Supplementary information to

A Unique LHCE Light-Harvesting protein Family is involved in Photosystem I and II Far-Red Absorption in *Euglena gracilis*

Héctor Miranda-Astudillo[1,2], Rameez Arshad[3], Félix Vega de Luna[1], Zhaida Aguilar-Gonzalez[2], Hadrien Forêt[1], Tom Feller[1], Alain Gervasi[1], Wojciech Nawrocki[1,4], Charles Counson[1,5], Pierre Morsomme[6], Hervé Degand[6], Denis Baurain[5], Roman Kouřil[3], Pierre Cardol[1]

[1] Genetics and Physiology of microalgae, InBioS/Phytosystems, University of Liège, Belgium.
[2] Present Address: Departamento de Biología Molecular y Biotecnología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Mexico City, Mexico.
[3] Faculty of Science, Department of Biophysics, Palacký University Olomouc, Czech Republic.
[4] Institute of Physical and Chemical Biology, French National Centre for Scientific Research, France.
[5] Eukaryotic Phylogenomics, InBioS–PhytoSYSTEMS, University of Liège, Belgium.
[6] Institut des Sciences de la Vie, Université Catholique de Louvain, Louvain-la-Neuve, Belgium.

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ids	mick	emilie	koziol	uniprot
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LHCE6-4_Koziol/LHCA6-4@191	EG_transcript_2508,EG_transcript	comp60656_c0_seq12	LHCA6-4	A7
LHCE6-5_Koziol/LHCA5-4@191			LHCA5-4	A10
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LHCE7-2_GEFR01002507.1/F-2/O1/P2@175	EG_transcript_2508		LHCA7-1	A11
LHCE7-3_Koziol/LHCA5-1@184	EG_transcript_32126	comp60527_c0_seq1	LHCA5-1	A10
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LHCSRL-3_HBDM01049636.1/F+2/O2/P1@338		comp3673_c0_seq1		

Supplementary Table S1. Corresponding nomenclature for *Euglena gracilis* LHC sequences. Column "protein name" corresponds to the new naming scheme proposed in this work, "protein identifier" provides the corresponding sequence identifier as appearing in the detailed phylogenetic tree of Suppl. Figure S48 (and built as follows: <name>_<accession>/<frame>/<orf#>/<segment#>@<length>; see Methods for details), "transcript identifier" gives the numeric part of the corresponding transcript accession(s) in the *Euglena gracilis* dataset used in Van Vlierberghe et al. (2021) (and originally downloaded from ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2019/01/PXD009998/Euglena_translated_transcriptome.fasta), "Koziol annotation(s)" and "UniProt annotation(s)" are the closest BLAST matches to the protein sequences described in Koziol and Durnford (2008) and to those available in the UniProt database (https://www.uniprot.org/), respectively, using an identity threshold of 100% from the perspective of the final protein fragments. Moreover, since most LHC sequences encode polyproteins (Koziol and Durnford, 2008), annotations greedily applied to the full-length sequences, as in the UniProt database (Koziol et al., 2007), are less accurate than those applied to the final protein fragments (i.e.,

References to Supplementary Table S1

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Koziol, A.G., Durnford, D.G., 2008. Euglena light-harvesting complexes are encoded by multifarious polyprotein mRNAs that evolve in concert. *Mol Biol Evol* **25**, 92–100.

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Supplementary Table S2. Quantitative Proteomic Analysis of Representative *Euglena Gracilis* Samples Using LC-ESI-Q-TOF-MS

A1				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
40	**20**	**153**	**LHCBM1-5**	**435530**	**435480**
27	**21**	**129**	**LHCBM6-6**	**292125**	**280648**
23	**23**	**147**	**LHCB4-CP29**	**281535**	**268402**
45	**43**	**200**	**PSBC-CP43**	**189103**	**187778**
63	**62**	**268**	**PSBB-CP47**	**179341**	**174607**
14	**8**	**97**	**LHCBM7-5**	**152378**	**154845**
53	**52**	**179**	**LHCE9-2**	**151339**	**152675**
20	**20**	**83**	**LHCBM5-11**	**108939**	**108990**
12	**12**	**74**	**PSBD-D2**	**93956**	**97203**
9	8	67	PSAB	93482	99937

A2				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
22	**21**	**121**	**LHCBM1-5**	**216038**	**216158**
48	**48**	**239**	**PSBB-CP47**	**135110**	**141268**
15	**15**	**112**	**LHCB4-CP29**	**133801**	**132445**
31	**31**	**163**	**PSBC-CP43**	**97094**	**102436**
36	**23**	**163**	**LHCE9-2**	**71760**	**75994**
22	**22**	**63**	**PSBA-D1**	**71213**	**55354**
20	**18**	**116**	**LHCBM6-7**	**71174**	**74319**
8	**5**	**69**	**LHCBM7-5**	**43861**	**45614**
9	9	61	PSAB	43389	44902
11	11	68	PSAA	38899	41586
9	**9**	**56**	**PSBD-D2**	**38259**	**40266**
13	**13**	**57**	**LHCBM5-13**	**34833**	**35840**

A3				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
34	10	118	**LHCE5-3**	217027	221040
34	34	130	**LHCBM8-2**	167901	169723
28	28	88	**LHCE11-1**	159113	164726
19	12	92	**LHCE10-2**	156839	155761
16	16	85	**LHCBM2-1**	154854	157320
38	37	132	**PSAA**	125847	130873
25	24	82	**LHCE6-5**	116950	123267
15	15	92	**PSAF**	112959	114694
15	5	83	**LHCE7-2**	96942	99359
16	16	116	LHCBM1-5	93079	93769
15	2	66	**LHCE13-7**	88524	90346

34	5	121	**LHCE5-7**	82747	82050
24	24	106	**PSAB**	81126	85385
20	20	112	**LHCBM8-4**	79330	78183
34	34	177	PSBB-CP47	75085	79888
22	8	108	**LHCE7-3**	73818	67562
13	13	88	LHCB4-CP29	70781	69436
27	27	156	PSBC-CP43	68453	71278
16	8	108	**LHCE8-2**	62973	65704
28	27	177	**PSAD**	61023	62046

A4				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
11	**11**	**65**	**PSAA**	**73198**	**71418**
13	**6**	**70**	**LHCE6-5**	**66278**	**70903**
14	**14**	**69**	**LHCE11-1**	**52229**	**50918**
6	6	28	LHCB4-CP29	48849	49421
23	**4**	**104**	**LHCE5-7**	**44212**	**44547**
11	**11**	**68**	**PSAF**	**43935**	**43973**
24	**5**	**110**	**LHCE5-3**	**42958**	**43283**
11	**10**	**61**	**LHCBM8-2**	**40557**	**37873**
4	**4**	**32**	**PSAB**	**37786**	**39524**
12	12	80	PSBB-CP47	34879	33172
7	**7**	**44**	**LHCBM2-1**	**33974**	**32868**
11	11	70	PSBC-CP43	29274	28693
13	**8**	**71**	**LHCAE7-3**	**27336**	**28647**
23	**22**	**133**	**PSAD**	**26199**	**26528**
4	**3**	**33**	**LHCE7-1**	**19236**	**19259**
17	**7**	**80**	**LHCE8-2**	**16337**	**16501**
10	**6**	**55**	**LHE10-2**	**16148**	**16078**

A5				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
7	7	27	**LHCBM1-4**	69267	75768
28	28	142	**PSBB-CP47**	61951	62876
12	12	88	**LHCBM1-5**	61207	63583
16	16	114	PSAD	59288	58060
25	25	136	**PSBC-CP43**	58589	58355
12	12	61	**PSBA-D1**	52719	56716
7	7	50	PSAA	32069	31767
21	21	127	**LHCE9-2**	25759	27856
5	5	31	LHCE3-5	18050	17379
6	6	37	**PSBD-D2**	16062	17721
10	9	49	PSAB	14592	15343

A6				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	

40	40	215	**PSBB-CP47**	133490	131562
27	26	162	**PSBC-CP43**	90215	88543
12	12	47	**PSBA-D1**	65284	60643
7	4	50	LHCE3-5	54338	52700
26	26	141	**LHCE9-2**	45416	44755
4	*4*	*23*	LHCE5-7	*41277*	*39864*
5	2	49	**LHCBM1-5**	26798	26786
10	10	32	**PSBD-D2**	26600	25868
6	1	58	LHCE1-7	25305	23898
10	10	52	**LHCB4-CP29**	18401	17622
5	5	45	LHCE4-1	16955	16290
11	11	65	LHCE12-2	12763	12555

A7

				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
17	**10**	**90**	**LHCE3-5**	**197199**	**199363**
21	**2**	**139**	**LHCE1-7**	**129910**	**131640**
21	**7**	**121**	**LHCE2-1**	**87273**	**85212**
31	**12**	**155**	**LHCE1-6**	**86606**	**86393**
15	**15**	**107**	**LHCE12-2**	**45053**	**44618**
3	3	13	PSBB-CP47	1755	1836
8	8	51	LHCBM1-5	38390	38055
21	**1**	**125**	**LHCE2-2**	**34051**	**33150**
15	**1**	**102**	**LHCE4-1**	**32711**	**32717**

A8

				sample 1	sample 2
Peptide count	Unique peptides	Confidence score	Description	Normalized abundance	
55	**54**	**135**	**LHCBM1-5**	**1004668**	**1002999**
7	**7**	**15**	**LHCBM1-1**	**175163**	**48792**
18	**1**	**90**	**LHCBM5-11**	**140005**	**139821**
10	**9**	**97**	**LHCBM6-7**	**113955**	**118107**
9	**8**	**71**	**LHCBM7-5**	**102344**	**102144**
9	9	48	LHCA1-2	73668	72432
5	1	54	LHCA2-1	60381	60041

Supplemental Table S2 : Table A1–A8 present mass spectrometry results for eight representative *Euglena gracilis* samples (Sample 1 and Sample 2 per group) following hrCN-PAGE separation and LC-ESI-Q-TOF-MS analysis. Only proteins with a normalized abundance ≥2.5% of the total were included. For each protein, the peptide count, number of unique peptides, identification confidence score, protein description, and normalized abundance in both samples are shown. Protein identification was performed using Progenesis software against public (UniProt) and *in-house* databases.

Supplemental Table S3. Composition of the photosystem I and II cores complex in *Euglena gracilis*

Protein	Identified by	E: Score/Identified Peptides	S: Score/Identified Peptides	Accession	References
Photosystem I					
PsaA	E/S/P	153/16	250/12	EG_transcript_158	(Sobotka et al., 2017); This work
PsaB	E/S/P	142/15	29/3	NP_041907.1	(Sobotka et al., 2017); This work
PsaC	E/S/P	15/4	14/5	NP_041934.1	(Sobotka et al., 2017); This work
PsaD	E/S/P	199/18	44/4	EG_transcript_12295/EG_transcript_3688	(Sobotka et al., 2017); This work
PsaE	E/P	82/9	—	EG_transcript_31070	(Sobotka et al., 2017); This work
PsaF	E/P	76/12	—	EG_transcript_10340	(Sobotka et al., 2017); This work
PsaJ	P	—	—	YP_002720092.1	(Sobotka et al., 2017); (Bennett and Triemer, 2015); This work
PsaM	P	—	—	NP_041896.1	(Schlunegger and Stutz, 1984); This work
Photosystem II					
PsbA (D1)	E/P	123/20	—	EG_transcript_13288/NP_041895.1	(Sobotka et al., 2017); This work
PsbB(CP47)	E/S/P	309/58	378/19	EG_transcript_899	(Sobotka et al., 2017); This work
PsbC (CP43) (VII) (34kDa)	E/S/P	212/29	415/19	NP_041892.1	(Sobotka et al., 2017); This work
PsbD (D2)	E/S/P	140/16	274/14	EG_transcript_10715/NP_041889.2	(Sobotka et al., 2017); This work
PsbE (cyt559α)	E/S/P	14/4	122/8	NP_041908.1	(Cushman et al., 1988); This work
PsbF (cyt559β)	S/P	—	25/2	NP_041909.1	(Cushman et al., 1988); This work
PsbH (10kDa)	E/P	16/2	—	NP_041944.1	(Sobotka et al., 2017); This work
PsbI	E/S/P	14/2	43/3	NP_041904.1	(Sobotka et al., 2017); This work
PsbJ	P	—	—	NP_041911.1	(Jenkins et al., 1995); This work
PsbK	P	—	—	NP_041898.1	(Jenkins et al., 1995); This work
PsbL	P	—	—	NP_041910.1	(Jenkins et al., 1995); This work
PsbM	E/S/P	86/8	68/3	EG_transcript_7656	This work
PsbN	P	—	—	NP_041943.1	(Hallick et al., 1993); This work
PsbO (OEE1)	E/P	12/2	—	EG_transcript_15767/EG_transcript_8709	(Sobotka et al., 2017); This work
PsbP (OEE2)	E/P	88/10	—	EG_transcript_13851/EG_transcript_14464/EG_transcript_17799	(Sobotka et al., 2017); This work
PsbQ (OEE3)	E/P	146/24	—	EG_transcript_25934	(Sobotka et al., 2017); This work
PsbR	P	—	—	EG_transcript_22790	This work
PsbT (PsbTc) (ycf8)	P	—	—	NP_041945.1	(Jenkins et al., 1995); This work
PsbW	E/P	16/5	—	EG_transcript_30510	This work
PsbX	P			EG_transcript_39502	This work
PsbY	P	—	—	EG_transcript_32529	This work
PsbZ (ycf9)	S/P	—	15/2	NP_041931.1	(Sobotka et al., 2017); This work

Psb27	E/P	42/5	—	EG_transcript_16063/EG_transcript_16166/EG_transcript_16389	(Sobotka et al., 2017); This work
Psb28	P	—	—	EG_transcript_28462	This work
Psb29	P	—	—	EG_transcript_17545	This work
Psb30 (ycf12)	P	—	—	NP_041897.1	(Bennett and Triemer, 2015); This work
Psb32	P	—	—	EG_transcript_17812/EG_transcript_20226	This work
Psb33	P	—	—	EG_transcript_22691	This work
Ycf48	P	—	—	EG_transcript_12174	(Sobotka et al., 2017); This work

E: Liquid chromatography-Electrospray-ionisation quadrupole time-of-flight mass spectrometry from complete band from CN-PAGE. S: Tandem mass spectrometry from isolated spots from the 3D gels. P: Phylogenomic approach for conserved subunits.

“Accession” gives either the NCBI accession number, or the numeric part of the corresponding transcript accession(s) in the Euglena gracilis dataset used in Van Vlierberghe et al. (2021) (and originally downloaded from ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2019/01/PXD009998/Euglena_translated_transcriptome.fasta),

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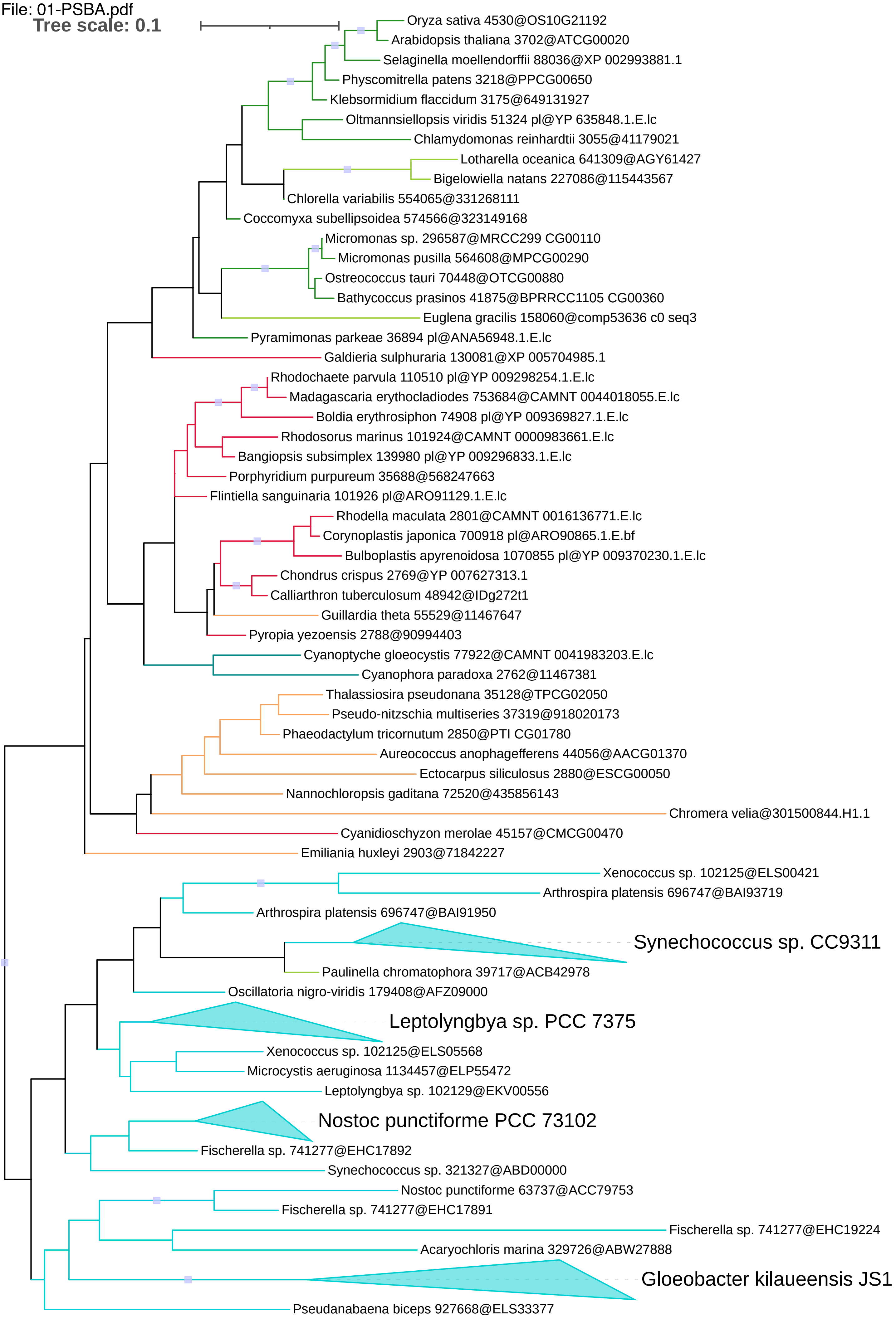

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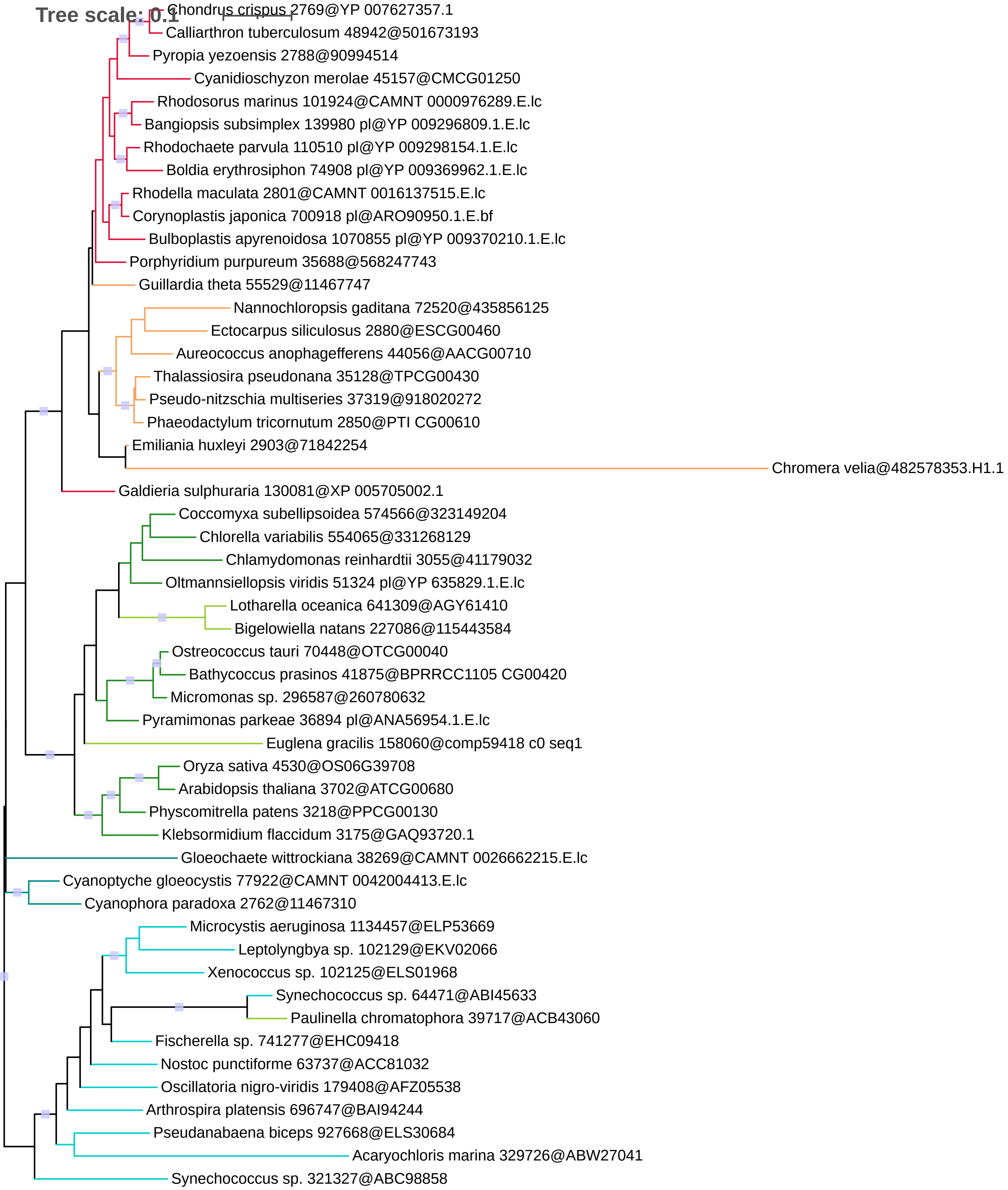

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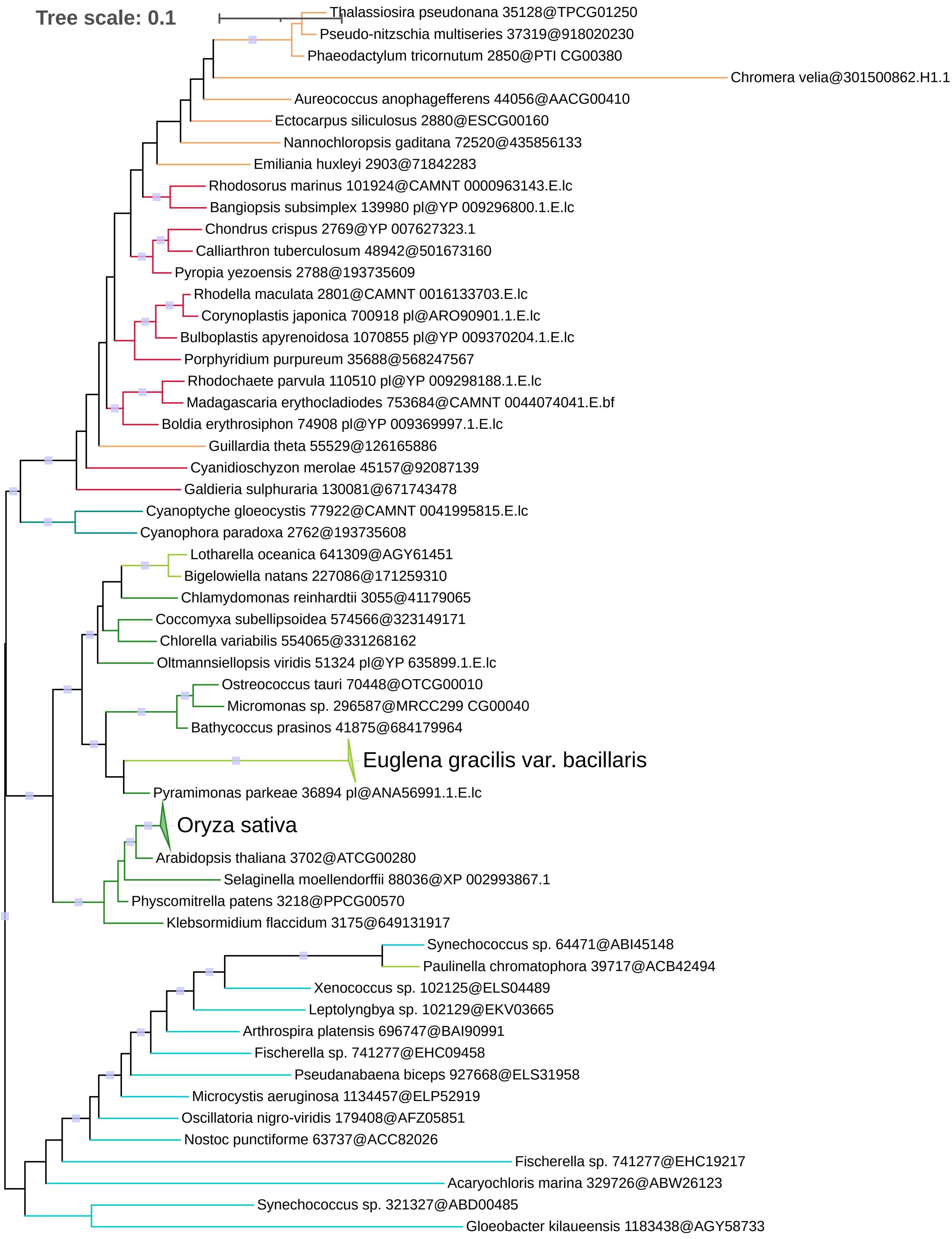

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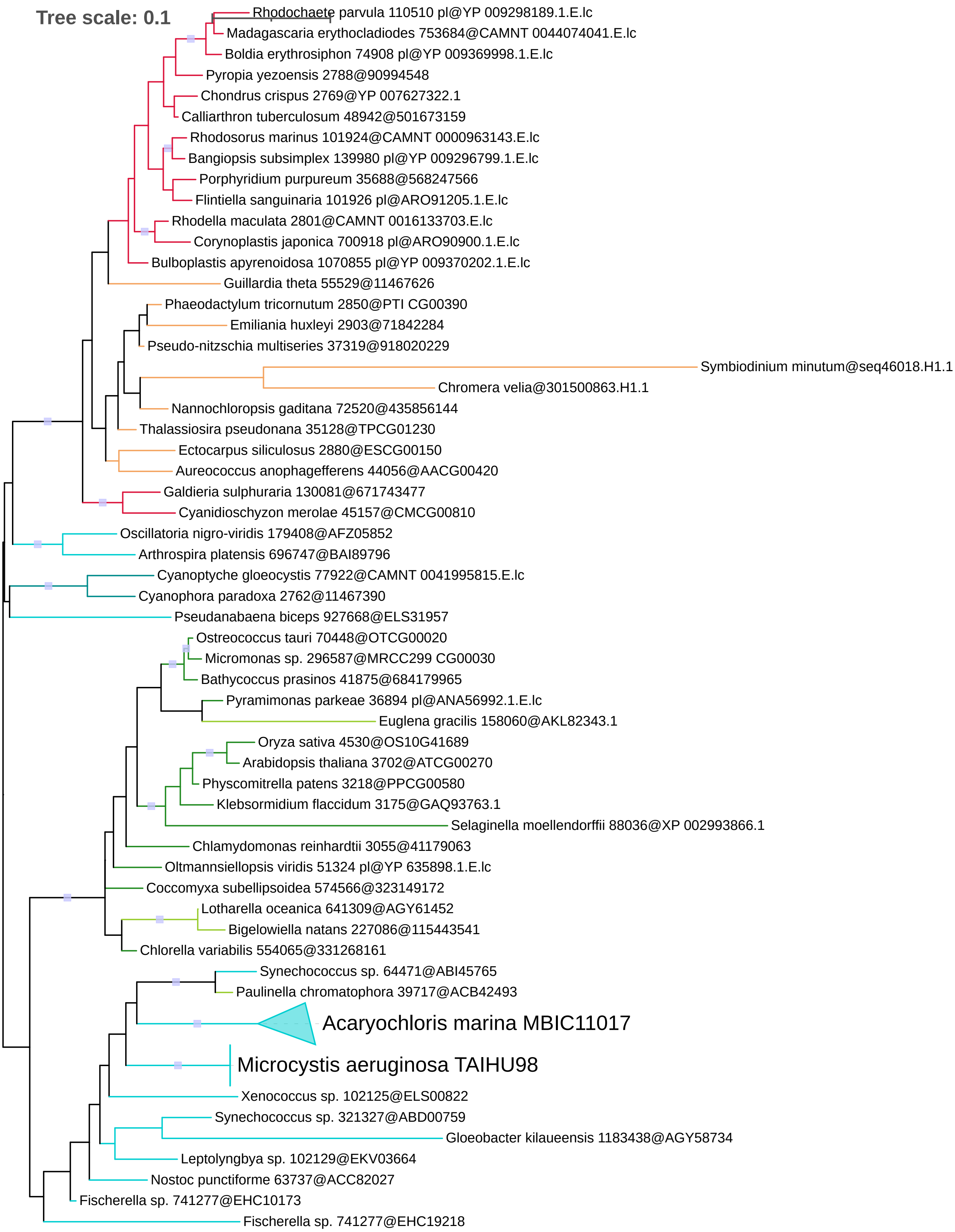

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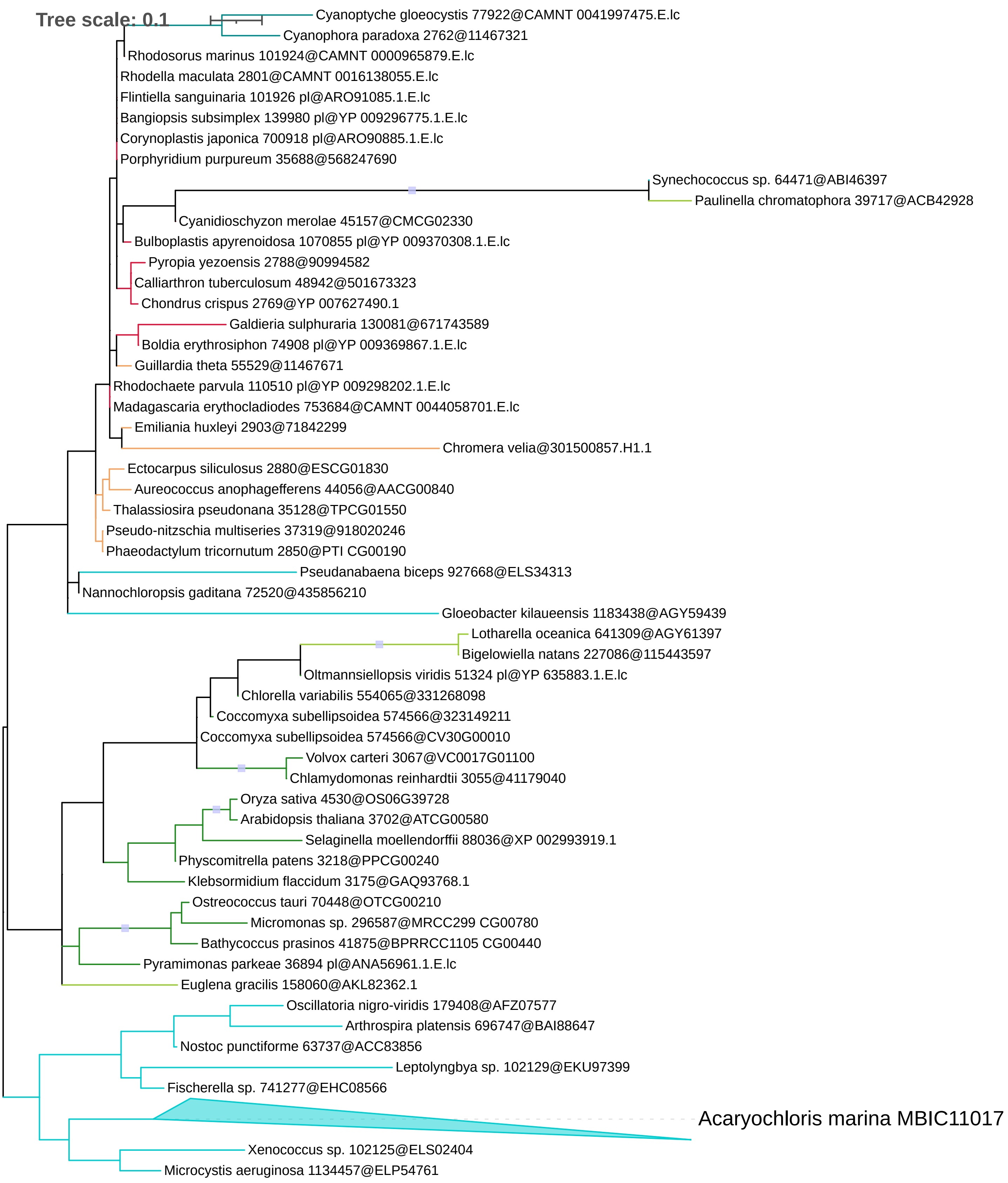

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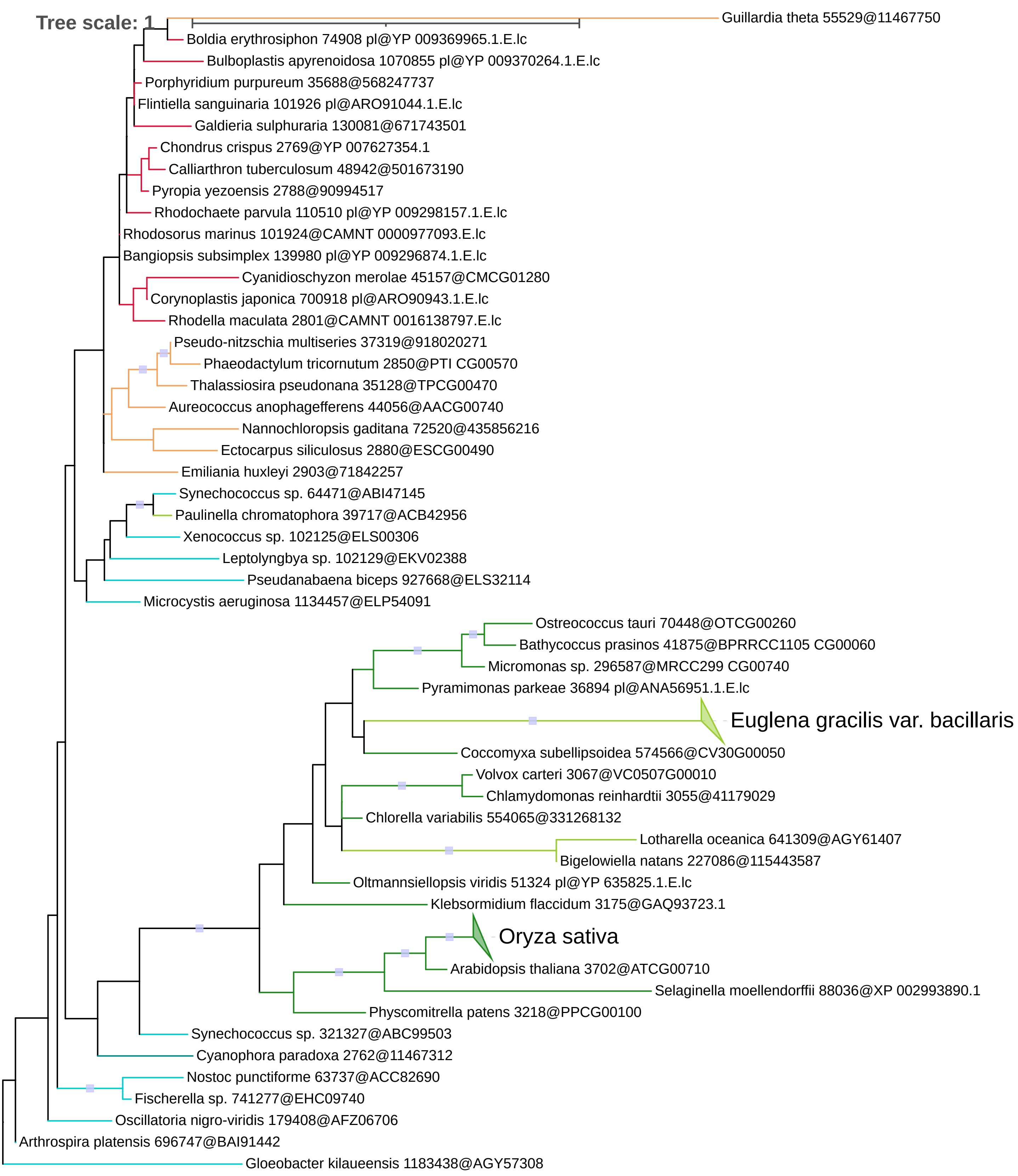

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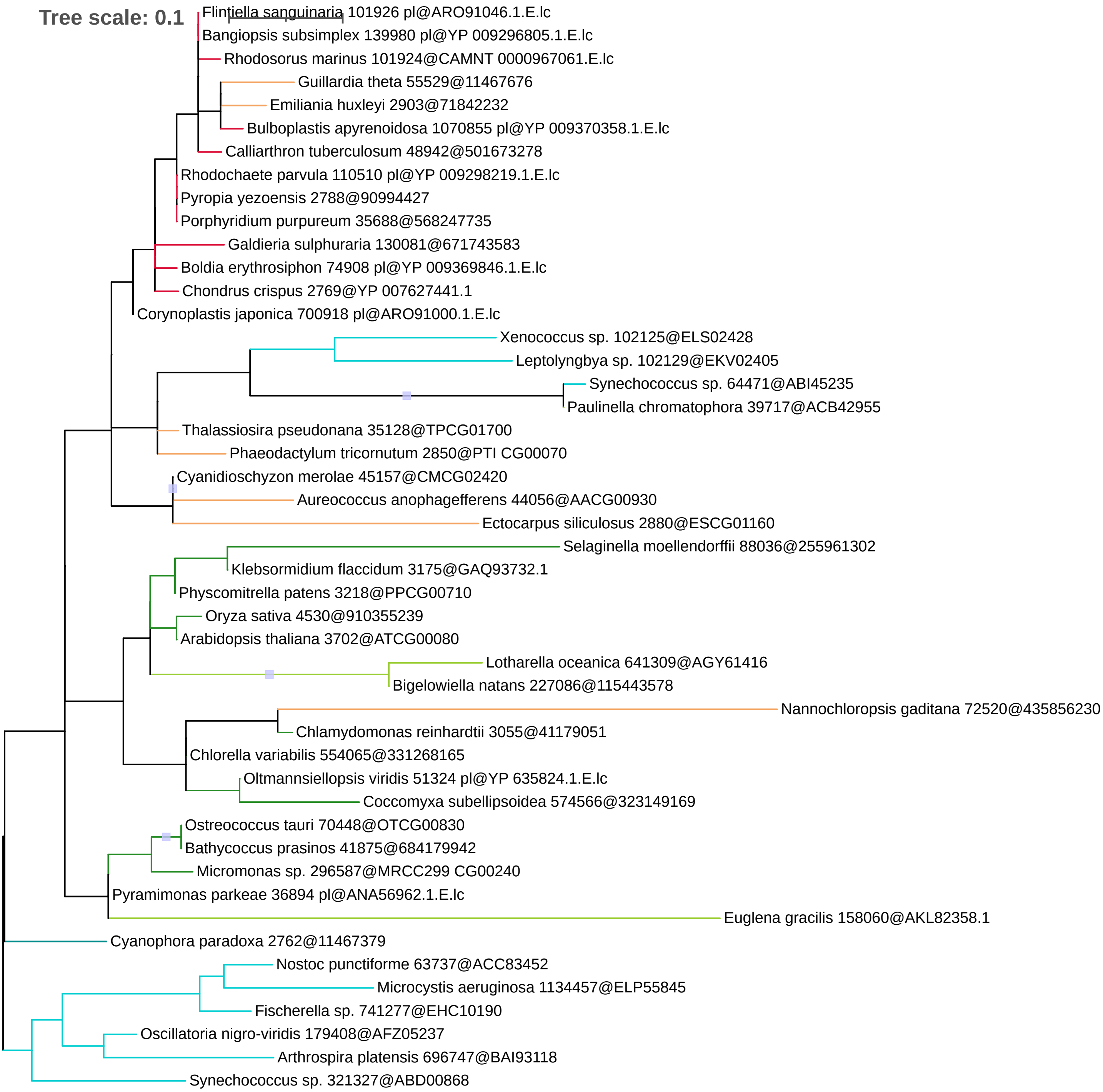

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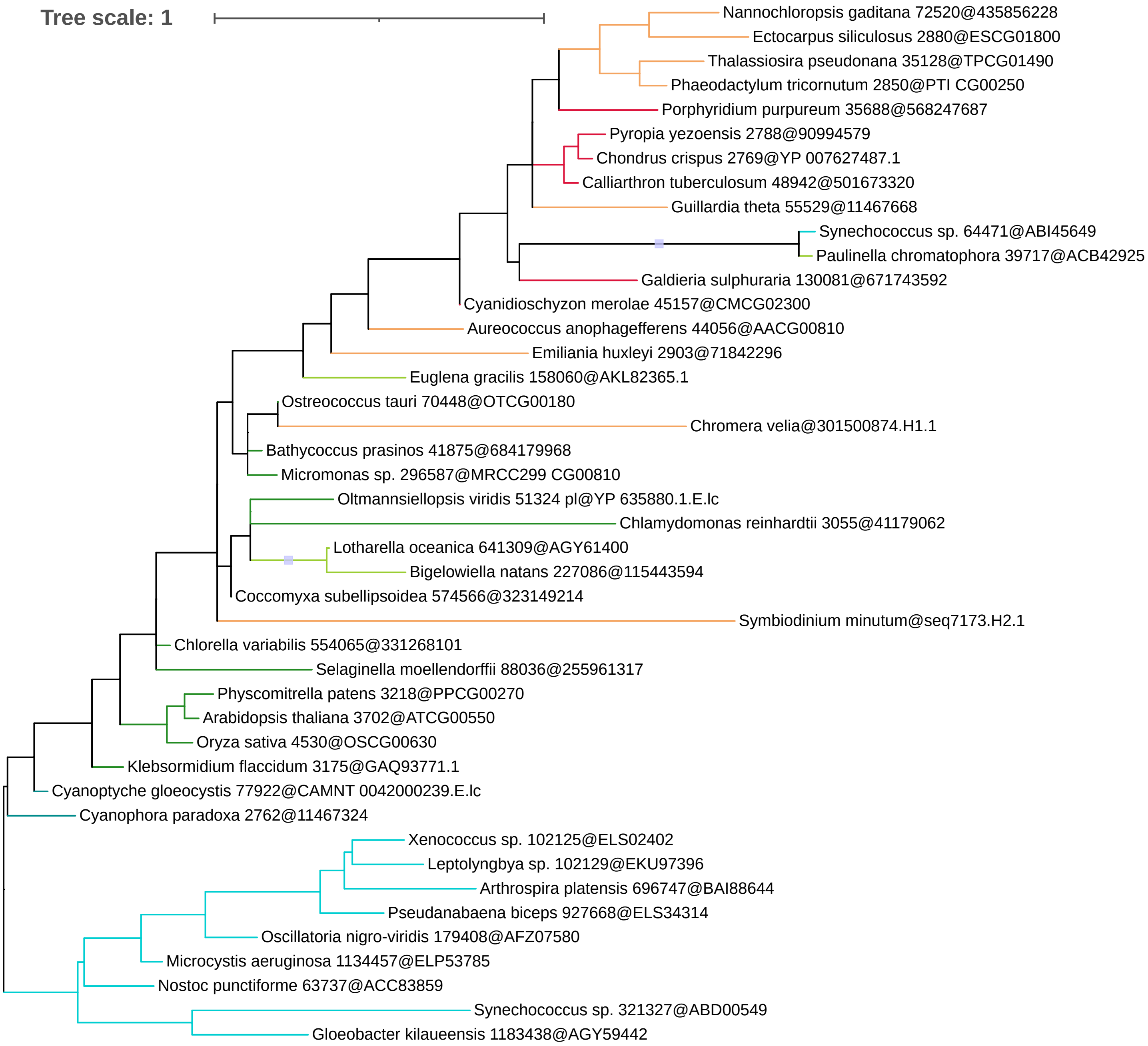

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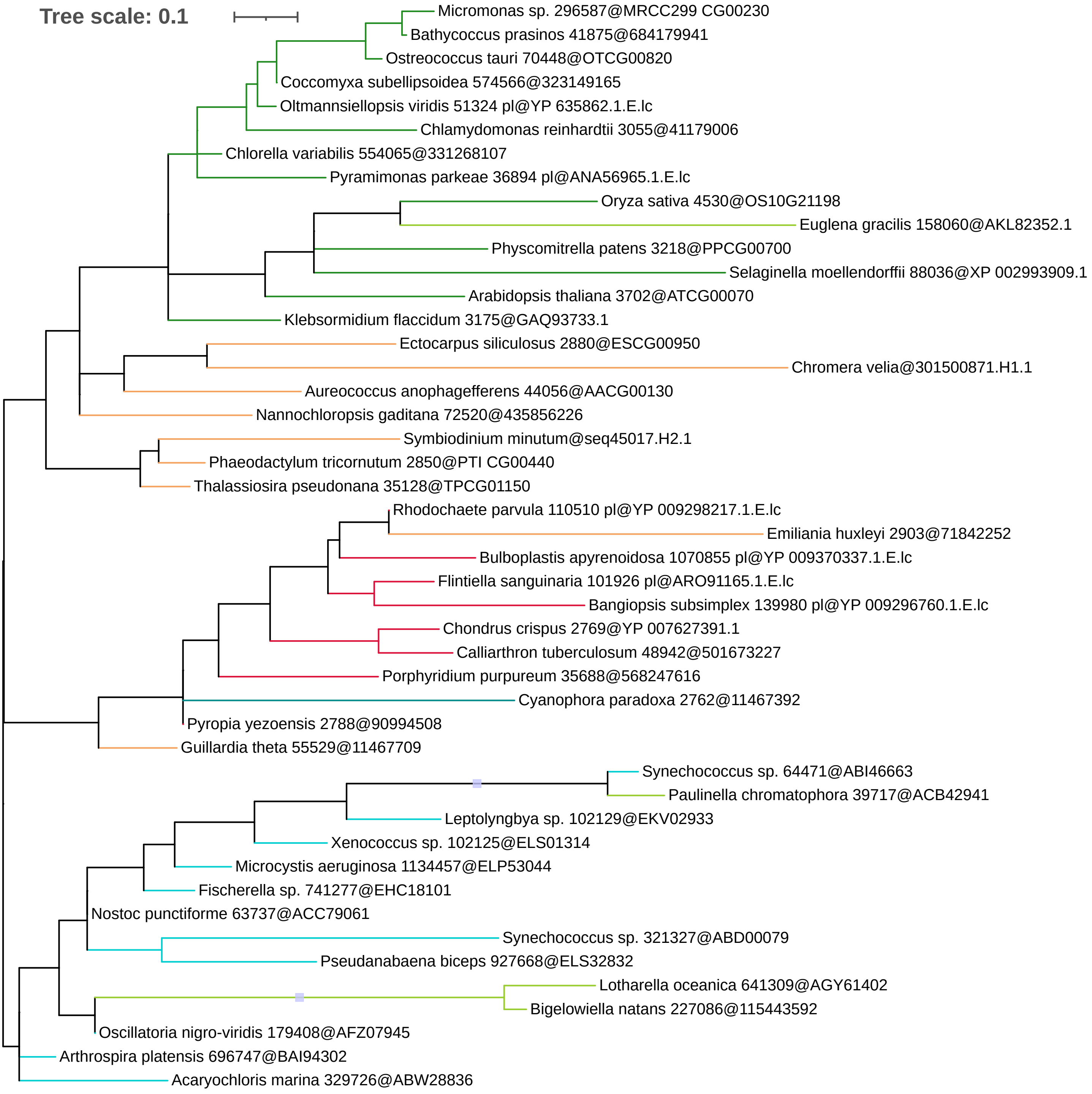

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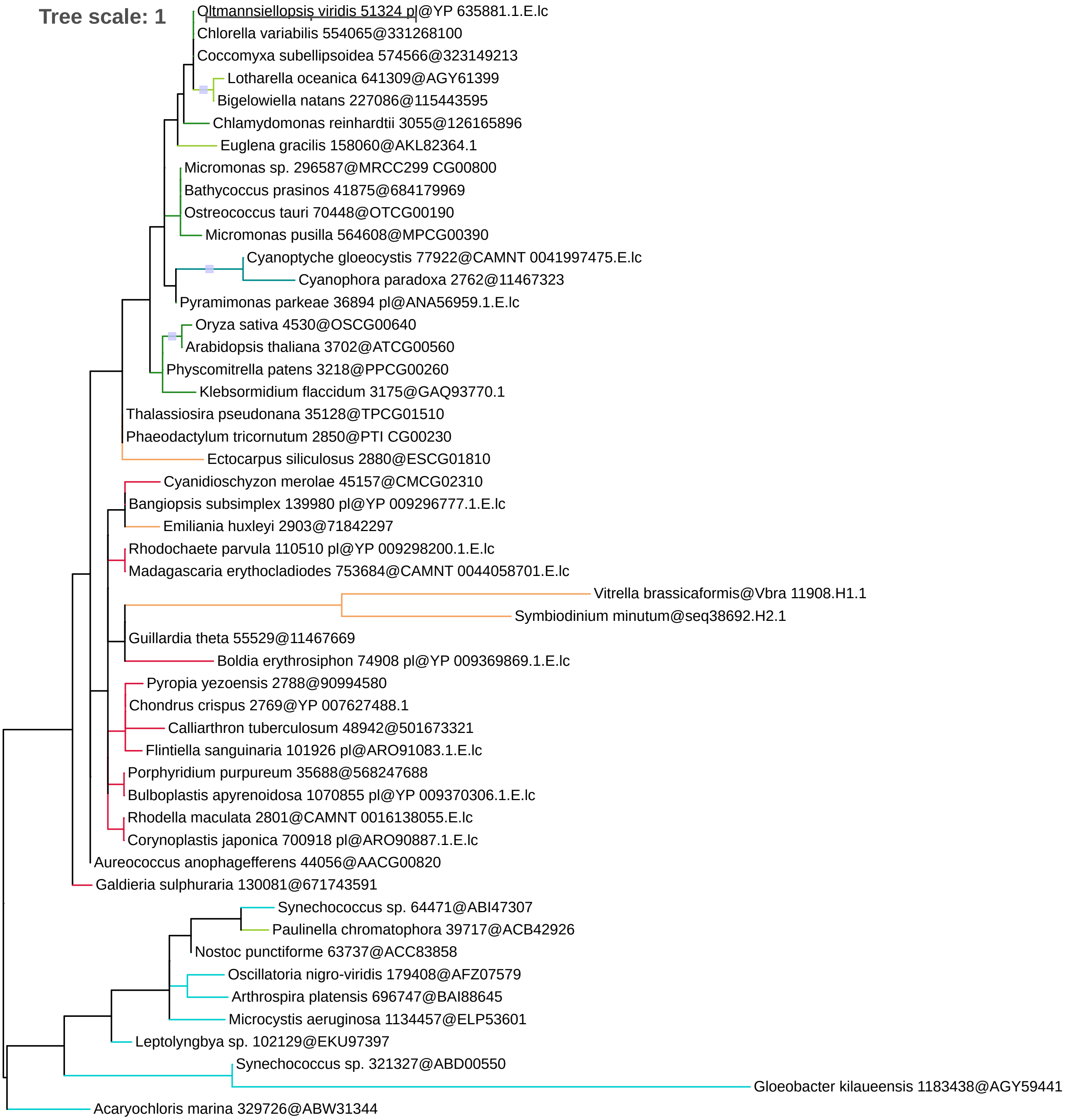

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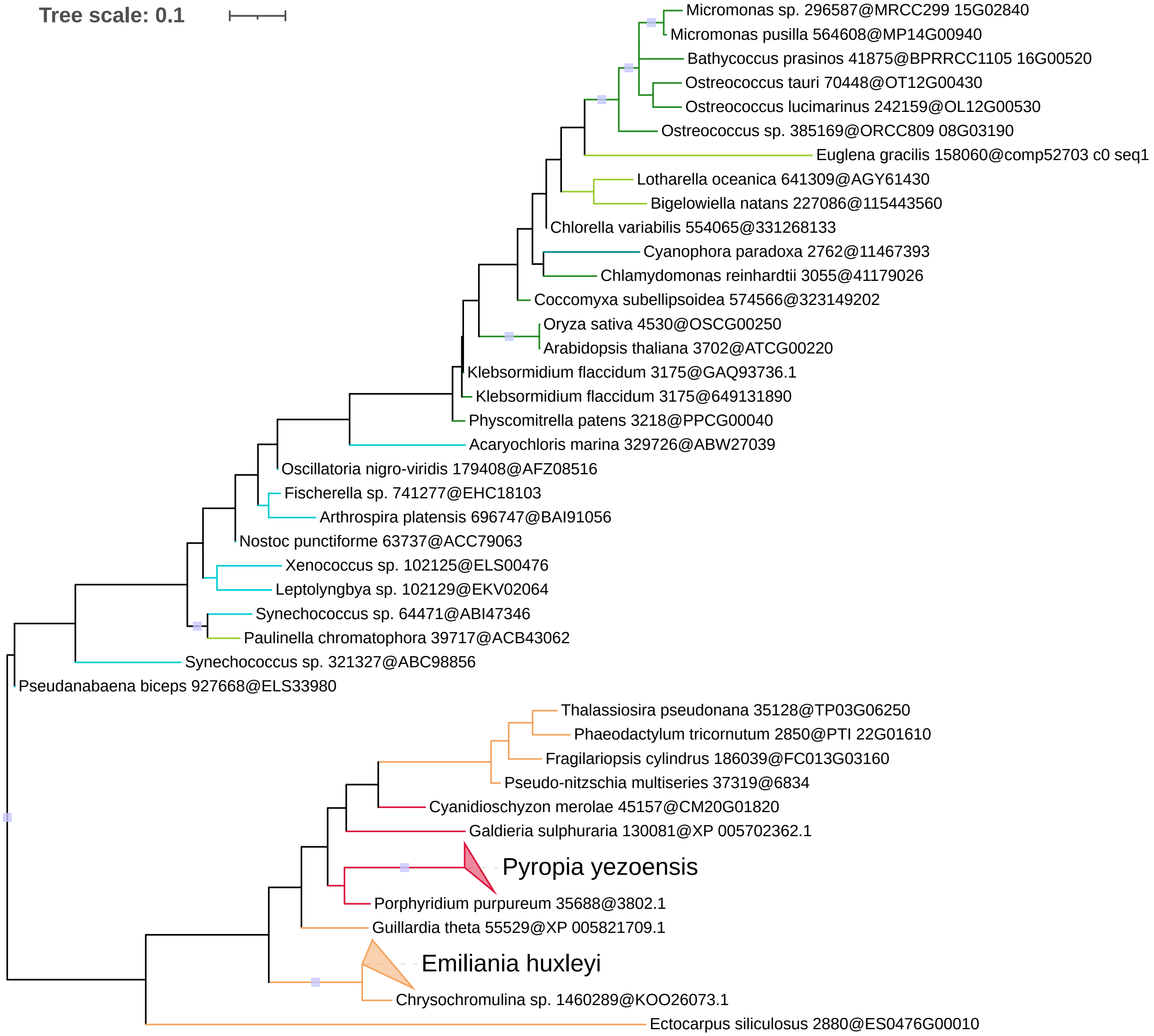

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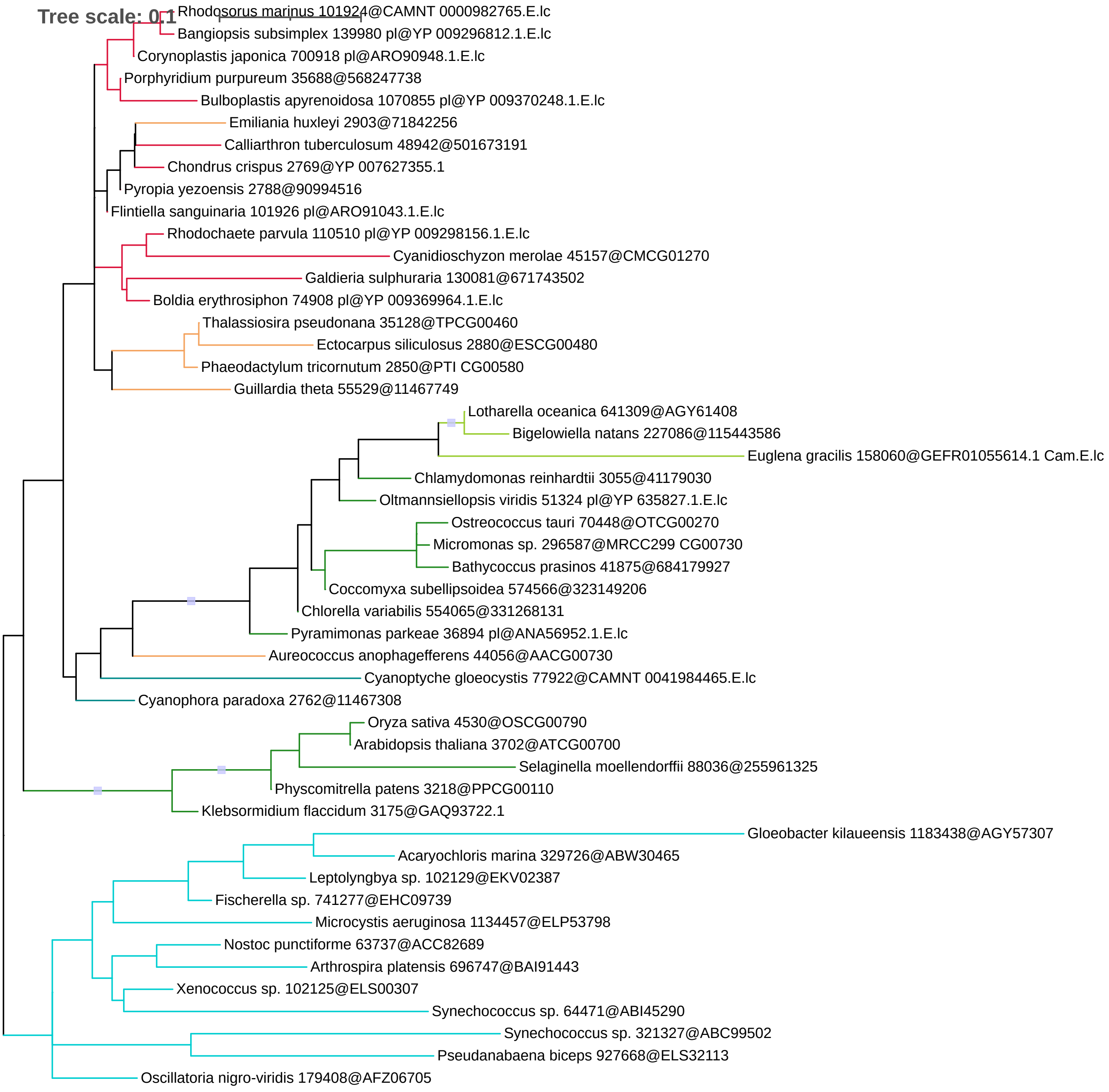

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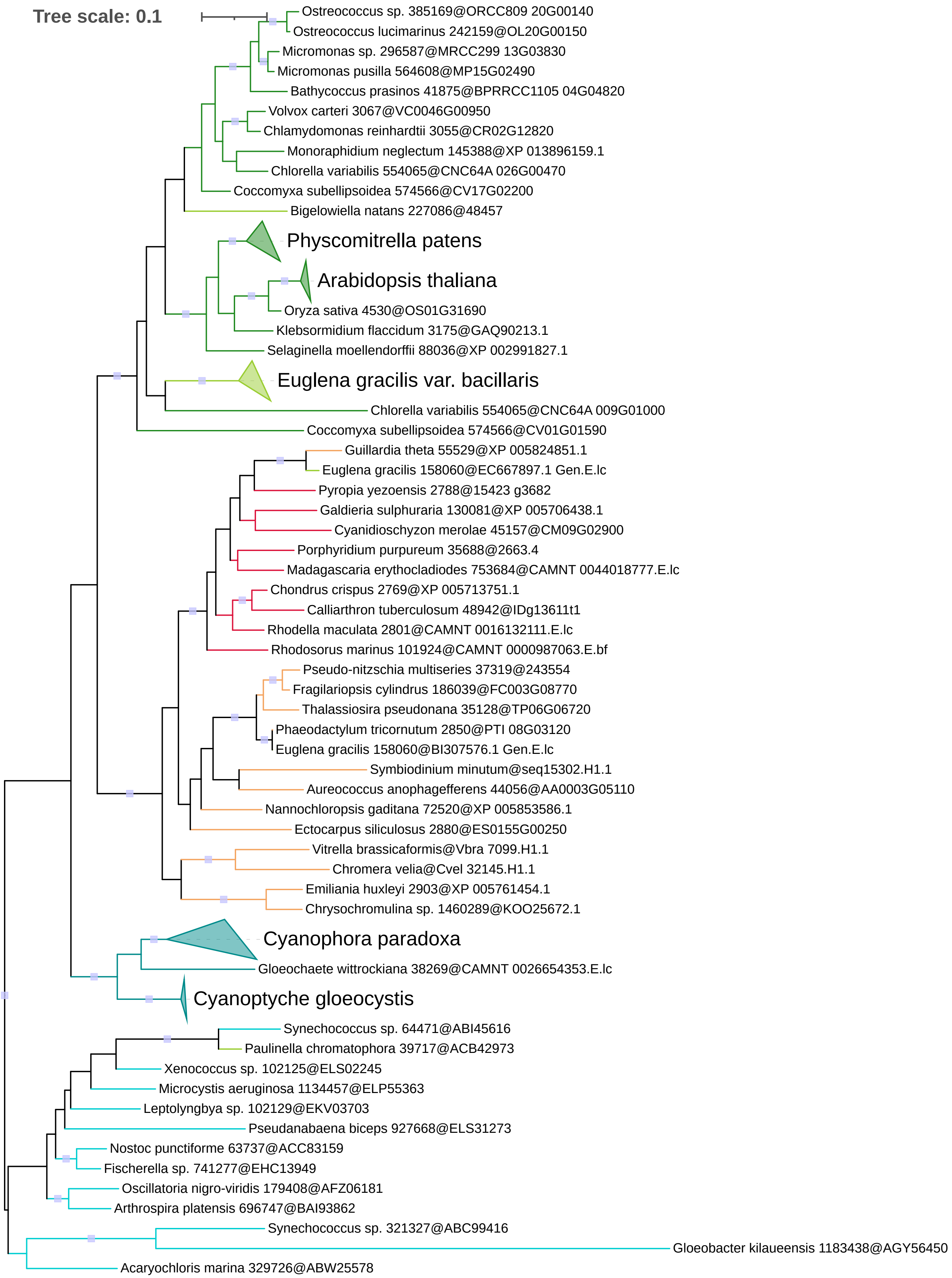

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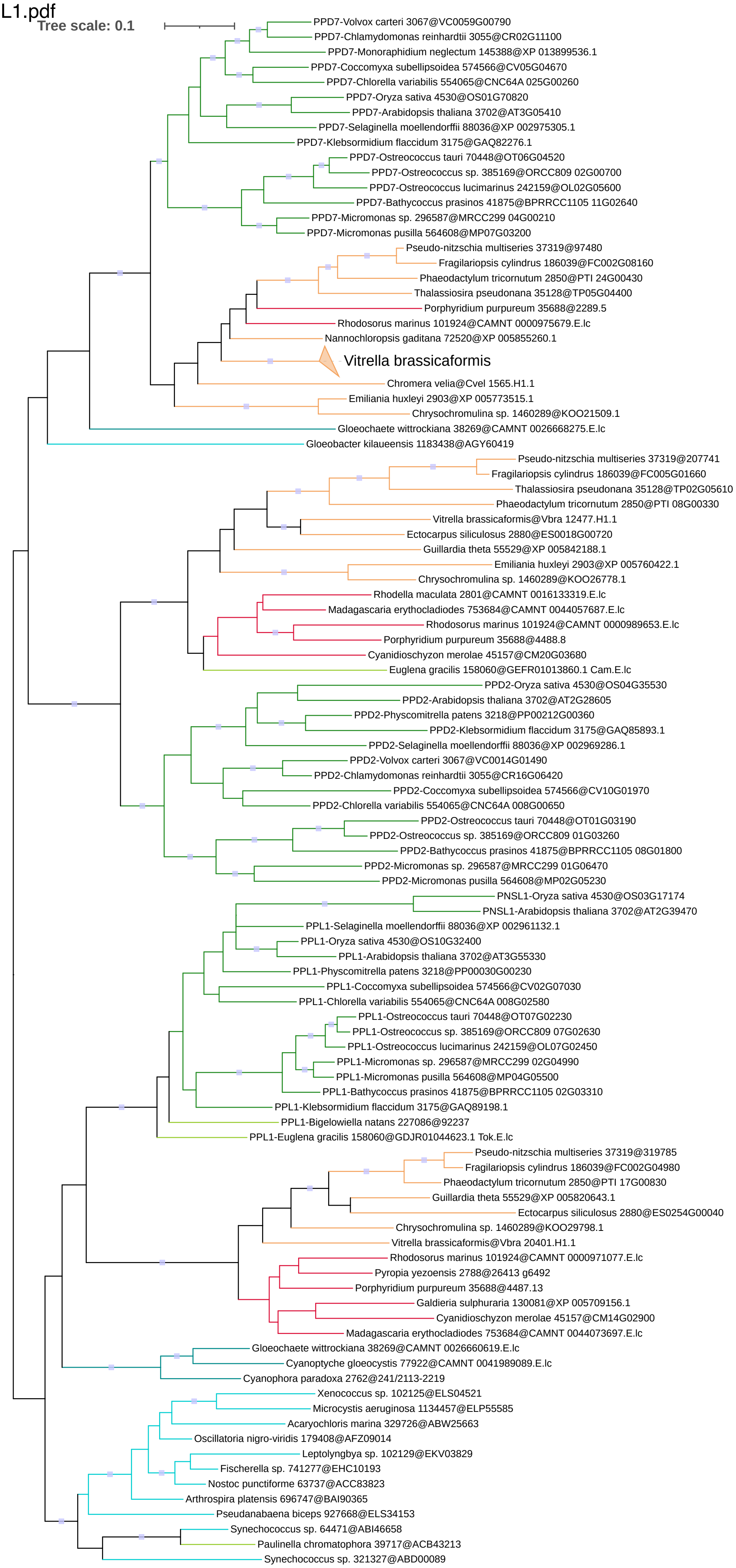

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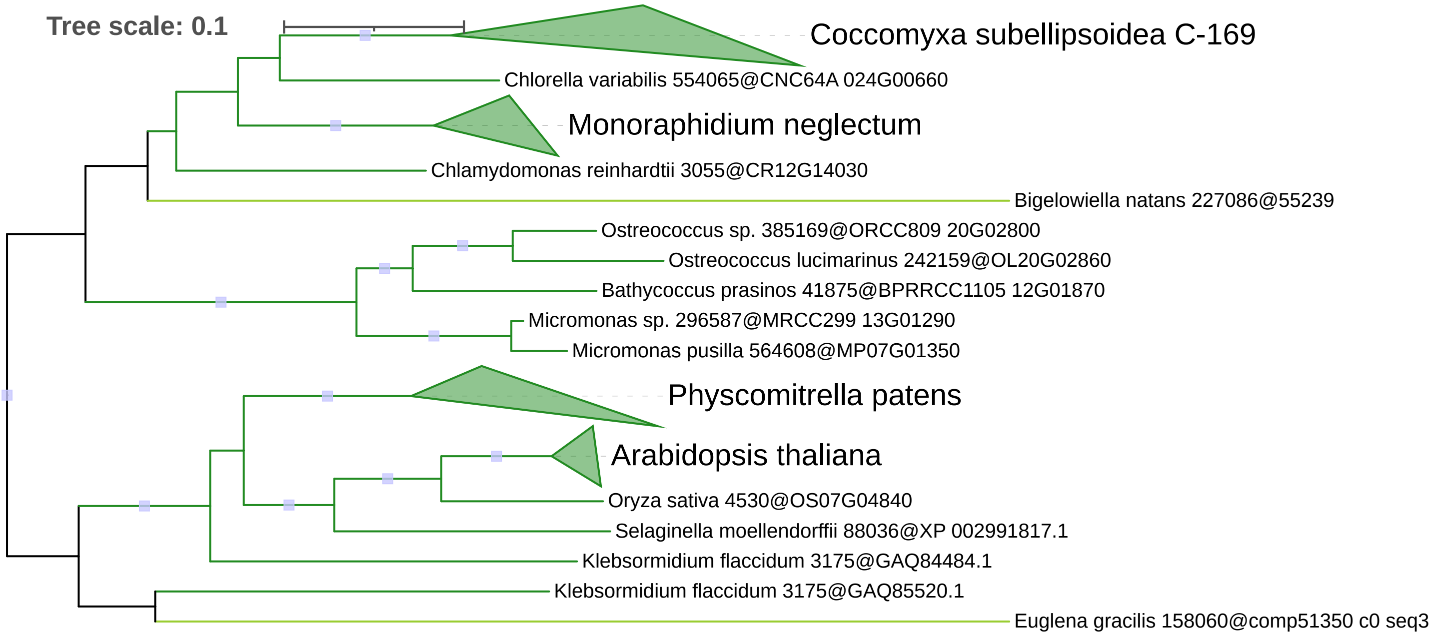

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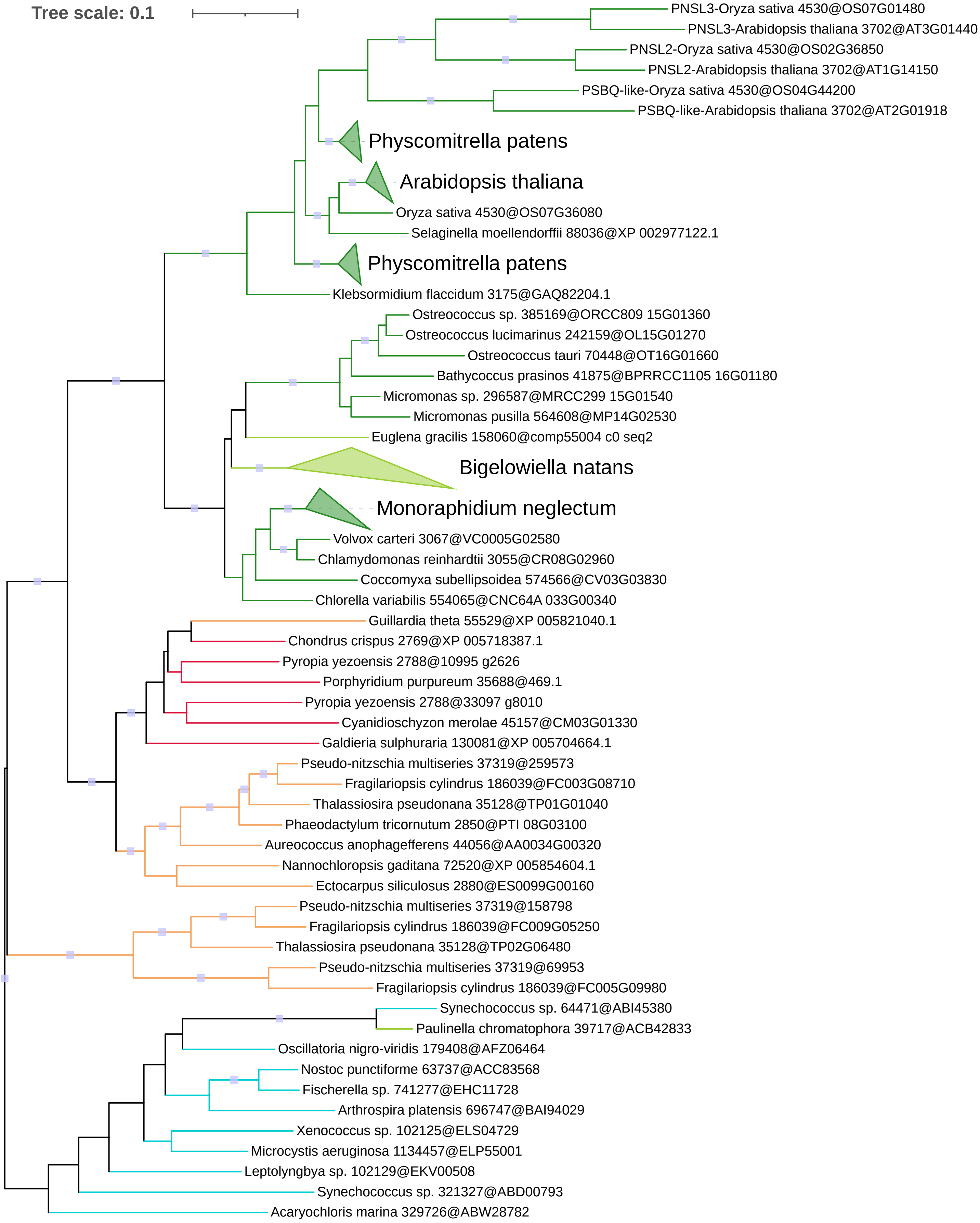

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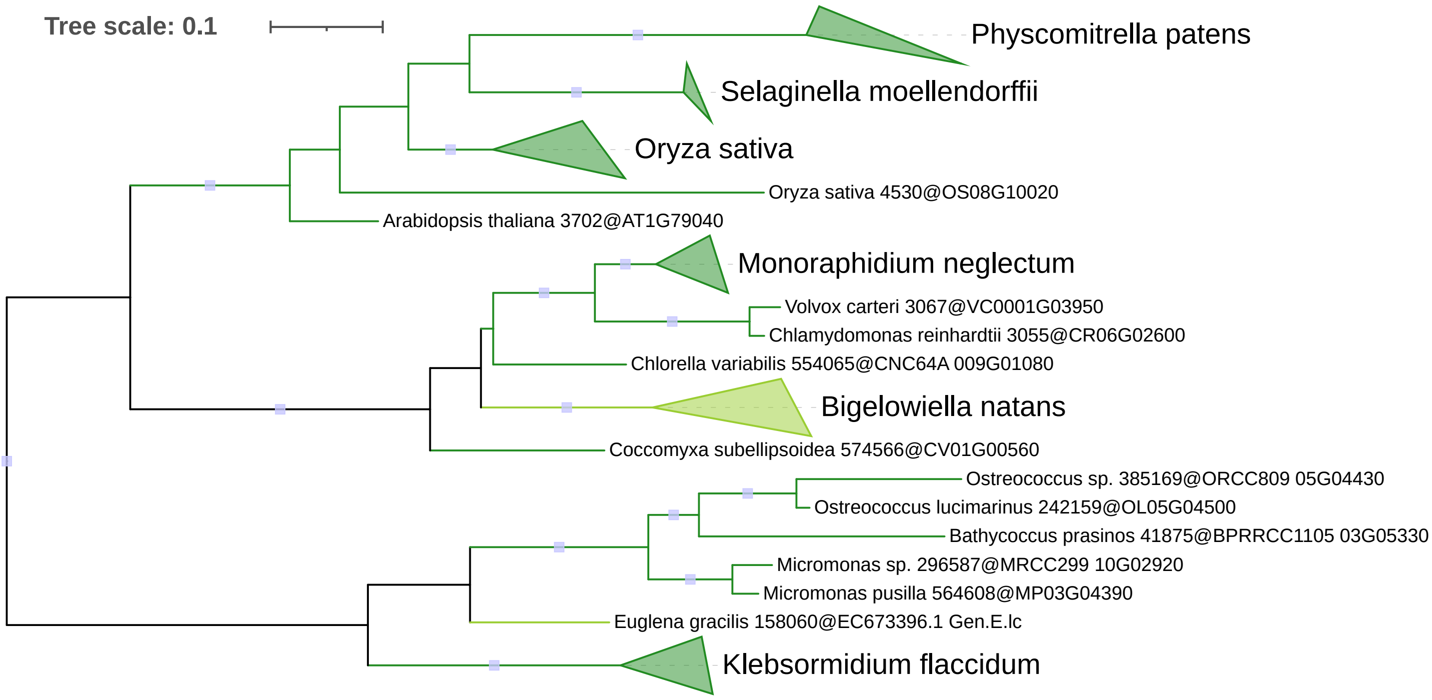

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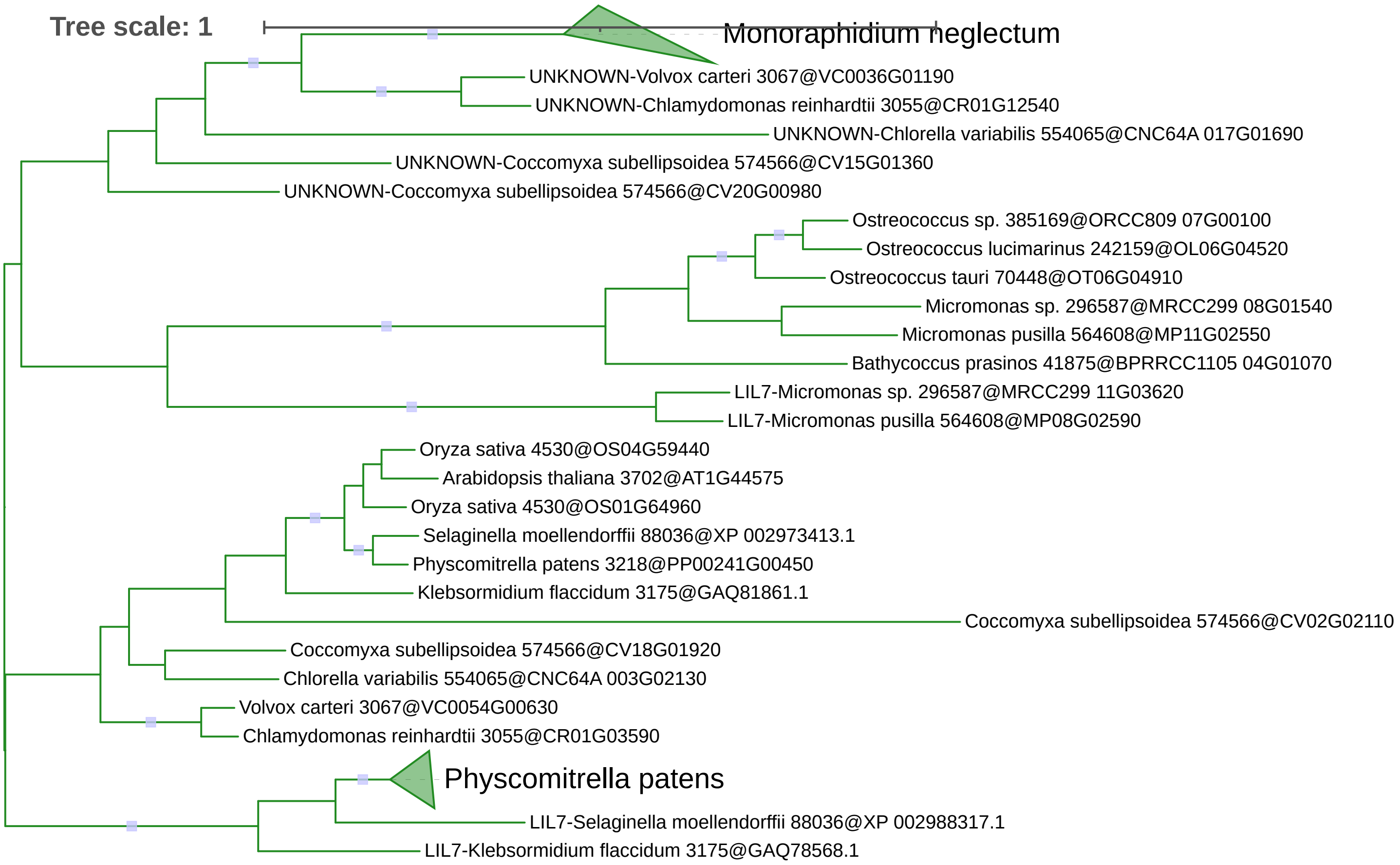

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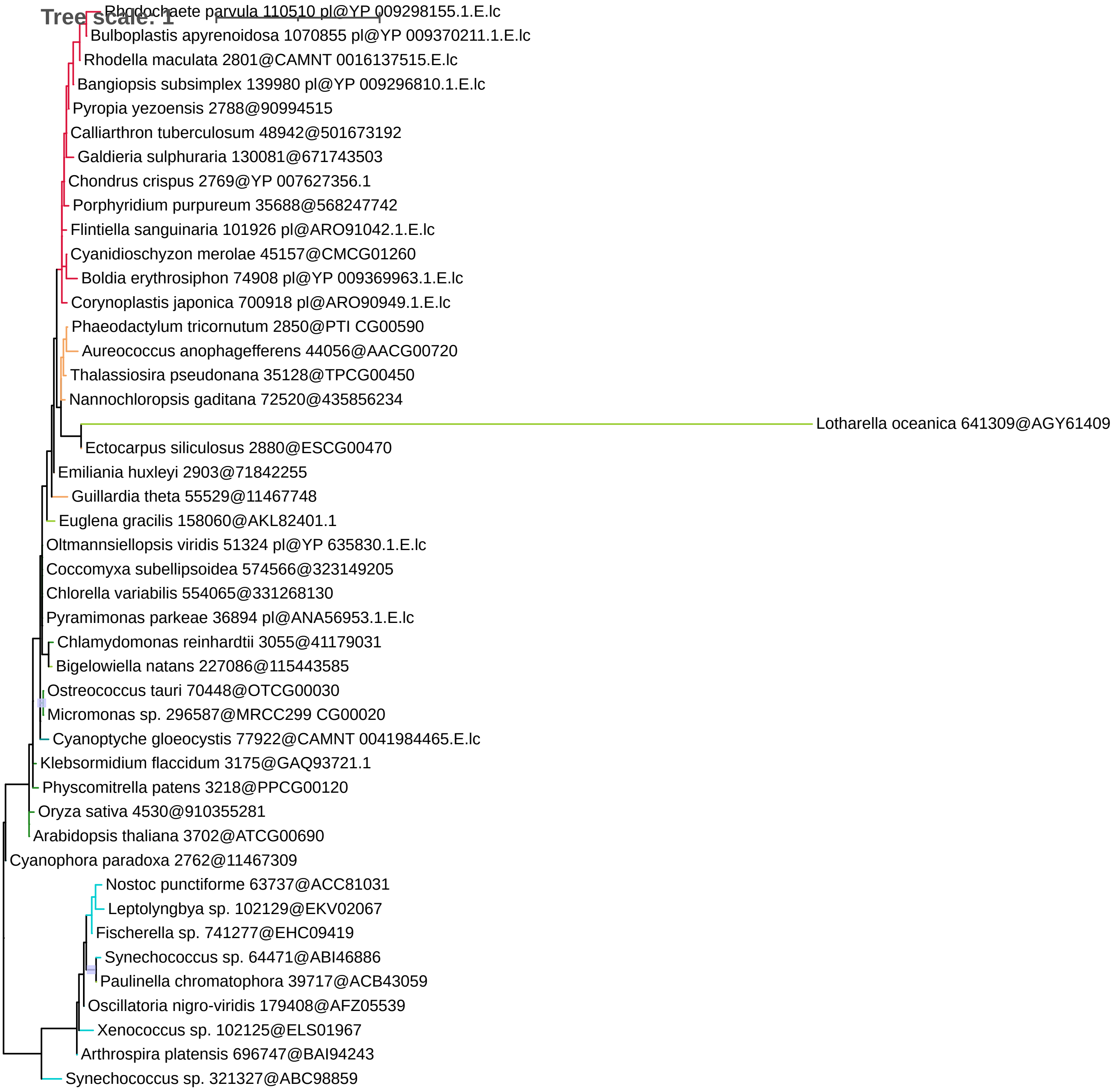

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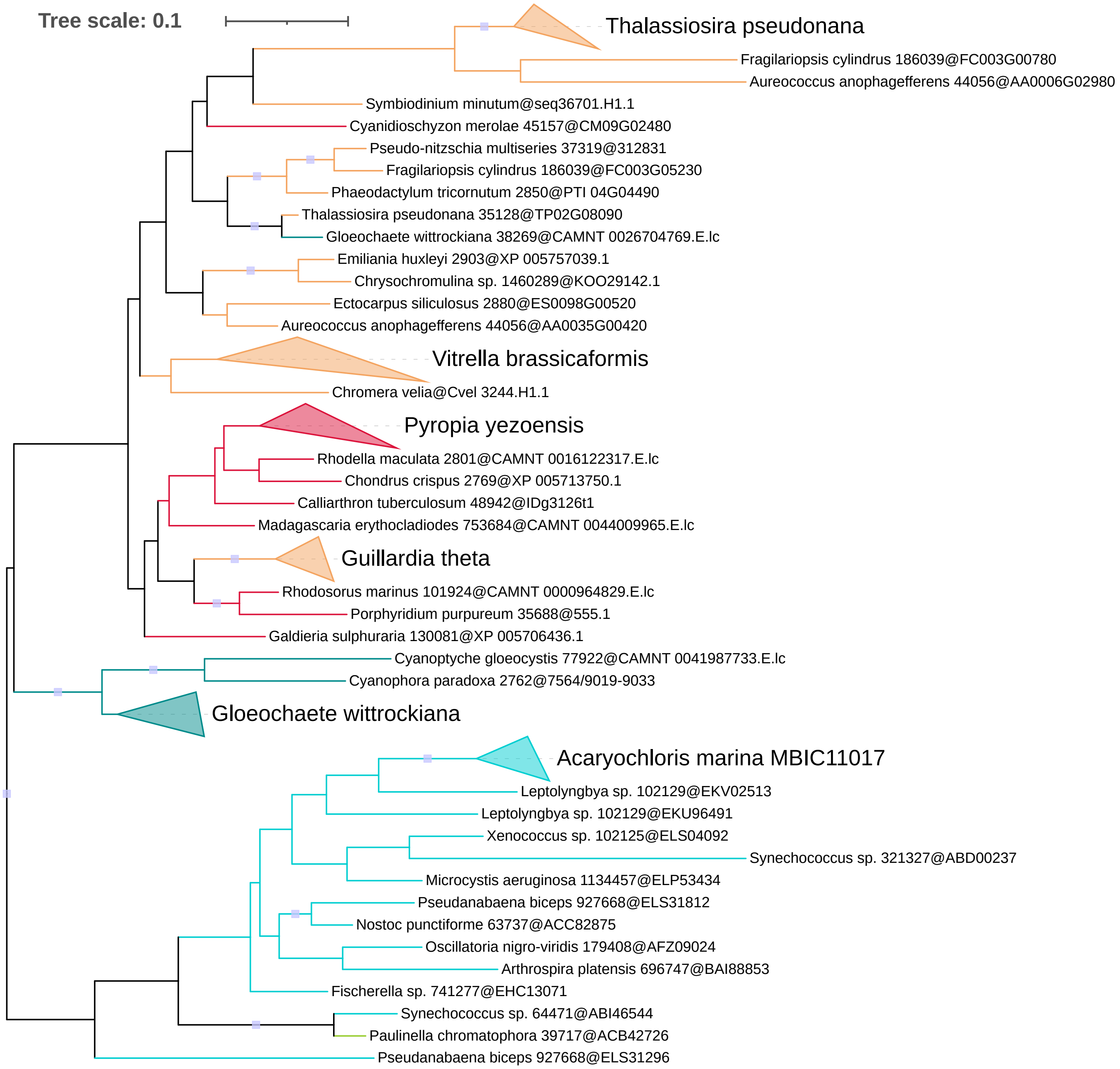

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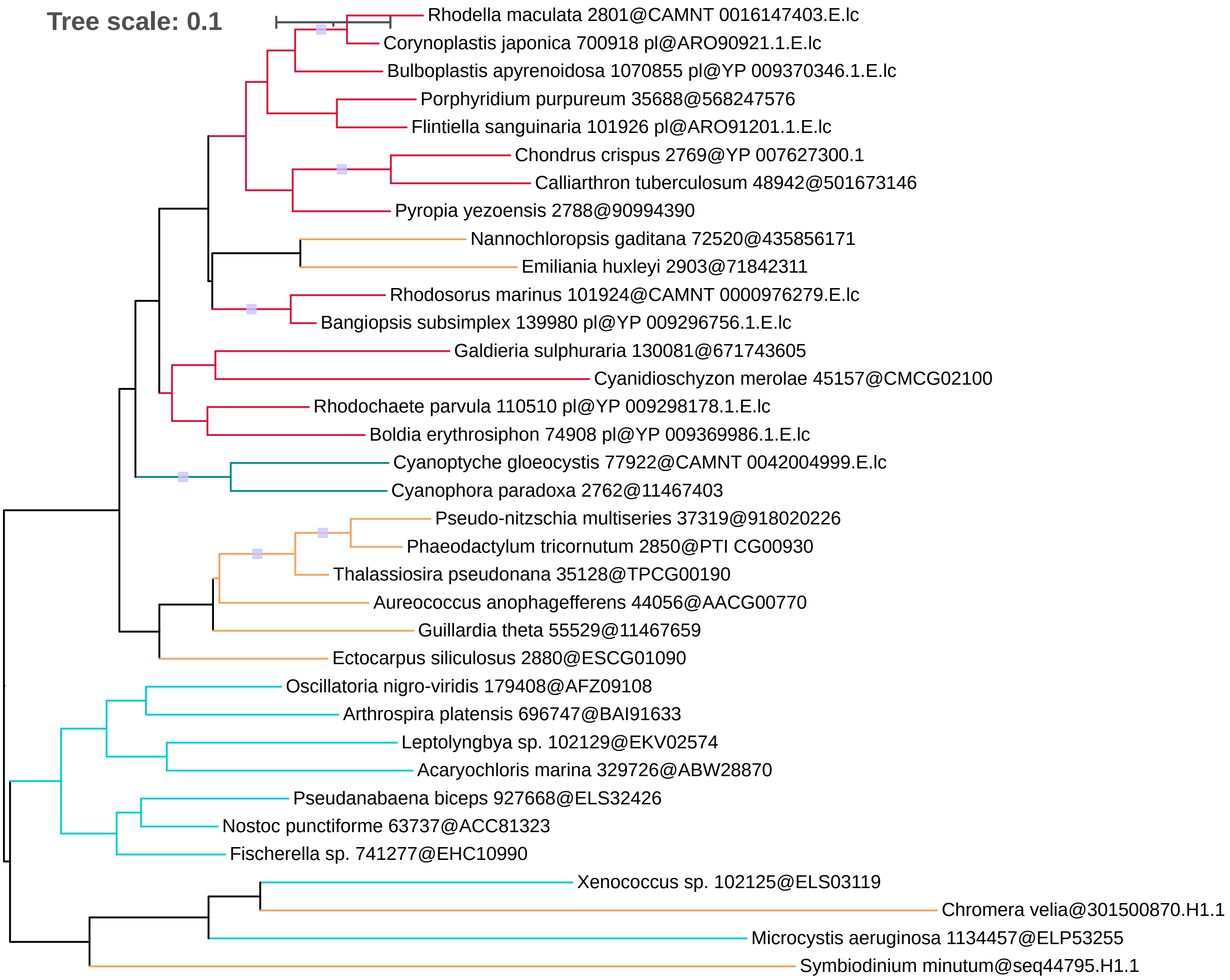

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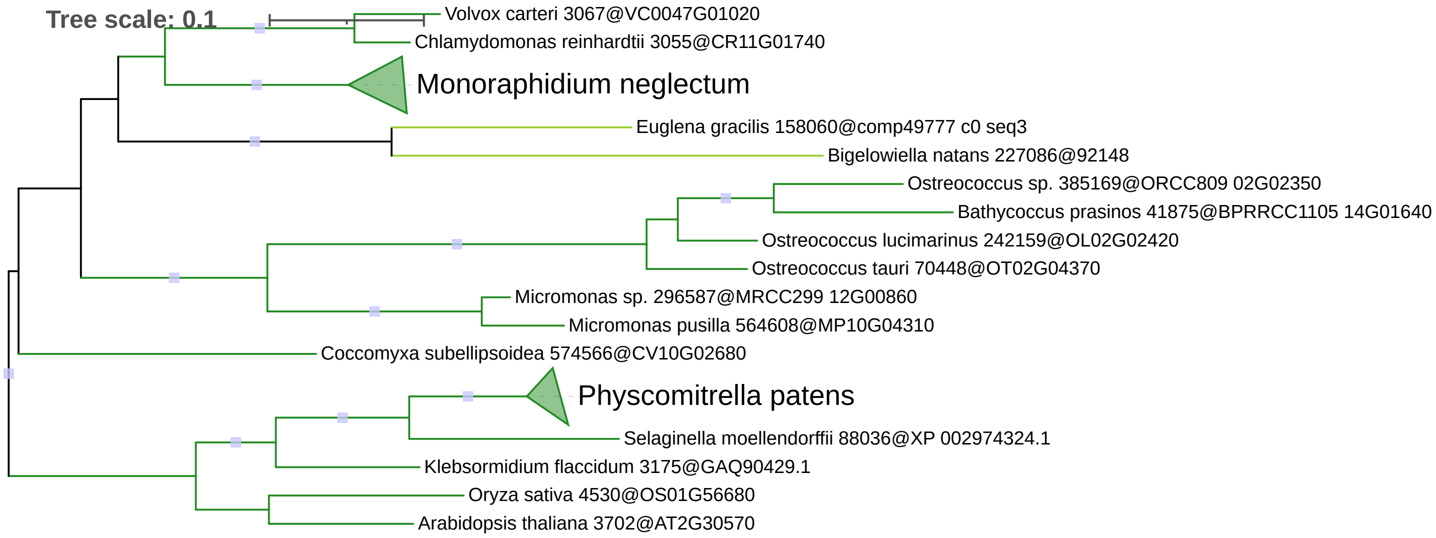

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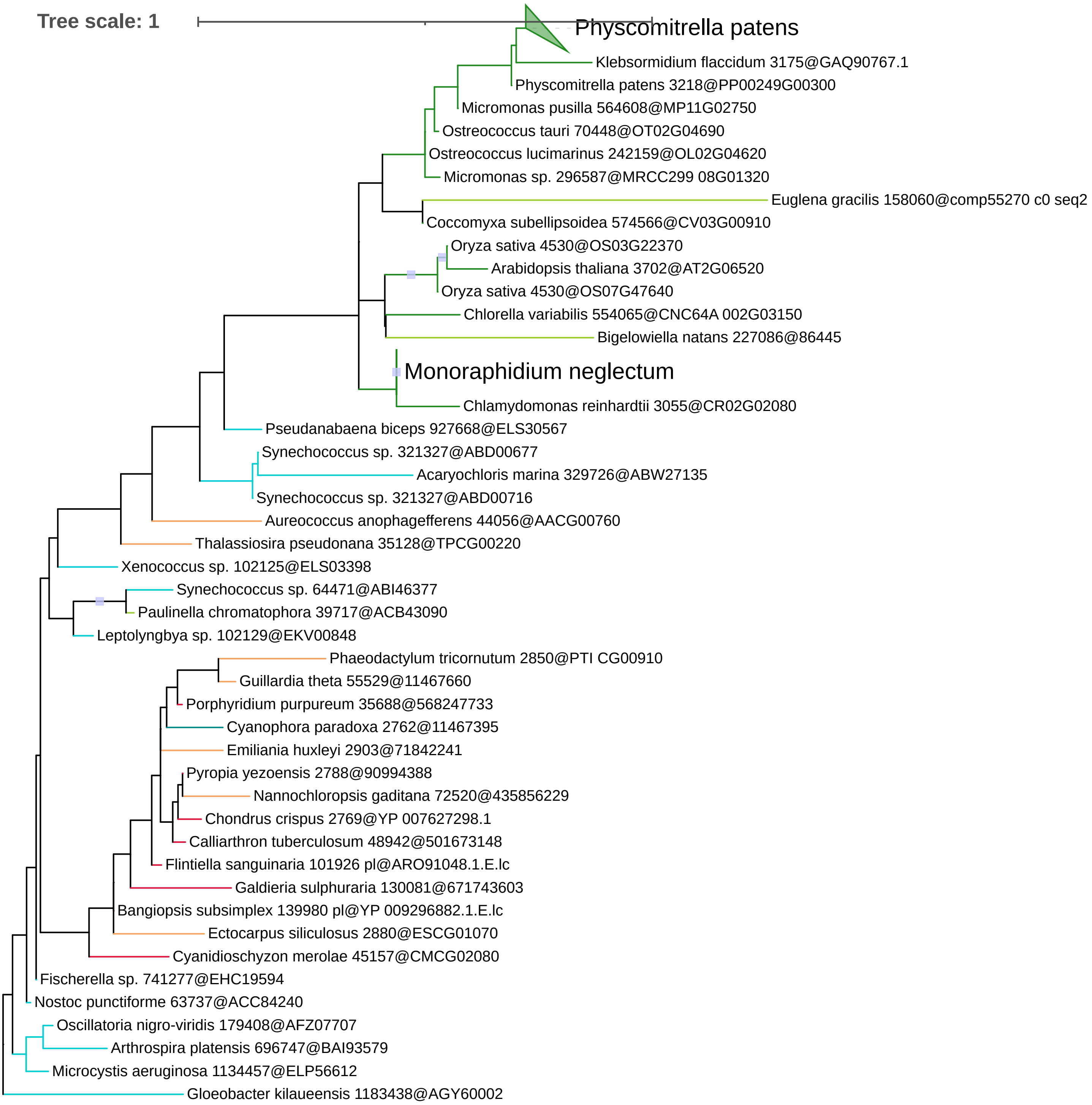

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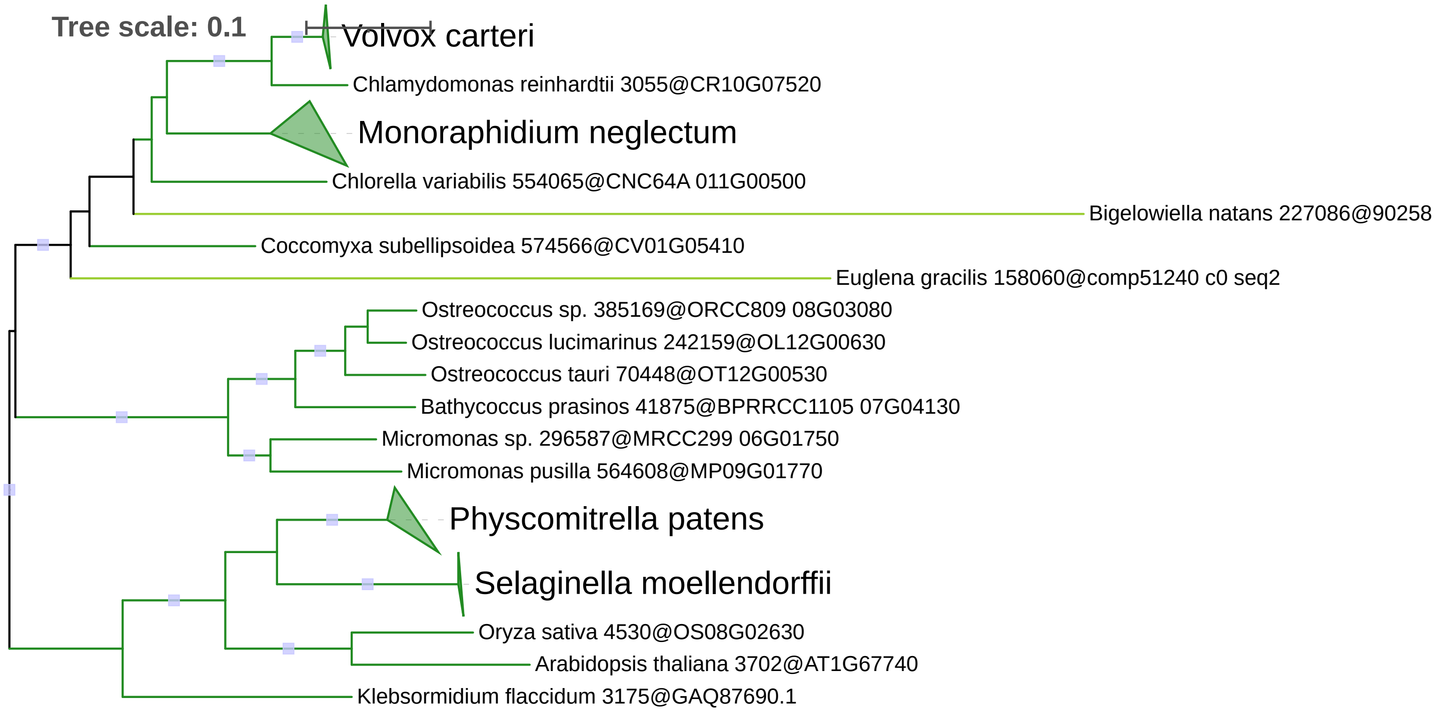

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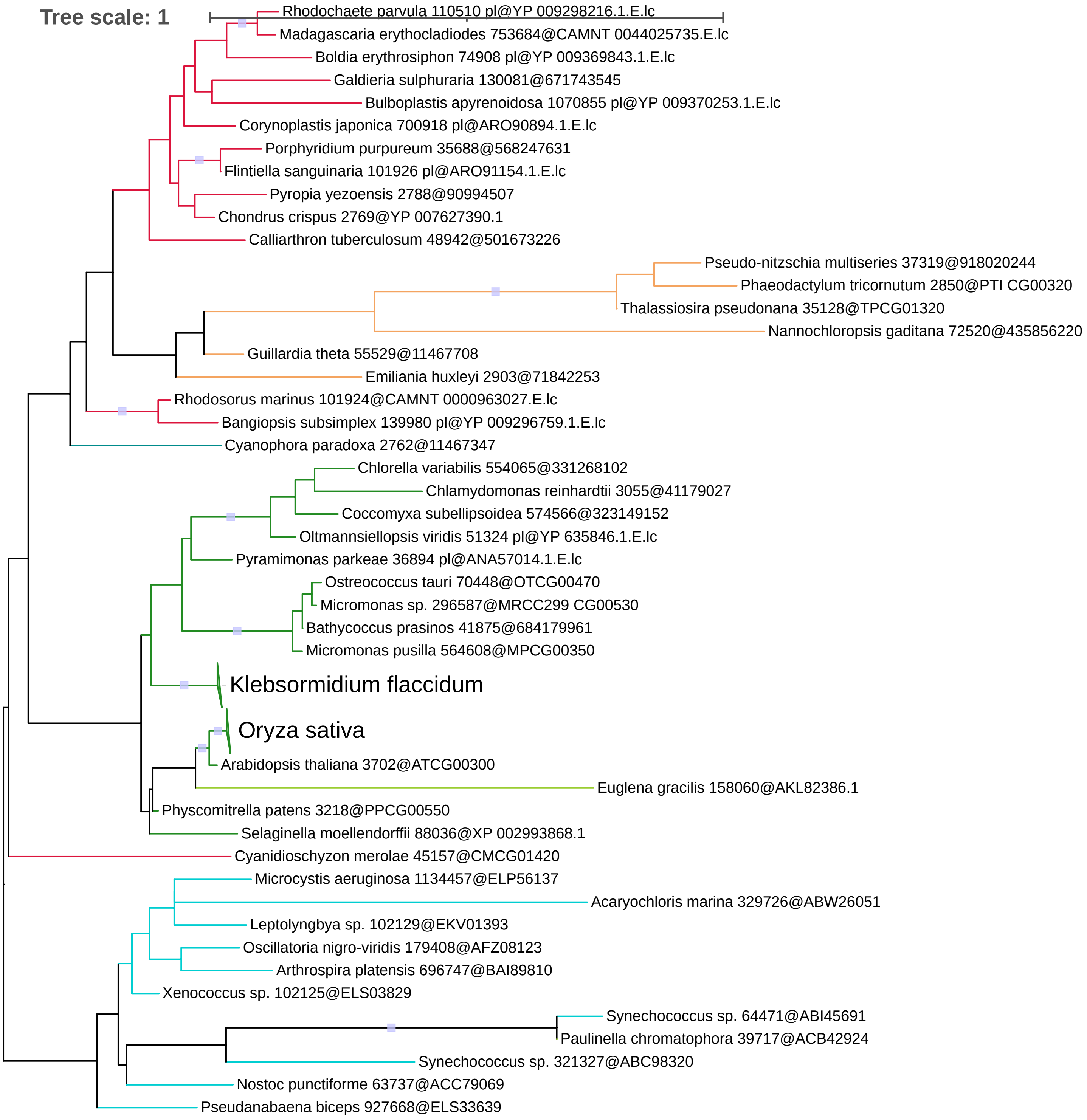

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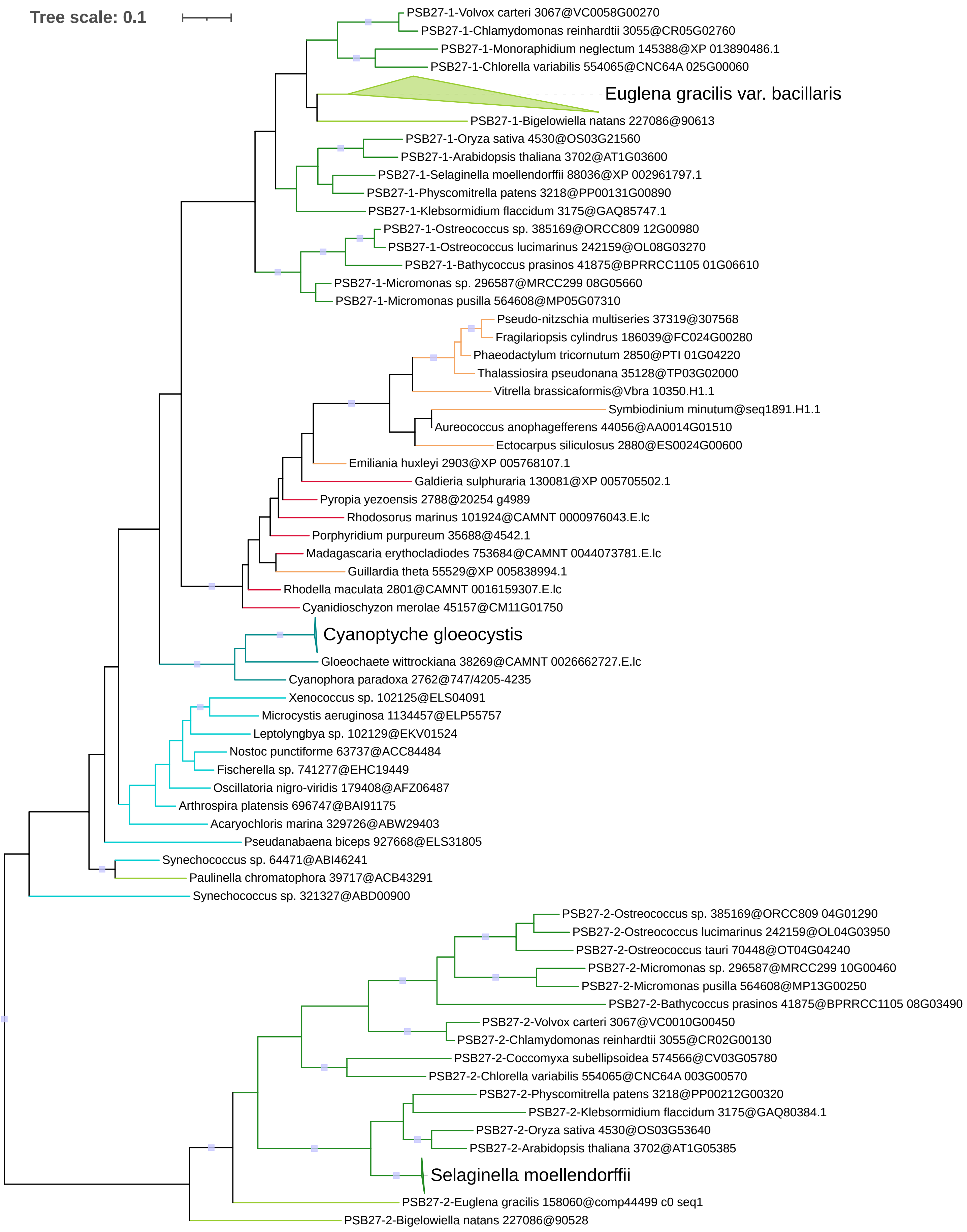

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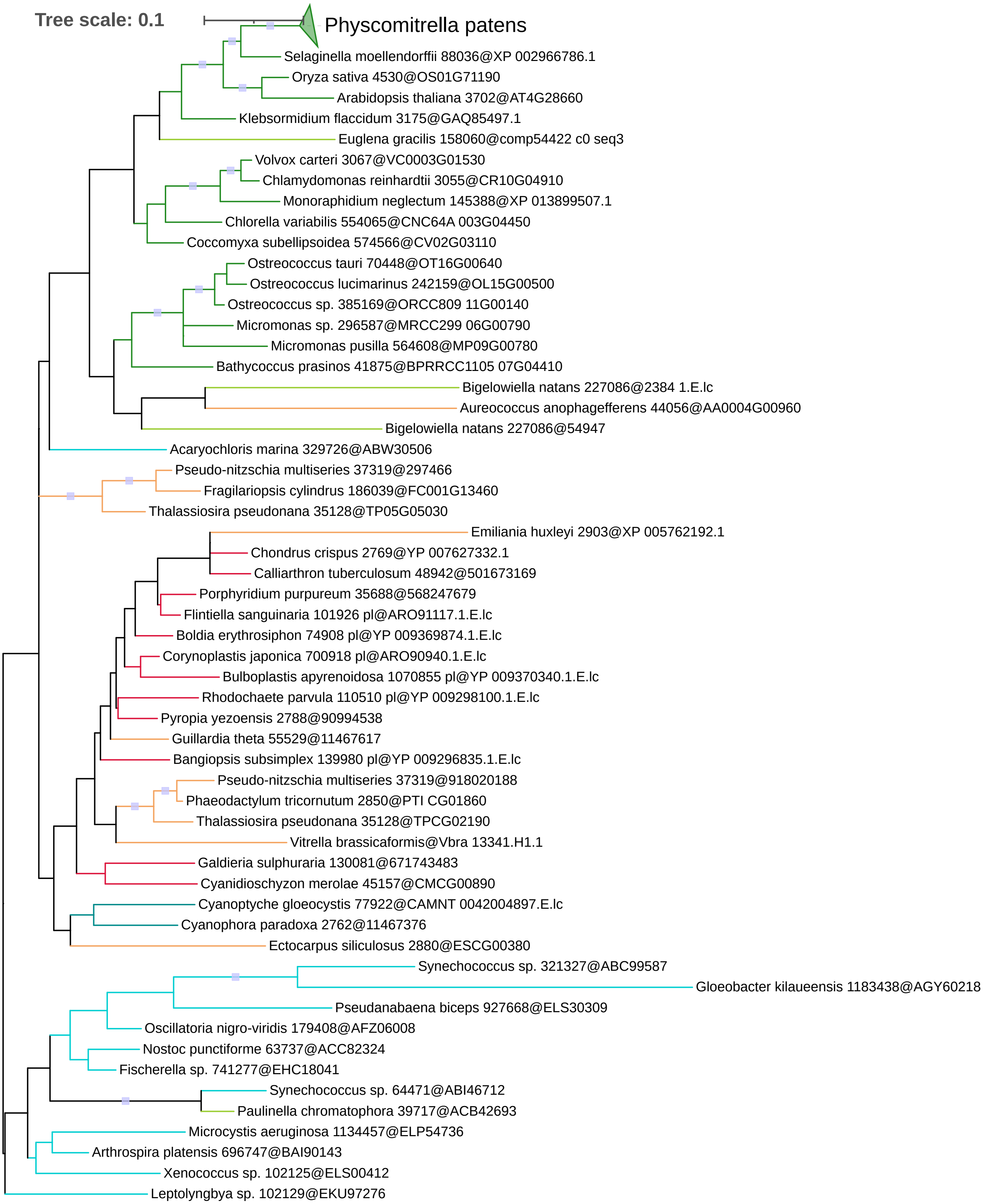

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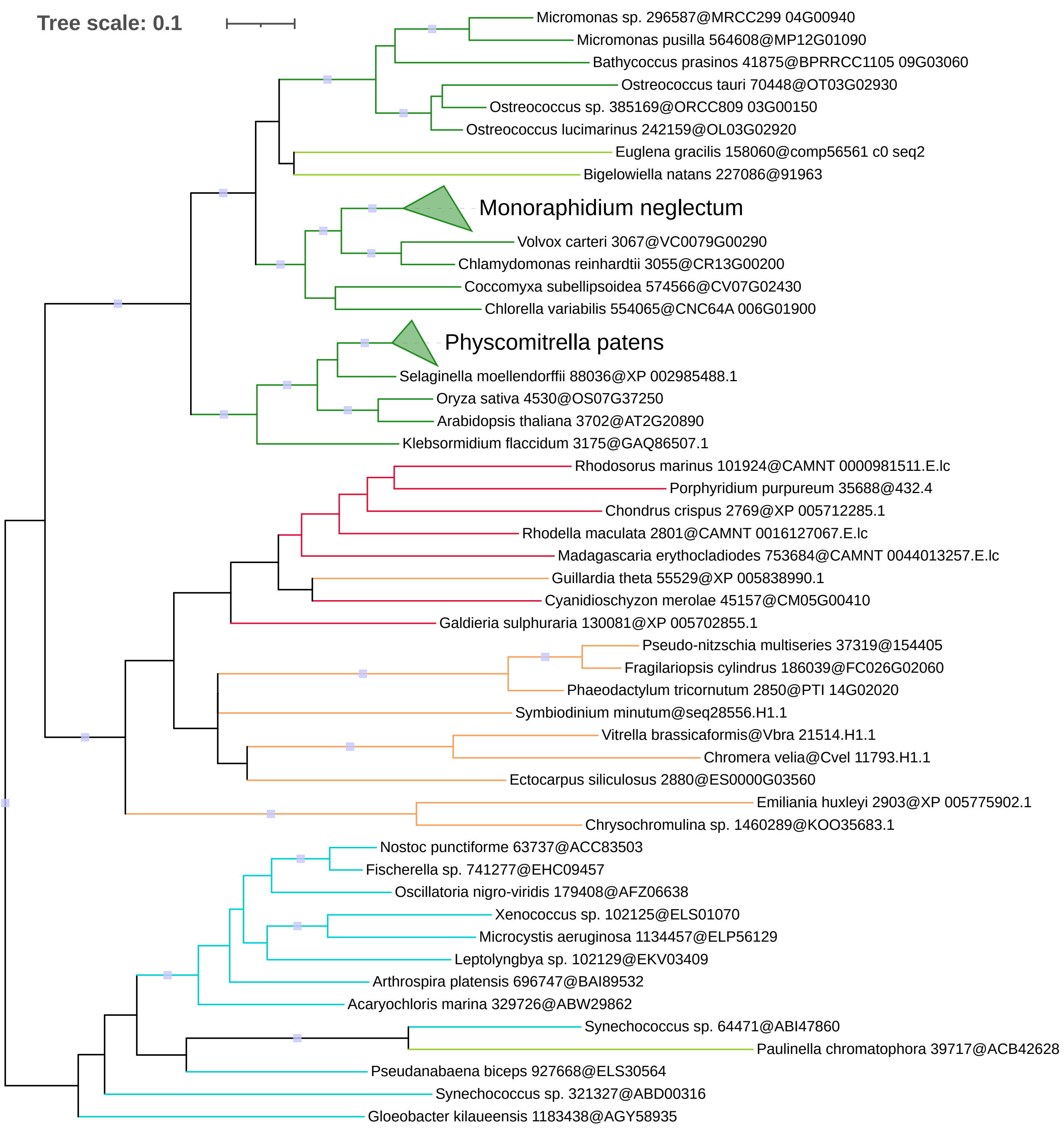

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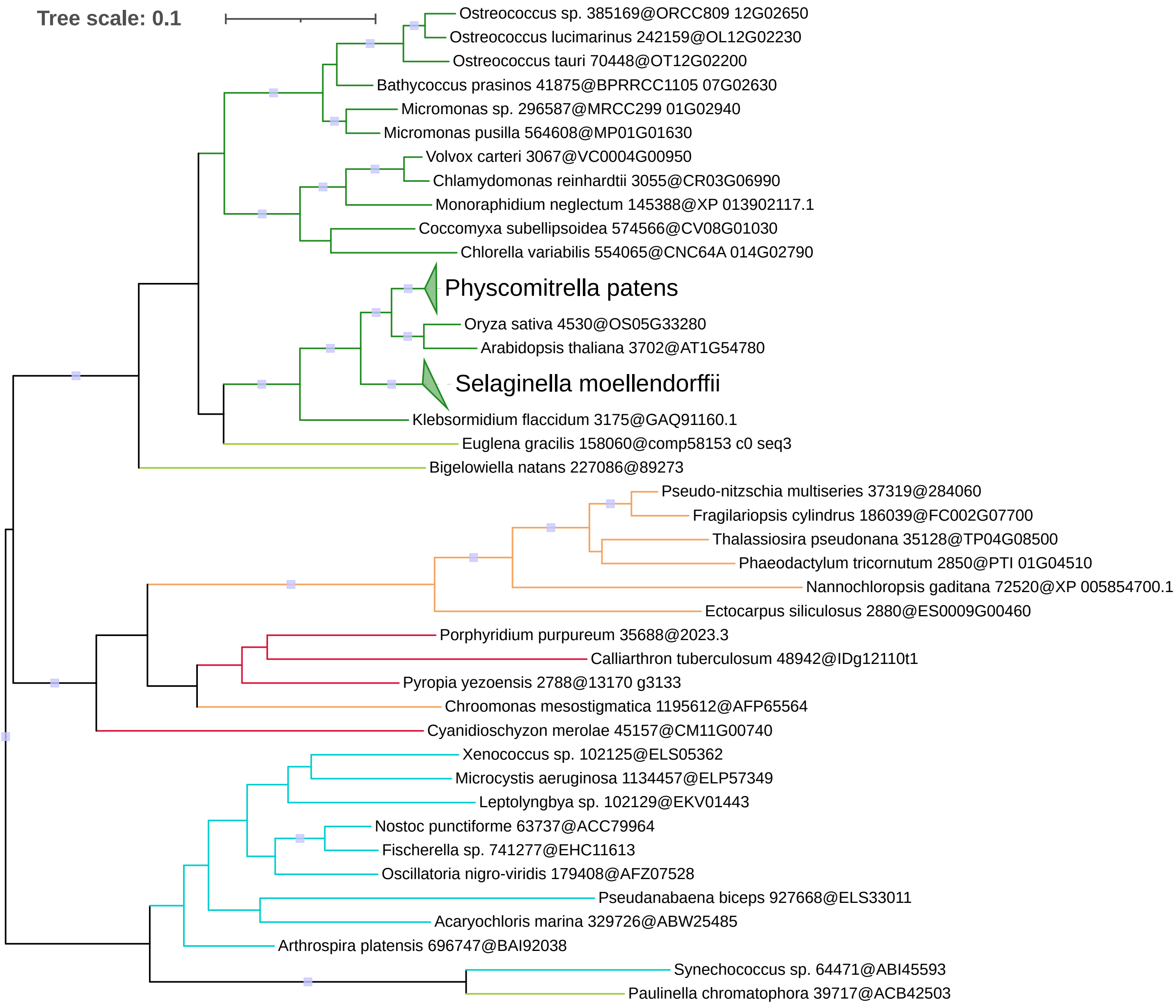

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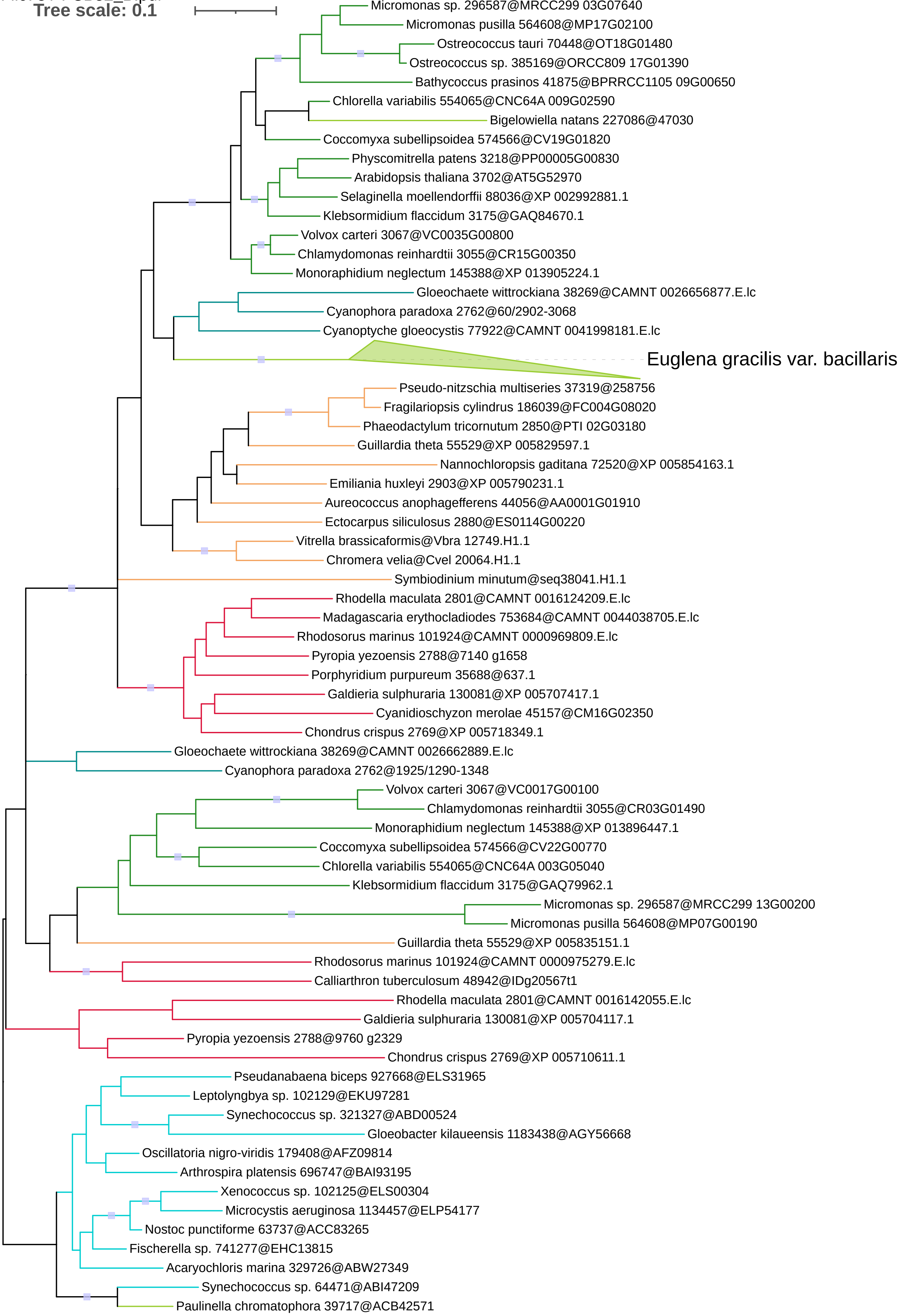

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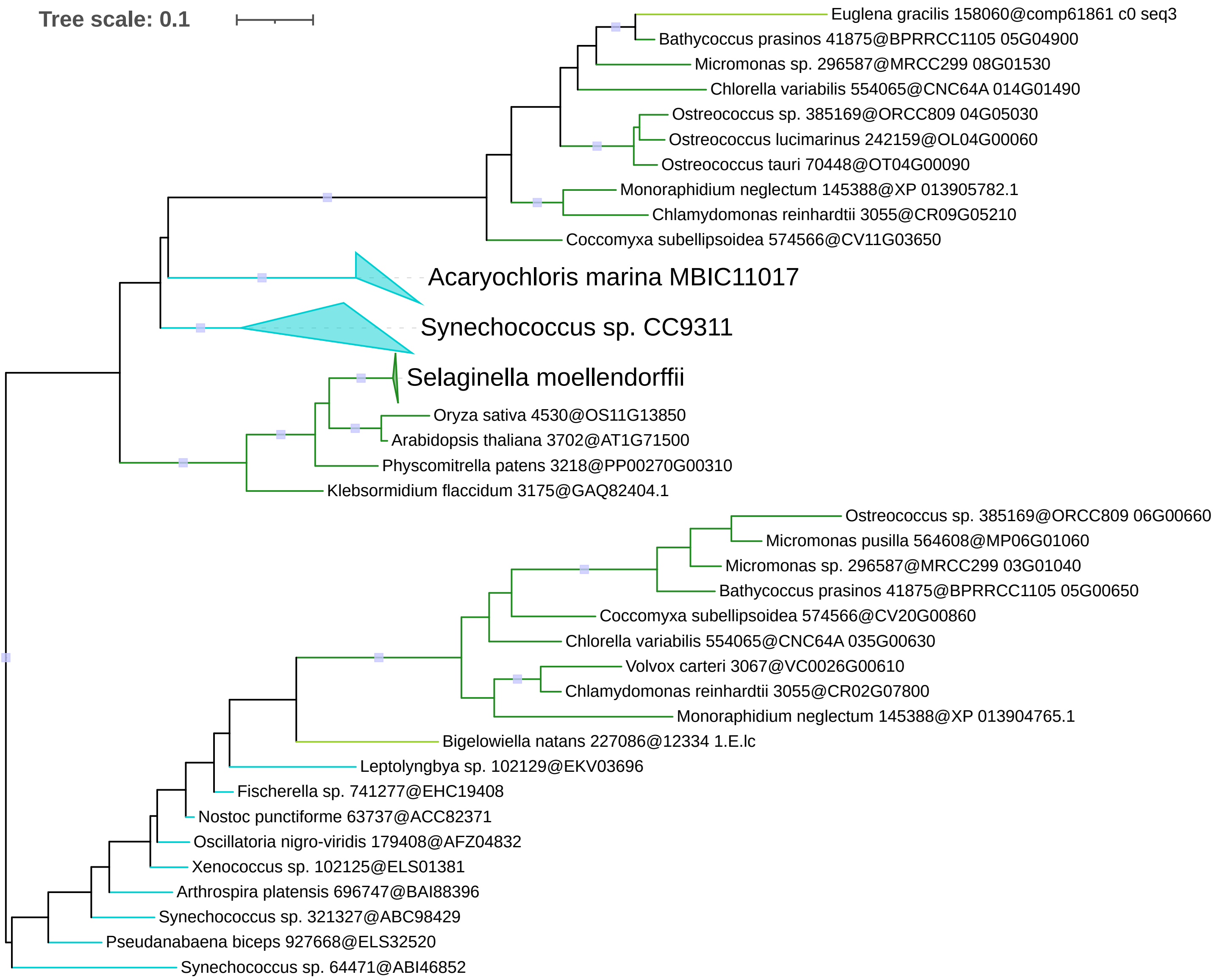

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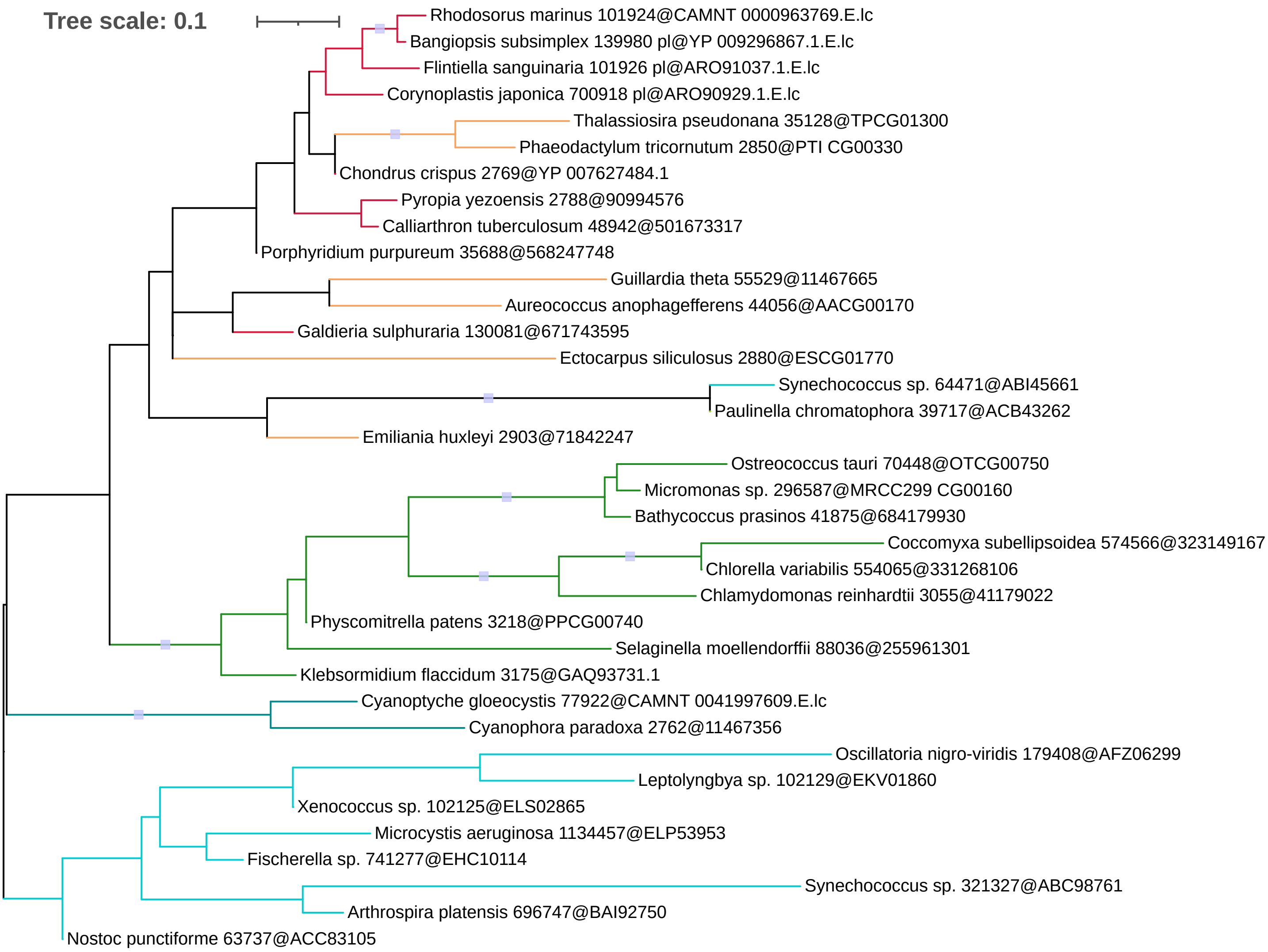

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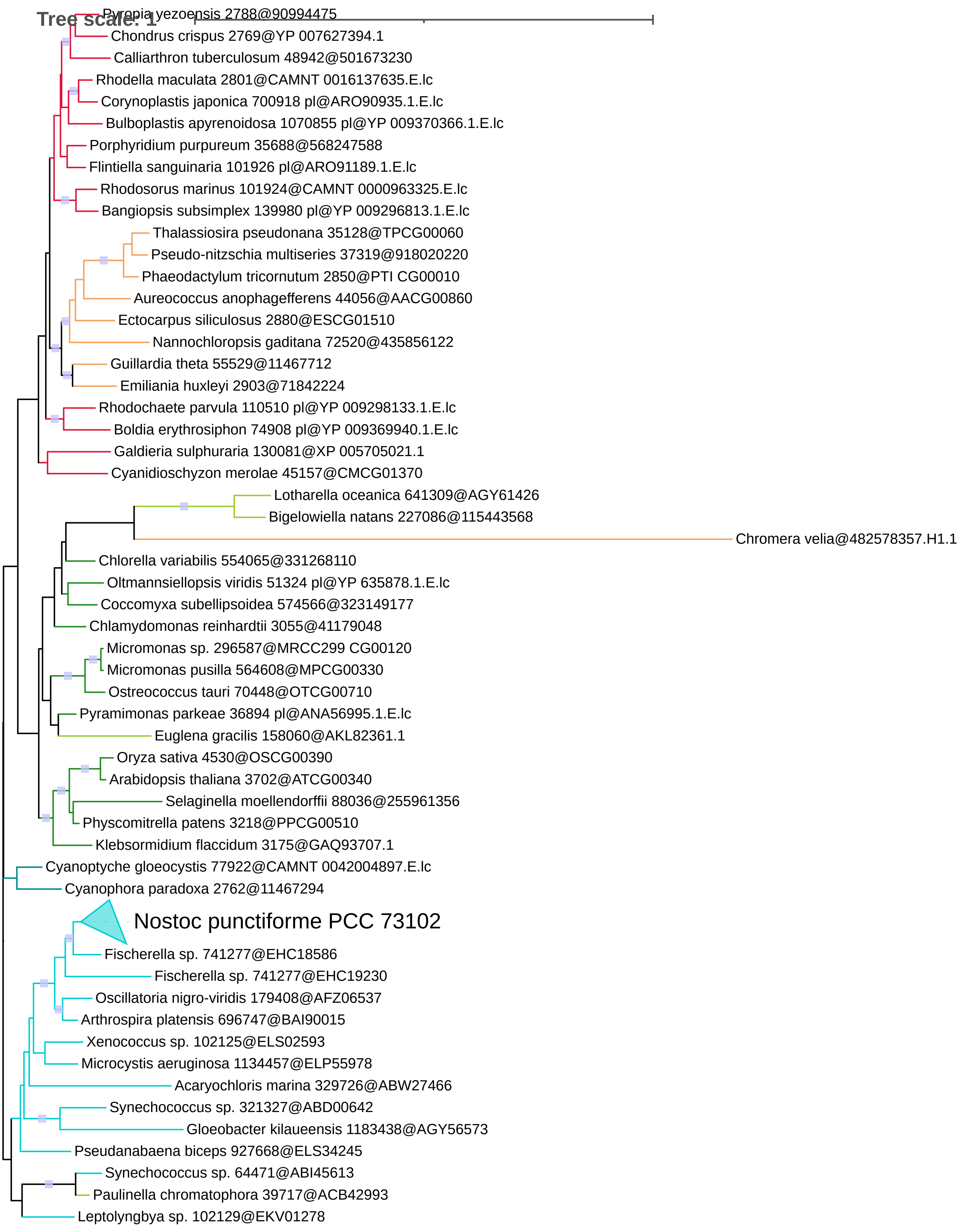

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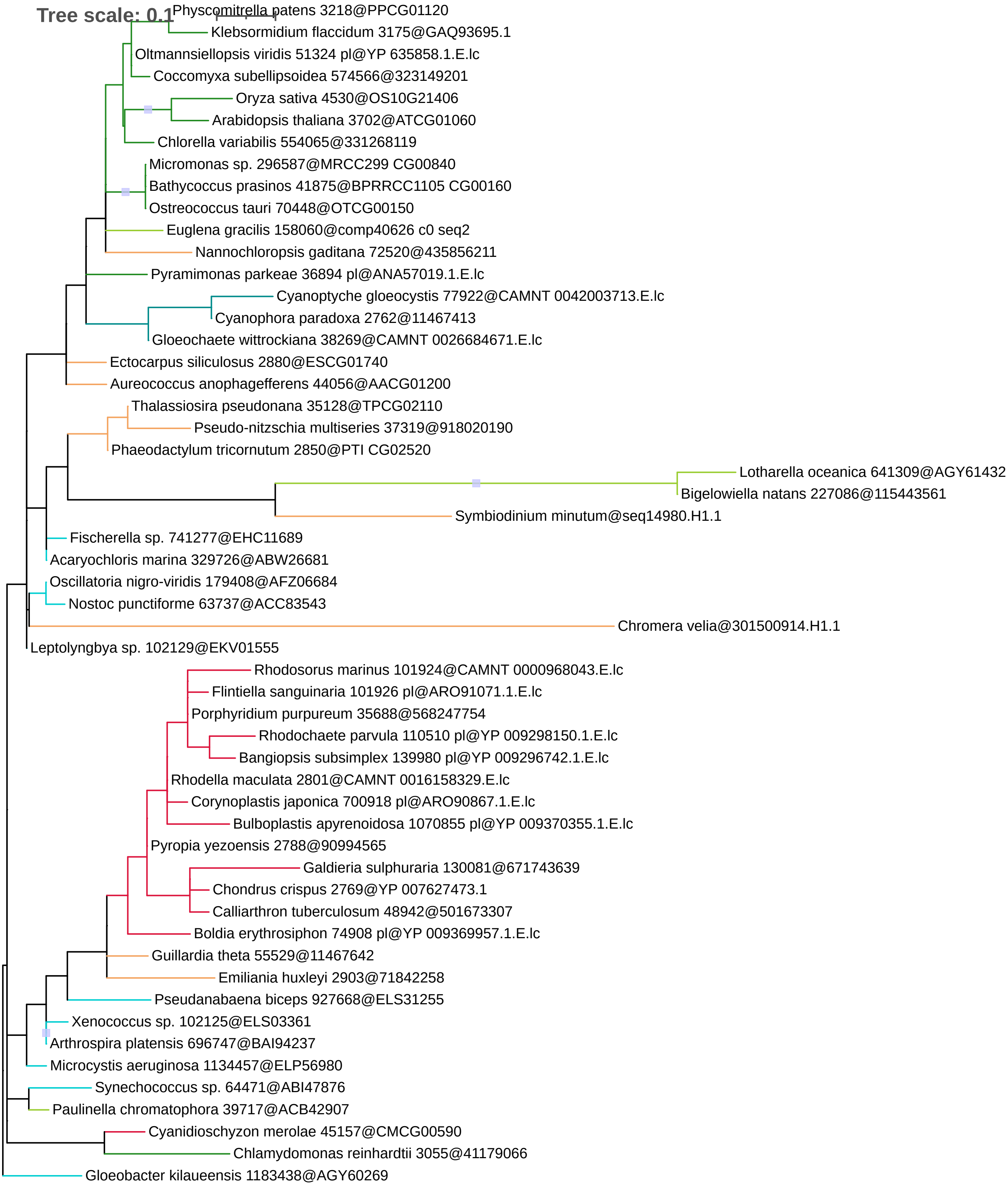

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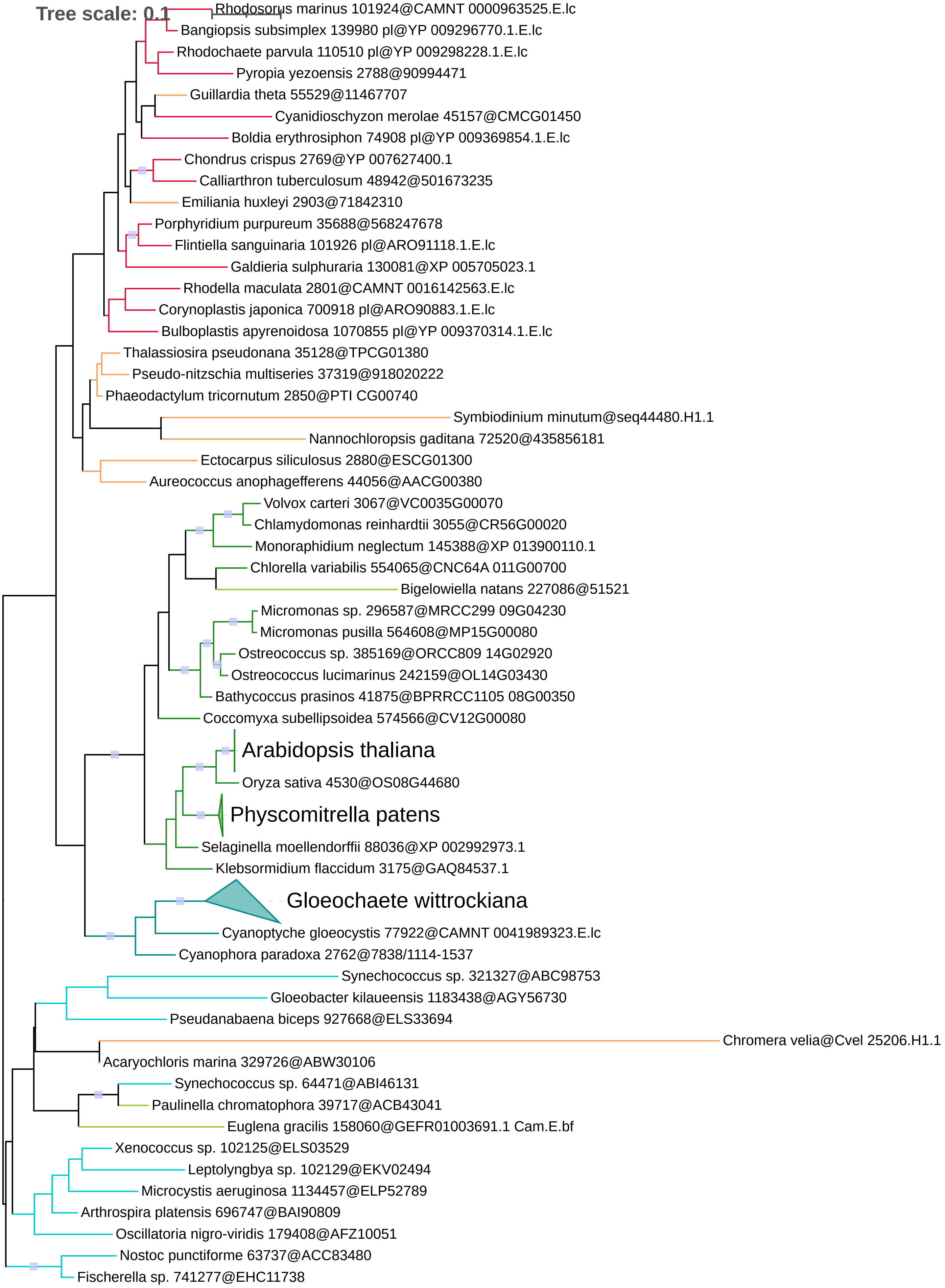

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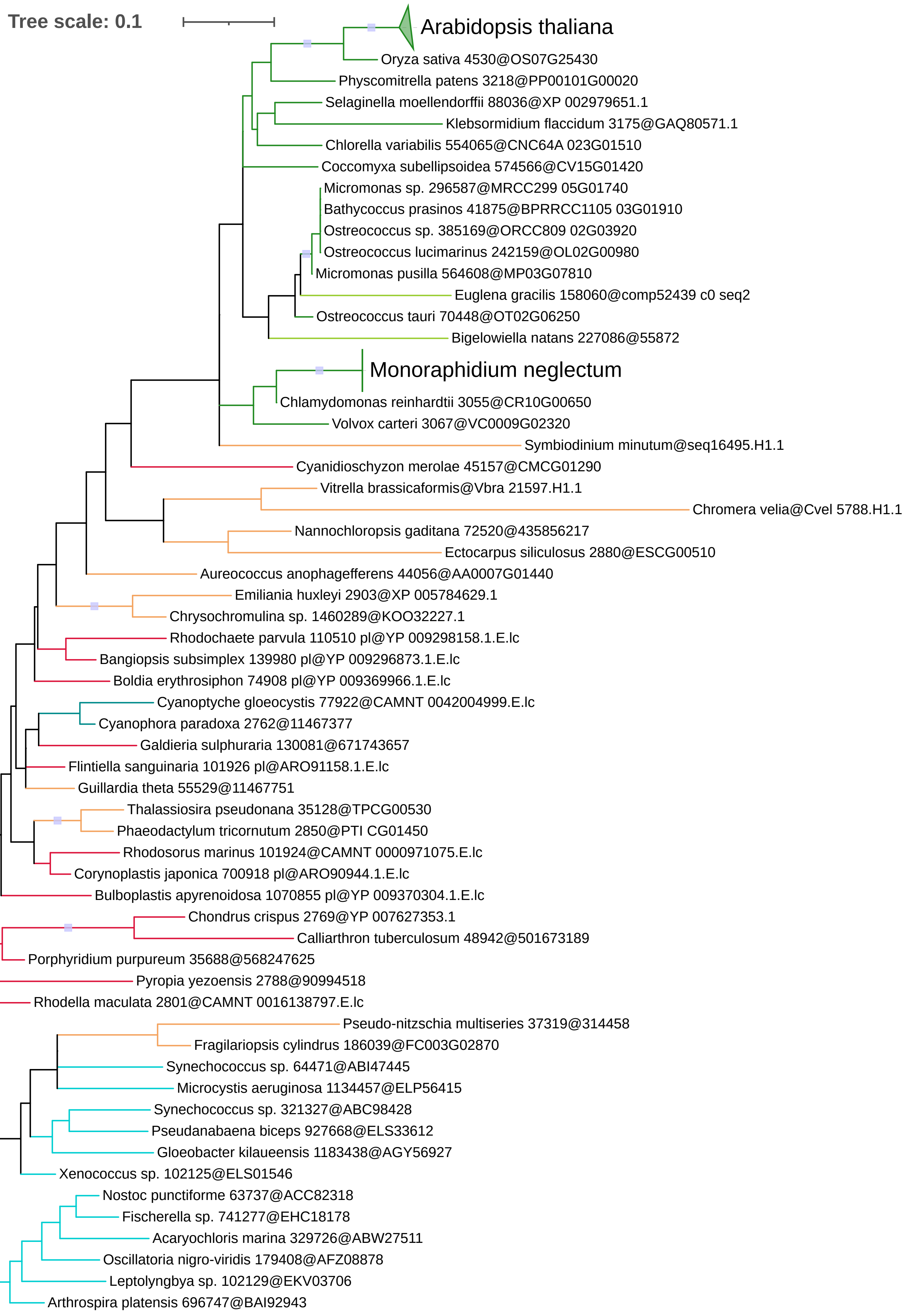

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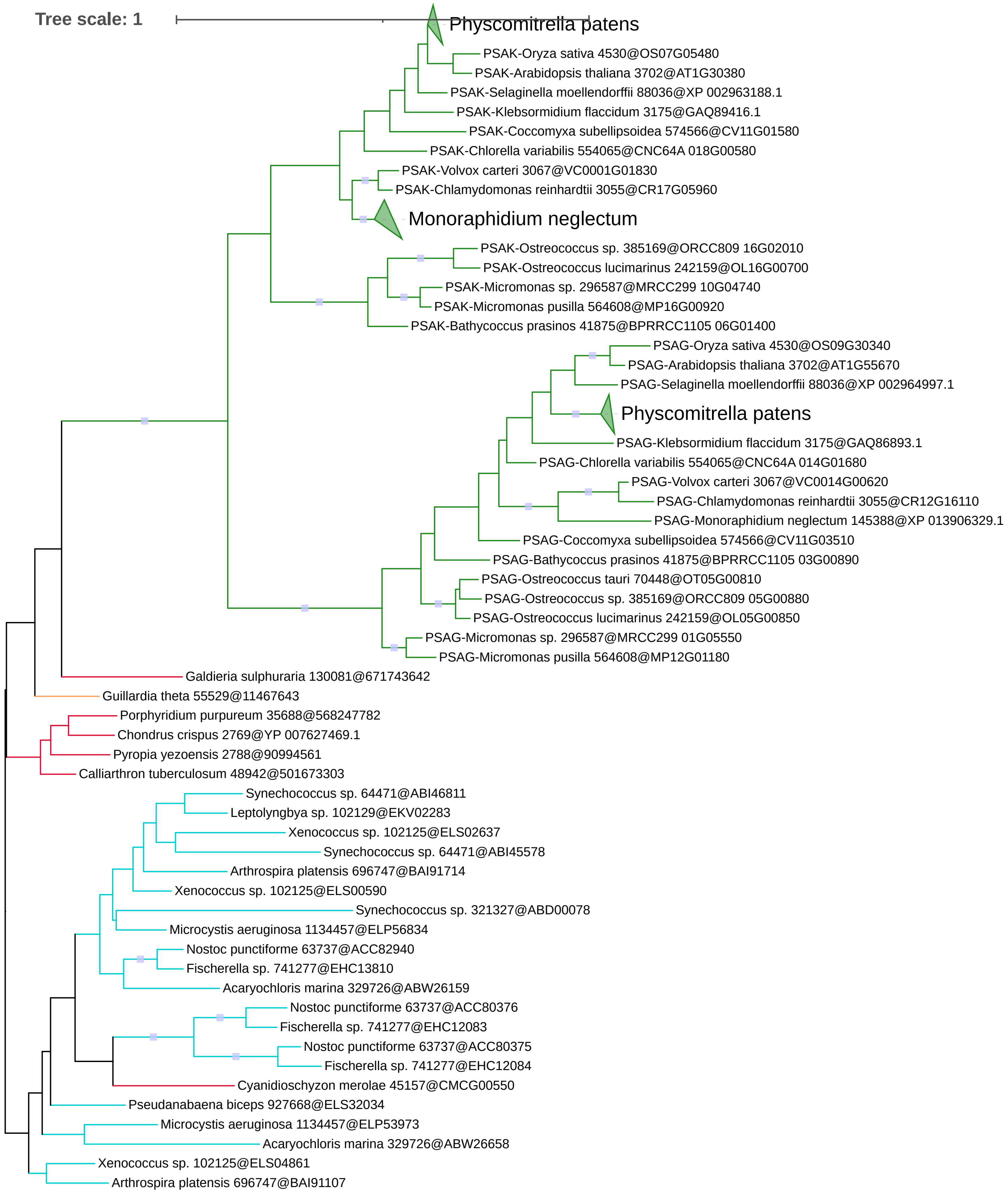

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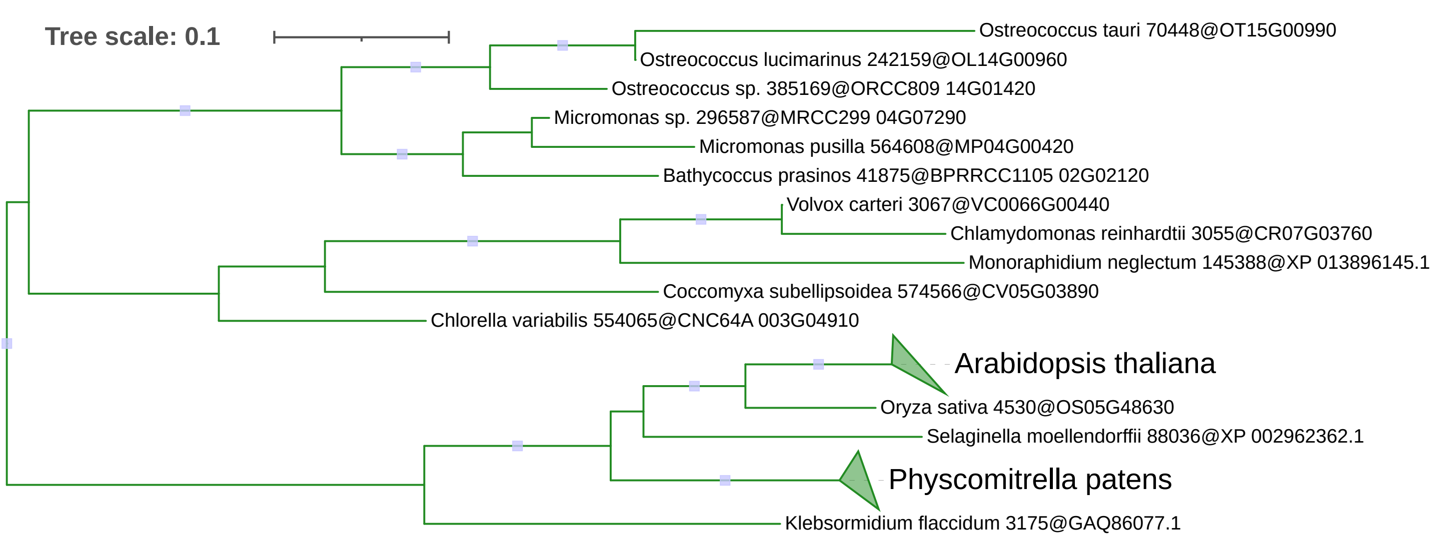

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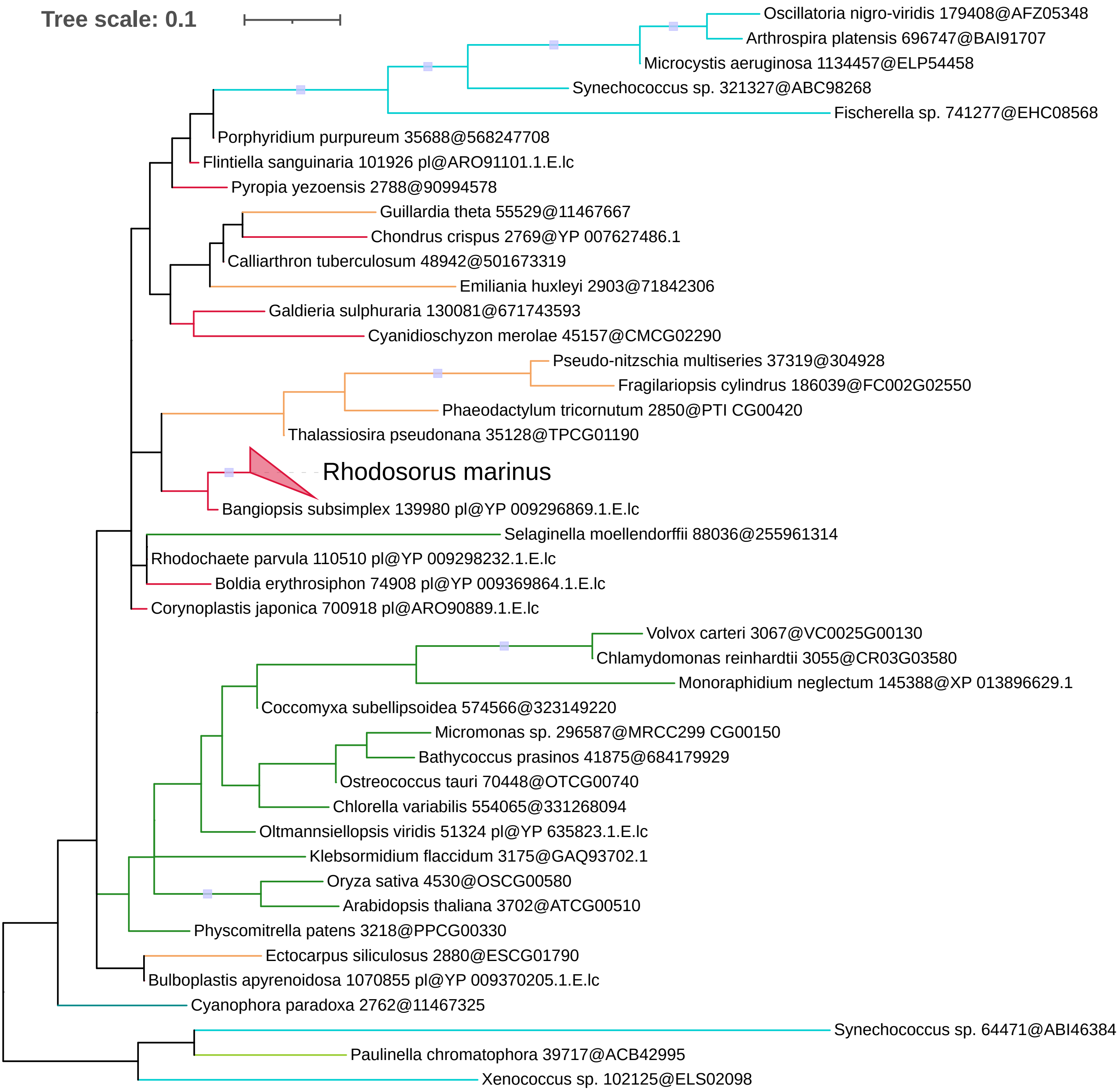

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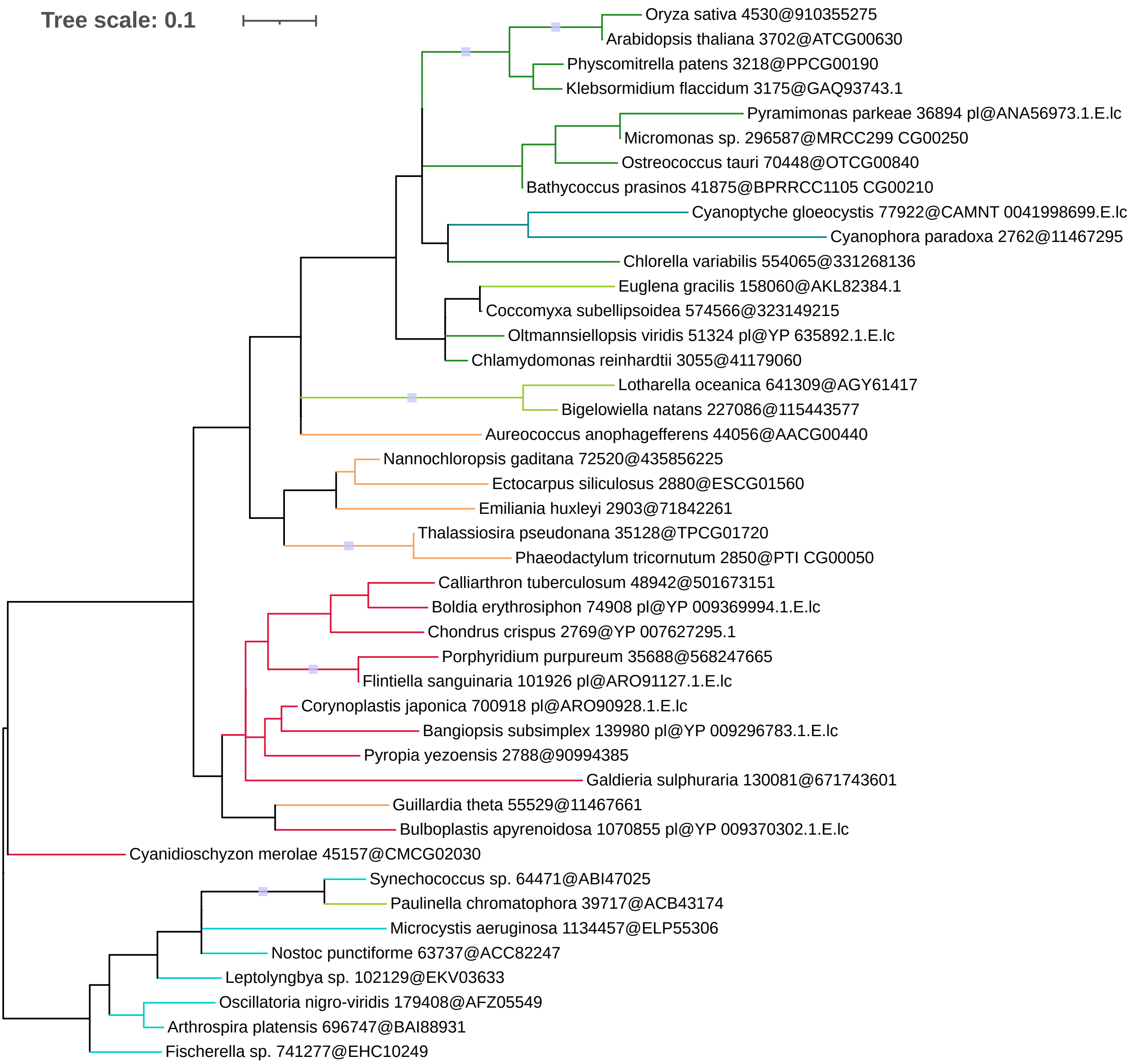

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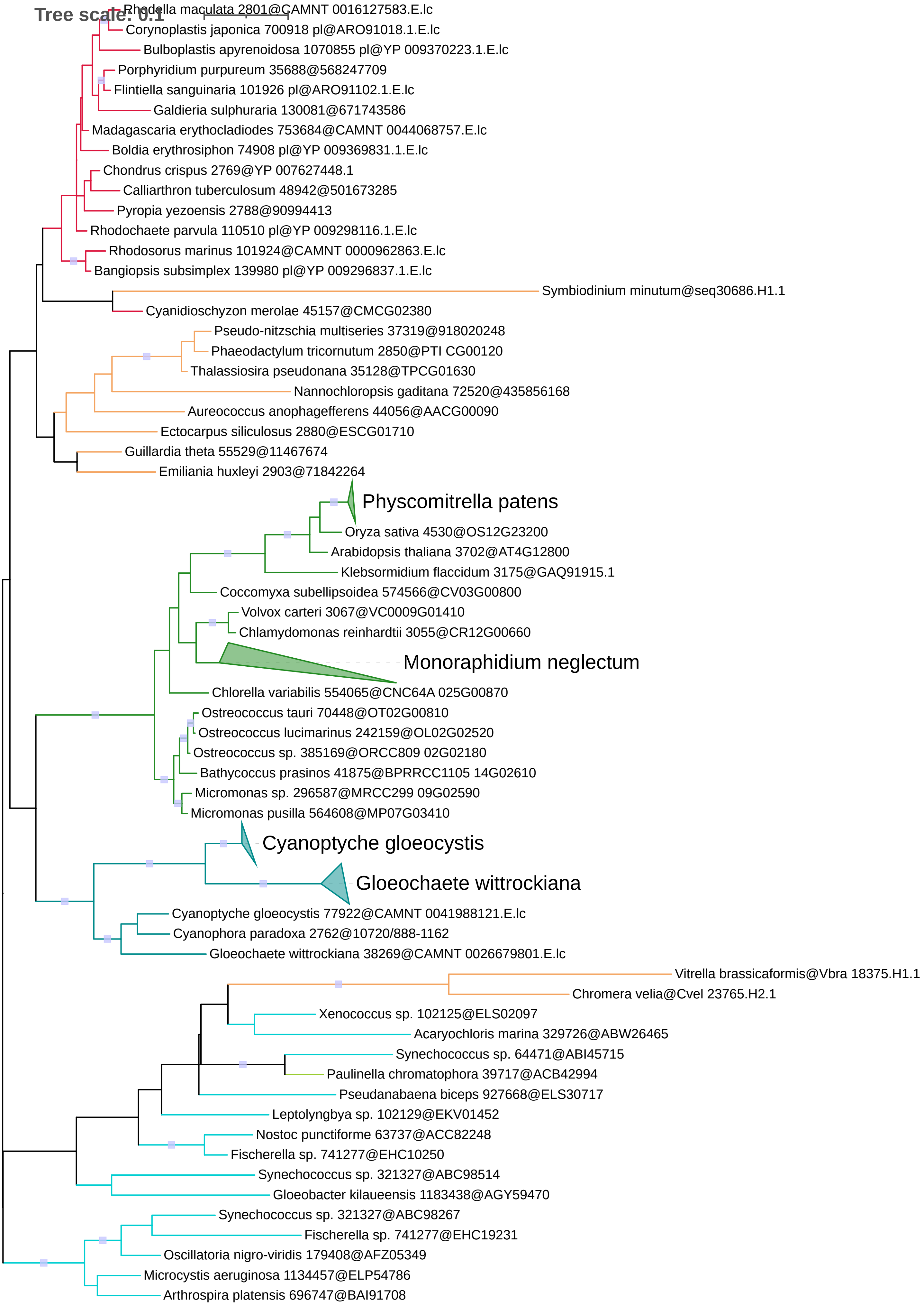

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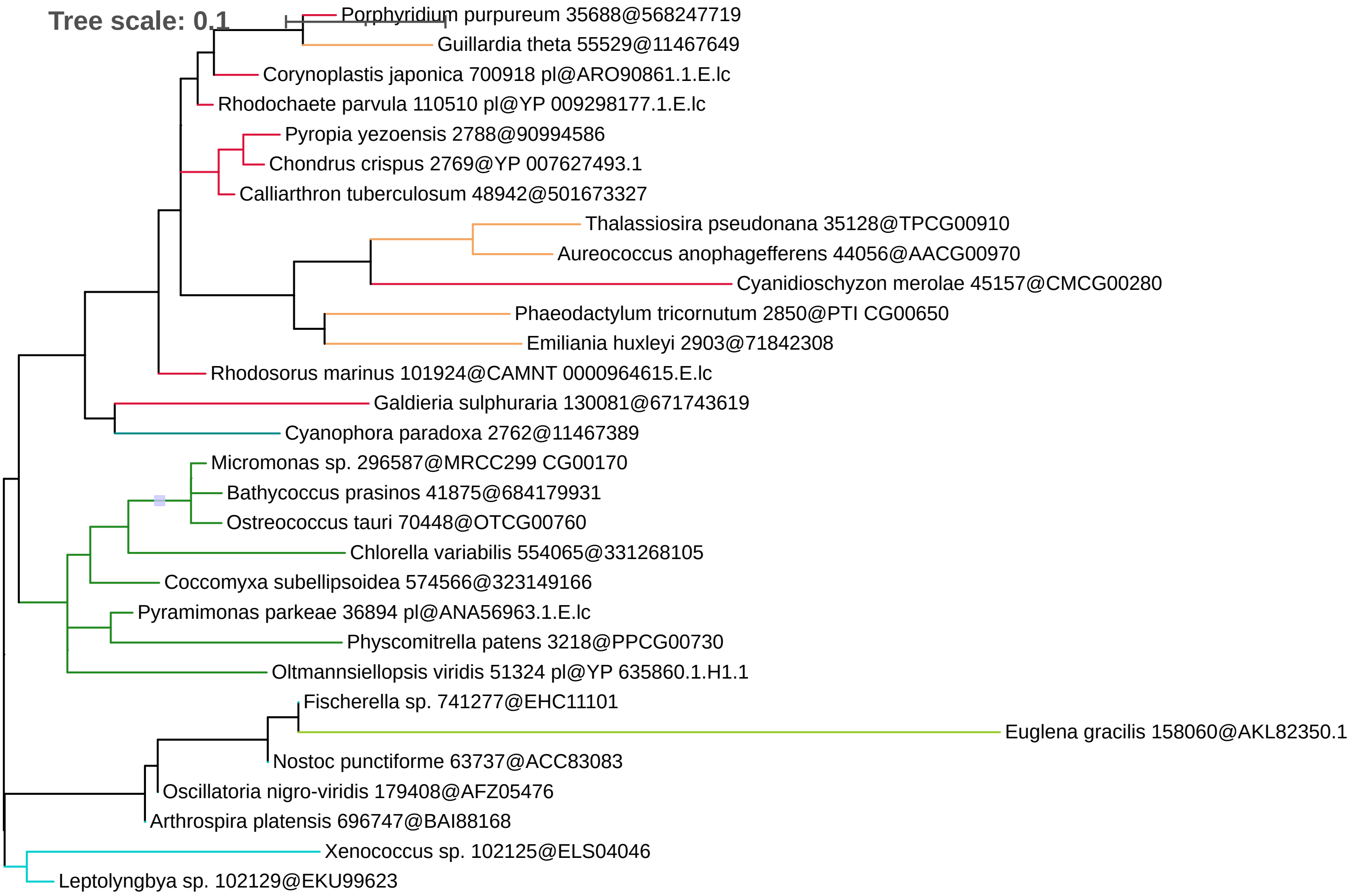

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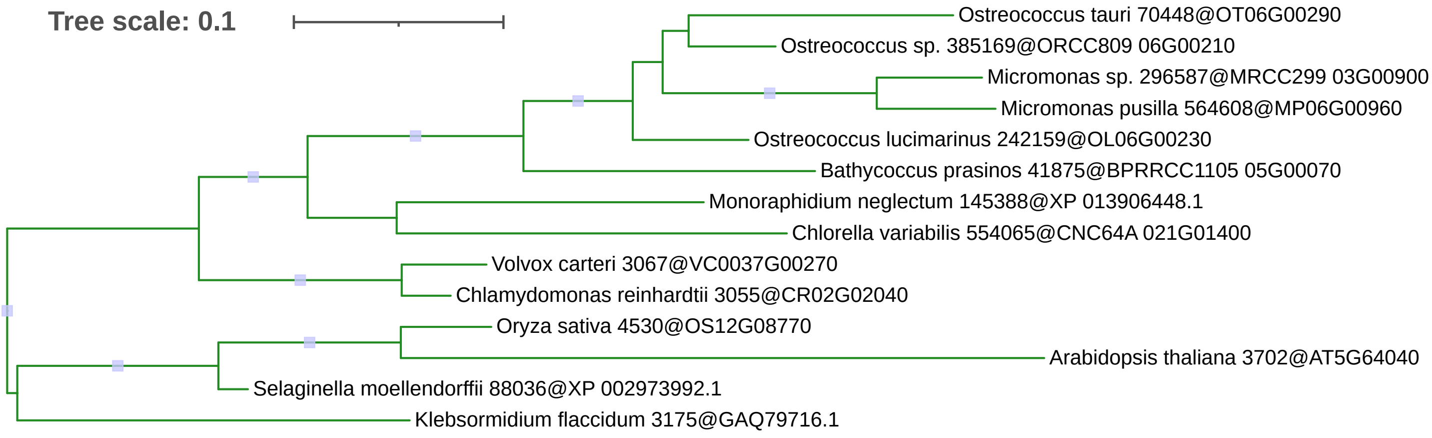
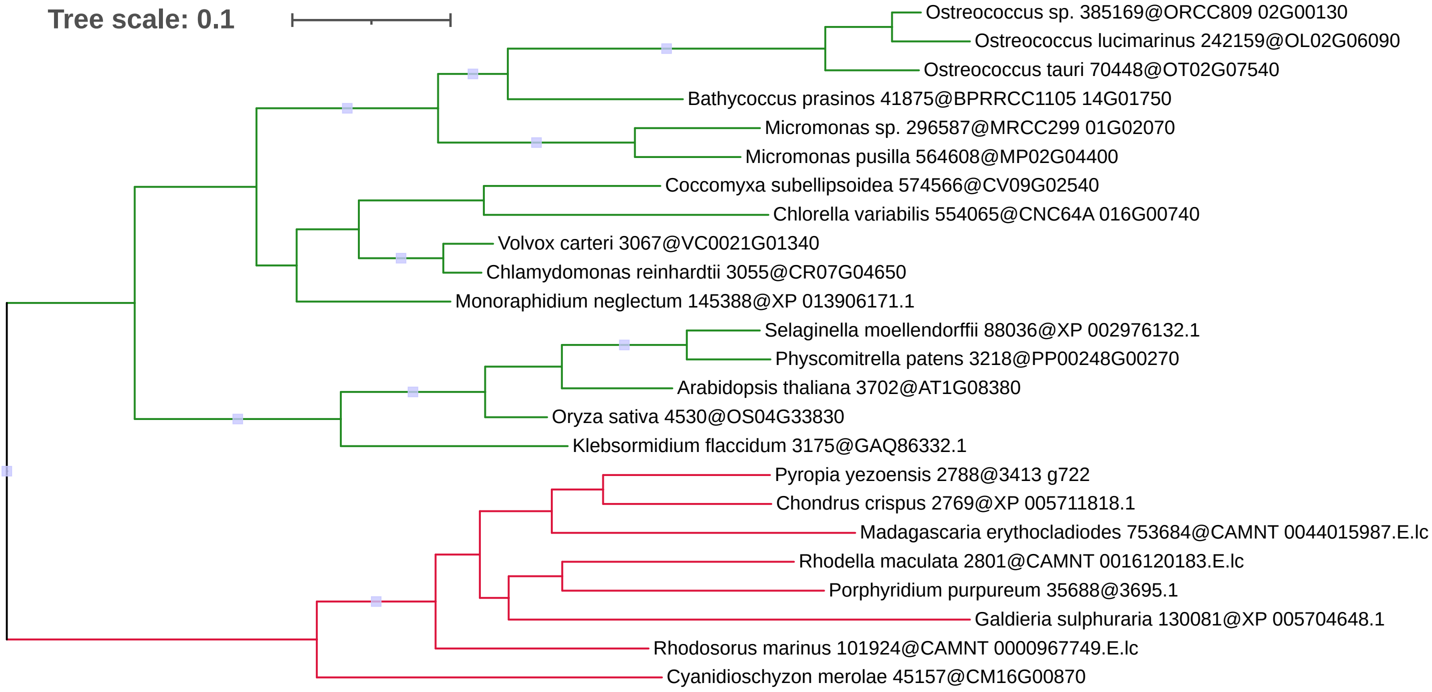
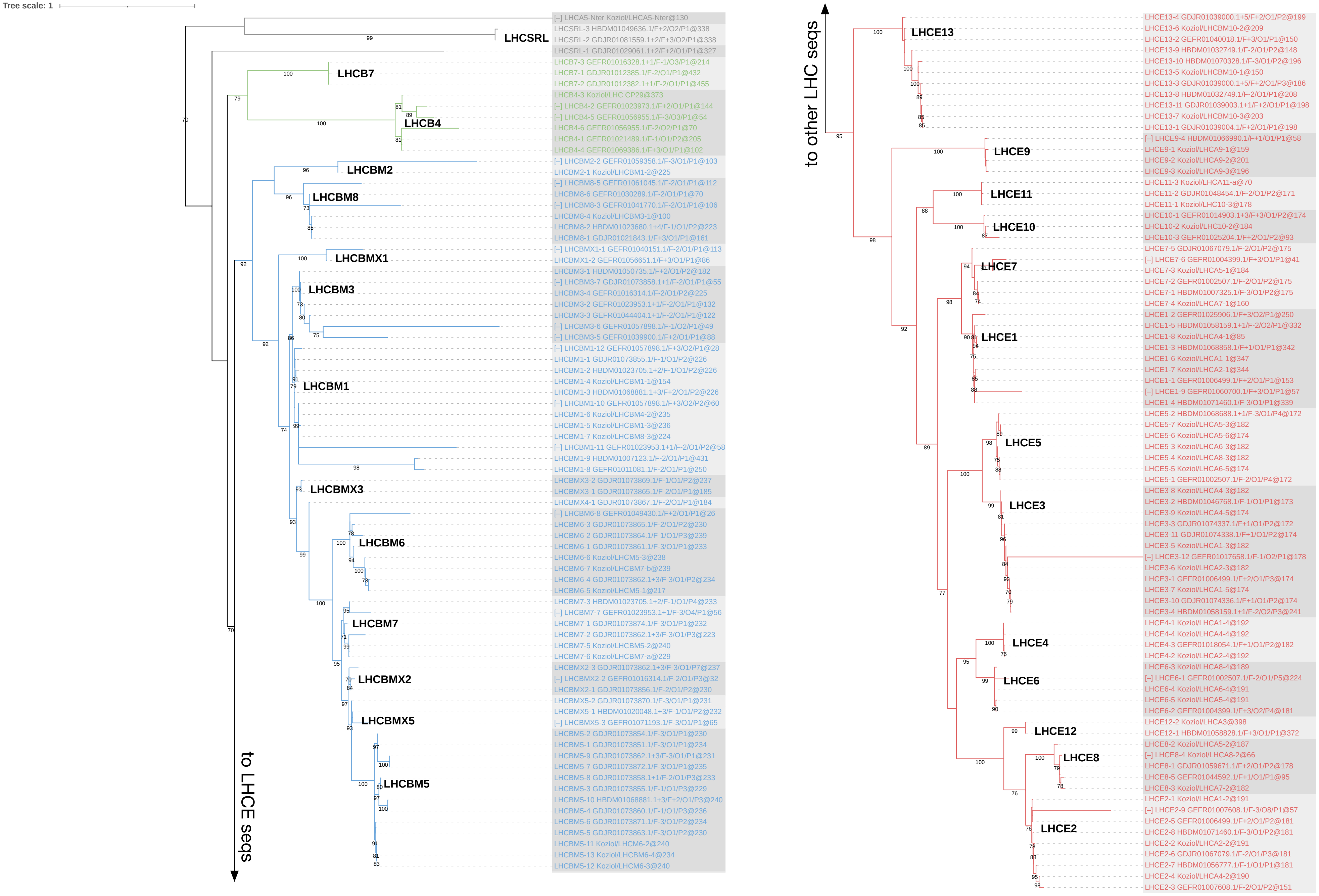


File: 47-PSAO.pdf



Supplementary Figures S1-47 : Phylogenetic trees of PSI/PSII subunits inferred with RAxML under the PROTGAMMALG4X model and 100 rapid bootstrap replicates. Branches are in substitutions per site and color-coded as follows: Cyanobacteria (light blue), Glaucophyta (turquoise), Rhodophyta (red), Viridiplantae (dark green), complex red algae (orange), complex green algae, including Euglena (light green). Nodes with bootstrap support values ≥70% are indicated by semi-transparent squares. When a species had multiple in-paralogous genes, the corresponding branches were collapsed in a triangle.

Supplementary Figure 1- PSBA
Supplementary Figure 2-PSBB
Supplementary Figure 3-PSBC
Supplementary Figure 4-PSBD
Supplementary Figure 5-PSBE
Supplementary Figure 6-PSBF
Supplementary Figure 7-PSBH
Supplementary Figure 8-PSBI
Supplementary Figure 9-PSBJ
Supplementary Figure 10-PSBK
Supplementary Figure 11-PSBL
Supplementary Figure 12-PSBM
Supplementary Figure 13-PSBN
Supplementary Figure 14-PSBO
Supplementary Figure 15-PSBP-PPL1
Supplementary Figure 16-PSBP2
Supplementary Figure 17-PNSL23-PSBQ
Supplementary Figure 18-PSBR
Supplementary Figure 19-PSBS
Supplementary Figure 20-PSBT
Supplementary Figure 21-PSBU
Supplementary Figure 22-PSBV
Supplementary Figure 23-PSBW
Supplementary Figure 24-PSBX
Supplementary Figure 25-PSBY
Supplementary Figure 26-PSBZ
Supplementary Figure 27-PSB27-1-2
Supplementary Figure 28-PSB28
Supplementary Figure 29-PSB29
Supplementary Figure 30-PSB32_A
Supplementary Figure 31-PSB32_B
Supplementary Figure 32-PSB33
Supplementary Figure 33-YCF12
Supplementary Figure 34-PSAA
Supplementary Figure 35-PSAB
Supplementary Figure 36-PSAC
Supplementary Figure 37-PSAD
Supplementary Figure 38-PSAE
Supplementary Figure 39-PSAF
Supplementary Figure 40-PSAG-PSAK
Supplementary Figure 41-PSAH
Supplementary Figure 42-PSAI
Supplementary Figure 43-PSAJ
Supplementary Figure 44-PSAL
Supplementary Figure 45-PSAM
Supplementary Figure 46-PSAN
Supplementary Figure 47-PSAO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LHCBM8
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LHCBM3
LHCBM1
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LHCBM6
LHCBM7
LHCBMX2
LHCBMX5
LHCBM5
to LHCE seqs
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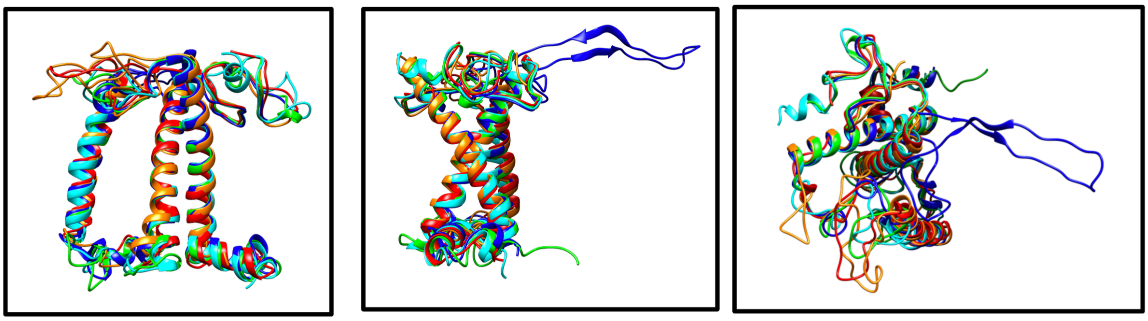
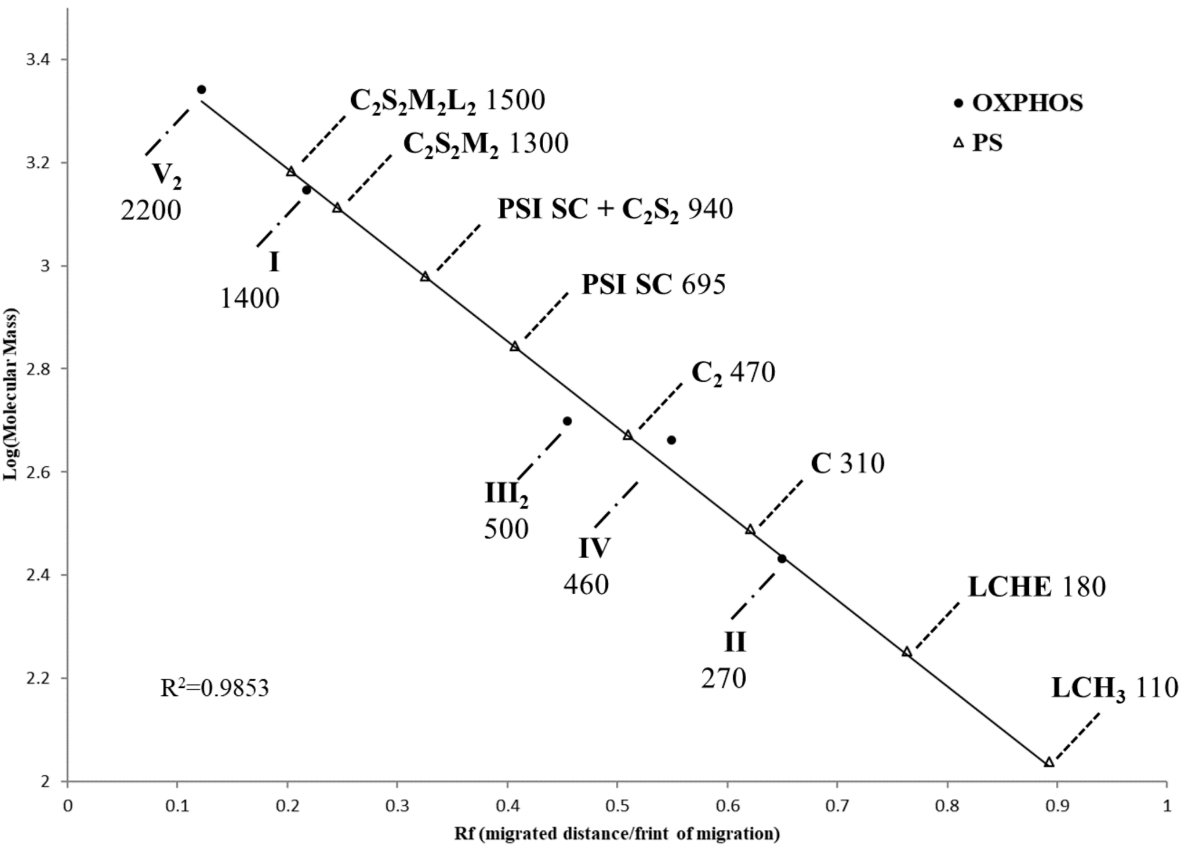
Supplementary Figure S48. Phylogenetic tree of *Euglena gracilis* Light-Harvesting Complex (Lhc) Proteins. (A) Phylogenetic tree of Lhc proteins in *Euglena gracilis*. The maximum likelihood phylogenetic tree was constructed using an expanded dataset of Euglena gracilis Lhc proteins. Bootstrap values are indicated at key nodes. Lhc proteins are grouped into distinct families, with major clades highlighted in different colors: LhcbM proteins (blue), LhcE proteins (red), Lhcb (green) other Lhc-related families (gray).



Supplementary Figure S49. Structural comparison of Light Harvesting Complexes proteins. Overlap of LHCII (green), CP24 (orange), CP26 (cyan), CP29 (blue), LhcE9 (red) structures. Left panel: side view, center panel: 90° rotation on the same plane view, right panel: upper view. Structures from LHCII, CP24, CP26 and CP29 were obtained from PSII-LHCII supercomplex from Pisum sativum (PDB: 5XNL (Su et al., 2017)). LhcE9 homology model were obtained with SWISS-MODEL (Waterhouse et al., 2018).

Su X, Ma J, Wei X, Cao P, Zhu D, Chang W, Liu Z, Zhang X, Li M. Structure and assembly mechanism of plant $C_2S_2M_2$-type PSII-LHCII supercomplex. Science. 2017 Aug 25;357(6353):815-820. doi: 10.1126/science.aan0327. PMID: 28839073.

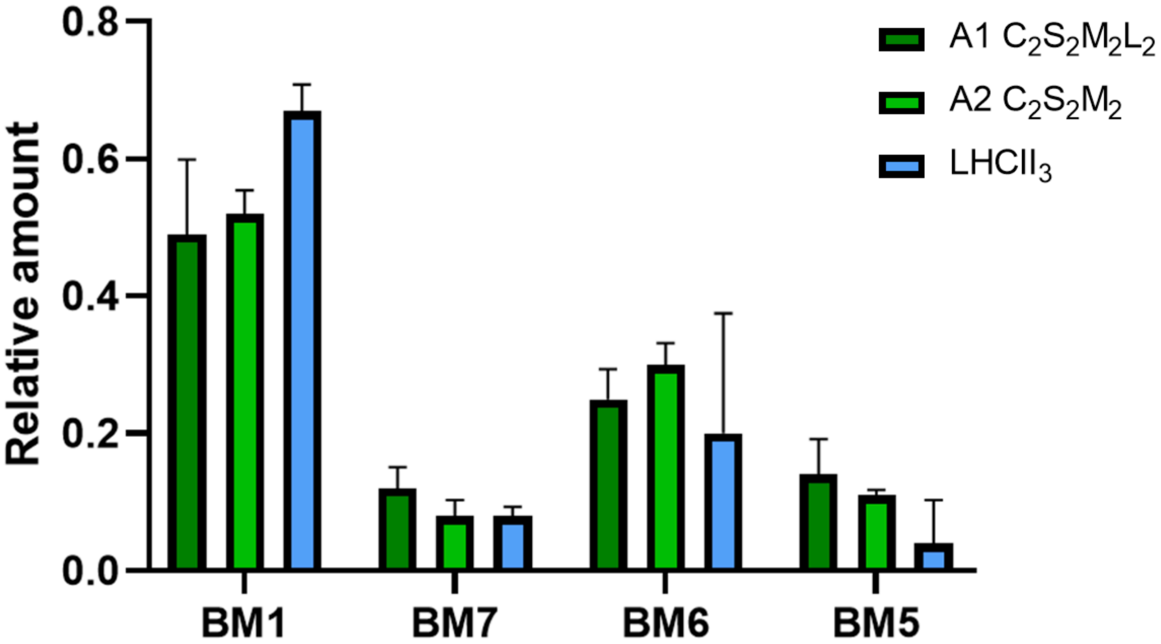
Waterhouse A, Bertoni M, Bienert S, Studer G, Tauriello G, Gumienny R, Heer FT, de Beer TAP, Rempfer C, Bordoli L, Lepore R, Schwede T. SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Res. 2018 Jul 2;46(W1):W296-W303. doi: 10.1093/nar/gky427. PMID: 29788355; PMCID: PMC6030848.



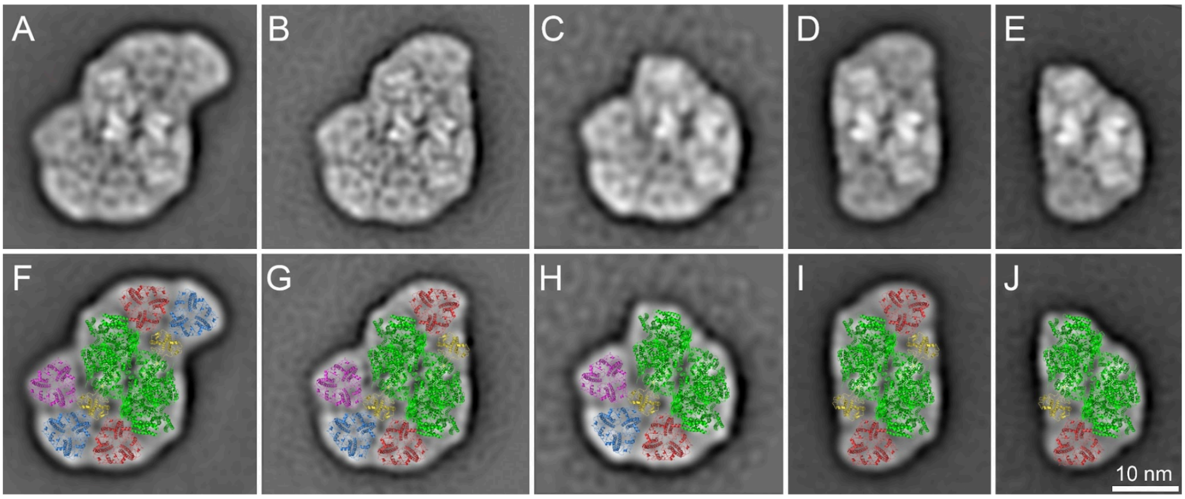
Supplementary Figure S50. Estimated molecular masses for the *Euglena gracilis* photosynthetic complexes. The logarithms of the molecular masses of previously characterized mitochondrial complexes (●) (V_2, I, III_2, IV) (Miranda-Astudillo et al., 2018; Yadav et al., 2017) were plotted against their migration distance in *hr*CN-PAGE ($R^2 = 0.9755$). Then, the migration distances of the *Euglena* photosynthetic complexes (Δ) were interpolated and their corresponding molecular masses inferred.

Yadav KNS, Miranda-Astudillo HV, Colina-Tenorio L, Bouillenne F, Degand H, Morsomme P, González-Halphen D, Boekema EJ, Cardol P. Atypical composition and structure of the mitochondrial dimeric ATP synthase from Euglena gracilis. Biochim Biophys Acta Bioenerg. 2017 Apr;1858(4):267-275. doi: 10.1016/j.bbabio.2017.01.007. Epub 2017 Jan 12. PMID: 28089911.

Miranda-Astudillo HV, Yadav KNS, Colina-Tenorio L, Bouillenne F, Degand H, Morsomme P, Boekema EJ, Cardol P. The atypical subunit composition of respiratory complexes I and IV is associated with original extra structural domains in Euglena gracilis. Sci Rep. 2018 Jun 26;8(1):9698. doi: 10.1038/s41598-018-28039-z. PMID: 29946152; PMCID: PMC6018760.

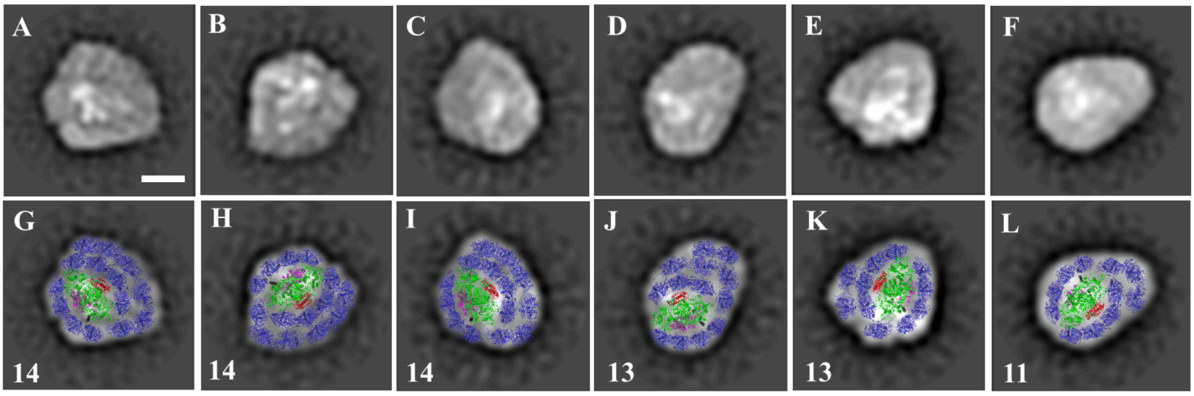


Supplementary Figure S51. Distribution of LhcbM in PSII-SC and Free LHCII Across Different PSII/LHCII Particles. The bar graph illustrates the relative amounts of LhcbM (BM-I, BM-VII, BM-VI, BM-V). The color-coded bars represent different PSII-LHCII compositions: $C_2S_2M_2N_2$ (dark green), $C_2S_2M_2$ (light green), and free $LHCII_3$ (blue). Error bars represent standard deviations.



Supplementary Figure S52. Projection maps and structural models of PSII supercomplexes from *Euglena gracilis* revealed by single particle electron microscopy. (A-E) Projection maps of several subforms of PSII supercomplex. (F-J) Structural models of different forms of the PSII supercomplexes obtained by fitting the high-resolution structure of the PSII supercomplex from green alga *Chlamydomonas reinhardtii* (PDB: 6AKD (Shen et al., 2019). The scale bar is 10 nm.

Shen L, Huang Z, Chang S, Wang W, Wang J, Kuang T, Han G, Shen JR, Zhang X. Structure of a $C_2S_2M_2N_2$-type PSII-LHCII supercomplex from the green alga *Chlamydomonas reinhardtii*. Proc Natl Acad Sci U S A. 2019 Oct 15;116(42):21246-21255. doi: 10.1073/pnas.1912462116. Epub 2019 Sep 30. PMID: 31570614; PMCID: PMC6800332.



Supplementary Figure S53. Structural models of PSI-LHC supercomplexes from Euglena gracilis revealed by single-particle electron microscopy. Structural models of different PSI-LHC supercomplex forms obtained through single-particle electron microscopy. Top rows: raw electron density projections. Bottom rows: corresponding fitted models with assigned structural components. Densities were assigned by fitting the high-resolution PSI structure from *Dunaliella salina* (PDB: 6RHZ, Perez-Boerema et al., 2020). Additional antenna proteins were modeled using copies of the Lhca1 subunit from *Dunaliella salina*. PSI core (green), PsaD subunit (violet); LHC (blue) belt at the PsaF side (red); Variable "flipper" region at the PsaM side (black). The scale bar represents 10 nm.

Perez-Boerema A, Klaiman D, Caspy I, Netzer-El SY, Amunts A, Nelson N. Structure of a minimal photosystem I from the green alga Dunaliella salina. Nat Plants. 2020 Mar;6(3):321-327. doi: 10.1038/s41477-020-0611-9. Epub 2020 Mar 2. PMID: 32123351.

Supplementary dataset 1. Reference sequences for LHH and PSI/PSII subunits (and a few other proteins) compiled from the literature for model organisms *C. reinhardtii*, *Arabidopsis thaliana*, *Ostreococcus tauri*, *Synechocystis* PCC 6803.

```
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AMLGAAGFIIPEALNKYGANCGPEAVWFKTGALLLDGNTLNYFGKNIPINLVLAVVAEVV
LLGGAEYYRITNGLDFEDKLHPGGPFDPLGLAKDPEQGALLKVKEIKNGRLAMFAMLGFF
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>LHCB5/CP26-Chlamydomonas_reinhardtii_3055@CR16G05320
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ANKFGSLAPPDLYPEFGTYPGGGESPVIPFGSEKNAEREIIHGRWAMLGVTGAWAAENGT
GIPWFTAGTLCTPDDCTAVADKFPGAVAPLAPAGSGYPNFWAVLAIEIFLVGSAECYRTG
LFENPFPELTQGDVTPGGRFDPLGFAEAGDLEELKIKELKHSRLAMFAWLGCIMQALATQ
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>LHCP/prasino-Ostreococcus_tauri_70448@OT16G00400
MSALLASSFVSRVAAFKAQKVQNKSVSTTVKADIYPEFGTYPGGGESPIIPFGSEKNAER
EVIHGRWAMLGVTGAWAAENGTGIPWFTAGTLCTPDDCTAVADKFPGAVAPLAPEGSGYP
SFWNVLIIEIVLVGAAEAYRTGISDSPFDDGLTVGDVNPGGRFDPLGLAESGDLEELKIK
ELKHCRLSMFAWLGCIFQALATQEGPIANWQSHVADPVHSNVLTNAAKGFGFY
>LHCSR-Chlamydomonas_reinhardtii_3055@CR08G01590
MAMMMRKAAAVPASSRRSVAVNSVSGKRTVSGKAGAPVPEDVLAYAKTLPGVTAPFDNVF
DPAGFLATASVKDVRRWRESEITHGRVAMLAALGFIVGEQLQDFPLFFNFDGRVSGPAIY
HFQQIGQGFWEPLLIAIGVAESYRVAVGWATPTGTGFNSLKDDYEPGDLGFDPLGLKPTD
PEELKTLQTKELNNGRLAMIAIAAFVAQELVEQTEIFEHLVLRFEKEVILELEDVERDLG
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>LHCSR-Chlamydomonas_reinhardtii_3055@CR08G01950
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SGPAIYHFQQIGQGFWEPLLIAIGVAESYRVAVGWATPTGTGFNSLKDDYEPGDLGFDPL
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>LHCSR-Ostreococcus_tauri_70448@OT05G01790
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IGSVIAIAESARVQAGWQDPGQSDKLFLLKDGYTPGDLSFDPLGLGNGKSAEELDALRLK
ELNNGRLAMIAISGMVAQELVDGLNILPADIALELGNGDLQKMEQACAGKVDEAACAKAF
EASLEAASRM
Haut du formulaire
>XP_001700736.1 uncharacterized protein CHLRE_05g243800v5 [Chlamydomonas reinhardtii]
MASITCSSGKAAVVSRAKTARPVARRMSVVASAAPQGNASRRELLGLSAVAASLLLSSRPAHAIFGFADD
NTALFDTYTAETSAILDKVKVTLALDKDDPAKEDSVKGLRKDINNWVAKYRREPKVSGKPSFGNTYSALN
ALAGHFNSFGATAPIPKKRLERLQKELDDATLLLTRNR

>NP_563687.1 photosystem II family protein [Arabidopsis thaliana]
MASASATATLLKPNLPPHKPTIIASSVSPPLPPPRRNHLLRRDFLSLAATSTLLTQSIQFLAPAPVSAAE
DEEYIKDTSAVISKVRSTLSMQKTDPNVADAVAELREASNSWVAKYRKEKALLGKASFRDIYSALNAVSG
HYVSFGPTAPIPAKRKARILEEMETAEKALTRGR

>CAL57287.1 Photosystem II Pbs27 [Ostreococcus tauri]
MNKARATFNVSASALFKRVAEDASRAESAPSTSRRFVALSLALAAASTASAPGANAQKFKEVCDPTEDGA
ECRANILAQDGIDVGAYEVGGSRSFKAANPTGAKTSLTTYQSDTLEFVGEVEALLAMDVYDGSREKAVAA
FQKKSNNWSGKYAPGGSSKMASGRAFYNALNQLAGHYSFNGLAPIPKSRLDVVETNIAKTKELIAAGR

>WP_041425825.1 MULTISPECIES: photosystem II protein Psb27 [unclassified Synechocystis]
MSFLKNQLSRLLALILVVAIGLTACDSGTGLTGNYSQDTLTVIATLREAIDLPQDAPNRQEVQDTARGQI
NDYISRYRRKGDAGGLKSFTTMQTALNSLAGYYTSYGARPIPEKLKKRLQLEFTQAERSIERGV

>XP_001693657.1 uncharacterized protein CHLRE_13g562850v5 [Chlamydomonas reinhardtii]
MLVAKHFVAPSVAPRPKAAPAPRSSLARKAVATPVLAATFKPPTVAETKAKFLSGYNKPIASIYSTVLQE
LLVQQHFMRYSKNYQYNPIFALGFVSVYEQILESLSAEERGAIFKAYVDALGEDADKYKRDASALEQAAN
GLTPESLTPNADGNEVQKALASISSASAAGAFSYNKFVAIGLFRLLELSGAKEPSALEKLVKAVGVKPEA
VNRDLLMYKGVLSKLAAAKELMREFVEREKRKQAERDAAKAAKAAGTESSPAQVQA

>NP_565491.1 photosystem II reaction center PSB29 protein [Arabidopsis thaliana]
MAATAISSLSFPALGQSDKISNFASSRPLASAIRICTKFSRLSLNSRSTSKSLIHCMSNVTADVPPVSET
KSKFLKAYKRPIPSIYNTVLQELIVQQHLMRYKKTYRYDPVFALGFVTVYDQLMEGYPSDQDRDAIFKAY
IEALNEDPKQYRIDAQKMEEWARSQTSASLVDFSSKEGDIEAVLKDIAGRAGSKEGFSYSRFFAVGLFRL

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LELASATDPTVLDKLCASLNINKKSVDRDLDVYRNLLSKLVQAKELLKEYVEREKKKQGERAQSQKANET
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>CEF97146.1 Photosystem II Psp29, biogenesis [Ostreococcus tauri]
MRAQLARVTAPKALGASRKAPTSARARCAAITRAQSGIYGVTVADTKRKFLEAYPYPIPSVWATVVQELL
VQGHFQKYNKKSEYNELASLGFVSVYDQLFEGFPSEEEKGKIFNAFLGALDEDAVRTRADAETLGAFATS
ANGVEGLKENAIFAKLAAKSAEGTLLYTKYIAIGMFRMLELAKATDPAALEALVTAGGLSMSKVSGDLSM
YKGLLSKLAAAKELQEEFLEREKRKTAERLAKKAEAEQKAEAEA

>BAA18023.1 sll1414 [Synechocystis sp. PCC 6803]
MTKIRTVSDAKRKFFTHYSRPISSIYRRFVEELLVEMHLLSVNIDFTYDPIFALGIVTSFNSFMQGYQPA
EQLPAIFNALCHGVDQNPDQVRQDAKNVAASAHHIGLDAWVTAAASEQASGDNLLLNTLTGIHQRHKFKY
SRLFAIGLYTLLADQDPEVKDNDEKRQDYLTRLSELLDLSLDKVVKDLDLYRSNLEKVDQLLKVLEDAAE
AERKKKEKQAASTTPAIEEAPVTTAESSES

>NP_958413.1 photosystem II protein D1 (chloroplast) [Chlamydomonas reinhardtii]
MTAILERRENSSLWARFCEWITSTENRLYIGWFGVIMIPCLLTATSVFIIAFIAAPPVDIDGIREPVSGS
LLYGNNIITGAVIPTSNAIGLHFYPIWEAASLDEWLYNGGPYQLIVCHFLLGVYCYMGREWELSFRLGMR
PWIAVAYSAPVAAASAVFLVYPIGQGSFSDGMPLGISGTFNFMIVFQAEHNILMHPFHMLGVAGVFGGSL
FSAMHGSLVTSSLIRETTENESANEGYRFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLAAWPV
IGIWFTALGLSTMAFNLNGFNFNQSVVDSQGRVLNTWADIINRANLGMEVMHERNAHNFPLDLASTNSSS
NN

>NP_051039.1 photosystem II protein D1 (chloroplast) [Arabidopsis thaliana]
MTAILERRESESLWGRFCNWITSTENRLYIGWFGVLMIPTLLTATSVFIIAFIAAPPVDIDGIREPVSGS
LLYGNNIISGAIIPTSAAIGLHFYPIWEAASVDEWLYNGGPYELIVLHFLLGVACYMGREWELSFRLGMR
PWIAVAYSAPVAAATAVFLIYPIGQGSFSDGMPLGISGTFNFMIVFQAEHNILMHPFHMLGVAGVFGGSL
FSAMHGSLVTSSLIRETTENESANEGYRFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLAAWPV
VGIWFTALGISTMAFNLNGFNFNQSVVDSQGRVINTWADIINRANLGMEVMHERNAHNFPLDLAAVEAPS
TNG

>YP_717233.1 photosystem II protein D1 (chloroplast) [Ostreococcus tauri]
MTATLERRANATVWGRFCSWITSTENRLYIGWFGVLMIPTLLTATSVFIVAFIAAPPVDIDGIREPVSGS
LMYGNNIISGAVIPTSNAIGLHFYPIWEAASLDEWLYNGGPYQLIVCHFFIGICSYMGREWELSFRLGMR
PWIAVAYSAPVAAATAVFLIYPIGQGSFSDGMPLGISGTFNFMIVFQAEHNILMHPFHMLGVAGVFGGSL
FSAMHGSLVTSSLIRETTENESANAGYKFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLAIWPV
MGIWFTALGISTMAFNLNGFNFNQSVVDSNGRVINTWADIVNRANLGMEVMHERNAHNFPLDLASVEAPS
INA

>AIE73589.1 photosystem II protein D1 (PsbA) [Synechocystis sp. PCC 6714]
MTTTLQQRESASLWEQFCQWVTSTNNRIYVGWFGTLMIPTLLTATTCFIIAFIAAPPVDIDGIREPVAGS
LLYGNNIISGAVVPSSNAIGLHFYPIWEAASLDEWLYNGGPYQLVVFHFLIGIFCYMGRQWELSYRLGMR
PWICVAYSAPVSAATAVFLIYPIGQGSFSDGMPLGISGTFNFMIVFQAEHNILMHPFHMLGVAGVFGGSL
FSAMHGSLVTSSLVRETTEVESQNYGYKFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLGAWPV
IGIWFTAMGVSTMAFNLNGFNFNQSILDSQGRVIGTWADVLNRANIGFEVMHERNAHNFPLDLASGEQAP
VALTAPAING

>NP_958388.1 photosystem II 47 kDa protein (chloroplast) [Chlamydomonas reinhardtii]
MGLPWYRVHTVVINDPGRLISVHLMHTALVSGWAGSMALFEISVFDPSDPVLNPMWRQGMFVLPFMTRLG
ITQSWGGWTISGETATNPGIWSYEGVAAAHIILSGALFLASVWHWTYWDLELFRDPRTGKTALDLPKIFG
IHLFLSGLLCFGFGAFHVTGVFGPGIWVSDPYGLTGRVQPVAPSWGADGFDPYNPGGIASHHIAAGILGV
LAGLFHLCVRPSIRLYFGLSMGSIETVLSSSIAAVFWAAFVVAGTMWYGSAATPIELFGPTRYQWDQGFF
QQEIQKRVQASLAEGASLSDAWSRIPEKLAFYDYIGNNPAKGGLFRTGAMNSGDGIAVGWLGHASFKDQE
GRELFVRRMPTFFETFPVLLLDKDGIVRADVPFRKAESKYSIEQVGVSVTFYGGELDGLTFTDPATVKKY
ARKAQLGEIFEFDRSTLQSDGVFRSSPRGWFTFGHVCFALLFFFGHIWHGARTIFRDVFAGIDDDINDQV
EFGKYKKLGDTSSLREAF

>NP_051084.1 photosystem II 47 kDa protein (chloroplast) [Arabidopsis thaliana]
MGLPWYRVHTVVLNDPGRLLAVHIMHTALVAGWAGSMALYELAVFDPSDPVLDPMWRQGMFVIPFMTRLG
ITNSWGGWNITGGTITNPGLWSYEGVAGAHIVFSGLCFLAAIWHWVYWDLEIFCDERTGKPSLDLPKIFG
IHLFLSGVACFGFGAFHVTGLYGPGIWVSDPYGLTGKVQPVNPAWGVEGFDPFVPGGIASHHIAAGTLGI
LAGLFHLSVRPPQRLYKGLRMGNIETVLSSSIAAVFFAAFVVAGTMWYGSATTPIELFGPTRYQWDQGYF
QQEIYRRVSAGLAENQSLSEAWAKIPEKLAFYDYIGNNPAKGGLFRAGSMDNGDGIAVGWLGHPVFRNKE
GRELFVRRMPTFFETFPVVLVDGDGIVRADVPFRRAESKYSVEQVGVTVEFYGGELNGVSYSDPATVKKY
ARRAQLGEIFELDRATLKSDGVFRSSPRGWFTFGHASFALLFFFGHIWHGARTLFRDVFAGIDPDLDAQV
EFGAFQKLGDPTTKRQAV
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>YP_717207.1 PsbB (chloroplast) [Ostreococcus tauri]
MTRLGVTNSWGGWTISGESTSNPGLWSYEGVAASHIILSGLLFLAAIWHWVFWDLELFRDPRTQQPALDL
PKIFGIHLFLSGVLCFGFGAFHVTGLFGPGIWVSDPYGLTGAVEPVAPAWGAEGFDPYNPGGIAAHHIAA
GIVGILAGLFHLSVRPPQRLYKALRMGNVETVLSSSIAAVFWAAFVVGGTMWYGCAATPIELFGPTRYQW
DQGFFQQEIEKRVQTSVAGGASLSTAWSTIPEKLAFYDYIGNNPAKGGLFRSGPMDNGDGIAAGWLGHAT
FTDKNGRELFVRRMPTFFETFPVILIDGDGVVRADVPFRRAESKYSIEQVGVNVTFYGGELDGLTFTDPA
TVKKYARRAQLGEVFEFDRATLQSDGVFRSSPRAWFTFAHVSFALLFFFGHIWHGARTIFRDVFAGIDPD
LDEQVEFGAFQKLGDVTTRRQAV

>BAA10458.1 photosystem II CP47 protein [Synechocystis sp. PCC 6803]
MGLPWYRVHTVVLNDPGRLISVHLMHTALVAGWAGSMALYELAIFDSSDAVLNPMWRQGMFVLPFMARLG
VTSSWNGWSVTGETGLDPGFWSFEGVAAAHIVLSGLLFLAAVWHWVFWDLELFVDPRTGESALDLPKMFG
IHLFLSGLLCFGFGAFHLTGVWGPGMWVSDPYGLTGHVQPVAPEWGPAGFNPFNPGGVVAHHIAAGIVGI
IAGLFHLTVRPPERLYKALRMGNIETVLSSSIAAVFFAAFVVAGTMWYGNATTPIELFGPTRYQWDKGYF
QEEIQRRVDSQLAEGASLSEAWSTIPEKLAFYDYVGNSPAKGGLFRTGAMNSGDGIAQEWIGHPIFKDKE
GRELEVRRMPNFFETFPVIMTDADGVVRADIPFRRSESKFSVEQTGVTVSFYGGALDGQTFSNPSDVKKF
ARKAQLGEGFDFDTETFNSDGVFRTSPRGWFTFGHAVFALLFFFGHIWHGSRTLFRDVFAGVDPGLEEQV
EFGVFAKVGDLSTRKEA

>NP_958422.1 photosystem II 44 kDa protein (chloroplast) [Chlamydomonas reinhardtii]
METLFNGTLTVGGRDQETTGFAWWSGNARLINLSGKLLGAHVAHAGLIVFWAGAMNLFEVSHFVPEKPMY
EQGLILLPHIATLGYGVGPGGEIIDTFPYFVSGVLHLISSAVLGFGGVYHSLIGPETLEESYPFFGYVWK
DKNKMTNILGYHLIMLGLGAWLLVWKAMYFGGVYDTWAPGGGDVRVITNPTTNAAVIFGYLVKSPFGGDG
WICSVDNMEDIIGGHIWIGTLEILGGIWHIYTTPWPWARRAFVWSGEAYLSYSLGAIGVMGFIACCMSWF
NNTAYPSEFYGPTGPEASQSQAFTFLVRDQRLGANVASAQGPTGLGKYLMRSPTGEIIFGGETMRFWDFR
GPWLEPLRGPNGLDLNKLKNDIQPWQERRAAEYMTHAPLGSLNSVGGVATEINAVNFVSPRSWLACSHFC
LGFFFFIGHLWHAGRARAAAAGFEKGIDRFDEPVLSMRPLD

>NP_051055.1 photosystem II 44 kDa protein (chloroplast) [Arabidopsis thaliana]
MKTLYSLRRFYHVETLFNGTLALAGRDQETTGFAWWAGNARLINLSGKLLGAHVAHAGLIVFWAGAMNLF
EVAHFVPEKPMYEQGLILLPHLATLGWGVGPGGEVIDTFPYFVSGVLHLISSAVLGFGGIYHALLGPETL
EESFPFFGYVWKDRNKMTTILGIHLILLGVGAFLLVFKALYFGGVYDTWAPGGGDVRKITNLTLSPSVIF
GYLLKSPFGGEGWIVSVDDLEDIIGGHVWLGSICIFGGIWHILTKPFAWARRALVWSGEAYLSYSLAALS
VCGFIACCFVWFNNTAYPSEFYGPTGPEASQAQAFTFLVRDQRLGANVGSAQGPTGLGKYLMRSPTGEVI
FGGETMRFWDLRAPWLEPLRGPNGLDLSRLKKDIQPWQERRSAEYMTHAPLGSLNSVGGVATEINAVNYV
SPRSWLSTSHFVLGFFLFVGHLWHAGRARAAAAGFEKGIDRDFEPVLSMTPLN

>YP_717204.2 photosystem II 44 kDa protein (chloroplast) [Ostreococcus tauri]
METLFNSTLVVGGRDQESTGFAWWAGNARLINLSGKLLGAHVAHAGLIVFWAGAMNLFEVAHFVPEKPMY
EQGLILLPHLAALGYGVGPGGEVLDTFPYFVSGVLHLISSAVLGFGGVYHSLIGPETLEESYPFFGYLWK
DKNKMTTILGIHLVLLGIGAWLLVWKAMYFGGVYDTWAPGGGDVRVISYPTYDPSVIFGYLLKSPFGGDG
WIISVDNMEDVIGGHIWIGTTLIIGGFFHIFTKPFAWARRAFVWSGEAYLSYSLASVSLMAFIAAVFVWF
NNTVYPSEFFGPTGPEASQAQAFTFLVRDQRLGANIASAQGPTGLGKYLMRSPTGEIIFGGETMRFWDMR
APWVEPLRGPNGLDLSKLKNDIQPWQERRSAEYMTHAPLGSLNSVGGVATEINSTNFVNPRSWLATSHYV
LGFFFFVGHLWHAGRARAAAAGFEKGIDRDTEPVLSMRPLD

>BAA17799.2 photosystem II CP43 protein [Synechocystis sp. PCC 6803]
MVTLSNTSMVGGRDLPSTGFAWWSGNARLINLSGKLLGAHVAHAGLIVFWAGAMTLFEVAHFIPEKPMYE
QGLILLPHIATLGWGVGPAGEVTDIFPFFVVGVLHLISSAVLGLGGIYHALRGPEVLEEYSSFFGYDWKD
KNQMTNIIGYHLILLGCGALLLVFKAMFFGGVYDTWAPGGGDVRVITNPTLNPAIIFGYLLKAPFGGEGW
IISVNNMEDIIGGHIWIGLICISGGIWHILTKPFGWARRALIWSGEAYLSYSLGALSLMGFIASVFVWFN
NTAYPSEFYGPTGMEASQSQAFTFLVRDQRLGANIASAQGPTGLGKYLMRSPSGEIIFGGETMRFWDFRG
PWLEPLRGPNGLDLDKLRNDIQPWQVRRAAEYMTHAPLGSLNSVGGVITDVNSFNYVSPRAWLATSHFVL
GFFFLVGHLWHAGRARAAAAGFEKGIDRETEPTLFMPDLD

>NP_958420.1 photosystem II protein D2 (chloroplast) [Chlamydomonas reinhardtii]
MTIAIGTYQEKRTWFDDADDWLRQDRFVFVGWSGLLLFPCAYFALGGWLTGTTFVTSWYTHGLATSYLEG
CNFLTAAVSTPANSMAHSLLFVWGPEAQGDFTRWCQLGGLWAFVALHGAFGLIGFMLRQFEIARSVNLRP
YNAIAFSAPIAVFVSVFLIYPLGQSGWFFAPSFGVAAIFRFILFFQGFHNWTLNPFHMMGVAGVLGAALL
CAIHGATVENTLFEDGDGANTFRAFNPTQAEETYSMVTANRFWSQIFGVAFSNKRWLHFFMLLVPVTGLW
MSAIGVVGLALNLRAYDFVSQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHERLVFPEEVLPRGN
AL

>NP_051054.1 photosystem II protein D2 (chloroplast) [Arabidopsis thaliana]
MTIALGKFTKDEKDLFDIMDDWLRRDRFVFVGWSGLLLFPCAYFALGGWFTGTTFVTSWYTHGLASSYLE
GCNFLTAAVSTPANSLAHSLLLLWGPEAQGDFTRWCQLGGLWAFVALHGAFALIGFMLRQFELARSVQLR
PYNAIAFSGPIAVFVSVFLIYPLGQSGWFFAPSFGVAAIFRFILFFQGFHNWTLNPFHMMGVAGVLGAAL
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LCAIHGATVENTLFEDGDGANTFRAFNPTQAEETYSMVTANRFWSQIFGVAFSNKRWLHFFMLFVPVTGL
WMSALGVVGLALNLRAYDFVSQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHENLIFPEEVLPRG
NAL

>YP_717205.1 photosystem II protein D2 (chloroplast) [Ostreococcus tauri]
MTIALGKVDEKRGWFDNVDDWLKRDRFVFVGWSGILLFPCAYFALGGWLTGTTFVSSWYTHGLASSYLEG
CNFLTSAVSTPSNSMAHSLLLLWGPEAQGDFTRWCQLGGLWTFVALHGAFGLIGFMLRQFEIARAVQIRP
YNAIAFSAPIAVFVSVFLIYPLGQSGWFFAPSFGVAGIFRFILFFQGFHNWTLNPFHMMGVAGVLGAALL
CAIHGATVENTLFEDGDGSNTFRAFNPTQAEETYSMVTANRFWSQIFGVAFSNKRWLHFFMLFVPVTGLW
MSALGVVGLALNLRAYDFVSQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHENLVFPEEVLPRGN
AL

>AAA85377.1 psbD [Synechocystis sp. PCC 6803]
MTIAVGRAPVERGWFDVLDDWLKRDRFVFIGWSGLLLFPCAFMALGGWLTGTTFVTSWYTHGLASSYLEG
ANFLTVAVSSPADAFGHSLLFLWGPEAQGNLTRWFQIGGLWPFVALHGAFGLIGFMLRQFEISRLVGIRP
YNAIAFSGPIAVFVSVFLMYPLGQSSWFFAPSFGVAGIFRFILFLQGFHNWTLNPFHMMGVAGILGGALL
CAIHGATVENTLFEDGEDSNTFRAFEPTQAEETYSMVTANRFWSQIFGIAFSNKRWLHFFMLFVPVTGLW
MSSVGIVGLALNLRAYDFVSQELRAAEDPEFETFYTKNILLNEGMRAWMAPQDQPHENFIFPEEVLPRGN
AL

>NP_958396.1 photosystem II protein V (chloroplast) [Chlamydomonas reinhardtii]
MAGKPVERPFSDILTSIRYWVIHSITVPALFIAGWLFVSTGLAYDVFGTPRPNEYFTEDRQEAPLITDRF
NALEQVKKLSGN

>NP_051076.1 photosystem II protein V (chloroplast) [Arabidopsis thaliana]
MSGSTGERSFADIITSIRYWVIHSITIPSLFIAGWLFVSTGLAYDVFGSPRPNEYFTESRQGIPLITGRF
DPLEQLDEFSRSF

>YP_717219.1 photosystem II protein V (chloroplast) [Ostreococcus tauri]
MSGSTGERPFSDIVTSIRYWVIHSVTIPSLFIAGWLFVSTGLAYDVFGTPRPNEYFTEERQELPLISDRY
GALAQLDDLVPN

>BAA17092.1 cytochrome b559 a subunit [Synechocystis sp. PCC 6803]
MSGTTGERPFSDIVTSIRYWVIHSITIPMLFIAGWLFVSTGLAYDAFGTPRPDEYFTQTRQELPILQERY
DINQEIQEFNQ

>NP_958399.1 photosystem II protein VI (chloroplast) [Chlamydomonas reinhardtii]
MTTKKSAEVLVYPIFTVRWLAIHGIAVPTIFFLGAITAMQFIQR

>NP_051075.1 photosystem II protein VI (chloroplast) [Arabidopsis thaliana]
MTIDRTYPIFTVRWLAVHGLAVPTVSFLGSISAMQFIQR

>YP_717218.1 photosystem II protein VI (chloroplast) [Ostreococcus tauri]
MSVKTYPIFTFRWLAVHALAVPTVFFLGSITAMQFIQR

>BAA17093.1 cytochrome b559 b subunit [Synechocystis sp. PCC 6803]
MATQNPNQPVTYPIFTVRWLAVHTLAVPSVFFVGAIAAMQFIQR

>NP_958385.1 photosystem II protein H (chloroplast) [Chlamydomonas reinhardtii]
MATGTSKAKPSKVNSDFQEPGLVTPLGTLLRPLNSEAGKVLPGWGTTVLMAVFILLFAAFLLIILEIYNS
SLILDDVSMSWETLAKVS

>NP_051087.1 photosystem II protein H (chloroplast) [Arabidopsis thaliana]
MATQTVEDSSRSGPRSTTVGKLLKPLNSEYGKVAPGWGTTPLMGVAMALFAVFLSIILEIYNSSVLLDGI
SVN

>YP_717221.1 photosystem II protein H (chloroplast) [Ostreococcus tauri]
MAAKDSKLAGTGKVTALGTALRPLNSEYGKVAPGWGTTILMSVFIGLFAVFIVILLEIYNKSLILDNVGV
NWLSSTGL

>BAA17629.1 photosystem II PsbH protein [Synechocystis sp. PCC 6803]
MAQRTRLGDILRPLNSEYGKVVPGWGTTPVMGVFMALFLVFLLIILQIYNSSLILEGFSVDWAG

>NP_958407.1 photosystem II protein I (chloroplast) [Chlamydomonas reinhardtii]
MLTLKIFVYTVVTFFVCLFIFGFLSNDPARNPGKNLD

>NP_051043.1 photosystem II protein I (chloroplast) [Arabidopsis thaliana]
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MLTLKLFVYTVVIFFVSLFIFGFLSNDPGRNPGREE

>YP_717260.1 photosystem II protein I (chloroplast) [Ostreococcus tauri]
MLTLKILVYTVVSFFVSLFIFGFLSNDPGRNPNSKDFE

>BAA10085.1 photosystem II PsbI protein [Synechocystis sp. PCC 6803]
MLTLKIAVYIVVGLFISLFIFGFLSSDPTRNPGRKDFE

>NP_958419.1 photosystem II reaction center protein J (chloroplast) [Chlamydomonas reinhardtii]
MSNTGTTGRIPLWLVGTEEGTLAIGAISCFFYGFLCWFRFFSIIKFKFFV

>NP_051073.1 photosystem II protein J (chloroplast) [Arabidopsis thaliana]
MADTTGRIPLWVIGTVAGILVIGLIGIFFYGSYSGLGSSL

>YP_717216.1 photosystem II protein J (chloroplast) [Ostreococcus tauri]
MSNTTTGRIPLWFVGMVGGLAALGLLAIFFYGSYVGLGSSL

>BAA17095.1 photosystem II PsbJ protein [Synechocystis sp. PCC 6803]
MFAEGRIPLWVVGVVAGIGAIGVLGLFFYGAYAGLGSSM

>NP_958361.1 photosystem II protein K (chloroplast) [Chlamydomonas reinhardtii]
MTTLALVLAKLPEAYAPFAPIVDVLPVIPVFFILLAFVWQAAVSFR

>NP_051042.1 photosystem II protein K (chloroplast) [Arabidopsis thaliana]
MLNIFNLICIFFNSTLFSSTFLVAKLPEAYAFLNPIVDVMPVIPLFFLLLAFVWQAAVSFR

>YP_717259.1 photosystem II protein K (chloroplast) [Ostreococcus tauri]
MTQIFLIGRLPEAYAPFDPIVDVLPIIPVLFLLLAFVWQASVSFR

>BAA17075.1 photosystem II PsbK protein [Synechocystis sp. PCC 6803]
METIYLLAKLPEAYQIFDPLVDVLPVIPLFFLALAFVWQAAVGFK

>CAA46978.1 psbL (chloroplast) [Chlamydomonas reinhardtii]
MFKNFFMARPNPNKQVVELNRTSLYWGLLLIFVLAVLFSSYIFN

>NP_051074.1 photosystem II protein L (chloroplast) [Arabidopsis thaliana]
MTQSNPNEQSVELNRTSLYWGLLLIFVLAVLFSNYFFN

>YP_717217.1 photosystem II protein L (chloroplast) [Ostreococcus tauri]
MTNPNPNKQTVELNRTSLYWGLLLIFVLAVLFSSYIFN

>BAA17094.1 photosystem II PsbL protein [Synechocystis sp. PCC 6803]
MDRNSNPNRQPVELNRTSLYLGLLLVAVLGILFSSYFFN

>NP_958382.1 photosystem II protein M (chloroplast) [Chlamydomonas reinhardtii]
MEVNIYGLTATALFIIIPTSFLLILYVKTASTQD

>NP_051053.1 photosystem II protein M (chloroplast) [Arabidopsis thaliana]
MEVNILAFIATALFILVPTAFLLIIYVKTVSQND

>XP_003082196.1 Photosystem II PsbM [Ostreococcus tauri]
MPALASALGLIPLARARATPRARARVVAPRASAGVKLAQKVQKAVVAAPAIVAAPAFAAQEAIEQVALDN
VNILGVVATALFIIIPTSFLIILYVKSASEGNVSGYSQEYYDKSKAAGNKKTNLAAALKGKGLGMRPEK

>BAA16708.1 photosystem II PsbM protein [Synechocystis sp. PCC 6803]
MQVNNLGFIASILFVLVPTVFLLILFIQTGKQSES

>NP_958386.1 photosystem II protein N (chloroplast) [Chlamydomonas reinhardtii]
MESPAFFFTFFLWFLLLSVTGYSVYVSFGPPSKKLRDPFEEHED

>NP_051086.1 photosystem II protein N (chloroplast) [Arabidopsis thaliana]
METATLVAIFISGLLVSFTGYALYTAFGQPSQQLRDPFEEHGD

>YP_717222.1 PsbN (chloroplast) [Ostreococcus tauri]
MENSAFFYGVFLWCLLISVTGYSIYIGFGPPSKELRDPFEEHED

>BAA17630.1 photosystem II PsbN protein [Synechocystis sp. PCC 6803]
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MESATVLSITFAVILIAITGLAVYTSFGPPSAELGDPFDDHED

>XP_001694699.1 uncharacterized protein CHLRE_09g396213v5 [Chlamydomonas reinhardtii]
MALRAAQSAKAGVRAARPNRATAVVCKAQKVGQAAAAAALATAMVAGSANALTFDEIQGLTYLQVKGSGI
ANTCPVLESGTTNLKELKAGSYKLENFCIEPTSFTVKEESQFKGGETEFVKTKLMTRLTYTLDAMSGSFK
VGSDGSAELKEDDGIDYAATTVQLPGGERVAFLFTIKQFDGKGTLDNIKGDFLVPSYRGSSFLDPKGRGG
STGYDNAVALPARADAEELLKENVKITKALKGSAVFSVAKVDPVTGEIAGVFESIQPSDTDLGAKPPKDI
KVTGLWYAQLK

>NP_201458.1 PS II oxygen-evolving complex 1 [Arabidopsis thaliana]
MAASLQSTATFLQSAKIATAPSRGSSHLRSTQAVGKSFGLETSSARLTCSFQSDFKDFTGKCSDAVKIAG
FALATSALVVSGASAEGAPKRLTYDEIQSKTYMEVKGTGTANQCPTIDGGSETFSFKPGKYAGKKFCFEP
TSFTVKADSVSKNAPPEFQNTKLMTRLTYTLDEIEGPFEVASDGSVNFKEEDGIDYAAVTVQLPGGERVP
FLFTVKQLDASGKPDSFTGKFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELVKENVKNTAA
SVGEITLKVTKSKPETGEVIGVFESLQPSDTDLGAKVPKDVKIQGVWYGQLE

>CEG01950.1 Photosystem II PsbO, manganese-stabilising [Ostreococcus tauri]
MASIARSAVFGNTAFAVRAKSAKRSAKAQAPKASLNEFAEKVSKATVSLGVAGAVLAQSASAVTYDELQG
LTYLQVKGTGLANTCPVVEGGVSGKDIKAGDYKLERFCMEPTSFTVKEESQFKAGESEFQKTRLMTRLTY
TLDGMTGDFKVGSDGSVQIKENDGLDYAPVTVQLPGGERVPFLFTLKEFTGKGNTSQFGGDFVVPSYRGS
SFLDPKGRGGSTGYDNAVALPARADSEELQKENNKSAAALKGSAVFNIAKYDPATGEIAGVFESIQPSDT
DLGAKVPKDVKITGLWYGNIAK

>BAA18474.1 photosystem II manganese-stabilizing polypeptide [Synechocystis sp. PCC 6803]
MRFRPSIVALLSVCFGLLTFLYSGSAFAVDKSQLTYDDIVNTGLANVCPEISSFTRGTIEVEPNTKYFVS
DFCMEPQEYFVKEEPVNKRQKAEYVKGKVLTRQTTSLEQIRGSIAVGADGTLTFKEKDGIDFQPITVLLP
GGEEVPFFFTVKNFTGTTEPGFTSINSSTDFVGDFNVPSYRGAGFLDPKARGLYTGYDNAVALPSAADKF
RTNKKETPLGKGTLSLQVTQVDGSTGEIAGIFESEQPSDTDLGAKEPLDVKVRGIFYGRVDTDV

>sp|P11471.1|PSBP_CHLRE RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; Flags:
Precursor
MATALCNKAFAAAPVARPASRRSAVVVRASGSDVSRRAALAGFAGAAALVSSSPANAAYGDSANVFGKVT
NKSGFVPYAGDGFALLLPAKWNPSKENDFPGVILRYEDNFDAVNNLVVIAQDTDKKAIADFGSQDKFLES
VSYLLGKQAYSGETQSEGGFAPNRVSAASLLDVSTTTDKKGKTYYKYELLVRSADGDEGGRHQLIGATVG
SDNKLYIIKIQIGDKRWFKGAKKEAMGAFDSFTVV

>NP_191224.1 thylakoid lumenal protein (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein)
[Arabidopsis thaliana]
MATASLVPTSKIFSVSPKSSASIKARSRVVVASSQQQQPRRRELLLKSAVAIPAILQLKEAPISAAREV
EVGSYLPLSPSDPSFVLFKAKPSDTPALRAGNVQPYQFVLPPNWKQLRIANILSGNYCQPKCAEPWIEVK
FENEKQGKVQVVASPLIRLTNKPNATIEDLGEPEKVIASLGPFVTGNSYDSDELLKTSIEKIGDQTYYKY
VLETPFALTGSHNLAKATAKGSTVVLFVVSATEKQWQSSQKTLEAILDSFQL

>XP_003083092.1 photosystem II oxygen-evolving complex 23 kDa protein, chloropla (IC) [Ostreococcus tauri]
METLHVILTLSLDARRRLRDGEGFARRAQVALLTLEPTLVTGLKLHDVQVAVAHGGGDQLVASAFVAIRG
AREDFILVVLLALVLAGTDFEHGGGGNLVRREPTFGSRFAGVRLLTEQVRDLFQERLRLAVVRDLALRGL
FDDDGDVRHRVKVILPVRVLVRERALLGRVVLRREQERVSIARVRDETYVFANTSTATPRGPTTSPNPIR
ERIFAKPIALGHPPVLHRARRTGRVRDTAPNVRGITIAPASVARLHRAIASRSRAYPSHASVSIAHPRRH
RR

>ALJ67700.1 PsbP [Synechocystis sp. PCC 6803]
MLKKSLSTAVVLVTLLLSFTLTACGGVGIASLQRYSDTKDGYEFLYPNGWIGVDVKGASPGVDVVFRDLI
ERDENLSVIISEIPSDKTLTDLGTATDVGYRFMKTVNDASQGDRQAELINAEARDEDGQVYYTLEYRVLV
GDNVERHDLASVTTNRGKLITFDLSTAEDRWDTVKSLFDTVASSFHVY

>XP_001701331.1 oxygen evolving enhancer protein 3 [Chlamydomonas reinhardtii]
MALASKVATRPAVASRRGAVVVRASGESRRAVLGGLLASAVAAVAPKAALALTPVDLFDDRSVRDRGFDL
IYEARDLDLPQNVREGFTQARASLDETKKRVKESEARIDADLDVFIQKSYWTEAREQLRRQVGTLRFDLN
TLASTKEKEAKKAALGLRKEFIQAVEDLDFALREKDQASAAKKLEITKAKLDSVLAAVL

>NP_001031687.1 photosystem II subunit QA [Arabidopsis thaliana]
MASMGGLHGASPAVLEGSLKINGSSRLNGSGRVAVAQRSRLVVRAQQSEETSRRSVIGLVAAGLAGGSFV
QAVLADAISIKVGPPPAPSGGLPAGTDNSDQARDFALALKDRFYLQPLPPTEAAARAKESAKDIINVKPL
IDRKAWPYVQNDLRSKASYLRYDLNTIISSKPKDEKKSLKDLTTKLFDTIDNLDYAAKKKSPSQAEKYYA
ETVSALNEVLAKLG

>CEG00370.1 Photosystem II PsbQ, oxygen evolving complex [Ostreococcus tauri]
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MSVAASTSTFAGKAIAQKAVVKTSKVSTVVKASANKALSLAAATAVVLSTGPAFANTAIELTDKRAEQQN
GLQLIYEARDLDLSNKPNAEGNSRFSFQKLGSTETAARARESVARINGDVGTYVEKKYWTQAANELRRQV
GTLRFDINNLVNEKGANAAEAKAFYKKLENLDFSIRQKDQAAATALLAEVQSTANTLISSLA

>WP_028947222.1 MULTISPECIES: photosystem II protein PsbQ [Cyanophyceae]
MSRLRSLLSLVLVLVTTVLVSCSSPQVEIPTTYSPEKIAQLQVYVNPIAVARDGMEKRLQGLIADQNWVD
TQTYIHGPLGQLRRDMLGLSSSLLPKDQDKAKTLAKEVFGHLERLDVAAKDRNSSQAKIQYQEALADFDA
FLNLLPQAS

>XP_001696588.2 uncharacterized protein CHLRE_06g261000v5 [Chlamydomonas reinhardtii]
MATMQISAKGLAPLRPRVSSRRVVKPVASGGGKTDITKVGLNSIEDPVVKQNLMGKSRFMNKKDWKDASG
RKGKGYGVYRYEDKYGANVDGYSPIYTPDLWTESGDSYTLGTKGLIAWAGLVLVLLAVGVNLIISTSQLG
A

>NP_178025.1 photosystem II subunit R [Arabidopsis thaliana]
MAASVMLSSVTLKPAGFTVEKTAARGLPSLTRARPSFKIVASGVKKIKTDKPFGINGSMDLRDGVDASGR
KGKGYGVYKYVDKYGANVDGYSPIYNENEWSASGDVYKGGVTGLAIWAVTLAGILAGGALLVYNTSALAQ

>CEF98147.1 Photosystem II PsbR [Ostreococcus tauri]
MSALTSSTFVTKSVAATATKSSRARRGALVVMNNSSGPKRGTKAAPAQRSVGYKGSTDAGSAPKTRSGKS
GYVYKLGLKNGKANVDEYSPIWTPQDFKSDGDKYEGNLTYWAITLAGIIGTGALAIILTSQL

>XP_001689923.1 uncharacterized protein CHLRE_01g016750v5 [Chlamydomonas reinhardtii]
MAMTLSTKAFAQRGVSARKNTVRVYAATTKVNPKLASKTEVERFKQATGLPAPAINGKQFPLKLGFTKTN
ELFVGRLAMVGFSASLIGEILTGKGALAQFGYETGLNGIEVDGLVIGLIAFNLIAAVLPTSQTFVPEEQD
TISERPAGPLQDPRITLLEPKKFFGVQGFGFTKENELFVGRAAQLGFAFSLIGEAVTGKGALAQFDIETG
LSLRDTEFGLVVFILFLLFAAINEGSGKFVDEESA

>NP_175092.1 Chlorophyll A-B binding family protein [Arabidopsis thaliana]
MAQTMLLTSGVTAGHFLRNKSPLAQPKVHHLFLSGNSPVALPSRRQSFVPLALFKPKTKAAPKKVEKPKS
KVEDGIFGTSGGIGFTKANELFVGRVAMIGFAASLLGEALTGKGILAQLNLETGIPIYEAEPLLLFFILF
TLLGAIGALGDRGKFVDDPPTGLEKAVIPPGKNVRSALGLKEQGPLFGFTKANELFVGRLAQLGIAFSLI
GEIITGKGALAQLNIETGIPIQDIEPLVLLNVAFFFFAAINPGNGKFITDDGEES

>XP_003080104.1 photosystem II 22 kda polypeptide (ISS) [Ostreococcus tauri]
MHARAIASSSVAHARPGSTRHARGGNGESVTSTSRPAARVRGKRAVARAVAPADEGERDVTDIEINLGRA
AMLGFLGTTLGDVITRGEGPIEQLEDEAAYVINHVNPVDLTRDALEVAGIYVESVILVWLLLGCALLLGV
SQGMRNPIRTVSGRTTKQPYETNVKEQKPYELFNGRLAMLGSAFALVGDVRTGGLGPLEQVQNEVGIPVI
DEEIFAVIFLGGVALNVVSTGITAFRRAYAKGRE

>NP_958387.1 photosystem II protein T (chloroplast) [Chlamydomonas reinhardtii]
MEALVYTFLLVGTLGIIFFSIFFRDPPRMIK

>NP_051085.1 photosystem II protein T (chloroplast) [Arabidopsis thaliana]
MEALVYTFLLVSTLGIIFFAIFFREPPKISTKK

>YP_717206.1 photosystem II protein T (chloroplast) [Ostreococcus tauri]
MEAIVYTFLLVGTLGIIFFAIFFREPPRIAK

>BAA10133.1 photosystem II PsbT protein [Synechocystis sp. PCC 6803]
MESVAYILVLTMALAVLFFAIAFREPPRIEK

>BAA16847.1 photosystem II 12 kD extrinsic protein [Synechocystis sp. PCC 6803]
MKFISRLLVACSLLIGLMGFLGADLAQALTPNPILAELNAVDAKLTTDFGQKIDLNNSDIRDFRGLRGFY
PNLASEIIKNAPYDTVEEVLDIPGLSETQKSRLEANLGSFTVTEPSIELTSGDDRINPGVY

>BAA18512.1 cytochrome c550 [Synechocystis sp. PCC 6803]
MKRFFLVAIASVLFFFNTMVGSANAVELTESTRTIPLDEAGGTTTLTARQFTNGQKIFVDTCTQCHLQGK
TKTNNNVSLGLADLAGAEPRRDNVLALVEFLKNPKSYDGEDDYSELHPNISRPDIYPEMRNYTEDDIFDV
AGYTLIAPKLDERWGGTIYF

>XP_001702016.1 photosystem II reaction center W protein [Chlamydomonas reinhardtii]
MQALSARAPRVAAKPVSRSGARSAVTVVCKATTVRSEVAKKVAMLSTLPATLAAHPAFALVDERMNGDGT
GRPFGVNDPVLGWVLLGVFGTMWAIWFIGQKDLGDFEDADDGLKL

>NP_180615.1 photosystem II reaction center W [Arabidopsis thaliana]
MASFTASASTVSAARPALLLKPTVAISAPVLGLPPMGKKKGGVRCSMETKQGNVSVMGAGVSAAATAALT

AVMSNPAMALVDERMSTEGTGLPFGLSNNLLGWILFGVFGLIWTFFFVYTSSLEEDEESGLSL

>CEG01031.1 Photosystem II PsbW, class 2 [Ostreococcus tauri]
MLTILSSLSPICNLSPRRAGPRQASNQRHGVTVRATPQEAGKQVFGTSMLISSMNTVLPALAIVDDRLNG
DGTGLPLGINDGALGIILASVPLAIFSLYFIAGKQDAGIENGGKNDDSGLSL

>CAO86551.1 psbW [Microcystis aeruginosa PCC 7806]
MAEIQFSRGLKEPVVPDIRLSRTKTGEKGSAKFYFDQPTILGDQQTEEITGMYLIDEEGEIVTREVKGKF
INGKPMAIEATVIFNSPAEWDRFMRFMERYGSENGLEFTKSS

>XP_001701704.1 4.1 kDa photosystem II subunit [Chlamydomonas reinhardtii]
MAAVCVSSKAVAVRPATRVASRPAARMVVRASAKPAQISEKAIAAGVSAAAAASLALAPIAEAAVTPSLK
NFLGSLIAGATVLGGIALAITAVSKFDKTIR

>NP_565335.1 photosystem II subunit X [Arabidopsis thaliana]
MASTSAMSLVTPLNQTRSSPFLKPLPLKPSKALVATGGRAQRLQVKALKMDKALTGISAAALTASMVIPE
IAEAAGSGISPSLKNFLLSIASGGLVLTVIIGVVVGVSNFDPVKRT

>CAL52344.1 Photosystem II PsbX [Ostreococcus tauri]
MVVYTSKLRSLAIPKAQVRNARKLGKTSAVSAKLAPAEGTFQFDGIESAKAKVGAAVSAAAVATISSPLA
AEASVTPSLRNTLLSVVAGGVVLAAIAVAVIGVSSFDKVSRK

>BAA10311.1 photosystem II PsbX protein [Synechocystis sp. PCC 6803]
MTPSLANFLWSLVLGAAIVLIPATVGLIFISQKDKITRS

>XP_001692627.1 ycf32-related polyprotein of photosystem II, partial [Chlamydomonas reinhardtii]
VGTVATLSSVAASWMMAGNAQAATELASLAASDNRAGILATLLVPVLGWVGFNIFGSLQAQLNQMDAKNK
RAVPAAVGMGAAASLLFAQSAEASTEIATLAASDNRVAILATLLVPVIGWVGFNIFGSLQAQLNQMDAKN
KRAVPAAVGMGAAASLLFAQSAEASTEIATLAASDNRVAILATLLVPVIGWVGFNIFGSLQAQLNQMDAK
NKRAVPAAVGMGAAASLLFAQSAEASTEIATLAASDNRVAILATLLVPVIGWVGFNIFGSLQAQLNQMDA
KNKRAVPAAVGMGAAASLLFAQSAEASTEIATLAASDNRVAILATLLVPVIGWVGFNIFGSLQAQLRQMD
AKNK

>NP_176940.1 photosystem II BY [Arabidopsis thaliana]
MAAAMATATKCMSLNPSPPKLQNQTKSKPFISLPTPPKPNVSLAVTSTALAGAVFSSLSYSEPALAIQQI
AQLAAANASSDNRGLALLLPIVPAIAWVLYNILQPAINQVNKMRESKGIVVGLGIGGGLAASGLLTPPPE
AYAAAEAAAASSDSRGQLLLIVVTPALLWVLYNILQPALNQINKMRSGD

>XP_003082206.1 manganese-binding protein PsbY precursor, photosystem II-associated-s (ISS) [Ostreococcus tauri]
MLCTVNVPALRASRAAPLAKRERRAKRTAIASKVATKVATIESDEIVTRGQTAAMSLAATMLFADQAHAA
QEVGDLAGIDGRIAIFFVFAPVLGWVAYNILGPGLRQFEDMQKKNAKSKGVLAGAGLSAAALLGMPEASD
AAEKLGDLAGIDGRIAIFFVFAPVLGWVAYNILGPGLRQFEDMQKKNAKSKGVLAGAGLSAAALLGMPEA
SDAAEKLGDLAGIDGRIAIFFVFAPVLGWVAYNILGPERGQEVDGLRRRSLQTPP

>BAA17722.1 ycf32 gene product [Synechocystis sp. PCC 6803]
MDWRVIVVVSPLLIAATWAAINIGAAAIRQLQDVLGREA

>NP_958383.1 photosystem II protein Z (chloroplast) [Chlamydomonas reinhardtii]
MTSILQVALLALIFVSFALVVGVPVVFATPNGWTDNKGAVFSGLSLWLLLVFVVGILNSFVV

>NP_051056.1 photosystem II protein Z (chloroplast) [Arabidopsis thaliana]
MTIAFQLAVFALIITSSILLISVPVVFASPDGWSSNKNVVFSGTSLWIGLVFLVGILNSLIS

>YP_717234.1 photosystem II protein Z (chloroplast) [Ostreococcus tauri]
MLFIFQLTLLAFIGLSLALVIGVPVLLASPEGWAQSKGLVFSGSALWMLLVFVVGALNSFVS

>BAA18462.1 photosystem II 11 kD protein [Synechocystis sp. PCC 6803]
MMSFLKNQLSRLLALILVVAIGLTACDSGTGLTGNYSQDTLTVIATLREAIDLPQDAPNRQEVQDTARGQ
INDYISRYRRKGDAGGLKSFTTMQTALNSLAGYYTSYGARPIPEKLKKRLQLEFTQAERSIERGV

>sp|P50370.1|PSB30_CHLRE RecName: Full=Photosystem II reaction center protein Psb30; AltName: Full=Photosystem II reaction center protein Ycf12
MNIELALTLVSLVLVVSAGPLVVVLLSARGGNL

>YP_717256.1 Ycf12 (chloroplast) [Ostreococcus tauri]
MNLELIGQLVTVALVVGAGPIIIGALFARGGNL

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>WP_009631668.1 photosystem II reaction center protein Ycf12/Psb30 [Synechocystis sp. PCC 7509]
MESLFDGLGSINWLVLAQLVSVGLIMISGPVVIFILAFRNGNL

>XP_001696125.1 uncharacterized protein CHLRE_08g365900v5 [Chlamydomonas reinhardtii]
MAMMMRKAAAVPASSRRSVAVNSVSGKRTVSGKAGAPVPEDVLAYAKTLPGVTAPFDNVFDPAGFLATAS
VKDVRRWRESEITHGRVAMLAALGFIVGEQLQDFPLFFNFDGRVSGPAIYHFQQIGQGFWEPLLIAIGVA
ESYRVAVGWATPTGTGFNSLKDDYEPGDLGFDPLGLKPTDPEELKTLQTKELNNGRLAMIAIAAFVAQEL
VEQTEIFEHLVLRFEKEVILELEDVERDLGLPLTPLPDNLKAI

>XP_001696064.1 uncharacterized protein CHLRE_08g367500v5 [Chlamydomonas reinhardtii]
MLANVVSRKASGLRQTPARATVAVKSVSGRRTTAAEPQTAAPVAAEDVFAYTKNLPGVTAPFEGVFDPAG
FLATASIKDVRRWRESEITHGRVAMLAALGFVVGEQLQDFPLFFNWDGRVSGPAIYHFQQIGQGFWEPLL
IAIGVAESYRVAVGWATPTGTGFNSLKDDYEPGDLGFDPLGLKPTDPEELKVMQTKELNNGRLAMIAIAA
FVAQELVEQTEIFEHLALRFEKEAILELDDIERDLGLPVTPLPDNLKSL

>NP_958375.1 photosystem I P700 chlorophyll a apoprotein A1 (chloroplast) [Chlamydomonas reinhardtii]
MTISTPEREAKKVKIAVDRNPVETSFEKWAKPGHFSRTLSKGPNTTTWIWNLHADAHDFDSHTSDLEEIS
RKVFSAHFGQLGIIFIWLSGMYFHGARFSNYEAWLSDPTHIKPSAQVVWPIVGQEILNGDVGGGFQGIQI
TSGFFQLWRASGITSELQLYTTAIGGLVMAAAMFFAGWFHYHKAAPKLEWFQNVESMLNHHLGGLLGLGS
LAWAGHQIHVSLPVNKLLDAGVDPKEIPLPHDLLLNRAIMADLYPSFAKGIAPFFTLNWSEYSDFLTFKG
GLNPVTGGLWLSDTAHHHVAIAVLFLVAGHMYRTNWGIGHSMKEILEAHRGPFTGEGHVGLYEILTTSWH
AQLAINLALFGSLSIIVAHHMYAMPPYPYLATDYGTQLSLFTHHTWIGGFCIVGAGAHAAIFMVRDYDPT
NNYNNLLDRVIRHRDAIISHLNWVCIFLGFHSFGLYIHNDTMSALGRPQDMFSDTAIQLQPVFAQWIQNT
HFLAPQLTAPNALAATSLTWGGELGAHGGKVAMMPISLGTSDFMVHHIHAFTIHVTVLILLKGVLFARSS
RLIPDKANLGFRFPCDGPGRGGTCQVSAWDHVFLGLFWMYNSLSIVIFHFSWKMQSDVWGTVTASGVSHI
TGGNFAQSANTINGWLRDFLWAQSSQVIQSYGSALSAYGLIFLGAHFVWAFSLMFLFSGRGYWQELIESI
VWAHNKLKVAPAIQPRALSITQGRAVGVAHYLLGGIATTWSFFLARIISVG

>NP_051059.1 photosystem I P700 chlorophyll a apoprotein A1 (chloroplast) [Arabidopsis thaliana]
MIIRSPEPEVKILVDRDPIKTSFEEWAKPGHFSRTIAKGPDTTTWIWNLHADAHDFDSHTSDLEEISRKV
FSAHFGQLSIIFLWLSGMYFHGARFSNYEAWLSDPTHIGPSAQVVWPIVGQEILNGDVGGGFRGIQITSG
FFQIWRASGITSELQLYCTAIGALVFAALMLFAGWFHYHKAAPKLAWFQDVESMLNHHLAGLLGLGSLSW
AGHQVHVSLPINQFLNAGVDPKEIPLPHEFILNRDLLAQLYPSFAEGATPFFTLNWSKYSEFLTFRGGLD
PVTGGLWLTDIAHHHLAIAILFLIAGHMYRTNWGIGHGIKDILEAHKGPFTGQGHKGLYEILTTSWHAQL
SLNLAMLGSLTIIVAHHMYSMPPYPYLATDYATQLSLFTHHMWIGGFLIVGAAAHAAIFMVRDYDPTNRY
NDLLDRVLRHRDAIISHLNWVCIFLGFHSFGLYIHNDTMSALGRPQDMFSDTAIQLQPVFAQWIQNTHAL
APGVTAPGETASTSLTWGGGELVAVGGKVALLPIPLGTADFLVHHIHAFTIHVTVLILLKGVLFARSSRL
IPDKANLGFRFPCDGPGRGGTCQVSAWDHVFLGLFWMYNAISVVIFHFSWKMQSDVWGSISDQGVVTHIT
GGNFAQSSITINGWLRDFLWAQASQVIQSYGSSLSAYGLFFLGAHFVWAFSLMFLFSGRGYWQELIESIV
WAHNKLKVAPATQPRALSIIQGRAVGVTHYLLGGIATTWAFFLARIIAVG

>YP_717254.1 photosystem I P700 chlorophyll a apoprotein A1 (chloroplast) [Ostreococcus tauri]
MTISPPEREIKTVKIVVDRDPVPTSFEKWAKPGHFSRTLAKGPATTTWVWDLHADAHDFDSHTTDLEDIS
RKVFSAHFGQLGVIFIWLSGMYFHGARFSNYEAWLSDPTHIKPSAQVVWPIVGQEILNGDVGGGFQGVQI
TSGFFQLWRGSGITSELQLYSTAIGALICAGLMFFAGWWHYHKAAPKLEWFQNVESMMNHHLAGLLGLGS
LAWAGHQIHIALPVNTLLDAGVDPKEIPLPHEFMLNRALMAELYPSFAKGLTPFFTFNWTEYSDFLTFRG
GLNPVTGGLWLTDMAHHHLAIAVLFLVAGHQYRTNWGIGHSMKEILEAHKGPFTGEGHKGLYEILTTSWH
AQLAINLALMGSLSIIVSHHMYSMPPYPYLATDYGTQLSLFTHHMWIGGFCICGAAAHAAIFMVRDYDPA
TNYNNVLDRVLRHRDAIISHLNWVCIFLGFHSFGLYIHNDTMSALGRPQDMFSDTAIQLQPIFAQFVQHT
HALAPELTAPTAAGSTSASWGGDIVAVGGKIAMMPISLGTSDFMVHHIHAFTIHVTVLILLKGVLFARSS
RLIPDKANLGFRFPCDGPGRGGTCQVSAWDHVFLGLFWMYNSISIVIFHFSWKMQSDVWGSVTGNGVSHI
TGGNFAQSANTINGWLRDFLWAQSSQVIQSYGSALSAYGLIFLGAHFIWAFSLMFLFSGRGYWQELIESI
VWAHNKLKVAPAIQPRALSITQGRAVGVAHYLLGGIATTWSFFLARIIAVG

>BAA17437.1 P700 apoprotein subunit Ia [Synechocystis sp. PCC 6803]
MTISPPEREAKAKVSVDNNPVPTSFEKWGKPGHFDRTLARGPKTTTWIWNLHANAHDFDSQTSDLEDVSR
KIFSAHFGHLAVVFVWLSGMYFHGAKFSNYEGWLADPTHIKPSAQVVWPIVGQGILNGDVGGGFHGIQIT
SGLFYLWRASGFTDSYQLYCTAIGGLVMAALMLFAGWFHYHVKAPKLEWFQNVESMMNHHLAGLLGLGSL
GWAGHQIHVSMPINKLLDAGVAPKDIPLPHEFILEPSKMAELYPSFAQGLTPFFTLNWGVYSDFLTFKGG
LNPVTGGLWLSDTAHHHLAIAVLFIIAGHMYRTNWGIGHSMKEILEAHKGPFTGEGHKGLYEILTTSWHA
QLAINLALLGSLTIIVAQHMYAMPPYPYQAIDYATQLSLFTHHMWIGGFLIVGAGAHGAIFMVRDYDPAK
NVNNLLDRMLRHRDAIISHLNWVCIFLGFHSFGLYIHNDTMRALGRPQDMFSDTAIQLQPIFAQWVQHLH
TLAPGATAPNALATASYAFGGETIAVAGKVAMMPITLGTADFMVHHIHAFTIHVTALILLKGVLYARSSR
LVPDKANLGFRFPCDGPGRGGTCQVSGWDHVFLGLFWMYNSLSVVIFHFSWKMQSDVWGTVSPDGSVTHV
TLGNFAQSAITINGWLRDFLWAQAANVINSYGSALSAYGIMFLAGHFVFAFSLMFLFSGRGYWQELIESI
VWAHNKLNVAPAIQPRALSIIQGRAVGVAHYLLGGIVTTWAFFLARSLSIG
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>NP_958404.1 photosystem I P700 chlorophyll a apoprotein A2 (chloroplast) [Chlamydomonas reinhardtii]
MATKLFPKFSQGLAQDPTTRRIWYGLAMAHDFESHDGMTEENLYQKIFASHFGQLSIIFLWTSGNLFHVA
WQGNFEQWVTDPVHIRPIAHAIWDPHFGQPAVEAFTRGGASGPVNISTSGVYQWWYTIGMRTNQDLYVGS
VFLALVSAIFLFAGWLHLQPNFQPSLSWFKDAESRLNHHLSGLFGVSSLAWTGHLVHVAIPESRGQHVGW
DNFLSVLPHPQGLTPFFTGNWAAYAQSPDTASHVFGTAQGSGQAILTFLGGFHPQTQSLWLTDMAHHHLA
IAVIFIVAGHMYRTNFGIGHRMQAILEAHTPPSGSLGAGHKGLFDTVNNSLHFQLGLALASVGTITSLVA
QHMYSLPPYAFQAIDFTTQAALYTHHQYIAGFIMCGAFAHGAIFFIRDYDPEQNKGNVLARMLDHKEALI
SHLSWVSLFLGFHTLGLYVHNDVMQAFGTPEKQILIEPVFAQWIQAAHGKALYGFDFLLSSKTSAAFANG
QSLWLPGWLDAINNNQNSLFLTIGPGDFLVHHAIALGLHTTTLILVKGALDARGSKLMPDKKDFGYSFPC
DGPGRGGTCDISAYDAFYLAVFWMLNTIGWVTFYWHWKHLTLWQGNVAQFDESSTYLMGWLRDYLWLNSS
QLINGYNPFGMNSLSVWAWTFLFGHLIYATGFMFLISWRGYWQELIETLVWAHEKTPLANLVYWKDKPVA
LSIVQARLVGLAHFSVGYIFTYAAFLIASTSGRFG

>NP_051058.1 photosystem I P700 chlorophyll a apoprotein A2 (chloroplast) [Arabidopsis thaliana]
MALRFPRFSQGLAQDPTTRRIWFGIATAHDFESHDDITEERLYQNIFASHFGQLAIIFLWTSGNLFHVAW
QGNFETWVQDPLHVRPIAHAIWDPHFGQPAVEAFTRGGALGPVNIAYSGVYQWWYTIGLRTNEDLYTGAL
FLLFLSALSLIGGWLHLQPKWKPRVSWFKNAESRLNHHLSGLFGVSSLAWTGHLVHVAIPASRGEYVRWN
NFLNVLPHPQGLGPLFTGQWNLYAQNPDSSSHLFGTSQGSGTAILTLLGGFHPQTQSLWLTDMAHHHLAI
AILFLIAGHMYRTNFGIGHSIKDLLEAHIPPGGRLGRGHKGLYDTINNSIHFQLGLALASLGVITSLVAQ
HMYSLPAYAFIAQDFTTQAALYTHHQYIAGFIMTGAFAHGAIFFIRDYNPEQNEDNVLARMLDHKEAIIS
HLSWASLFLGFHTLGLYVHNDVMLAFGTPEKQILIEPIFAQWIQSAHGKTSYGFDVLLSSTSGPAFNAGR
SIWLPGWLNAINENSNSLFLTIGPGDFLVHHAIALGLHTTTLILVKGALDARGSKLMPDKKDFGYSFPCD
GPGRGGTCDISAWDAFYLAVFWMLNTIGWVTFYWHWKHITLWQGNVSQFNESSTYLMGWLRDYLWLNSSQ
LINGYNPFGMNSLSVWAWMFLFGHLVWATGFMFLISWRGYWQELIETLAWAHERTPLANLIRWKDKPVAL
SIVQARLVGLAHFSVGYIFTYAAFLIASTSGKFG

>YP_717253.1 photosystem I P700 chlorophyll a apoprotein A2 (chloroplast) [Ostreococcus tauri]
MATKFPKFSQGLASDPTTRRIWFGIATAHDFETHDGMTEEKLYQKIFASHFGQLAIIFLWTSGNLFHVAW
QGNFEKWGEDPLHVRPIAHTIWDPHFGQPAVEAFTRGGASAPVNIAYSGVYQWWYTIGMRTNVDLYNGSL
FLLFVAGLFLFAGWLHLQPTFAPAVSWFKNAESRLNHHLSGLFGVSSLAWTGHLVHVAIPASRGETVRWD
NFLTTLPHPAGLAPFFTGQWAVYAQNPDTAGHIFGTSEGAGTAILTFLGGFHPQTQSLWLTDMAHHHLAI
AVVFIIAGHQYRTNFGIGHSMKEILEAHTAPSGRLGAGHTGLFDTVNNSLHFQLGLALASVGVLCSLTAQ
HMYSMPPYAFLAQDFTTQAALYSHHQYIAGFIMCGAFAHGAIFFIRDYDPEANKGNVLARMLEHKEAIIS
HLSWVSLFLGFHTLGLYVHNDVMQAFGTPEKQILIEPVFAQWIQAAQGKALYGFDILLSGDNAATAAGNS
IYLPGWLAGINSSTNSLFLPIGPGDFLVHHAIALGLHTTTLILVKGALDARGSKLMPDKKDFGYSFPCDG
PGRGGTCDISAWDAFYLAVFWELNTVSWTVFYFHWKHLALWQGNSAQFDESSTYIMGWLRDYLWLNSSQL
INGYNPFGMNSLSVWAWMFLFGHLIYATGFMFLISWRGYWQELIETLVWAHERTPLANFVKWNDKPVALS
IVQARLVGLTHFAVGFVLTYAAFVIASTSGKFG

>BAA17438.1 P700 apoprotein subunit Ib [Synechocystis sp. PCC 6803]
MATKFPKFSQDLAQDPTTRRIWYGIATAHDFETHDGMTEENLYQKIFASHFGHIAIIFLWTSGTLFHVAW
QGNFEQWIKDPLNIRPIAHAIWDPHFGEGAVNAFTQAGASNPVNIAYSGVYHWFYTIGMTTNQELYSGAV
FLLVLASLFLFAGWLHLQPKFRPSLAWFKNAESRLNHHLAGLFGVSSLAWAGHLVHVAIPEARGQHVGWD
NFLSTPPHPAGLMPFFTGNWGVYAADPDTAGHIFGTSEGAGTAILTFLGGFHPQTESLWLTDIAHHHLAI
AVIFIIAGHMYRTNWGIGHSIKEILNAHKGPLTGAGHTNLYDTINNSLHFQLGLALASLGVITSLVAQHM
YSLPSYAFIAQDHTTQAALYTHHQYIAGFLMVGAFAHGAIFFVRDYDPVANKDNVLARMLEHKEALISHL
SWVSLFLGFHTLGLYVHNDVVVAFGTPEKQILIEPVFAQWIQATSGKALYGFDVLLSNPDSIASTTGAAW
LPGWLDAINSGTNSLFLTIGPGDFLVHHAIALGLHTTALILIKGALDARGSKLMPDKKDFGYSFPCDGPG
RGGTCDISAWDAFYLAMFWMLNTLGWLTFYWHWKHLGVWSGNVAQFNENSTYLMGWFRDYLWANSAQLIN
GYNPYGVNNLSVWAWMFLFGHLVWATGFMFLISWRGYWQELIETIVWAHERTPLANLVRWKDKPVALSIV
QARLVGLAHFTVGYVLTYAAFLIASTAGKFG

>NP_958423.1 photosystem I subunit VII (chloroplast) [Chlamydomonas reinhardtii]
MAHIVKIYDTCIGCTQCVRACPLDVLEMVPWDGCKASQMASAPRTEDCVGCKRCETACPTDFLSVRVYLG
SESTRSMGLSY

>NP_051110.1 photosystem I subunit VII (chloroplast) [Arabidopsis thaliana]
MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVGCKRCESACPTDFLSVRVYLW
HETTRSMGLAY

>YP_717214.1 photosystem I subunit VII (chloroplast) [Ostreococcus tauri]
MSHAVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASAPRTEDCVGCKRCEAACPTDFLSVRVYLG
SETTRSMGLAY

>BAA10036.1 photosystem I subunit VII [Synechocystis sp. PCC 6803]
MSHSVKIYDTCIGCTQCVRACPLDVLEMVPWDGCKAAQIASSPRTEDCVGCKRCETACPTDFLSIRVYLG
AETTRSMGLAY
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>XP_001697722.1 uncharacterized protein CHLRE_05g238332v5 [Chlamydomonas reinhardtii]
MAVMMRTQAPAATRASSRVAVAARPAARRAVVVRAEAEAAPAAAKKAAEKPAWTVPTLNPDTPSPIFGGS
TGGLLRKAQTEEFYVITWEAKKEQIFEMPTGGAAIMRQGPNLLKFGKKEQCLALTTQLRNKFKLTPCFYR
VFPDGKVQYLHPADGVYPEKVNAGRVGANQNMRRIGQNVNPIKVKFSGRMMSPAEI

>NP_192186.1 photosystem I subunit D-1 [Arabidopsis thaliana]
MATQAAGIFNSAITTAATSGVKKLHFFSTTHRPKSLSFTKTAIRAEKTDSSAAAAAAPATKEAPVGFTPP
QLDPNTPSPIFAGSTGGLLRKAQVEEFYVITWNSPKEQIFEMPTGGAAIMREGPNLLKLARKEQCLALGT
RLRSKYKITYQFYRVFPNGEVQYLHPKDGVYPEKANPGREGVGLNMRSIGKNVSPIEVKFTGKQSYDL

>CEG01861.1 Photosystem I PsaD [Ostreococcus tauri]
MSVTHAPARAVAKPTAMRTRKSARSATIVRAEEAKAKTESAAPAVWTAPKLDPNTPSPIFGGSTGGLLRK
AQVEEFYVLTWEAKKEAIFEMPTGGAAIMRKGPNLLKLARKEQCLALLNTFRSKMKLDGCIYRVFPSGEV
QYLHPKDGVYPEKVNKGRVGANQNMRSIGKNTNPAKIKFQGKLGPFEV

>BAA16688.1 photosystem I subunit II [Synechocystis sp. PCC 6803]
MTELSGQPPKFGGSTGGLLSKANREEKYAITWTSASEQVFEMPTGGAAIMNEGENLLYLARKEQCLALGT
QLRTKFKPKIQDYKIYRVYPSGEVQYLHPADGVFPEKVNEGREAQGTKTRRIGQNPEPVTIKFSGKAPYE
V

>XP_001702611.1 uncharacterized protein CHLRE_10g420350v5 [Chlamydomonas reinhardtii]
MQALSSRVNIAAKPQRAQRLVVRAEEVKAAPKKEVGPKRGSLVKILRPESYWFNQVGKVVSVDQSGVRYP
VVVRFENQNYAGVTTNNYALDEVVAAK

>NP_567818.2 Photosystem I reaction centre subunit IV / PsaE protein [Arabidopsis thaliana]
MAMTTASTVFVLPANVTSVAGASSSRSSVSFLPMRNAGSRLVVRAAEDPAPASSSSKDSPAAAAAPDGAT
ATKPKPPPIGPKRGSKVKILRRESYWFKNVGSVVAVDQDPKTRYPVVVRFAKVNYANISTNNYALDEVEE
VAA

>CAL52500.2 Photosystem I PsaE, reaction centre subunit IV [Ostreococcus tauri]
MFACTKVQANVFAVKTTKTVRRSTVTRAEGEAAKPAAKPQVGPPRGTMVKILRPESYWFNDYGKVISVDQ
TGVRYPVVVRFEKVNYAGVSTNNYALDEVEY

>BAA18383.1 photosystem I subunit IV [Synechocystis sp. PCC 6803]
MALNRGDKVRIKRTESYWYGDVGTVASVEKSGILYPVIVRFDRVNYNGFSGSASGVNTNNFAENELELVQ
AAAK

>XP_001696798.1 uncharacterized protein CHLRE_09g412100v5 [Chlamydomonas reinhardtii]
MALTMRNPAVKASSRVAPSSRRALRVACQAQKNETASKVGTALAASALAAAVSLSAPSAAMADIAGLTPC
SESKAYAKLEKKELKTLEKRLKQYEADSAPAVALKATMERTKARFANYAKAGLLCGNDGLPHLIADPGLA
LKYGHAGEVFIPTFGFLYVAGYIGYVGRQYLIAVKGEAKPTDKEIIIDVPLATKLAWQGAGWPLAAVQEL
QRGTLLEKEENITVSPR

>NP_174418.1 photosystem I subunit F [Arabidopsis thaliana]
MSLTIPANLVLNPRSNKSLTQSVPKSSARFVCSDDKSSSSTPQSMKAFSAAVALSSILLSAPMPAVADIS
GLTPCKDSKQFAKREKQQIKKLESSLKLYAPESAPALALNAQIEKTKRRFDNYGKYGLLCGSDGLPHLIV
NGDQRHWGEFITPGILFLYIAGWIGWVGRSYLIAISGEKKPAMKEIIIDVPLASRIIFRGFIWPVAAYRE
FLNGDLIAKDV

>XP_003078706.1 Photosystem I PsaF, reaction centre subunit III [Ostreococcus tauri]
MHAHAQAQLTSKVTVSGLKRSARVQTRAVKTVAHCSAVDFSKKAASLAVAAAVAAAPLVAVEEAFARDVQ
PYAGLTPCKTSKAFAKREKTELKALEKRLKKYDPESAPALALQATMEKTKTRFANYGESGLLCGKDGLPH
LIVDGNLEHLGEFAIPGLGFLYVAGWIGYAGRSYIQENKTASKPTEGEIIIDVPKALGLMFQAGAWPLLA
GLELKNGTLTAPESEITVSPR

>BAA18108.1 photosystem I subunit III [Synechocystis sp. PCC 6803]
MKHLLALLLAFTLWFNFAPSASADDFANLTPCSENPAYLAKSKNFLNTTNDPNSGKIRAERYASALCGPE
GYPHLIVDGRFTHAGDFLIPSILFLYIAGWIGWVGRSYLIEIRESKNPEMQEVVINVPLAIKKMLGGFLW
PLAAVGEYTSGKLVMKDSEIPTSPR

>CAA33257.1 polypeptide 35 precursor [Chlamydomonas reinhardtii]
MQTLASRPSLRASARVAPRRAPRVAVVTKAALDPQIVISGSTAAFLAIGRFVFLGYQRREANFDSTVGPK
TTGATYFDDLQKNSTIFATNDPAGFNIIDVAGWGALGHAVGFAVLAINSLQGANLS

>NP_175963.1 photosystem I subunit G [Arabidopsis thaliana]
MATSASALLSPTTFSTAISHKNPNSISFHGLRPLRLGGSSSALPKLSTTGRKSSSAVVRAELSPSIVISL

STGLSLFLGRFVFFNFQRENVAKQGLPEQNGKTHFEAGDDRAKEYVSLLKSNDPIGFNIVDVLAWGSIGH
IVAYYILATSSNGYDPSFFG

>CAL53836.1 Photosystem I PsaG/PsaK protein [Ostreococcus tauri]
MLARTALPTKTTASFNGRVAKQTRTAKRGAKVAARAFDDVNVVMSASNALALYLGRFVFLPYQRAQVERV
GMPTQNGQTHFAAGDTRAEEASFITSTNDPAGFNLVDVFAWGSIGHAIGFLALASQSAQQML

>XP_001690629.1 uncharacterized protein CHLRE_07g330250v5 [Chlamydomonas reinhardtii]
MALVARPVLSARVAASRPRVAARKAVRVSAKYGENSRYFDLQDMENTTGSWDMYGVDEKKRYPDNQAKFF
TQATDIISRRESLRALVALSGIAAIVTYGLKGAKDADLPITKGPQTTGENGKGGSVRSRL

>NP_188235.1 photosystem I subunit H-1 [Arabidopsis thaliana]
MASLATVAAVKPSAAIKGLGGSSLAGAKLSIKPSRLSFKPKSIRANGVVAKYGDKSVYFDLEDLGNTTGQ
WDVYGSDAPSPYNPLQSKFFETFAAPFTKRGLLLKFLILGGGSLLTYVSATSTGEVLPIKRGPQEPPKLG
PRGKL

>CEG01722.1 Photosystem I PsaH, reaction centre subunit VI [Ostreococcus tauri]
MAHVKVHTWTQIARNTTTPPTTTTTTTRERPARQSSMVAHAKTTAFATGAALARSTPTTRRARATVMTRA
KYGDESVYFDLSDVEATTGSWDVYGVDSASRYPEQQAAFFEAAAQGLGRREAVYSVLAVSAGLLTVAYGV
KGAKDAKLPITVGPQQPAQVGPRDRI

>XP_001703367.1 uncharacterized protein CHLRE_03g165100v5 [Chlamydomonas reinhardtii]
MALRAVSAKSAVRPTVARASVKPVAALKPAQKMALAGAASVALLAASSSSAEASQVIATVASAAQGYPFV
PPSWAPSVFVPLTGLVLPAIAMATLFVYIEKEAPSS

>NP_051069.1 photosystem I subunit VIII (chloroplast) [Arabidopsis thaliana]
MTTFNNLPSIFVPLVGLVFPAIAMASLFLHIQKNKIF

>YP_717255.1 photosystem I subunit VIII (chloroplast) [Ostreococcus tauri]
MAASLLPSIFVPLVGLVFPAVAMASLFLYIEKEQVS

>BAA19609.1 PsaI [Synechocystis sp. PCC 6803]
MDGSYAASYLPWILIPMVGWLFPAVTMGLLFIHIESEGEG

>NP_958417.1 photosystem I subunit IX (chloroplast) [Chlamydomonas reinhardtii]
MKDFTTYLSTAPVIATIWFTFTAGLLIEINRYFPDPLVFSF

>NP_051079.1 photosystem I subunit IX (chloroplast) [Arabidopsis thaliana]
MRDLKTYLSVAPVLSTLWFGSLAGLLIEINRLFPDALTFPFFSF

>YP_717261.1 PsaJ (chloroplast) [Ostreococcus tauri]
MKNFQIYLSTAPVLAAVWFTVLAGILIELNRFFPDALSFPLT

>BAA18107.1 photosystem I subunit IX [Synechocystis sp. PCC 6803]
MDGLKSFLSTAPVMIMALLTFTAGILIEFNRFYPDLLFHP

>XP_001697230.1 uncharacterized protein CHLRE_17g724300v5 [Chlamydomonas reinhardtii]
MQALATRPSAIRPTKAARRSSVVVRADGFIGSSTNLIMVASTTATLAAARFGLAPTVKKNTTAGLKLVDS
KNSAGVISNDPAGFTIVDVLAMGAAGHGLGVGIVLGLKGIGAL

>NP_174327.1 photosystem I subunit K [Arabidopsis thaliana]
MASTMMTTLPQFNGLRATKISAAPVQGLASVQPMRRKGNGALGAKCDFIGSSTNLIMVTSTTLMLFAGRF
GLAPSANRKATAGLRLEARDSGLQTGDPAGFTLADTLACGTVGHIIGVGVVLGLKNIGAI

>BAA16719.1 photosystem I subunit X [Synechocystis sp. PCC 6803]
MHSFLLATAVPATLSWSPKVAGVMIACNILAIAFGKLTIKQQNVGTPMPSSNFFGGFGLGAVLGTASFGH
ILGAGVILGLANMGVL

>XP_001691084.1 uncharacterized protein CHLRE_12g486300v5 [Chlamydomonas reinhardtii]
MAVAMRSSTGLRATAARRQMPLGLGRVSTVRVCAADTKKAQVISPVNGDPFVGMLETPVTSAPIVATYLS
NLPAYRTGVAPVLRGVEIGLAHGFLLAGPFIKLGPLRNVPETAEIAGSLSAAGLVLILALCLSIYGSAQF
QSTPSIGVKTLSGRSVARDPLFSADGWSEFAAGFLVGGEAGVAWAYVCTQILPYYS

>NP_193016.1 photosystem I subunit l [Arabidopsis thaliana]
MAASASPMASQLRSSFSSASLSQRLAVPKGISGAPFGVSPTKRVSSFTVRAVKSDKTTFQVVQPINGDPF
IGSLETPVTSSPLIAWYLSNLPGYRTAVNPLLRGVEVGLAHGFFLVGPFVKAGPLRNTAYAGSAGSLAAA
GLVVILSMCLTIYGISSFKEGEPSIAPSLTLTGRKKQPDQLQTADGWAKFTGGFFFGGISGVTWAYFLLY

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VLDLPYFVK

>CEG00928.1 Photosystem I PsaL, reaction centre subunit XI [Ostreococcus tauri]
MVLASKLTLDVRSCIGAKSLRTERPRNSAIGSNKTSRRQTKVSASSDKVQIVKPINGDPFIGMLETPVTS
SPDVANFLSNLPAYRTGVAPLLRGVEVGLAHGFFVTGPFIKLGPLRSTDAAELAGCLSGAGLVLILTACL
SIYGATAFQREEVVGLKTLSGRTIAKDPLQSSEGWASFTSGWLVGGLSGVAWSYVLTQVLPYYS

>BAA18773.1 photosystem I subunit XI [Synechocystis sp. PCC 6803]
MAESNQVVQAYNGDPFVGHLSTPISDSAFTRTFIGNLPAYRKGLSPILRGLEVGMAHGYFLIGPWTLLGP
LRDSEYQYIGGLIGALALILVATAALSSYGLVTFQGEQGSGDTLQTADGWSQFAAGFFVGGMGGAFVAYF
LLENLSVVDGIFRGLFN

>YP_717257.1 photosystem I subunit XII (chloroplast) [Ostreococcus tauri]
MPLSDTQVFTALFVALITGILSLRLGTQLYK

>BAA17005.1 photosystem I PsaM subunit [Synechocystis sp. PCC 6803]
MALSDTQILAALVVALLPAFLAFRLSTELYK

>XP_001701700.1 photosystem I reaction center subunit N [Chlamydomonas reinhardtii]
MAISARSSIKMQAARPARATTVVVRASAGRRELLGLGALALGLTMTLAPVANAGVVSDLQAKSAANKALN
DKKRLATSYANLARSRTVYDGTCTFPENFFGCEELAFNKGVKFIAEDIKIECEGKTAKECGSKFTLRSN

>NP_201209.1 photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) [Arabidopsis
thaliana]
MAAMNSSVLTCSYAIAGSGSVELNQKVGLVNSSVGFGQKKQMIMPVIKAQRVVGDDVDGSNGRRSAMVFL
AATLFSTAAVSASANAGVIDEYLERSKTNKELNDKKRLATSGANFARAFTVQFGSCKFPENFTGCQDLAK
QKKVPFISEDIALECEGKDKYKCGSNVFWKW

>CEF98203.1 Photosystem I PsaN, reaction centre subunit N [Ostreococcus tauri]
MYTVCGANIIAAKAPTAAKKQDKVKRAVSLGLAGLAAATVSVAPAHADLTADLLARTEANKSLNDQKRAA
TSSANFERSRLVTDGFCQFPQNIFGCQNAAEKGSVKFLSDDMAIECEGTADGKTCSSKAPGAYPSFLGL

>XP_001700109.1 uncharacterized protein CHLRE_07g334550v5 [Chlamydomonas reinhardtii]
MAVAMRSAAMPSLASRPRVSSRRSVVVRAEASNKSFPRDWVKTDPLVPVLGFAGWTIPANIGVSAFGGQS
LFGLFTQSIGENLAHFPTGPALDDKFWLYLITYHLGLFLTITLGQIGVQGRKQGYW

>NP_563815.1 photosystem I subunit O [Arabidopsis thaliana]
MAATFATPSTVIGLGGSSITTKPFSSSFLKPTLSAKNPLRLAGASGGRVTCFERNWLRRDLNVVGFGLIG
WLAPSSIPAINGKSLTGLFFDSIGTELAHFPTPPALTSQFWLWLVTWHLGLFLCLTFGQIGFKGRTEDYF
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Supplementary dataset 2. Comprehensive set of 158 predicted Lhc proteins in *E. gracilis.*

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>LHCA5-Nter_Koziol/LHCA5-Nter@130
FFSDKKMYGTVSASSSNKATSTVAVCACAAVFAVAGFVAVQPRSLYAPAAVRPVVQATMT
TVPVAHSVQSNTVAAQIQSRPLNVESNVFAQVGSTFAPIALGVGALAAFVAALIHKGQQP
VAMAASSGER
>LHCB4-1_GEFR01021489.1/F-1/O1/P2@205
GKAPAAAKGGRPLWFPSAVAPDYLDGSLPGDRGFDPWGFAKPEELLQYTTGTADITLSKN
KDEEYVGKVKEERDVLTGEPLVPWSSAFGLKRLRECELIHGRWAMLFVLGALVGEAVTGV
AWQNAGLVEAREGYTYFGFSLPFSGAQITWFEVLTMGFVEIFRNTEMNIEKRVYPGGAFD
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>LHCB4-2_GEFR01023973.1/F+2/O1/P1@144
LQLPHEIQKFMKIFELVSEVTCIHGTSPNPGVGLVEAREGYTYFGFSLPFSGSQITWFEV
LTMGFVEIFRNTEMNIEKRVYPGGAFDPLGLASKDAETTFRLKEAEIKHARLAMVAFLGF
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>LHCB4-3_Koziol/LHC_CP29@373
FRSIFFRFTKMYSEQTSYSRVAAAALLAVSAGACVGVAIAPAASSFYAPAAVRPISSQVA
VMNVPRMQLGAVNAPYYAENAATEVQAVDGTSNVNAWTILSGGLFAAAAAMAAFAFKGSR
TETSEQIAMLAAAGKKGKAPAAAKGGRPLWFPSAVAPDYLDGSLPGDRGFDPWGFAKPEE
LLQYTTGTADITLSKNKDEEYVGKVKEERDVLTGEPLVPWSSAFGLKRLRECELIHGRWA
MLFVLGALVGEAVTGVAWQNAGLVEAREGYTYFGFSLPFSGSQITWFEVLTMGFVEIFRN
TEMNIEKRVYPGGAFDPLGLASKDAETTFRLKEAEIKHARLAMVAFLGFATAAAKTGAGA
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>LHCB4-4_GEFR01069386.1/F+3/O1/P1@102
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LPFLSGFAKPEELLQYTTGTADITLSKNKDEEYVGKVKEERD
>LHCB4-5_GEFR01056955.1/F-3/O3/P1@54
MQKPGIFLCCQLPKQLIAVQLSLPQITLKRTTFRLKEAEIKHARLAMVAFLGFA
>LHCB4-6_GEFR01056955.1/F-2/O2/P1@70
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>LHCB7-1_GDJR01012385.1/F-2/O1/P1@432
SIFFREMKLFCFAVVAFVICLSFSSSLMHPFPQLICTSVDGKLCFRISFRKKTTPLHQLT
SLSRTPRESVWLSPRSRTTVGQASKPNDPADPPSSSTSRRWASFLTGVGASPLFYVSIGA
LAAAAAVKGSADSSAVVLTLAGLPVVGLTILKNLSVGESLRATLDQQLPQLEEAVALRLQ
AQAEAQRGSRYYGPSRVGRLFPAPPHLDGTLPGDAGFDPLGLARSDSRPKLPDTLASCRL
LMHKRRVALGLEAAPGAADTRPTLERLLDCEVLHGRWAQLAVVGCLVPSKLAEEAATLDY
LGIPGLHIAGGQGIAIIAACQFFLMGGPEYARYVGLRGLEPVGIFLDGTDVTYPGGQLFD
PLGLAKDPVAFQEQRVAEVKHGRLAMVAMAGMAAQALATRAGPVENLADFLADPGHNNVL
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>LHCB7-2_GDJR01012382.1+1/F-2/O1/P1@455
SIFFREMKLFCFAVVAFVICLSFSSSLMHPFPQLICTSVDGKLCFRISFRKKTTPLHQLT
SLSRTPRESVWLSPRSRATVGQASKPNDPADPPSSSTSRRWASFLTGVGASPLFYVSIGA
LAAAAAVKGSADSSAVVLTLAGLPVVGLTILKNLSVGESLRATLDQQLPQLEEAVALRLQ
AQAEAQRGSRYYGPSRVGRLFPAPPHLDGTLPGDAGFDPLGLARSDSRPKLPDTLASCRL
LMHKRRVALGLEAAPGAADTRPTLERLLDCEVLHGRWAQLAVVGCLVPEALGRALGSSVQ
FGETVWWKVGASKLAEEAAALDYLGIPGLHIAGGQGIAIIAACQFFLMGGPEYARYVGLR
GLEPVGIFLDGTDVTYPGGQLFDPLGLAKDPVAFQEQRVAEVKHGRLAMVAMAGMAAQAL
ATRAGPVENLADFLADPGHNNVLRSLHTFSHAFAS
>LHCB7-3_GEFR01016328.1+1/F-1/O3/P1@214
MYKRRVALGLEAAPGAADTRPTLERLLDCEVLHGRWAQLAVVGCLVPEALGRALGSSVQF
GETVWWKVGASKLAEEAAALDYLGIPGLHIAGGQGIAIIAACQFFLMGGPEYARYVGLRG
LEPVGIFLDGTDVTYPGGQLFDPLGLAKDPVAFQEQRVAEVKHGRLAMVAMAGMAAQALA
TRAGPVENLADFLADPGHNNVLRSLHTFSHAFAS
>LHCBM1-1_GDJR01073855.1/F-1/O1/P2@226
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EVIHARWAMLGALGVVTPELLAGNGVPFGEGAVWYKAGAQIFSADGLNYLGNPSLIHAQS
VVLTFLSTLAIMGAVEAYRYGGGVGDFGRELDTLYPGGPFDPLGLANDPDALAELKVKEL
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>LHCBM1-2_HBDM01023705.1+2/F-1/O1/P2@226
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Supplementary Dataset S3. PSI and PSII subunit amino acid sequences in *E. gracilis*.

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