QPLWILLPMV	GFGIAWSSIL	TIPYSILSRT	LTSKNTGLYM
EcSB	327	VGLISLVFVD	QPLLALLPMI	GFGIAWSSIL	AIPYSILSQT	VTSQNIGLYM
EpSB	342	IGLISLVFVD	RPLLVLFPMI	GFGIAWSSIL	AIPYSILSRT	LTGQNTGLYM
C51142	334	VGLISLLWVN	RPIYALFSMV	GFGIAWSSTL	VIPYSMLSHI	IPEKNMGLYM
consensus	451	.*:*. :		.*:***:	* ::::	:: :: * **:
MalT-LacRe	394	GLFNGSICLP	QIIASLLS-F	ALFPLFGHSQ	AHMFILAGIV	MALGALSVAT
MalT-SheOn	470	GIFNFFIVIP	QLLAASVLGL	ILNGLFDGQP	IYALITGGVF	MLCAGIAVLF
MalY-CauCr	482	GIFNVFIVVP	QLLAATLLGL	MLKTFFGNQS	IFALVLGALS	FALAAAATFL
RgSb	380	GIFNAFIVLP	QIFAALGLGW	IMKIFLESNS	LLVVVIGGFS	LLLA AVL VHF
RaSb	381	GIFNVFIVLP	QIFAALGLGW	IIKIFFKKNC	LLVVVLGGFS	LLLA AVL VHF
EcSB	377	GIFNAFIVIP	QIFAALGLGW	IMKIFLDSNC	LLVVVVGGFS	LLLAAMLVHF
EpSB	392	GIFNAFIVLP	QIFAALGLGW	IMKIFFNSNC	LLVVVVGGFS	LLLA AVL IYF
C51142	384	GLFNAFIVIP	QIIAALGLGS	IMDYFLNNNR	LLVVVLGGVS	ILLAAICIHV
consensus	501	*:** * :*	*::**:	: :: .	:: ...	: ..
MalT-LacRe	443	IKETYAE---	-----			
MalT-SheOn	520	VEQPKALTPH	-----			
MalY-CauCr	532	VRDRVAGAPA	-----			
RgSb	430	VDEPETLEQT	SIQPEILSPS			
RaSb	431	VDEPETSEKT	SIQPEILSPS			
EcSB	427	VDKPETSEKT	SIQPEILSPS			
EpSB	442	VEEY-----	-----			
C51142	434	VDDIETASTN	NQALEVQPTV			
consensus	551	: .				

Supplemental Fig. S11: α -Glucosidase phylogeny

