Supplemental data

# Photosynthetic trichomes contain a specific Rubisco with a modified pH-dependent activity

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Spot <sup>1</sup>	EST accession <sup>2</sup>	Corresponding protein name
Metabolism		······································
20	FG175097	Glutamine synthetase
4	EB432526	Nucleoside diphosphate kinase
24	FG194360	3-isopropylmalate dehydrogenase large subunit
22	FG194360	3-isopropylmalate dehydrogenase large subunit
26	FG139607	D-cysteine desulfhydrase
42	DV157962	Rubisco small subunit
15	EB679897	NAD-dependent dehydrogenase
43	EB679897	NAD-dependent dehydrogenase
Energy		
27	DV162381	Phosphoglycerate kinase
33g	FG133688	ATP synthase $\beta$ subunit
33d	FG135901	ATP synthase $\beta$ subunit
3d	FS414373	ATP synthase d subunit
30	EB680336	Aspartate aminotransferase
13	FG198580	Light harvesting chlorophyll a/b-binding protein
Protein destination and storage		
34d	DW000222	Chaperonin-60 beta subunit
Disease/defense	D0007666	
1	FS38/666	Putative PR-10 type pathogenesis-related protein
2 3g	F\$387666	Putative PR-10 type pathogenesis-related protein
5g 6	FS387666	Putative PR-10 type pathogenesis-related protein
32	AM817165	Pathogenesis-related protein
9	FG194579	Thioredoxin peroxidase
100	FG194579	Thioredoxin peroxidase
5	FS429935	Thioredoxin peroxidase
19	EB677336	Fe-superoxide dismutase
18	EB677336	Fe-superoxide dismutase
8	EH622457	Superoxide dismutase
7	EH624278	Glutathione peroxidase
17	FS374016	Glutathione S-transferase
16	FS374016	Glutathione S-transferase
14b	FS411447	Glutathione S-transferase
14h	FS411447	Glutathione S-transferase
44	EB447814	Glutathione S-transferase
10d	EB440026	Peroxiredoxin
11	EB440026	Peroxiredoxin
Secondary metabolism		
34g	FG187107	Cembratrienol synthase 2b
35	FG187107	Cembratrienol synthase 2b
36	FG187107	Cembratrienol synthase 2b
37	FG187107	Cembratrienol synthase 2b
28	EH615865	Chalcone synthase
12	EB426860	Chalcone isomerase
25	FG175910	1-deoxy-D-xylulose-5-phosphate reductoisomerase
23	DV998901	1-hydroxy-2-methyl-butenyl 4-diphosphate reductase
21	FG187212	1-hydroxy-2-methyl-butenyl 4-diphosphate reductase
38	FG175170	(E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase
39 40	FG149054 EG140054	(E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase (E) 4 hydroxy 3 methylbut 2 anyl diphosphate synthese
40 41	FG149054 FG149054	(E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase
TI Unknown	1 0147034	(E)-+-nyuroxy-5-methytout-2-enyt uphosphate synthase
29	AM816756	No identification
31	AM816756	No identification
1	2	

Supplemental Table S1 – MS-MS identification of the 49 most abundant trichomespecific protein spots.

<sup>1</sup>Numbering corresponds to that of Supplemental Fig 2. <sup>2</sup>Closest EST from the translated *N. tabacum* NCBI EST database

**Supplemental Table S2** – **List of the protein sequences used for the phylogenetic analysis of the RbcS.** A, a protein BLAST search was performed (5 May 2015) using the Nt-RbcS-T mature protein sequence as a query. All of the proteins displaying a score higher than 200 are listed. Although the rice Rubisco small subunit, OsRbcS1 displays a BLAST score lower than the 200 threshold, its sequence was added to this analysis since its corresponding gene also exhibits a specific expression pattern (Morita *et al.*, 2014). Because, no sequence from C4 plants was obtained through the BLAST analysis, the two RbcS sequences of *Zea mays*, a C4 plant, were also included. The "Secretory organs" column mentions whether glandular trichomes (GT), trichomes without more information (T) secretory cavities (SC), nectaries (N) or colleters (C) have been reported for each species. B, for each species listed in A, the RbcS protein showing the highest identity with the protein listed in A was retrieved. In addition, all of the RbcS sequences from *Arabidopsis* were listed.

Abbreviation	Accession number	Species	Secretory	<b>References</b> <sup>1</sup>
	(NCBI)		organs	
A. Cluster T				
NtRbcS-t	DV157962.1	Nicotiana tabacum	GT	1
Nsy-t	XP_009794031.1	Nicotiana sylvestris	GT	1
Nto-t	XP_009608851.1	Nicotiana tomentosiformis	GT	1
Stu-t	XP_006344531.1	Solanum tuberosum	GT	2
Sly-t	XP_004243079.1	Solanum lycopersicum	GT	3
Egr-t	XP_010046977.1	Eucalyptus grandis	SC	4
Lja-t1	AFK34410.1	Lotus japonicus	Т	5
Cca-t	CDP02988.1	Coffea canephora	GC	6
Egu-t	EYU37322.1	Erythranthe guttata	Т	7
Csi-t1	KDO43856.1	Citrus sinensis	SC	8
Jcu-t1	XP_012074043.1	Jatropha curcas	Т	9
Ccl-t1	XP_006453353.1	Citrus clementina	SC	8
Jcu-t2	KDP36388.1	Jatropha curcas	Т	9
Ccl-t2	XP_006453352.1	Citrus clementina	SC	8
Csi-t2	KDO43855.1	Citrus sinensis	SC	8
Lja-t2	AFK37376.1	Lotus japonicus	Т	5
Gra-t	KJB20540.1	Gossypium raimondii	GT	10
Gar-t	KHG02980.1	Gossypium arboreum	GT	10
Atr-t	XP_006856657.1	Amborella trichopoda	Т	11
Peu-t	XP_011043951.1	Populus euphratica	GT	12
Ptr-t	ABK96070.1	Populus trichocarpa	GT	12
Vvi-t	XP 002270117.1	Vitis vinifera	GT	13
Sin-t	XP_011069924.1	Sesamum indicum	GT	14
Ppe-t	XP_007223576.1	Prunus persica	С	15
Mno-t	XP 010094223.1	Morus notabilis	GT	16
Fve-t	XP_004296442.1	Fragaria vesca	GT	17
Tca-t	XP_007014245.1	Theobroma cacao	GT	18
Pmu-t	XP 008223772.1	Prunus mume	С	15
Pbr-t	XP_009336182.1	Pyrus bretschneideri	Ν	19
Gso-t	KHN22693.1	Glycine soja	GT	20
Nnu-t	XP_010275523.1	Nelumbo nucifera	GT	21
Mtr-t	XP_003610095.1	Medicago truncatula	GT	22
Gma-t	NP 001235868.1	Glycine max	GT	23
Pda-t	XP_008803597.1	Phoenix dactylifera	Т	24
Egi-t	XP 010914155.1	Elaeis guineensis	Т	25
Tha-t	XP_010526347.1	Tarenaya hassleriana	GT	26
OsRbcS1	BAD38596.1	Oryza sativa	-	27
B. Cluster M				
Nta	CAA26208.1	Nicotiana tabacum		
Nsy	P22433.1	Nicotiana sylvestris		
Nto	XP 009625434.1	Nicotiana tomentosiformis		
Stu	ABY21254.1	Solanum tuberosum		
Sly	BAA01888.1	Solanum lycopersicum		
Egr	XP_010044264.1	Eucalyptus grandis		

CcaCBY05833.1Coffea canephoraEguEYU38174.1Erythranthe guitataCaiXP_006482254.1Citrus sinensisJcuADB85091.1Jatropha curcasCclXP_006430779.1Citrus clementinaGraAFS41724.1Gossypium raimondiiGarAFS41722.1Gossypium raimondiiGarAFS41722.1Gossypium raimondiiAtrXP_006842277.2Amborella trichopodaPeuXP_001035062.1Populus euphraticaPurXP_002305162.2Populus trichocarpaVviXP_002276967.1Vitis viniferaSinXP_010103758.1Morus notabilisFveXP_007215051.1Prinus persicaMnoXP_010103758.1Morus notabilisFveXP_0093270.1Theobroma cacaoPmuXP_009357812.1Pyrus bretschneideriGsoKHN47663.1Glycine sojaNnuXP_003618735.1Medicago truncatulaGmaAAG24884.1Glycine maxPdaXP_005197838.1Phoenix dactyliferaEgiXP_010521010.1Tarenaya hasslerianaOsRbcS2BAT16784.1Oryza sativaOsRbcS5BAT16784.1Oryza sativaOsRbcS5BAT16784.1Oryza sativaOsRbcS4BAT16784.1Oryza sativaOsRbcS5BAT16784.1Oryza sativaOsRbcS4BAT16784.1Oryza sativaOsRbcS4BAT16784.1Oryza sativaOsRbcS5BAT16784.1Oryza sativaOsRbcS5	Lja-1	AFK45650.1	Lotus japonicus
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	Ath-2	CAA32702.1	Arabidopsis thaliana
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Ath-4 CAA31948.1 Arabidopsis thaliana	Ath-4	CAA31948.1	Arabidopsis thaliana

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**Supplemental Figure S1** – 2D-DIGE of soluble proteins of tall glandular trichomes compared to other tissues. Proteins of tall glandular trichomes were compared to proteins from roots (A), germinating seeds (B), leaves (C), seed pods (D), stems (E, and flowers (F). Soluble proteins (20  $\mu$ g) isolated from trichomes and other tissues were labeled with the Cy3 (green) and Cy5 (red) fluorescent dyes, respectively. As an internal control, 10  $\mu$ g of both compared protein samples were mixed and tagged with the Cy2 (blue) fluorescent dye (not shown).



**Supplemental Figure S2** – Preparative 2-DE of soluble tall glandular trichome proteins. Proteins (500  $\mu$ g) from tall glandular trichomes were analyzed by 2D gel electrophoresis and stained with colloidal blue. Spots that are numbered correspond to trichome-specific proteins and were analyzed by mass spectrometry. Their identification is given in Supplemental Table S1.

ATGATGACCTGGAACCCGATCGACAACAAGAAGTTCGAGACCCTGTCCTACCTGCCGCCGCTGTCCG AGGACTCCATCGCCAAGGAGGTCGACTACATGATCCAGAAGGGCTGGATCCCGTGCCTGGAGTTCGA CCAGGTCGGCTACGTCCGCCGCGGAGAACTCCTCCATGCCGGGCTACTACGACGGCCGCTACTGGACC CTGTGGAAGCTGCCGATGTTCGGCTGCAACGACTCCTCCCAGGTCCTGAACGAGATCCAGGAGTGCA AGAAGGCCTACCCGAACGCCTTCATCCGCTGCCTGGCCTTCGACAACGTCAAGCAGGTCCAGTGCAT GGCCTTCCTGATCCAGAAGCCGGCCGCCGCCTAA

#### В

А

ATGATGGTCTGGCCGCCGATCAACAAGAAGAAGAAGTACGAGACCCTGTCCTACCTGCCGGACCTGTCCC AGGAGCAGCTGCTGTCCGAGGTCGAGTACCTGCTGAAGAACGGCTGGGTCCCGTGCCTGGAGTTCGA GACCGAGCACGGCTTCGTCTACCGCGAGGAACAACAAGTCCCCGGGCTACTACGACGGCCGCTACTGG ACCATGTGGAAGCTGCCGATGTTCGGCTGCACCGACGCCACCCAGGTCCTGGCCGAGGTCGAGGAGG CCAAGAAGGCCTACCCGCAGGCCTGGATCCGCCATCATCGGCTTCGACAACGTCCGGCCAGGTCCAGTG CATCTCCTTCATCGCCTACAAGCCGGAGGGCTACTAA

**Supplemental Figure S3.** Synthetic coding sequences of NtRbcS-T and Nt-RbcS-M for expression in *Chlamydomonas*. The coding sequences for the mature small subunit NtRbcS-T (A) and NtRbcS-M (B) were optimized for expression in *Chlamydomonas*, and engineered to replace the plant Lys2 and Gln2, respectively, with the *Chlamydomonas* Met to facilitate transit-peptide processing. These sequences were used to exactly replace the *Chlamydomonas rbcS1* mature-protein coding sequence of pSS1-ITP (Genkov *et al.*, 2010) to generate the plasmids pSS1-NtRbcS-T and pSS1-NtRbcS-M.

#### 8



**Supplemental Figure S4.** Engineered plasmids containing the wild-type *Chlamydomonas rbcS1* gene (pSS1-CrRbcS1) and the *N. tabacum* mesophyll- and trichome-expressed *rbcS* cDNA sequences (pSS1-NtRbcS-M and pSS1-NtRbcS-T). The regions encoding the transit peptide and mature small subunit are shown as *gray* and *black boxes*, respectively, and introns are denoted by black lines. Introns are inserted into the transit peptide-encoding region. White boxes represent part of the plasmid. Figure adapted from Genkov *et al.*, 2010.



**Supplemental Figure S5.** Electrophoretic analysis of the purified Rubisco from *Chlamydomonas* transformants. A, Purified Rubisco (1  $\mu$ g) from the strain expressing pSS1-CrRbcS1 (C), pSS1-NtRbcS-M (M), or pSS1-NtRbcS-T (T) were analyzed by SDS-PAGE and gel stained with Coomassie blue. B, Example of Rubisco quantification on gel. Increasing quantities of Rubisco and bovine serum albumin (BSA) used a standard were analyzed by SDS-PAGE. The gel pictures were then analyzed using ImageJ software.

	Le	eaf	Trichome	
Amount of soluble proteins (µg):	0.30	0.45	2.0	4.0
	<i>Winnersonger</i>	encourse,	ana ana	entresenter.

**Supplemental Figure S6**. Comparison of the Rubisco amount in trichome and leaf samples of N. *tabacum*. Soluble proteins (pool of the four biological repetitions of Fig. 6B) from leaves cleared of trichomes and from trichomes were analyzed by SDS-PAGE and western blotting using an anti-RbcL antibody. Relative quantification of the Rubisco determined in both samples using ImageJ software showed that trichome samples contains 4.5 times less Rubisco that leaf samples.

## Cluster T

		10	20	30	40	50	60 70
Consensus	MK WNPI	NKKFE	LSYLPPLS	SIAKE YM	KGW PCLEFD	G R NS	PGYYDGRYWTLWK
Nt-RbcS-t	T	DT	ГЕ	DVD	Q	QV. YVR. E S	M
Nsy-t	T	DT	ГЕ	DVDI	QI	QV.YVR.ES	Μ
Nto-t	<u>T</u>	DT	「E	DVD	Q	QV.YVR.E.S	M
Stu-t		יייט ד ח	Q.E	E.G.VD.I	KI K V	QV.YVH.EP	чм
Egr-t	T	N T	rD	DIDL	κν	EV.YVR.E.F	RM
Lja-t1	т	N . R T	гто	E V D L	к	EL.HIR.EF	RM
Cca-t	T	ΝΤ	ГD	DR.IDL	KN	AD.FVH.E	(MHM
Egu-t	.QT	N1	E	E.VIDI	KI	KL.YVY.EF	RM . N
Jcu-t1	T	N T	ζ	DNIDI	KM I	EV. HVR. E F	RM
Ccl-t1	т	N	λSD	DIDL	кі	EV.YVH.E.F	RM
Gra-t	<b>T</b>	ΝΤ	「D	DIDM	КІ	EV.AVH.E	<b>1</b>
Gar-t	<u>T</u>	N T	[D	D	KI	EV.AVH.E.S	
Atr-t	· · · T · · · ·	S1	「D	EID	SI.S	EV.YVS.QF	RM
Ptr-t	T	N	E	D	K I	EV.SVR.EH.F	RM
Vvi-t	т	ΝΤ	ГD	DIDL	КІ	EV.YVF.KC	21
Sin-t	Т	ΝΤ	ГІЕ	QIEI	КVІ	EV.YVY.EF	RM . N
Ppe-t	V	ΝΤ	「D	DIDL	КІ	EI.HIY.E1	М
Mno-t	T	NRT	ГР.D	DIDL	KN	ER.HVH.E.F	RI
Tca_t		NT	r	D	K	EV. TVQ.E P	<ivi< th=""></ivi<>
Pmu-t	v	ΝΤ	r D	DIDL	κ	EI. HVY. E 1	Μ
Pbr-t	V	ΝΤ	г <b>D</b>	DIDL	к	EV.YVY.E	М
Gso-t	T	ΝΤ	ГD	E I D L	КІ	EL.CVR.EH	IM
Nnu-t	<u>T</u>	N A	λD	EIE.II	RII	EV.HVH.S.F	RM
Gma_t		NT	r	F ID I	K. K. I	EF.CTH.AG	(M) F
Pda-t	T	N	AAE	EVDL	SI.A	EV.EVH.A.F	RN
Egi-t	Т	ΝΑ	λ <mark>S</mark> Ε	E . V V E L	SI.G	EV. EVH. T F	81
Tha-t	T M	K.RRY.T	「ED	DQIDL	KI.A	EE.RIE.E.F	R
OsRbcS1	. QT F	T. RRY. A	АМА	KSIEFIM	S V	KE.EIH.SF	RM
		80	90	100	110	120	130
		80 	90 •   • • • •   • • •	100 •   • • •   • • • •	110   · · · ·   · · · ·	120	130 · · · ·   · · ·
Consensus	LPMFGC		EI EC Y	100 -     PNA IRC AFD	110    Q QCM F	120 	150 • • • • I • • •
Consensus Nt-RbcS-t Nsy-t	LPMFGC	80 D VL .SSQ .SSQ	90 EIECY N.Q.KKA.	100 •   • • •   • • • • PNA IRC AFD • • • F • • • L • • •	110 Q QCM F NVK.VA.L NVK.VA.L	120 I KP Q. AAA	130 · · · · I · · ·
Consensus Nt-RbcS-t Nsy-t Nto-t	L P M F G C	0 D VL .SSQ .SSQ	90 EIECY QKKA. Q.KKA.	100 PNA IRC AFD FL FL	110 Q QCM F NVK.VA.L NVK.VA.L NVK.VA.L	120 I KP .Q.AAA .Q.XAA	130
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t	LPMFGC	80 D VL .SSQ .SSQ .SSQ	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL	110 Q QCM F NVK.VA.L NVK.VA.L NVK.VA.L NVK.AA.L	120 I KP Q. AAA Q. AAA Q. VA Q. AA	130
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Stu-t Sly-t Erret	L PMFGC	0 VL .SSQ .SSQ .SSQ .SSQ	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL	110 Q QCM F NVK V A . L NVK V A . L NVK A A . L NVK . A A . L	120 	130
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Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Sly-t Egr-t Lja-t1 Cca-t	L PMFGC	80 D VL .SSQN .SSQN .SSQN .SSQN .SSQN .SSQN	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL FL YV.L Y.L	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NVK.VA.V	120 	130
Consensus Nt-RbcS-t Nto-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t	L PMFGC N N N N N N N	80 55 Q N 55 Q N	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL FL YV.L Y.L	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NVK.VA.V	120 	
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Csi-t1	LPMFGC N N N N N N N N N N N N N N N N N N N	0 5 5 5 5 5 5 5 5 5 5 5 5 5	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL YV.L Y.L Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NYK.VA.V NIK.AA.V NIK.AA.V	120 	
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Cca t	LPMFGC N N N N N N N N N N N N N N N N N N N	0 5 5 5 5 5 5 5 5 5 5 5 5 5	9 EI EC Y Q. KKA. Q. KKA.	100 PNA IRC AFD FL FL FL Y.L Y.L Y.L.N Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NHRHM.S.A.I NIK.AA.V NIK.AA.V NIK.AS.I NKK.CS.I NKK.C.S.I	120 I KP Q. AAA Q. AA Q. AA	
Consensus Nt-RbcS-t Nsy-t Stu-t Sly-t Egr-t Lja-t1 Cca-t Egu-t Ccsi-t1 Jcu-t1 Gra-t	L PMFGC N 	80         VL         SSQ	50 EI EC Y N. Q. KKA Q. KKA N. Q. KKA	100 PNA IRC AFD FL FL FL YV.L YL YL YL YL	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NHRHM.S.A.V NIK.AA.V NIK.AS.I NQK.GS.L NQK.G.S.L NKH.A.S.V	120 I KP Q. AAA Q. AA Q. AA	
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Siy-t Egr-t Lja-t1 Cca-t Egu-t Cca-t Jcu-t1 Cci-t1 Gra-t Gar-t	L PMFGC N N N N N N N N N N N N N N N N N N N	0     VL       .SSQ     N	50 EI EC Y N. Q. KKA N. Q. KKA	100 PNA IRC AFD FL FL FL YV.L Y.L Y.L Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NKN.GA.I NHRHM.S.A.I NHRHM.S.A.I NKK.GS.L NKK.CS.L NKK.GS.L NKH.AS.V	120 I KP Q. AAA Q. AA Q. AA	
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Sly-t Egr-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Ccl-t1 Gra-t Gar-t Atr-t	L PMFGC N N N N N N N N N N N N N N N N N N N	0     VL       .SSQ     N	90 EI EC Y N. Q. KKA. Q. KKA. N. Q. KKA. MH. KKA. C. H. KKA. C. H. KKA.	100 PNA IRC AFD FL FL FL YV.L Y.LN Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.YA.V NIK.AA.V NIK.AS.L NKK.CS.L NKK.CS.L NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V	120       I     KP       Q.     AAA       Q.     TTS       Q.     TTTTST       Q.     TTTTST       H.     N       H.     N       Q.     SQA	
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Cca-t1 Jcu-t1 CcI-t1 Gra-t Gar-t Atr-t Peu-t	L PMFGC N N N N N N N N N N N N N N N N N N N	00         VL         SSQ	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. S. KKA. N. Q. KKA.	100 PNA IRC AFD FL FL FL Y.L Y.L.N Y.L.N Y.L.N Y.L.N Y.L Y.L Y.L Y.L Y.L Y.L Y.L	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NKN.GA.I NKK.C.S.I NQK.G.S.L NKK.C.S.I NKK.C.S.I NKK.C.S.L NKK.C.S.L NKK.S.L NKK.AA.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V	120         I       KP         Q.       AAA         Q.       AAA         Q.       AAA         Q.       AAA         Q.       AA         Q.       NTAS         Q.       TTTTST         Q.       TTTTST         H.       N         H.       N         Q.       SQA         Q.       SN	
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Sty-t Egu-t Cca-t Egu-t Cca-t Egu-t Cci-t1 Gra-t Gar-t Atr-t Peu-t Ptr-t Voi t	L PMFGC N N N N N N N N N N N N N	00         VL         SSQ.	90 EI EC Y N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. S. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. N. Q. KKA. S. E. KKA. S. H. KKA. S. E. KKT. S. E. KKA.	100 PNA IRC AFD FL FL FL Y.L Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NKN.GA.I NKN.GA.I NKK.CS.I NQK.GS.L NKK.CS.I NKK.CS.L NKK.AS.V NKH.AS.V NKH.AS.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V NKH.AA.V	120         I       KP         Q.       AAA         Q.       AAA         Q.       AAA         Q.       AA         Q.       NTS         Q.       NTTST         Q.       Q.         Q.       TTTTST         H.       N         Q.       SQA         Q.       SN         Q.       GN	
Consensus Nt-RbcS-t Nsy-t Nto-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Cca-t1 Gra-t Gar-t Atr-t Peu-t Prr-t Vvi-t Sin-t	L PMFGCNN	0     VL       .SSQ     N       .SSQ	90 EI EC Y . Q. KKA. . Q. KKA. . Q. KKA. . Q. KKA. . S. KKA. . Q. KKA. . Q. KKA. . Q. KKA. . Q. KKA. . Q. KKA. . Q. KKA. . H. KKA. . H. KKA. . H. KKA. . H. KKA.	100 PNA IRC AFD FL FL FL FL Y.L Y.L.N	110 Q QCM F NVK.VA.L NVK.VA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.L NVK.AA.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AS.V NKH.AA.V NKH.AA.V NKH.AS.V NKH.AS.V NKH.AA.V	120       I     KP       Q.     AAA       Q.     AAA       Q.     AA       Q.     AS       Q.     NTAS       Q.     NTAS       Q.     Q.       Q.     TTTTST       Q.     SQA       Q.     SN       Q.     SN       Q.     SN       Q.     CS       Q.     SN	
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Cci-t1 Gra-t Gra-t Gar-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ppe-t	LPMFGC N N N N N N N N N N N N N	0     VL       .SSQ     N       .SSQ	90 EI EC Y N. Q. KKA. N. H. KKA. N. H. KKA. N. H. KKA. N. Q. KKA. N. H. KKA. N. H. KKA.	100 PNA IRC AFD FL FL FL FL YV.L Y.L	110       Q     QCM       F       NVK.VA.L       NVK.VA.L       NVK.VA.L       NVK.VA.L       NVK.GA.L       NVK.AA.L       NVK.VA.L       NVK.VA.L       NVK.AA.L       NVK.AA.L       NKN.GA.L       NKK.GS.L       NKK.CS.L       NKH.AS.V       NKH.AS.V       NKH.AS.V       NKH.AA.L       NKR.A.A.L       NKR.A.A.L       NKR.A.A.L       NKR.A.A.L       NKR.A.A.L       NKR.A.A.L       NKH.GA.L       NKH.A.L       NKH.A.L	120       I     KP       Q.     AAA       Q.     AAA       Q.     AA       Q.     SA       Q.     TTTTST       H.     N       Q.     SQA       Q.     SN       Q.     GN       Q.     TCS       Q.     NN       Q.     AAATITT	130 1
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Egr-t Lja-t1 Cca-t Csi-t1 Jcu-t1 Ccl-t1 Gra-t Gra-t Gra-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t	L PMFGC N N N N N N N N N N N N N	80       VL       SSQ	50 EI EC Y Q. KKA. Q. KKA. KA. KKA. Q. KKA. KA. KKA. KA. KKA. KA. KKA. KA. KKA. KA. KKA. KA. KKA.	100 PNA IRC AFD FL FL FL FL YV.L Y.L	110       Q     QCM       F       NVK.VA.L       NVK.VA.L       NVK.VA.L       NVK.VA.L       NVK.GA.L       NVK.VA.L       NVK.VA.L       NVK.GS.L       NKK.CS.L       NKK.CS.L       NKK.GS.L       NKK.AA.V       NKK.AA.V       NKK.GS.L       NKK.AA.L       NKH.AS.V       NKH.GA.L       NKH.GA.V       NKH.GA.V       NKH.GA.V       NKH.GA.V	120       I     KP       Q.     AAA       Q.     AP       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     NTAS       Q.     Q.       Q.     TTTTST       Q.     SQA       Q.     SQA       Q.     SN       Q.     SN       Q.     TCS       QN     NN       Q.     TTTTTT	130 130 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Consensus Nt-RbcS-t Nsy-t Stu-t Sly-t Egr-t Lja-t1 Cca-t Egu-t Cci-t1 Gra-t Gra-t Gra-t Gra-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t	L PMFGC 	0     VL       .SSQ     SSQ	50 EI EC Y Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. MH. KKA. MH. KKA. MH. KKA. C. H. KKA.	100 PNA IRC AFD FL FL FL FL YL	110       Q    Q	120       I       KP       Q.       AA       Q.       AA       Q.       AA       Q.       AA       Q.       AA       Q.       Q.       AA       Q.       AP       Q.       AA       Q.       AA       Q.       AA       Q.       AA       Q.       AA       Q.       MTAS       Q.       MTAS       Q.       MTAS       Q.       MTTTST       Q.       Q.       SQA       Q.       Q.       Q.       MA       Q.       MA       Q.       Q.       MA       Q.       MA       Q.       MI       Q.       MA       Q. <th>130 1</th>	130 1
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Cca-t1 Gra-t Gra-t Gra-t Gra-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t Tca-t Pmu.t	L PMFGCNN	0     VL       .SSQ     N	50 EI EC Y Q. KKA. Q. KKA.	100 PNA IRC AFD FL FL FL YV.L YV.L Y.L Y.L.N Y.L.N Y.L.N Y.L.S S	110       Q       <	120       I       KP       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AANTITT       Q.       Q.       MTAS       Q.       Q.       MTAS       Q.       Q.       MTAS       Q.       Q.       Q.       Q.       Q.       Q.       Q.       Q.       Q.       MAATITT       Q.	130 1
Consensus Nt-RbcS-t Nsy-t Stu-t Siy-t Egr-t Lja-t1 Cca-t Egu-t Cca-t Jcu-t1 Cci-t1 Gra-t Gar-t Atr-t Pu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t Tca-t Pbr-t	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     SSQ       .SSQ     NSSQ       .SSQ     NSSQ       .SSQ     NSSQ       .SSQ     NSSQ       .SSQ     NSSQ       .SSQ     NSSQ	50 EI EC Y 4. Q. KKA 4. Q. KKA 5.	100       PNA     IRC     AFD        F     L        F     L        F     L        F     L        F     L        Y	110       Q       <	120       I     KP       Q.     AAA       Q.     TTST       Q.     TTTST       Q.     SQA       Q.     SQA       Q.     SN       Q.     SQA       Q.     SN       Q.     SQA       Q.     SN       Q.     SQA       Q.     SN       Q.     SN       Q.     AAATITT       Q.     AAATITTT       Q.     NIAATTS       Q.     TATAAATTS	130 130 130 130 130 130 130 130
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Cca-t1 Jcu-t1 Ccl-t1 Gra-t Ccl-t1 Gra-t Pu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t Tca-t Pbu-t Gso-t	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     N	90 EI EC Y I. Q. KKA. I. MH. KKA. I. H. KKA. I. H. KKA. I. H. KKA. I. H. KKA. I. H. KKA. I. H. KKA. I. R. KEA. I. R. KEA. I. R. KEA. I. R. KKA. I. R	100       PNA     IRC     AFD        F     L        F     L        F     L        F     L        F     L        Y	110       Q       <	120       I     KP       Q.     AAA       Q.     TTS       Q.     NTAS       Q.     TTTTST       Q.     QL       Q.     TTTTST       Q.     SQA       Q.     TTTTTT       Q.	130 1
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Stu-t Stu-t Stu-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Ccl-t1 Ccl-t1 Gra-t Gar-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t Tca-t Pmu-t Gso-t Nnu-t	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     SSQ	90 EI EC Y I. Q. KKA. . H. KKA. . H. KKA. . H. KKA. . YQ. KTA. . Q. KKT. . H. KKA. . Q. KKT. . H. KKA.	100 PNA IRC AFD FL FL FL Y.L	110       Q     QCM       NVK.VA.L       NKN.GA.I       NKN.GS.L       NQK.G.S.L       NKK.C.S.S.I       NKK.C.S.S.L       NKK.G.A.S.V       NKH.A.S.V       NVK.A.A.L       NVK.A.A.L       NVN.G.A.I       NVN.G.S.I       NVN.G.S.A.I       NVR.G.A.I       NVR.G.A.I       NVR.G.A.I       NVR.G.A.I	120       I     KP       Q.     AAA       Q.     TTTTST       Q.     TTTTST       H.     N       Q.     SQA       Q.     <	130 130 130 140 140 140 140 140 140 140 14
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Cci-t1 Gra-t Gra-t Gra-t Gra-t Atr-t Ptr-t Vvi-t Sin-t Ptr-t Vvi-t Sin-t Ppe-t Mno-t Fve-t Tca-t Ptr-t Sin-t Ptr-t Sin-t Nnu-t Mtr-t	LPMFGC N N N N N N N N N N N N N	0     VL       .SSQ     SSQ       .SSQ     SSQ   <	90 EIEC Y N.Q.KKA Q.KKA Q.KKA V.Q.KTA V.Q.KKA V.Q.KTA V.Q.KTA V.Q.KTA V.Q.KTA V.Q.KTA V.K.KA V.Q.KTA V.K.KA V.Q.KTA V.K.KA V.K.KA V.K.KA V.K.KA V.K.KA V.K.KA V.K.KA V.K.KA V.KA	100 PNA IRC AFD FL FL FL FL YV.L YL	110     I       Q     QCM       P     VK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.A.A.L       NVK.A.A.L       NVK.A.A.L       NVK.A.A.L       NVK.A.A.L       NKN.G.A.I       NKK.A.A.V       NKK.G.S.L       NKK.G.S.L       NKK.A.A.V       NKH.A.S.V       NKH.A.S.V       NKH.A.S.V       NKH.A.S.V       NKK.A.A.L       NKK.A.A.V       NKK.A.A.V       NKH.G.A.V       NKH.G.A.V       NKH.G.A.I       NKH.A.S.V       NVNG.S.A.I       NVNG.S.A.I	120       I     KP       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AA       Q.     AAA       Q.     AA       Q.     AA       Q.     AA       Q.     AA       Q.     AA       Q.     AA       Q.     NTAS       Q.     TTTTST       Q.     TTTTST       H.     N       Q.     SQA       Q.     SQA       Q.     SQA       Q.     SQA       Q.     SQA       Q.     SN       Q.     SN       Q.     SN       Q.     TCS       Q.     TATAAA       Q.     TATAAAA       YH.     DITTT       Q.     STASTTT       H.     TTTTN	130 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Csi-t1 Cci-t1 Cci-t1 Gra-t Gra-t Gra-t Gra-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Pu-t Tca-t Por-t Fve-t Nnu-t Nnu-t Mtr-t Gma-t	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     .SSQ       .SSQ <td< th=""><th>50 EI EC Y Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. M. Q. KKA. M. Q. KKA. M. Q. KKA. M. Q. KKA. M. KKA. M. Q. KKA. M. KA. M. KA.</th><th>100 PNA IRC AFD FL FL FL FL YV.L Y.L.N Y.L.N Y.L.N Y.L.N Y.L</th><th>110       Q       &lt;</th><th>120       I     KP       Q.     AAA       Q.     AAA       Q.     XAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AP       Q.     AP       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     TTTTST       Q.     QL       Q.     SQA       Q.     TTTTTT       Q.     TATAAAT       Q.     TATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA</th><th>130 130 130 130 130 130 130 130</th></td<>	50 EI EC Y Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. Q. KKA. M. Q. KKA. M. Q. KKA. M. Q. KKA. M. Q. KKA. M. KKA. M. Q. KKA. M. KA. M. KA.	100 PNA IRC AFD FL FL FL FL YV.L Y.L.N Y.L.N Y.L.N Y.L.N Y.L	110       Q       <	120       I     KP       Q.     AAA       Q.     AAA       Q.     XAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AP       Q.     AP       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     AAA       Q.     TTTTST       Q.     QL       Q.     SQA       Q.     TTTTTT       Q.     TATAAAT       Q.     TATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	130 130 130 130 130 130 130 130
Consensus Nt-RbcS-t Nsy-t Stu-t Stu-t Lja-t1 Cca-t Egu-t Csi-t1 Jcu-t1 Cci-t1 Gra-t Gar-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Pu-t Pre-t Fve-t Tca-t Pu-t Pbr-t Gso-t Nnu-t Mtr-t Gma-t Equ-t Csi-t Sin-t Ptr-t Sin-t Sin-t Ptr-t Sin-t Si	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     SSQ       .SSQ     NSSQ       .SSQ     NSSQ       .SSQ     SSQ       .SSQ     NSSQ       .SSQ     SSQ	50 EI EC Y I.Q. KKA I.Q. KKA I.KA I.KKA I.H. KKA I.H. KKA	100       PNA     IRC       AF     L       F     L       F     L       F     L       F     L       Y	110     I       Q     QCM       P     VK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.V.A.L       NVK.G.S.L       NKK.G.S.L       NKK.G.S.L       NKK.G.S.L       NKK.G.S.L       NKK.A.S.V       NKK.A.S.V       NKK.A.S.V       NKK.A.S.V       NKH.A.S.V       NKR.A.A.A.V       NKR.A.A.V       NKRHM.A.A.V       NKRAM.A.A.V       NKRHM.A.A.V       NKRHM.A.A.V       NKRHM.A.A.V	120       I       KP       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       Q.       AP       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAATITTST       Q.       Q.       MAA       Q.       M.       Q.       YH.       Q.       Q.       YH.       Q.       YH.       Q.       YH.       Q.       YATSAM   <	150 150 150 150 150 150 150 150
Consensus Nt-RbcS-t Nsy-t Stu-t Sty-t Egr-t Lja-t1 Cca-t Egu-t Cci-t1 Gra-t Gra-t Gra-t Gra-t Atr-t Peu-t Ptr-t Vvi-t Sin-t Ptr-t Vvi-t Sin-t Ptr-t Gso-t Nnu-t Mtr-t Gma-t Egi-t Tha-t	L PMFGC N N N N N N N N N N N N N	0     VL       .SSQ     .SSQ       .SSQ <td< th=""><th>50 EI EC Y I. Q. KKA I. MH. KKA I. H. KKA I. H. KKA I. H. KKA I. H. KKA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. Q. KKT I. H. KKM I. Q. KKT I. YQ. KTA I. Q. KKT I. RRV I. N. KKT I. N.</th><th>100 PNA IRC AFD FL FL FL YV.L YL</th><th>110       Q       &lt;</th><th>120       I       KP       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AANTTTI       Q.       Q.       MAA       Q.       M.       Q.       M.       Q.       Q.       TATAAAA       YH.       DITTT       Q.       M.       Q.       AATTATAAAA</th><th>150 150 150 150 150 150 150 150</th></td<>	50 EI EC Y I. Q. KKA I. MH. KKA I. H. KKA I. H. KKA I. H. KKA I. H. KKA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. YQ. KTA I. Q. KKT I. H. KKM I. Q. KKT I. YQ. KTA I. Q. KKT I. RRV I. N. KKT I. N.	100 PNA IRC AFD FL FL FL YV.L YL	110       Q       <	120       I       KP       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AAA       Q.       AANTTTI       Q.       Q.       MAA       Q.       M.       Q.       M.       Q.       Q.       TATAAAA       YH.       DITTT       Q.       M.       Q.       AATTATAAAA	150 150 150 150 150 150 150 150

#### Cluster M

		10	20	30	40	50	60 70
Consensus	M VWP	K ETL	SYLP L	L E YL	W PCLEF	GVR	SPGYYDGRYWTMW
Nta	.QPIN	<mark>КК.Ү</mark>	D . SQEC	Q. LS. VE LI	(NG . V E	TEH.F.Y.EN	INK
Nsy	.QPIN		D.SEEC	Q. LR. VE LI		TEH.F.Y.EN	NK
Stu	.QPIN		D. TDEC	. LK. VE L	(NG . V E	TEH.F.Y.EN	IHK.
Sly	.Q PIN	МК.Ү	D. SDEC	. LS . I E LI	(NG . V E	TEH.F.Y.EN	ΙНК
Egr	.QPIG	S <mark>KK</mark> .F	P . SPES	5. AK . V D L F	R <mark>SG</mark> .VE	LEH.F.Y.E	IHS
Lja-1	.QPIG	SKK.F	P.TVEC	Q.AK.VEIF	RKG . V E	TEK.F.Y.EN	NHK
Eca	.QPIG	INK Y	P TREC	LK.IDII	RNG.IE	LEK.H.Y.EY	INS
Csi	. K PTG	SLK.F		. LK. IS LF	RSG . I	LEK.W.Y.E	HS
Ccl	. <mark>K</mark> PTG	GLK.F	P . SDE /	A. LK. IS IF	R <mark>SG</mark> . I E	ELE <mark>K</mark> .W.Y.EF	HR
Jcu	. K TQG	SLK.F	P.TREC	AK.VE.L	RSG . V E	LEH.F.Y.EN	INR
Atn-1 Gra	.QPIG	SKK.F	D TPVC	. AK. VD H	KNK.IVE PSK I F	LEH.F.Y.EP	1GN
Gar	.QPT0	KK.F	D.TPV0	. AK . VD LF	RSK.VE	LEE.F.H.KY	(SSL.T
Atr	. K EPYN	NQRF	P.NKKA	A. AK. VD I F	RNG. I	)-VK.W.S.DN	INR
Peu	.QPT0	GLK.F	D . TEAE	. AK. ID LF	RSK.VE	LEK.W.Y.EN	IHR
Ptr	.QPTG	SLK.F	D.TEEL	E.AK.ID.LI	RSK.VE	ELEK.W.Y.EF	HS
Sin		SKK.F	D. TRFC	AS. ID IF	RSK.I.V.F	LEH.F.Y.FN	HR
Рре	. K TVG	SLK.F		AK.VD.LF	RKN. V E	LEK.F.Y.EN	IHR
Mno	. Q P R G	6 <mark>KL</mark> .F	D . TDEC	Q. LK. ID LF	R <mark>SN.I</mark> E	VGKAHIY. EN	INR
Fve	.QPVG	SLK.F	P.TSES	AK.VDF.LF	RNK . V E	LEK.F.Y.EN	инк
l ca Prnu	.QPLO	SKK.F	D.TREF	KIFKIVELILE SAK VD I I	KINK.VE RKNV -	LEH.F.Y.EN	ILKIC.I
Pbr	.QPLG	SLK.F		. AK . VD LF	RKN . V E	LET.F.Y.EN	инк
Gso	.QPIG	SKK.F	D. DDAG	AK.VE.L	RKG. I E	LEH.F.Y.E	INR
Nnu	. Q P I A	<u>КК.</u> Г	P . SPES	6. AK . V D L F	RMG . I E	ELEH.F.Y.EN	INR
Mtr	.QPIG	SKK.F	P.TEDO	Q.AK.VEIF	RKG . V E	LEK.F.Y.EN	IHS
Gma Pda	.QPVG	SVK F	P PIE4	LKOLE LE		CLEH.F.Y.ER	1NR
Egi	. K I E G	SLK.F	P.SIE4	LKQIE.LI	RSG. I	C-KV.F.S.DN	INR
Tha	.QTT0	G <mark>LR</mark> .F	D . SDT 8		RNN.IE	LGNAF.Y.EN	IHR
OsRbcS2	. Q I E G	61K.F	P.TVEC	D. LKQIE LF	RSK.V	6 - KV . F . Y . EN	IHR
		••••••••		100	· · ·   · · ·	120	
Consensus	KLPMFGC1	D QV	E E F	RIIGF	ON RQVQCISF	TA KP	
Nta			VE AKKAY.	QAWI	V	YEGY	
Nto		. AT LA	VE. AKKAY.	QAWI	. V	YEGY	
Stu		. AT LA	. VQ. CKKSY.	QAWI	. v	YEGY	
Sly		. AT LA	. VQ. AKKAY.	QAWV	. V	YEGY	
Egr	· · · · · · · · · · · · · · · · · · ·		LE.AKKAY.	TAFI	K	YPGF	
Cca		AT LK	VR CLKEY	NGWV	V	A KGF	
Egu		. AV VN	. LD. AIKAY.	EGF1	N. LK D	Y AGY	
Csi	<b>Y</b>	. AT LK	. VG. VQKEY.	HSFV	К	L.A PGV	
Ccl	<b>Y</b>	. AT LK	. VG . VQKEY .	HSFV	К		
JCU Ath_1		AV LN	VE CKKEY	NGEV	т.	V PSETO	
Gra		. SA LK	LE.CKKEY	NAFI	. V		
Gar		. S A L E	. LE. CKKAY.	NAF1	. V	Y PGF	
Atr		. SS MA	. LE. ATKSY.	DCYH	. К	L.Y. PPPPS	
Peu		EAS.LV	. LQ. AKKAY.	NAFI	V	AQAA	
Pu <sup>r</sup> Vvi		SA IK	VO ARTAY		N A	Y S	
Sin	Y	. SA LL	. VD. AVRAH	DAFV	. V		
Ppe		. <mark>S S</mark> L K	. LE. AKKAN.	NSF1	V		
Mno		. AT LA	. VQ. TKKAY.	DAHV	<mark>N</mark>	YPAK	
Fve Tca			LE.AKKAY.	TAFI	V	V POVEN	
Pmu			LE. AKKAN	NSFI	. V		
Pbr		. SS LK	LE.AKKAY	NAF1	. V	Y AGY	
Gso		. A <mark>S</mark> L K	. LQ. AKTAY.	NGF1	. V	Y PGF	
Nnu		. SS LA	. LE. AKKAY.	NAFI	<mark>K</mark>	YPGF	
Mtr	LA.		LA. AKAAY.	NGEL	V	V PCY	
Pda	N	I. AT AK	LE. CKKEY	DAFI	. V		
Egi	N	. AT AK	. LE. CKKEY	DAF1	. V	YPSY	
Tha		. SA MK	. LQ. AKTTH.	DAHI	. V	YKAT	
OsRbcS2		AT IK	IF AKKAY	DAEV	V	Y PGCEF	SGGN

**Supplemental Figure S7.** Alignment of the RbcS amino acid sequences. Amino acid sequences of the mature proteins from clusters T and M as listed in Table S2 were separately aligned using the ClustalW Multiple alignment, and a consensus sequence was generated for positions where at least 85% of the residues are conserved. Similar residues are in blue, identical residues are in black, and different residues are in red. Residues identical to the consensus sequence are indicated with a dot.