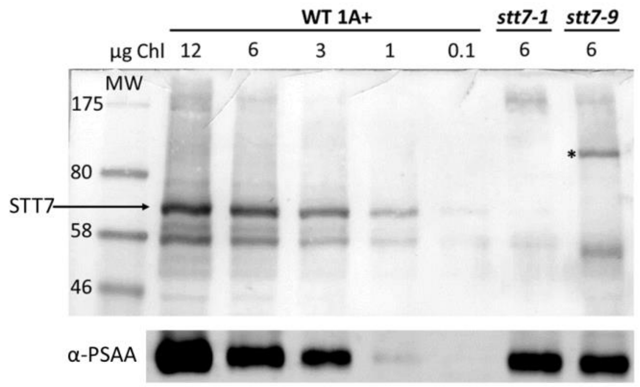
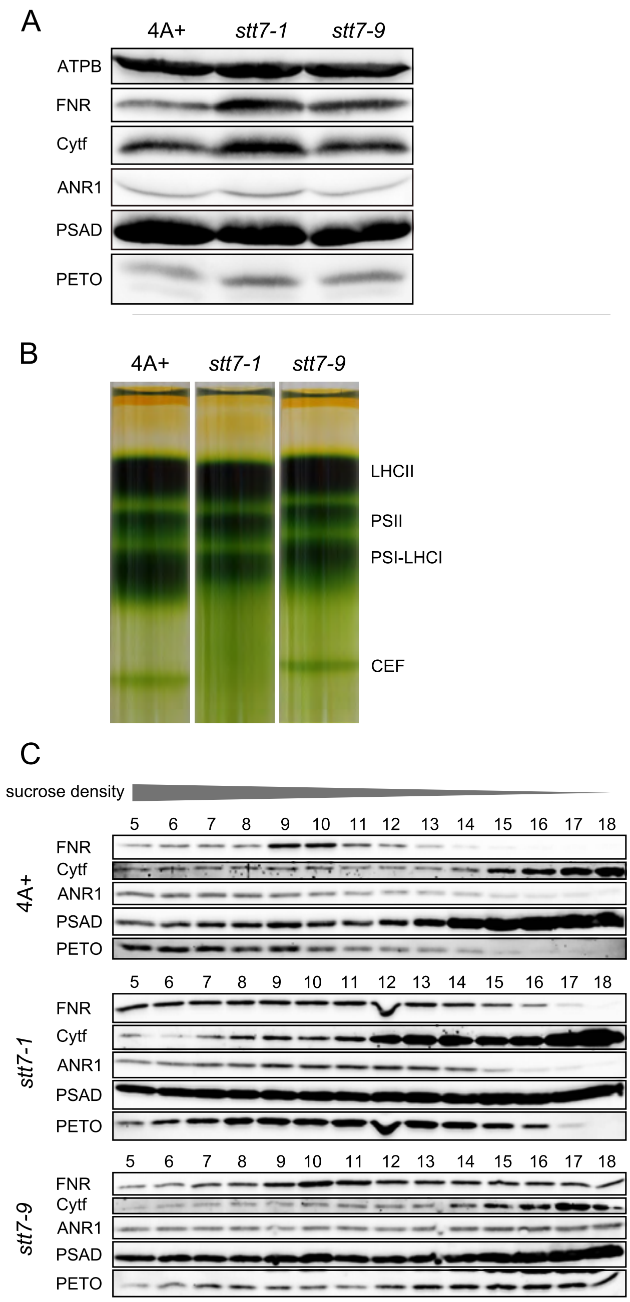


Supplemental Figure 1: Immunoblot detection of STT7 protein from *C. reinhardtii* thylakoid extracts using polyclonal α-STT7 antibodies (prepared in rabbit against purified recombinant STT7) and alkaline phosphatase conjugated secondary antibody.

The putative STT7-Arg7 fusion protein in *stt7-9* is indicated with *. The membrane was probed with α-PSAA antibodies and detected with chemiluminescence as a loading control.

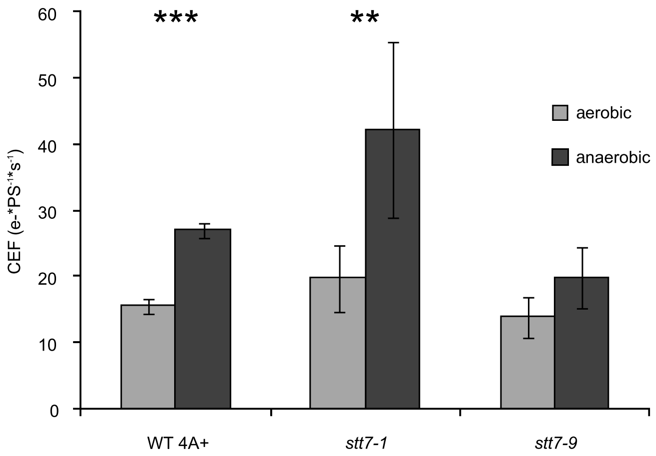


Supplemental Figure 2: STT7 deficiency alters organization and protein association of photosynthetic complexes.

A: Immunoblot analyses of thylakoid membranes (10 µg chlorophyll) isolated from anaerobic wt 4A+, *stt7-1* and *stt7-9* cells grown photo-heterotrophically in low light.

B: SDG separation of β-solubilized thylakoids from 4A+, *stt7-1* and *stt7-9*

C: Polypeptides in SDG-fractions 5-18 were analyzed by immunoblotting using the indicated antibodies. 40 µl volume of each fraction were loaded.



Supplemental Figure 3: CEF rates are significantly increased under anaerobic conditions in wt 4A+ and *stt7-1*. Results represent the average of three experiments. Significance was calculated using Student's t-test and is indicated as asterisks; **: p ≤ 0,01; ***: p ≤ 0,001.

Supplemental Table 1: All phosphoproteins identified from Chlamydomonas thylakoids

Figures given indicate the number of MS/MS events that led to phosphopeptide identifications (spectrum counts at 5 % posterior error probability). They do not permit quantitative interpretations. Phosphoproteins that were identified with a total of less than ten spectrum counts across all experiments were omitted. AN, anaerobic; HL, high-light; Lit, localization according to Terashima et al., 2012; Pred, localization as predicted by PredAlgo (C: chloroplast, M: mitochondria, SP: secretory pathway, O: other); n/a, not available.

					Treatment					
			Localization		**AN**			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre03.g175200.t1.1	TOC75	75 kDa chloroplast membrane translocon	C	C	75	76	81	106	83	119
Cre17.g720250.t1.1	Lhcb4	Lightharvesting chlorophylla/b binding protein Lhcb4	C	C	91	43	63	122	56	90
Cre09.g416850.t1.1	-	*(no conserved domains)*	C	M	79	75	129	54	48	79
Cre06.g300550.t1.1	-	*Pfam: MORN repeat*	n/a	O	85	64	50	105	91	65
Cre02.g081250.t1.1	-	*(no conserved domains)*	C	C	89	78	73	87	38	58
Cre13.g601050.t1.2	-	*KOG:0978 E3 ubiquitin ligase involved in syntaxin degradation*	n/a	C	68	81	96	72	86	16
Cre10.g457650.t1.1	-	*(no conserved domains)*	n/a	C	65	63	61	61	56	56
Cre01.g004400.t1.1	-	*(no conserved domains)*	n/a	SP	47	33	55	67	39	102
Cre18.g748950.t1.1	-	*(no conserved domains)*	n/a	C	47	48	49	61	54	52
Cre26.g773100.t1.1	-	*Pfam:04755 PAP_Fibrillin*	C	C	49	47	46	41	28	66
Cre06.g261000.t1.1	PsbR	Photosystem II 10 kDa polypeptide	C	C	39	44	49	55	35	43
Cre10.g459200.t1.1	PMA2	Plasma membranetype proton ATPase	n/a	O	21	16	18	71	78	51
Cre01.g058700.t1.1	TEF11	S-Isoprenylcysteine O-methyltransferase	C	C	48	46	44	37	50	17
Cre61.g792450.t1.2	-	*(no conserved domains)*	n/a	M	50	40	51	41	11	44
Cre17.g700750.t1.1	-	*Pfam:01184 GPR1/FUN34/yaaH family; KEGGORTH:07034 mannosyl-3-phosphoglycerate phosphatase; GO:0016020 membrane*	n/a	O	3	6	1	78	89	48
Cre02.g097950.t1.1	-	*(no conserved domains)*	n/a	O	50	36	49	19	9	59
Cre06.g263250.t1.2	-	*(no conserved domains)*	n/a	O	75	64	28	27	5	19
Cre16.g675300.t1.2	MFT9	*Major facilitator superfamily transporter*	n/a	C	50	32	35	37	34	30
Cre14.g611300.t1.2	COP3	Light-gated proton channel rhodopsin	n/a	SP	60	53	35	49	18	2
DAA00966.1	CP43	Photosystem II 44 kDa reaction center protein	C	C.e.	20	23	50	28	25	68
Cre12.g556250.t1.1	SEP1	Septinlike protein	C	O	35	70	41	19	22	19
DAA00964.1	D2	Photosystem II reaction center protein D2	C	C.e.	13	19	46	32	31	60
Cre12.g559450.t1.2	-	*Pfam:00168 C2 domain*	n/a	O	43	29	46	32	24	26

					Treatment					
			Localization		**AN**			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre13.g570350.t1.2	AKC4	ABC1like Kinase	n/a	C	41	54	54	12	15	23
Cre03.g186200.t1.1	PCT1	Phosphatidate cytidylyltransferase	n/a	O	35	32	31	25	28	42
Cre12.g540700.t1.2	-	hypothetical protein *(no conserved domains)*	n/a	C	23	28	30	53	38	18
Cre06.g269050.t1.1	CrTic62-NAD-1	*Extended shortchain dehydrogenase similar to the NADbinding domain of Tic621*	n/a	C	29	28	28	40	28	36
Cre16.g668350.t1.1	-	*Pfam:07889 Protein of unknown function*	n/a	M	32	29	31	40	18	33
Cre20.g759250.t1.1	-	*Pfam:07059 Protein of unknown function (DUF1336)*	n/a	O	33	40	33	36	15	16
Cre16.g663600.t1.1	-	Carbohydrate transporter	n/a	O	31	31	28	30	26	19
Cre01.g021650.t1.1	-	*(no conserved domains)*	n/a	O	35	41	35	15	17	21
Cre04.g221550.t1.1	-	*Panther:13847 FAD NAD BINDING OXIDOREDUCTASES; Panther:13847:SF34 DEAMINASE-RELATED*	n/a	C	10	17	35	27	18	53
Cre33.g782800.t1.1	NDA2	TypeII calciumdependent NADH dehydrogenase	n/a	C	36	34	36	25	13	16
Cre12.g530850.t1.2	-	*(no conserved domains)*	n/a	SP	35	29	42	15	18	12
Cre07.g325450.t1.2	-	*Pfam:06966 Â Protein of unknown function (DUF1295); KOG:4650 Predicted steroid reductase*	n/a	O	29	29	29	21	22	20
Cre12.g538700.t1.1	-	*Pfam:07766 LETM1-like protein; Panther:14009 LEUCINE ZIPPER-EF-HAND CONTAINING TRANSMEMBRANE PROTEIN*	C	C	18	24	20	36	14	37
Cre08.g367500.t1.1	LHCSR3	Stressrelated chlorophyll a/b binding protein 2	C	C	0	0	0	129	14	0
Cre10.g452450.t1.1	TIC110	*110 kDa translocon of chloroplast envelope inner membrane*	n/a	C	49	61	28	2	0	0
Cre06.g261750.t1.1	-	*Pfam:01062 Bestrophin, KOG:4090 Uncharacterized conserved protein*	n/a	O	39	40	18	11	11	21
Cre07.g336750.t1.2	-	*KOG:0978 E3 ubiquitin ligase involved in syntaxin degradation*	n/a	O	47	34	27	15	0	14
Cre01.g044600.t1.1	-	*Panther:10774:SF28; Panther:10774 CALCIUM-DEPENDENT LIPID-BINDING PROTEIN (CALB RELATED); KOG:4744 Uncharacterized conserved protein*	n/a	O	36	22	11	38	9	20
Cre07.g340450.t1.2	PKHD1-1	Fibrocystinlike protein	n/a	SP	29	11	47	36	0	11
Cre11.g477950.t1.2	-	*(no conserved domains)*	n/a	SP	28	30	9	28	14	23
Cre12.g552550.t1.2	-	*(no conserved domains)*	n/a	O	18	19	20	24	22	24
Cre01.g071450.t1.2	-	*Pfam:00069 Protein kinase domain; Pfam:01846 FF domain*	n/a	C	37	24	33	12	4	9
Cre14.g614000.t1.2	CGL17	Predicted protein	n/a	C	12	12	9	31	40	10
Cre06.g259100.t1.2	-	*KEG0978 E3 ubiquitin ligase involved in syntaxin degradation*	n/a	C	15	20	21	18	30	9
Cre10.g436550.t1.1	LCI5	lowCO2inducible protein	n/a	C	12	12	37	8	7	35
Cre12.g498550.t1.2	CHLM	*Mg protoporphyrin IX S-adenosyl methionine Omethyl transferase*	C	O	25	47	25	7	7	0

					Treatment					
			Localization		**AN**			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre05.g244900.t1.2	-	*Pfam:01594 Domain of unknown function DUF20; Panther:21716 TRANSMEMBRANE PROTEIN*	n/a	C	17	22	20	18	16	16
Cre12.g558600.t1.1	-	*(no conserved domains)*	C	O	21	15	17	26	6	23
Cre05.g247950.t1.1	-	*(no conserved domains)*	n/a	M	29	33	19	12	14	0
Cre14.g617300.t1.1	PSL3	Signal peptide peptidaselike protein	C	C	20	19	12	18	21	16
Cre01.g061800.t1.1	GSD1	Glutamicgammasemialdehyde dehydrogenase	n/a	C	23	21	18	17	18	7
Cre12.g500400.t1.1	-	*KOG:0977 Nuclear envelope protein lamin, intermediate filament superfamily*	n/a	O	30	23	21	11	2	15
Cre12.g500500.t1.2	SMT1	SterolC24methyltransferase	n/a	O	35	34	13	12	6	0
Cre07.g330250.t1.1	PSAH	Subunit H of photosystem I	C	C	24	16	30	8	14	7
Cre09.g398400.t1.1	TRP5	Transient receptor potential ion channel protein	n/a	O	16	12	0	14	53	0
Cre17.g729450.t1.1	-	*Pfam:00571 CBS domain; Pfam:00654 voltage gated chloride channel*	n/a	C	17	19	15	22	18	4
Cre06.g281600.t1.1	LCI23	LowCO2inducible protein	n/a	M	0	0	0	28	1	65
Cre01.g026900.t1.1	SSA14	Monooxygnase	C	C	13	15	16	18	19	13
1) Cre05.g243550.t1.1 2)Cre05.g243650.t1.1	-	*1) Hypothetical protein (no conserved domains) 2) (no conserved domains)*	1)C	1)O 2)O	15	11	11	30	21	5
Cre15.g645000.t1.1	MRP2	*ABC transporter, multidrug resistance associated protein*	n/a	O	19	17	17	18	18	4
Cre10.g448650.t1.2	-	*Pfam:00781 Diacylglycerol kinase catalytic domain (and others..)*	n/a	O	12	19	2	20	21	18
Cre29.g778350.t1.1	-	*(no conserved domains)*	n/a	M	34	9	9	25	10	4
Cre03.g199000.t1.1	PHOT	Phototropin	n/a	C	24	20	23	8	10	6
Cre02.g094250.t1.1	-	*Pfam:00153 Mitochondrial carrier protein*	n/a	O	19	12	10	17	31	2
Cre02.g076900.t1.1	CGK2	cGMPdependent Protein Kinase	n/a	O	13	27	8	12	15	15
Cre12.g539000.t1.1	ECT1	CDPEthanolamine synthase	n/a	SP	21	9	16	15	17	12
Cre17.g708000.t1.2	FAP260	Flagellar Associated Membrane Protein	n/a	C	16	18	21	17	5	13
Cre01.g038100.t1.1	-	*Pfam:01062 Bestrophin*	n/a	C	5	9	1	33	29	12
Cre12.g492350.t1.1	-	*Pfam: 01963 TraB family*	C	O	16	29	23	1	12	8
Cre04.g229300.t1.2	RCA1	Rubisco activase	n/a	C	9	7	15	20	15	22
Cre03.g171100.t1.2	-	*(no conserved domains)*	n/a	C	25	25	17	11	6	2
Cre12.g485900.t1.1	-	*(no conserved domains)*	n/a	O	19	16	18	18	9	4
Cre16.g657850.t1.1	SEC63	ERtargeted preprotein translocase subunit	C	SP	21	21	11	11	9	9
Cre03.g155100.t1.1	-	*(no conserved domains)*	n/a	M	28	45	8	0	0	0
Cre12.g488500.t1.1	ARC6	ARC6like protein	n/a	C	16	45	14	0	6	0

					Treatment					
			Localization		**AN**			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre01.g044650.t1.1	-	*Panther:10774 CALCIUM-DEPENDENT LIPID-BINDING PROTEIN (CALB RELATED)*	n/a	C	17	16	9	13	9	17
Cre07.g325550.t1.1	KDG3	diacylglycerol kinase	n/a	O	18	25	10	13	6	8
1) Cre02.g120250.t1.1 **2)Cre02.g120200.t1.1**	STT7	*Chloroplast protein kinase required for LHCII phosphorylation and state transition*	1)C	1)C 2)C	27	14	0	28	11	0
Cre12.g490700.t1.1	MIN1	Minieyespot protein	n/a	O	17	30	23	6	0	3
Cre06.g280950.t1.1	PYK2	Pyruvate kinase	n/a	O	31	9	8	18	6	6
Cre06.g262900.t1.1	PFK1	Phosphofructokinase family protein	C	C	14	8	10	16	20	9
Cre09.g402950.t1.2	CGL21	Conserved protein of unknown function	n/a	C	17	16	8	21	12	2
Cre17.g726350.t1.2	-	*Pfam:01940 Integral membrane protein DUF92 (...and more)*	n/a	C	15	22	18	8	7	6
Cre02.g102450.t1.1	-	*Pfam:00400 WD domain, G-beta repeat (...and others)*	n/a	SP	17	15	15	10	6	13
Cre02.g140700.t1.1	-	*Pfam:02656 Domain of unknown function DUF; Pfam:03105 SPX domain; Pfam:09359 VTC domain; Panther:10783 XENOTROPIC AND POLYTROPIC MURINE LEUKEMIA VIRUS RECEPTOR; Panther:10783:SF20; KOG:1161 Protein involved in vacuolar polyphosphate accumulation, contains SPX domain*	C	O	15	16	12	14	8	11
Cre06.g281900.t1.1	ZIL2	ZIP family transporter	n/a	SP	15	13	20	8	8	9
Cre16.g678650.t1.1	-	*(no conserved domains)*	n/a	O	22	35	15	0	0	0
Cre16.g653700.t1.2	-	*Pfam:01237 Oxysterol-binding protein*	n/a	M	24	15	12	5	3	13
Cre06.g273250.t1.1	-	*Pfam:01553 Acyltransferase*	n/a	C	15	17	12	11	8	9
Cre07.g352350.t1.1	-	*Pfam:01434 Peptidase family M41; Pfam:00004 ATPase family associated with various cellular activities (AAA); Panther:23076 METALLOPROTEASE M41 FTSH (...and others)*	n/a	C	11	1	25	8	9	17
Cre02.g130650.t1.1	-	Inorganic pyrophosphatase	C	SP	2	6	5	22	16	18
Cre13.g604150.t1.1		*Pfam:00664 ABC transporter transmembrane region (...and more)*	n/a	M	14	12	16	11	8	8
Cre12.g507750.t1.2	-	Protein kinase	n/a	M	18	29	5	1	15	0
Cre07.g350750.t1.1	PTOX1	Alternative oxidase	C	O	13	15	23	8	6	0
Cre04.g221050.t1.1	-	*Pfam:07059 Protein of unknown function (DUF1336)*	n/a	O	11	11	13	15	2	11
Cre12.g558900.t1.1	PETO	Cytochrome b6f complex subunit V	C	C	31	4	0	24	4	0
Cre02.g132550.t1.1	-	*Pfam:00583 Acetyltransferase (GNAT) family; Panther:13947 N-ACETYLTRANSFERASE CAMELLO; GO:0008080 N-acetyltransferase activity*	n/a	O	14	16	17	6	1	9
DAA00959.1		Hypothetical Protein *(no conserved domains)*	n/a	C.e.	26	10	14	5	0	6

					Treatment					
			Localization		AN			HL		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre07.g337650.t1.1	PDC1	*Mitochondrial pyruvate dehydrogenase complex, E1 component, alpha subunit*	n/a	M	16	12	4	11	14	4
Cre09.g413650.t1.2	-	*Pfam:04437 RINT-1 / TIP-1 family*	n/a	O	14	10	4	11	3	19
Cre01.g057900.t1.1	PYK4a	Pyruvate kinase	n/a	O	17	8	12	8	6	9
Cre12.g560450.t1.2	-	*KOG:0978 E3 ubiquitin ligase involved in syntaxin degradation*	n/a	O	25	18	11	4	1	1
Cre12.g527050.t1.1	-	*Pfam:03765 CRAL/TRIO, N-terminus; Pfam:00650 CRAL/TRIO domain; Panther:23324 SEC14 RELATED PROTEIN; Panther:23324:SF5 SEC14 CYTOSOLIC FACTOR-RELATED; KOG:1471 Phosphatidylinositol transfer protein SEC14 and related proteins*	n/a	O	23	15	11	3	3	4
Cre12.g532100.t1.1	-	*(no conserved domains)*	C	O	7	8	5	23	11	5
Cre17.g701500.t1.1	DNJ1	DnaJlike protein	n/a	O	10	12	13	4	6	14
Cre05.g236050.t1.2	-	*KOG:4674 Uncharacterized conserved coiled-coil protein*	n/a	O	4	0	7	0	1	46
Cre06.g283500.t1.2	-	*KOG: 0963 Transcription factor/CCAAT displacement protein CDP1*	n/a	O	2	0	5	4	0	47
Cre11.g471250.t1.2	-	*Pfam:04857 CAF1 family ribonuclease; Panther:15092 POLY(A)-SPECIFIC RIBONUCLEASE/TARGET OF EGR1, MEMBER 1*	n/a	C	14	11	9	11	5	8
Cre17.g715350.t1.1	-	*Pfam:01412 Putative GTPase activating protein for Arf*	n/a	O	23	17	12	0	1	4
Cre03.g196900.t1.1	-	Predicted protein (*Pfam:00635 MSP (Major sperm protein) domain; Panther:10809 VESICLE-ASSOCIATED MEMBRANE PROTEIN (VAMP)*)	n/a	O	8	12	10	12	14	1
Cre03.g201050.t1.1	ZNJ2	DnaJlike Zincfinger protein	n/a	C	11	11	10	8	10	7
Cre02.g132800.t1.1	PsbO	*Oxygen-evolving enhancer protein 1 of photosystem II*	n/a	C	12	12	21	4	3	4
Cre50.g790000.t1.1	-	*(no conserved domains)*	n/a	O	0	0	0	22	18	15
Cre03.g210900.t1.2	NAR1.3	Formate nitrite transporter	n/a	C	31	24	0	0	0	0
Cre07.g357157.t1.1	-	*Pfam:00067 Cytochrome P450*	n/a	O	6	22	7	5	11	4
Cre02.g074900.t1.2	-	*Pfam:00168 C2 domain; Panther:10774:SF2 CALCIUM LIPID BINDING PROTEIN*	n/a	M	16	17	5	8	3	6
Cre08.g379900.t1.2	-	*Pfam:01544 CorA-like Mg2+ transporter protein (...and more)*	n/a	O	4	10	2	8	18	13
1)Cre03.g164600.t1.1 2)Cre03.g165050.t1.1	1)PMH1 2)-	1) Plasma membrane hydrogen ATPase 2)	n/a (1+2)	1)O 2)O	22	15	6	7	1	4
Cre03.g197850.t1.2	-	*Pfam:11267 Protein of unknown function (DUF3067)*	n/a	M	10	13	7	5	12	8
Cre03.g177500.t1.2		Predicted protein *(Pfam:03134 TB2/DP1, HVA22 family)*	n/a	O	13	8	10	12	8	3
Cre12.g517500.t1.2		Hypothetical Protein *(Panther:13815:SF4 GOLGIN-84 (...and more))*	n/a	O	16	15	16	1	0	5

					Treatment					
			Localization		AN			HL		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre41.g786900.t1.1		Putative chloroplast lycopene beta cyclase	n/a	C	12	13	27	0	0	0
Cre01.g060900.t1.1	TEF10a	Predicted protein	n/a	C	16	20	2	6	8	0
Cre08.g360600.t1.2	ERM4	ERD4related membrane protein	n/a	SP	15	15	4	10	6	0
Cre12.g547300.t1.2	-	*Pfam:01061 ABC-2 type transporter; Pfam:00005 ABC transporter*	C	C	9	21	8	4	7	1
Cre17.g724150.t1.1	DRP3	Dynamin-related GTPase	n/a	O	13	14	8	7	1	7
Cre05.g247450.t1.1	CGL56	Putative rhodanese-like protein	C	C	8	8	12	9	4	9
Cre16.g664850.t1.1	-	*Pfam:00069 Protein kinase domain*	n/a	C	15	13	1	8	6	7
Cre02.g082450.t1.1	-	*(no conserved domains)*	n/a	M	10	13	8	11	7	1
Cre07.g318450.t1.1	SEC61B	SEC61beta subunit of ERtranslocon	n/a	C	12	9	10	9	4	6
Cre17.g696250.t1.2	-	*Pfam:02854 MIF4G domain; Panther:23253 EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (...and more)*	n/a	O	4	5	9	2	1	28
Cre13.g607650.t1.2	-	*Panther:10891 CALMODULIN*	n/a	O	0	0	9	4	0	35
Cre11.g474900.t1.1	-	*(no conserved domains)*	n/a	C	20	12	1	14	0	1
Cre12.g512400.t1.2	-	Nitrogen assimilation regulatory protein	n/a	O	15	13	13	4	3	0
Cre83.g796250.t1.1	SPT1	Component of serine palmitoyltransferase	n/a	O	24	12	6	2	0	0
Cre16.g661150.t1.1	CGL5	Predicted protein	n/a	C	5	13	9	8	9	0
Cre16.g672950.t1.1	LCI2	Low CO2 inducible gene	n/a	C	2	0	2	25	8	6
Cre14.g611700.t1.2	PLAP4	Plastid lipid associated protein	n/a	C	30	5	3	4	0	0
Cre12.g561550.t1.1	CDS1	*mitochondrial halfsize ABC transporter, membrane protein*	n/a	SP	8	7	0	16	11	0
Cre14.g608050.t1.2	-	predicted protein *(Pfam:10351 Golgi-body localisation protein domain)*	n/a	SP	11	9	8	8	5	0
Cre13.g583600.t1.1	DGD1	Galactolipid galactosyltransferase	n/a	O	15	7	5	7	5	2
Cre10.g459950.t1.2	-	*(no conserved domains)*	n/a	O	9	26	3	0	2	0
Cre06.g294700.t1.2	-	*Pfam:01477 PLAT/LH2 domain; Panther:10877 POLYCYSTIN-RELATED (...and more)*	n/a	C	1	2	6	0	0	30
Cre06.g251650.t1.2	PTC1	Lowaffinity phosphate transporter	C	O	17	4	4	9	2	2
Cre17.g702950.t1.1	-	*Pfam:01184 GPR1/FUN34/yaaH family; KEGGORTH:07034 mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]*	n/a	O	6	6	0	13	13	0
Cre07.g318350.t1.1	CGL64	Predicted protein *(Pfam:12576 Protein of unknown function (DUF3754))*	n/a	O	19	7	0	10	2	0
Cre03.g171850.t1.2	-	*(no conserved domains)*	n/a	O	2	0	1	0	0	34
Cre03.g162950.t1.1	-	*(no conserved domains)*	n/a	O	6	0	9	1	1	20
Cre06.g284100.t1.1	RHP1	Rh protein, CO_2 responsive	n/a	O	6	26	0	0	5	0

			Localization		**Treatment**					
					AN			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre10.g444400.t1.2	-	*Panther:13371 GLYCINE-, GLUTAMATE-, THIENYLCYCLOHEXYLPIPERIDINE-BINDING PROTEIN*	n/a	O	6	4	15	3	0	9
Cre17.g702900.t1.1		*Pfam:01184 GPR1/FUN34/yaaH family; KEGGORTH:07034 mannosyl-3-phosphoglycerate phosphatase [EC:3.1.3.70]; GO:0016020 membrane*	n/a	O	0	0	0	18	18	0
Cre16.g671800.t1.1	-	*(no conserved domains)*	n/a	C	5	8	9	5	8	0
Cre12.g547550.t1.2		*KOG:1003 Actin filament-coating protein tropomyosin*	n/a	M	1	0	3	3	0	27
Cre10.g450850.t1.2	-	*Pfam:00168 C2 domain*	n/a	O	7	10	4	5	8	0
Cre10.g436100.t1.1	MLK1	mixed lineage protein kinase	n/a	O	16	9	1	5	2	0
Cre03.g189550.t1.2	ZIP3	ZIP family transporter	n/a	SP	6	7	1	12	7	0
Cre17.g727100.t1.1		predicted protein *(no conserved domains)*	C	O	10	12	11	0	0	0
Cre01.g038550.t1.2	SQD2	sulfolipid synthase	n/a	C	9	11	7	5	0	0
Cre03.g156900.t1.1	LHCBM5	chlorophyll ab binding protein of LHCII	n/a	C	18	0	1	13	0	0
Cre01.g043350.t1.1	CAO	Chlorophyll a oxygenase	n/a	C	11	9	11	0	0	0
Cre07.g325500.t1.1	CHLH1	Magnesium chelatase subunit H	C	C	10	16	5	0	0	0
Cre10.g460050.t1.2	-	*FLU chloroplast precursor, alternative spliced version lFLP*	n/a	C	2	13	14	2	0	0
Cre10.g444450.t1.2	SSA17	predicted protein (*Pfam:00397 WW domain; Panther:21715 UNCHARACTERIZED; KOG:0977 Nuclear envelope protein lamin, intermediate filament superfamily; GO:0005515 protein binding)*	n/a	O	0	2	7	0	0	21
Cre12.g560950.t1.1	PSAG	photosystem I reaction center subunit V	C	C	9	0	0	19	0	0
Cre06.g282850.t1.2	-	*(no conserved domains)*	n/a	M	1	5	14	0	0	8
Cre03.g173750.t1.2	-	*KOG:3544 Collagens (type IV and type XIII), and related proteins*	n/a	O	0	0	2	4	3	19
Cre03.g161750.t1.1	-	*(no conserved domains)*	n/a	SP	9	6	11	1	1	0
Cre06.g286550.t1.1	-	*(no conserved domains)*	n/a	M	13	9	5	1	0	0
Cre10.g466250.t1.1		*Pfam:00400Â WD domain, G-beta repeat; Pfam:04192 Utp21 specific WD40 associated putative domain; Panther:13889:SF2 gb def: putative pre-mrna splicing factor [schizosaccharomyces pombe]; Panther:13889 WD40 REPEAT PROTEIN; KOG:1539 WD repeat protein; KEGGORTH:14554 U3 small nucleolar RNA-associated protein 21*	n/a	O	14	6	8	0	0	0
Cre16.g681900.t1.1	SECY1	Preprotein translocase secY subunit	C	C	7	2	3	11	2	2

			Localization		**Treatment**					
					AN			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre08.g379500.t1.2		*Pfam:07714Â Protein tyrosine kinase; Panther:23257:SF347; Panther:23257 SERINE-THREONINE PROTEIN KINASE; KOG:0192 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs; GO:0004672 protein kinase activity; GO:0006468 protein amino acid phosphorylation*	n/a	O	6	18	2	0	0	1
Cre03.g192050.t1.1	FTR1	Iron permease, membrane protein	n/a	O	14	7	6	0	0	0
DAA00933.1	CP47	Photosystem II P680 chlorophyll A apoprotein	C	C.e.	10	5	3	6	2	1
Cre16.g672200.t1.2	-	*(no conserved domains)*	n/a	C	1	0	2	0	0	23
Cre06.g257300.t1.1	-	*(no conserved domains)*	n/a	O	3	0	3	0	0	19
Cre12.g525150.t1.1	-	*(no conserved domains)*	n/a	M	9	10	1	2	3	0
Cre12.g551100.t1.1	-	*Pfam:07172 Glycine rich protein family*	n/a	O	6	4	2	7	6	0
Cre12.g505950.t1.1		*Pfam:03031 NLI interacting factor-like phosphatase; Panther:12210:SF3 PLASMA MEMBRANE SODIUM RESPONSE PROTEIN; Panther:12210 NUCLEAR LIM INTERACTOR-INTERACTING FACTOR-RELATED; KOG:2832 TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation); GO:0005515 protein binding*	n/a	M	4	5	5	7	4	0
Cre02.g097800.t1.2	HLA3	ABC transporter	n/a	O	0	0	0	6	6	12
Cre11.g479350.t1.2	-	*KOG:4462 WASP-interacting protein VRP1/WIP, contains WH2 domain*	n/a	O	9	6	7	0	0	2
Cre02.g085257.t1.1	COP4	chlamyopsin 4 lightgated ion channel	n/a	O	3	1	14	0	1	5
Cre01.g071650.t1.2	-	Reticulonlike protein	n/a	O	8	8	7	1	0	0
Cre03.g205550.t1.2	-	*(no conserved domains)*	n/a	SP	8	11	4	0	0	0
Cre16.g692300.t1.1	-	*Pfam:00664 ABC transporter transmembrane region;* *Pfam:00005Â ABC transporter;* *Panther:24221;Â* *Panther:24221:SF122;Â* *KOG:0058 Peptide exporter, ABC superfamily;* *GO:0055085 transmembrane transport*	n/a	SP	5	9	3	0	2	3
1) Cre08.g367500.t1.1 2) Cre08.g365900.t1.1	1) LHCSR3 2) LHCSR1	Stressrelated chlorophyll a/b binding protein 1	1+2)C	1+2)C	0	0	2	11	7	2
Cre19.g751700.t1.1	LHL3	low molecular mass early lightinduced protein	n/a	C	10	7	4	0	0	1

			Localization		**Treatment**					
					AN			**HL**		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre24.g769650.t1.2	-	hypothetical protein (*Pfam:00999 Sodium/hydrogen exchanger family; Panther:11584:SF4 LIM KINASE-RELATED; Panther:11584 SERINE/THREONINE PROTEIN KINASE; GO:0055085 transmembrane transport; GO:0016021 integral to membrane; GO:0015299 solute:hydrogen antiporter activity; GO:0006812 cation transport)*	n/a	SP	0	0	0	2	0	19
Cre16.g655750.t1.1	-	*Tektin, flagellar protein associated with inner arm dynein*	n/a	O	0	0	0	11	5	5
Cre12.g551250.t1.1	-	*Pfam:00069 Protein kinase domain*	n/a	O	0	0	0	6	6	9
DAA00905.1		Cytochrome b6/f subunit IV	n/a	C.e.	12	0	0	9	0	0
Cre12.g506650.t1.1		*Pfam:07064Â RIC1; Panther:22746 FAMILY NOT NAMED; Panther:22746:SF4 SUBFAMILY NOT NAMED*	n/a	O	8	4	8	0	0	0
Cre01.g003550.t1.2	-	*Pfam:00581 Rhodanese-like domain*	n/a	C	0	0	1	15	3	1
Cre09.g392850.t1.2	-	*(no conserved domains)*	n/a		5	1	3	0	0	11
Cre12.g549350.t1.1	-	*(no conserved domains)*	C	C	8	6	6	0	0	0
Cre19.g753050.t1.1	-	*Pfam:00179 Ubiquitin-conjugating enzyme*	n/a	O	13	2	2	2	0	0
Cre07.g321000.t1.2	CYG14	guanylate cyclase	n/a	M	12	6	1	0	0	0
Cre09.g392800.t1.2	-	*(no conserved domains)*	n/a	O	0	1	5	0	1	12
Cre19.g754700.t1.1	EGY1	*membrane associated metalloprotease involved in plastid development*	n/a	C	2	7	2	2	6	0
Cre02.g114850.t1.1	-	*Pfam:00515 Tetratricopeptide repeat; Pfam:01425 Amidase, Panther:22904 CHAPERONE BINDING PROTEIN, KOG:1308 Hsp70-interacting protein* *Hip/Transient component of progesterone receptor complexes and an Hsp70-binding protein*	n/a	M	8	6	5	0	0	0
Cre01.g053450.t1.2	-	*Pfam:00211 Adenylate and Guanylate cyclase catalytic domain; Panther:16305:SF7; Panther:16305 TESTICULAR SOLUBLE ADENYLYL CYCLASE; GO:0009190 cyclic nucleotide biosynthesis; GO:0016849 phosphorus-oxygen lyase activity; GO:0035556*	n/a	O	6	5	1	3	4	0
Cre07.g346050.t1.1	CRD1	Copper response defect 1 protein	n/a	C	10	9	0	0	0	0
Cre02.g073750.t1.1	KLP1	Kinesinlike protein	n/a	O	6	4	6	2	1	0
DAA00906.1		*Lightindependent protochlorophyllide reductase subunit B*	n/a	C.e.	6	10	2	0	0	0
Cre23.g768350.t1.1	PP2Ab	*Ser/Thr specific protein phosphatase regulatory subunit*	n/a	O	0	0	0	2	0	16
Cre11.g481450.t1.1	ATPG	CF0 ATP synthase subunit II precursor	n/a	C	6	2	0	5	5	0
Cre07.g340200.t1.2	TEF3	predicted protein *(no conserved domains)*	C	C	1	2	1	6	8	0
Cre02.g127450.t1.2		*Pfam:08241 Methyltransferase domain*	n/a	C	1	0	0	9	6	2

					Treatment					
			Localization		AN			HL		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre17.g702250.t1.2	TRP4	Transient receptor potential ion channel protein	n/a	C	7	7	4	0	0	0
Cre32.g781500.t1.2		*Pfam:00560 Leucine Rich Repeat;* *Panther:23155 LEUCINE-RICH REPEAT-CONTAINING PROTEIN;* *GO:0005515 protein binding*	n/a	O	5	5	0	4	4	0
Cre01.g048950.t1.1	PYR5	uridine 5' monophosphate synthase	n/a	C	5	7	5	1	0	0
Cre07.g329050.t1.1	AOC5	cationic amino acid transporter	n/a	O	0	0	1	0	0	16
Cre05.g244050.t1.2	-	*(no conserved domains)*	n/a	O	0	0	2	1	0	14
Cre01.g048400.t1.2	-	*Panther:12042:SF3 ZINC FINGER, C2H2 TYPE CONTAINING PROTEIN-RELATED; Panther:12042 LACTOSYLCERAMIDE 4-ALPHA-GALACTOSYLTRANSFERASE (ALPHA- 1,4-GALACTOSYLTRANSFERASE); KOG:0982 Centrosomal protein Nuf*	n/a		2	1	9	0	0	5
Cre12.g483650.t1.1	STL1	Serine/threonine protein kinase	C	O	10	5	0	1	1	0
Cre16.g668600.t1.1	-	*(no conserved domains)*	C	C	0	0	0	11	5	0
Cre07.g339600.t1.1	-	*Panther:20932 LOC443603 PROTEIN-RELATED*	n/a	O	14	1	1	0	0	0
Cre16.g649100.t1.1	MAPKKK13	Mitogen Activated Protein Kinase Kinase Kinase 13	n/a	O	7	9	0	0	0	0
Cre13.g588600.t1.2	-	*Pfam:00225 Kinesin motor domain (and other kinesin related)*	n/a	O	0	0	1	0	0	15
Cre10.g428650.t1.1	CDPKK1	*Calcium/Calmodulin Dependent Protein Kinase Kinase 1*	n/a	O	3	10	1	1	0	1
Cre18.g751100.t1.1	FAP15	Flagellar Associated Protein	n/a	O	0	0	0	7	1	8
Cre07.g350050.t1.2	-	*(no conserved domains)*	n/a	SP	0	0	0	4	5	7
Cre02.g077550.t1.1	-	predicted protein *(no conserved domains)*	n/a	SP	4	9	2	0	0	0
Cre02.g086300.t1.2	-	*(no conserved domains)*	n/a	C	6	3	5	0	0	0
Cre11.g469150.t1.1	-	*(no conserved domains)*	C	C	2	4	8	0	0	0
Cre10.g443000.t1.1	ATM3	halfsize ABC transporter, membrane protein	n/a	SP	0	0	0	0	0	13
Cre17.g734250.t1.2	-	*Pfam:00069 Protein kinase domain;Pfam:07714 Protein tyrosine kinase*	n/a	O	5	8	0	0	0	0
Cre05.g245550.t1.2	PIK1	Phosphatidylinositol 4kinase	n/a	O	0	0	1	0	1	11
Cre06.g303850.t1.2		TBC1 domain protein	n/a	M	5	4	0	3	1	0
Cre11.g480200.t1.2	-	*(no conserved domains)*	n/a	O	0	0	1	1	0	10
Cre10.g452800.t1.1	LCIB	lowCO2inducible protein	C	C	0	0	0	6	6	0
Cre03.g178000.t1.1	-	*(no conserved domains)*	n/a	O	0	0	0	0	0	12
Cre01.g043050.t1.1	-	*Pfam:09335 SNARE associated Golgi protein; Panther:12677 UNCHARACTERIZED*	n/a	M	0	0	6	0	1	5

					Treatment					
			Localization		AN			HL		
Protein ID (Augustus U10.2)	**Short name**	**Protein description (JGI3) or *conserved domains***	**Lit**	**Pred**	**WT**	**STT7-9**	**STT7-1**	**WT**	**STT7-9**	**STT7-1**
Cre26.g773750.t1.2	-	*Pfam:00069 Protein kinase domain; Panther:23257 SERINE-THREONINE PROTEIN KINASE;KOG:0192 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs*	n/a	M	2	7	3	0	0	0
Cre13.g598900.t1.1	LHCA1	Lightharvesting protein of photosystem I	1+2) n/a	C	2	4	6	0	0	0
Cre16.g661950.t1.1	-	*(no conserved domains)*	n/a	O	0	0	4	0	0	7
Cre11.g468400.t1.2		*Pfam:07466 Protein of unknown function (DUF1517)*	n/a	C	5	3	0	3	0	0
Cre04.g227350.t1.2	CCR4	Notcomplex component	n/a	O	0	0	0	0	0	11
Cre12.g518650.t1.1	BHSD1	Steroid dehydrogenase	n/a	O	3	4	4	0	0	0
Cre05.g242000.t1.1	CHLD	Magnesium chelatase subunit D	n/a	C	2	4	5	0	0	0
Cre07.g345350.t1.2	-	*Pfam:00249 Myb-like DNA-binding domain*	n/a	O	0	0	0	0	0	10
Cre01.g070900.t1.1	-	*(no conserved domains)*	n/a	M	0	0	1	0	0	9
Cre01.g024950.t1.1	-	*Panther:12444 Uncharacterized*	n/a	O	3	6	1	0	0	0
Cre05.g234100.t1.1	CYP745A1	cytochrome P450	n/a	SP	5	4	1	0	0	0
Cre06.g255950.t1.2	-	WD40 repeat protein	n/a	O	8	2	0	0	0	0
Cre15.g645950.t1.1	CYP97A5	*Cytochrome P450. CYP97A3 of Arabidopsis is a carotenoid betaring hydroxylase [PMID: 16492736]. CYP97C1 of Arabidopsis (LUT1) is a carotenoid epsilonring hydroxylase [PMID: 14709673]*	n/a	C	5	4	1	0	0	0

References

Tardif, M., Atteia, A., Specht, M., Cogne, G., Rolland, N., Brugiere, S., Hippler, M., Ferro, M., Bruley, C., Peltier, G., Vallon, O., and Cournac, L. (2012). PredAlgo: a new subcellular localization prediction tool dedicated to green algae. Molecular biology and evolution **29,** 3625-3639.

Terashima, M., Specht, M., and Hippler, M. (2011). The chloroplast proteome: a survey from the Chlamydomonas reinhardtii perspective with a focus on distinctive features. Current genetics **57,** 151-168.

Supplemental Table 2: Provided seperately as compressed file

Supplemental Table 3: Representative phosphopeptides derived from photosynthetic complexes and other proteins relevant to the manuscript.

Peptides quantified by pyQMS are highlighted in bold. Subscripts denote the position of phosphorylation sites within the polypeptide sequences. Ambiguous phosphorylation sites (PhosphoRS site probabilities <95%) are indicated by italic letters. Phosphorylation sites with probabilities < 5 % are not annotated. Site probabilities are presented for every possible acceptor with numbers given in brackets indicating their positions within respective peptides. #P, number of phosphorylations.

			PhosphoRS	
Protein	**Peptide**	**# P**	**Peptide Score**	**Site Probabilities**
PSAG	EANFD*S*$_{65}$*T*$_{66}$VGPK	1	121.058711	S(6): 94.0; T(7): 6.0
	EANFDST$_{66}$VGPK	1	115.722028	S(6): 0.5; T(7): 99.5
	EANFDS$_{65}$T$_{66}$VGPK	2	92.9285023	S(6): 100.0; T(7): 100.0
	T$_{71}$T$_{72}$GATYFDDLQK	1	148.237485	T(1): 5.0; T(2): 95.0; T(5): 0.0; Y(6): 0.0
PSAH	**YFDLQDM(ox)EN*T*$_{47}$*T*$_{48}$G*S*$_{50}$WDM(ox)YGVDEK**	1	127.592236	Y(1): 0.0; T(10): 8.7; T(11): 82.5; S(13): 8.7; Y(17): 0.0
	YFDLQDMENTTGS$_{50}$WDMYGVDEK	1	254.909514	Y(1): 0.0; T(10): 0.0; T(11): 0.0; S(13): 100.0; Y(17): 0.0
	YFDLQDMENT$_{47}$*T*$_{48}$G*S*$_{50}$WDMYGVDEK	2	123.392283	Y(1): 0.0; T(10): 99.9; T(11): 90.5; S(13): 9.6; Y(17): 0.0
	YFDLQDMENTT$_{48}$GS$_{50}$WDMYGVDEK	2	215.596742	Y(1): 0.0; T(10): 0.1; T(11): 100.0; S(13): 100.0; Y(17): 0.0
PSBB (CP47)	LGDTSS$_{503}$LREAF	1	160.650097	T(4): 0.0; S(5): 0.0; S(6): 100.0
PSBC (CP43)	***Ac*-T$_{3}$LFNGTLTVGGR**	1	109.558396	T(1): 100.0; T(6): 0.0; T(8): 0.0
	Ac-T$_{3}$LFNGT$_{8}$LTVGGR	2	93.2852333	T(1): 100.0; T(6): 99.9; T(8): 0.1
	GIDRFDEPVLS$_{456}$MRPLD	1	218.012454	S(11): 100.0
	GIDRFDEPVLS$_{456}$M(ox)RPLD	1	271.487046	S(11): 100.0
PSBD (D2)	**T$_{2}$IAIGTYQEK**	1	145.509962	T(1): 100.0; T(6): 0.0; Y(7): 0.0
	***Ac*-T$_{2}$IAIGTYQEK**	1	106.207208	T(1): 100.0; T(6): 0.0; Y(7): 0.0
	***Ac*-T$_{2}$IAIGTYQEKR**	1	151.864527	T(1): 100.0; T(6): 0.0; Y(7): 0.0
PSBO	**LTYTLDAM(ox)SGS$_{138}$FK**	1	176.240501	T(2): 0.0; Y(3): 0.0; T(4): 0.0; S(9): 0.0; S(11): 100.0
	VGS$_{143}$DGSAELKEDDGIDYAATTVQLPGGER	1	206.182797	S(3): 100.0; S(6): 0.0; Y(17): 0.0; T(20): 0.0; T(21): 0.0
PSBR	***T*$_{31}$DI*T*$_{34}$KVGLNSIEDPVVK**	1	192.884307	T(1): 94.5; T(4): 5.5; S(10): 0.0
	TDITKVGLNS$_{40}$IEDPVVK	1	209.641177	T(1): 0.0; T(4): 0.0; S(10): 100.0
	VGLNS$_{40}$IEDPVVK	1	157.800229	S(5): 100.0
	VGLNS$_{40}$IEDPVVKQNLMGK	1	241.265723	S(5): 100.0
	VGLNS$_{40}$IEDPVVKQNLM(ox)GK	1	205.191116	S(5): 100.0

STT7	*T*$_{489}$A*S*$_{491}$LQH*S*$_{495}$LSGSFEATVSTAAAATSTALTAAGK	1	99.5789068	T(1): 71.0; S(3): 13.1; S(7): 13.1; S(9): 2.5; S(11): 0.1; T(15): 0.1; S(17): 0.0; T(18): 0.0; T(23): 0.0; S(24): 0.0; T(25): 0.0; T(28): 0.0
	DAGLAS$_{533}$MEEAILK	1	209.096439	S(6): 100.0
	DAGLAS$_{533}$M(ox)EEAILK	1	197.119206	S(6): 100.0
	EGSQT$_{571}$IAWWQER	1	137.095954	S(3): 0.0; T(5): 100.0
STL1	**LQADDQGVT$_{126}$QR**	1	73.3515186	T(21): 97.3; S(23): 2.7
Cre01.g071450.t1.2 (STN8)	**SSGGS$_{426}$IDLTPAAAAASNR**	1	157.630963	S(1): 0.1; S(2): 0.1; S(5): 99.8; T(9): 0.1; S(16): 0.0
	S$_{422}$*S*$_{423}$GGS$_{426}$IDLTPAAAAASNR	2	127.685977	S(1): 50.0; S(2): 50.0; S(5): 100.0; T(9): 0.0; S(16): 0.0
	RQPS$_{753}$ATPEQVQAQAAAAQQQQAAPQR	1	203.063475	S(4): 0.9; T(6): 99.1
	AGS$_{814}$SSQSAAQPQQQMPR	1	169.538124	S(3): 99.6; S(4): 0.4; S(5): 0.0; S(7): 0.0
PGRL1	KDDGYIS$_{50}$EDEGLGNVAADYCAIDGAGK	1	148.687556	T(9): 100.0
LHCSR3	*S*$_{26}$V*S*$_{28}$GRRTTAAEPQTAAPVAAEDVFAYTK	1	254.906376	S(1): 50.0; S(3): 50.0; T(7): 0.0; T(8): 0.0; T(14): 0.0; Y(26): 0.0; T(27): 0.0
	S$_{26}$VS$_{28}$GRRTTAAEPQTAAPVAAEDVFAYTK	2	270.541763	S(1): 99.0; S(3): 99.0; T(7): 1.0; T(8): 1.0; T(14): 0.0; Y(26): 0.0; T(27): 0.0
	***S*$_{26}$V*S*$_{28}$GRRTT$_{33}$AAEPQTAAPVAAEDVFAYTK**	2	227.116185	S(1): 49.8; S(3): 49.8; T(7): 1.2; T(8): 99.2; T(14): 0.0; Y(26): 0.0; T(27): 0.0
	S$_{26}$V*S*$_{28}$GRRT$_{32}$T$_{33}$AAEPQTAAPVAAEDVFAYTK	3	225.242936	S(1): 50.2; S(3): 50.2; T(7): 99.6; T(8): 100.0; T(14): 0.0; Y(26): 0.0; T(27): 0.0
	***T*$_{32}$*T*$_{33}$AAEPQTAAPVAAEDVFAYTK**	1	182.489305	T(1): 6.8; T(2): 92.6; T(8): 0.5; Y(20): 0.0; T(21): 0.0
	R*T*$_{32}$*T*$_{33}$AAEPQTAAPVAAEDVFAYTK	1	213.488758	T(2): 93.5; T(3): 6.5; T(9): 0.0; Y(21): 0.0; T(22): 0.0
	R*T*$_{32}$*T*$_{33}$AAEPQT$_{39}$AAPVAAEDVFAYTK	2	229.517291	T(2): 93.7; T(3): 6.3; T(9): 100.0; Y(21): 0.0; T(22): 0.0
	RT$_{32}$T$_{33}$AAEPQTAAPVAAEDVFAYTK	2	252.243546	T(2): 100.0; T(3): 100.0; T(9): 0.0; Y(21): 0.0; T(22): 0.0
	EAILELDDIERDLGLPVTPLPDNLKS$_{258}$L	1	215.522415	T(18): 0.0; S(26): 100.0
	DLGLPVTPLPDNLKS$_{258}$L	1	221.09868	T(7): 0.0; S(15): 100.0
	DLGLPVT$_{250}$PLPDNLKS$_{258}$L	2	121.2829635	T(7): 100.0; S(15): 100.0
LHCA6	**KPGS$_{137}$VDQDPIFSQYK**	1	151.029756	S(4): 100.0; S(12): 0.0; Y(14): 0.0
LHCB4	Ac-VFKFPT$_{7}$PPGTQK	1	77.0006581	T(6):100.0;T(10):0.0
	Ac-VFKFPTPPGT$_{11}$QK	1	74.4817163	T(6):0.0;T(10):100.0
	Ac-VFKFPT$_{7}$PPGT$_{11}$QK	2	82.4913734	T(6):100.0;T(10):100.0
	FPTPPGT$_{11}$QK	1	170.7701	T(3):0.0;T(7):100.0
	FPT$_{7}$PPGTQK	1	134.146695	T(3):100.0;T(7):0.0
	FPT$_{7}$PPGT$_{11}$QK	2	146.61926	T(3): 100.0; T(7): 100.0
	AGT$_{17}$TATKPAPK	1	132.887942	T(3):100.0;T(4):0.0;T(6):0.0
	AGT$_{17}$T$_{18}$ATKPAPK	2	64.8200002	T(3):99.8;T(4):98.6;T(6):1.6
	AT$_{27}$T$_{28}$KKVATSTGTR	2	112.125371	T(2): 100.0; T(3): 100.0; T(8): 0.0; S(9): 0.0; T(10): 0.0; T(12): 0.0
	KVATS$_{35}$*T*$_{36}$GTRSGGVGYR	2	104.915493	T(4): 1.0; S(5): 98.3; T(6): 91.7; T(8): 9.0; S(10): 0.0; Y(15): 0.0
	VATS$_{35}$TGT$_{38}$RSGGVGYR	2	148.307042	T(3):0.5;S(4):99.1;T(5):0.5;T(7):99.5;S(9):0.5;Y(14):0.0
	VAT$_{34}$*ST*$_{36}$G*T*$_{38}$RSGGVGYR	2	151.074686	T(3): 99.5; S(4): 0.5; T(5): 6.4; T(7): 93.5; S(9): 0.0; Y(14): 0.0
	Gs$_{103}$VEAIVQATPDEVSSENR	1	177.527749	S(2): 100.0; T(10): 0.0; S(15): 0.0; S(16): 0.0
	GSVEAIVQATPDEVS$_{116}$SENR	1	147.370844	S(2):0.0;T(10):0.0;S(15):99.5;S(16):0.5

	NNKGS$_{103}$VEAIVQATPDEVSSENR	1	285.651331	S(5):100.0;T(13):0.0;S(18):0.0;S(19):0.0
	NNKGS$_{103}$VEAIVQATPDEV*S*$_{116}$*S*$_{117}$ENR	1	213.018701	S(5): 100.0; T(13): 0.0; S(18): 93.6; S(19): 6.4
Lhcbm5	**AAPASAQKKT$_{33}$IR**	2	178.131485	S(5): 0.0; T(10): 100.0
PetO	KAEVVE*S*$_{107}$*T*$_{108}$*S*$_{109}$GGLDPR	1	166.048475	S(7): 33.3; T(8): 33.3; S(9): 33.3
	IDGS$_{139}$FNDWFM(ox)EAVVR	1	130.074065	S(4): 100.0
	DSNNYAGYEAT$_{161}$LKSENGVTFPK	1	217.76082	S(2): 0.0; Y(5): 0.0; Y(8): 0.0; T(11): 100.0; S(14): 0.0; T(19): 0.0
	DSNNYAGYEATLKS$_{164}$ENGVTFPK	1	247.254223	S(2): 0.0; Y(5): 0.0; Y(8): 0.0; T(11): 0.0; S(14): 100.0; T(19): 0.0
	DSNNYAGYEAT$_{161}$LKS$_{164}$ENGVTFPK	2	176.332496	S(2): 0.0; Y(5): 0.0; Y(8): 0.0; T(11): 100.0; S(14): 100.0; T(19): 0.0
	SENGVT$_{169}$FPK	1	105.89249	S(1): 0.0; T(6): 100.0
	AATGS$_{187}$KKGGFPFGGK	1	95.2531449	T(3): 0.0; S(5): 100.0
	AAT$_{185}$GS$_{187}$KKGGFPFGGK	2	116.605432	T(3): 100.0; S(5): 100.0
Cytb6f-IV	**SVT$_{4}$KKPDLSDPVLK**	1	160.98424	S(1): 0.3; T(3): 99.7; S(9): 0.0
TEF23 (EGY1)	TLEGLDALLGIDPNDPKAGT$_{71}$GSSASTK	1	176.091281	T(1): 0.0; T(20): 97.9; S(22): 1.0; S(23): 1.0; S(25): 0.1; T(26): 0.0
	S$_{79}$ATAVAESVSSDAAR	1	118.678653	S(1): 99.2; T(3): 0.8; S(8): 0.0; S(10): 0.0; S(11): 0.0
	SATAVAES$_{86}$VSSDAAR	1	170.883664	S(1): 0.0; T(3): 0.0; S(8): 99.7; S(10): 0.3; S(11): 0.0
TEF1	TGGS$_{812}$VDQLLEEVTRR	1	89.5860978	T(1): 0.0; S(4): 100.0; T(13): 0.0
	HALGLTEAEASEIAVTAS$_{995}$LDEAAGGPK	1	203.909006	T(6): 0.0; S(11): 0.0; T(16): 0.0; S(18): 100.0
TEF10a	QGS$_{55}$MPNQMEMVR	1	135.992544	S(3): 100.0
Rh protein	**S$_{483}$HHNQSVSVGQLNPIR**	1	186.107204	S(1): 99.6; S(6): 0.4; S(8): 0.0
	SHHNQS$_{488}$VSVGQLNPIR	1	141.380957	S(1): 0.5; S(6): 99.5; S(8): 0.0
	SHHNQS$_{488}$VS$_{490}$VGQLNPIR	2	160.23552	S(1): 0.0; S(6): 100.0; S(8): 100.0
	SHHNQSVS$_{490}$VGQLNPIR	1	209.083848	S(1): 0.0; S(6): 0.0; S(8): 100.0
Cre09.g398400.t1.1 (TRP5)	TDGGATAEGQPMAATYGS$_{339}$FR	1	180.821621	T(1):0.0;T(6):0.0;T(15):0.0;Y(16):0.0;S(18):100.0
	T$_{342}$N*S*$_{344}$GVNGEAEDSNAFASVASHGLQIGENQDSGR	1	89.9056245	T(1):84.9;S(3):15.1;S(12):0.0;S(17):0.0;S(20):0.0;S(31):0.0
	QGD*T*$_{610}$AS$_{612}$*S*$_{613}$AVLDQAVEIEADTR	2	122.575676	T(4):91.1;S(6):99.1;S(7):9.8;T(20):0.0
	ADLDRTS$_{640}$RPLS$_{644}$VPNMPENLR	2	160.482517	T(6):0.8;S(7):99.2;S(11):100.0
	ADLDRTS$_{640}$RPLSVPNMPENLR	1	79.9466685	T(6):2.0;S(7):95.9;S(11):2.0
	TSRPLS$_{644}$VPNMPENLR	1	176.396511	T(1):0.0;S(2):0.0;S(6):100.0
	ADQVS$_{1058}$IGLAS$_{1063}$DDESNPILQHPR	2	220.305797	S(5):100.0;S(10):100.0;S(14):0.0
	ADQVSIGLAS$_{1063}$DDESNPILQHPR	1	229.866278	S(5):0.0;S(10):100.0;S(14):0.0
LCI2	**EYREDTGEVTAPGAS$_{57}$QTTR**	1	161.549477	Y(2):0.0;T(6):0.0;T(10):0.0;S(15):99.9;T(17):0.1;T(18):0.1
	EYREDTGEVTAPGASQT$_{59}$TR	1	156.844873	Y(2):0.0;T(6):0.0;T(10):0.0;S(15):0.7;T(17):99.3;T(18):0.1
	EYREDTGEVTAPGASQT$_{59}$T$_{60}$RR	2	93.0978002	Y(2):0.0;T(6):0.0;T(10):0.0;S(15):0.4;T(17):99.8;T(18):99.8
	RES$_{64}$DGLYVNADGPRPVPR	1	107.791414	S(3):100.0;Y(7):0.0
ALB3	APAT$_{325}$AGSSTPIVKPK	1	109.003645	T(4): 100.0; S(7): 0.0; S(8): 0.0; T(9): 0.0
	RNDDGEEVEDVEVEVVSSGSSSSSGSNGAS$_{384}$GR	1	233.551481	S(17): 0.0; S(18): 0.0; S(20): 0.0; S(21): 0.0; S(22): 0.0; S(23): 0.0; S(24): 0.0; S(26): 0.1; S(30): 99.9

	AASTVSAGAGGS$_{414}$EEGKDNSA	1	207.799917	S(3): 0.0; T(4): 0.0; S(6): 0.0; S(12): 100.0; S(19): 0.0
Cre12.g540700.t1.2	**KTAASSTPSTPGGS$_{63}$PPGTASSRPPPPPR**	1	189.470532	T(2): 0.0; S(5): 0.0; S(6): 0.0; T(7): 0.0; S(9): 0.0; T(10): 0.0; S(14): 100.0; T(18): 0.0; S(20): 0.0; S(21): 0.0
	KTAASSTPSTPGGS$_{63}$PPGT$_{67}$ASSRPPPPPR	2	147.246889	T(2): 0.0; S(5): 0.0; S(6): 0.0; T(7): 0.0; S(9): 0.2; T(10): 0.2; S(14): 99.6; T(18): 99.8; S(20): 0.2; S(21): 0.0
	KTAASSTPSTPGGSPPGT$_{67}$ASSRPPPPPR	1	195.195174	T(2): 0.0; S(5): 0.0; S(6): 0.0; T(7): 0.0; S(9): 0.0; T(10): 0.0; S(14): 0.0; T(18): 100.0; S(20): 0.0; S(21): 0.0
	TAASSTPSTPGGS$_{63}$PPGTASSRPPPPPR	1	153.717857	T(1): 0.0; S(4): 0.0; S(5): 0.0; T(6): 0.0; S(8): 0.0; T(9): 0.1; S(13): 99.8; T(17): 0.0; S(19): 0.0; S(20): 0.0
	TAASSTPSTPGGS$_{63}$PPGT$_{67}$ASSRPPPPPR	2	153.382944	T(1): 0.0; S(4): 0.0; S(5): 0.0; T(6): 0.0; S(8): 0.0; T(9): 0.2; S(13): 99.8; T(17): 99.8; S(19): 0.2; S(20): 0.0
	TA**ASSTPS$_{58}$T$_{59}$PGGSPPGT$_{67}$ASSRPPPPPR**	3	174.66505	T(1): 0.0; S(4): 0.0; S(5): 0.0; T(6): 0.2; S(8): 98.8; T(9): 98.8; S(13): 2.1; T(17): 100.0; S(19): 0.0; S(20): 0.0
Cre17.g724150	**ALDGASSLDDVLLGTGS$_{597}$R**	1	235.317382	S(6): 0.0; S(7): 0.0; T(15): 0.0; S(17): 100.0
	ALDGASS$_{587}$LDDVLLGTGS$_{597}$R	2	197.994692	S(6): 0.0; S(7): 100.0; T(15): 0.0; S(17): 100.0
Cre16.g668600.t1.1	VSLDQTPDS$_{219}$PLGSVNSIDQLLGTVSDSEETIGDK	1	185.449621	S(2): 0.0; T(6): 0.0; S(9): 99.8; S(13): 0.2; S(16): 0.0; T(23): 0.0; S(25): 0.0; S(27): 0.0; T(30): 0.0
	VSLDQTPDS$_{219}$PLGSVNSIDQLLGTVSDSEETIGDKLALK	1	175.122161	S(2): 0.0; T(6): 0.0; S(9): 99.7; S(13): 0.3; S(16): 0.0; T(23): 0.0; S(25): 0.0; S(27): 0.0; T(30): 0.0
	VSLDQTPDS$_{219}$PLGSVNSIDQLLGTVS$_{235}$DSEETIGDKLALK	2	133.725948	S(2): 0.0; T(6): 0.0; S(9): 99.4; S(13): 0.3; S(16): 0.3; T(23): 0.3; S(25): 97.8; S(27): 1.9; T(30): 0.0
	VSLDQTPDSPLGS$_{223}$VNSIDQLLGTVS$_{235}$DSEETIGDK	2	96.1133108	S(2): 0.0; T(6): 0.1; S(9): 0.4; S(13): 96.9; S(16): 2.5; T(23): 2.5; S(25): 95.0; S(27): 2.5; T(30): 0.0
PGM1b	**AVGLPSDADMGNS$_{148}$EVGHNALGSGQVVDQGAR**	1	164.404607	S(6): 0.0; S(13): 100.0; S(22): 0.0
Cre26.g773100.t1.1 (Fibrillin)	KLESAAT$_{296}$VAER	1	132.01026	S(4): 0.0; T(7): 100.0
	VAVAP*S*$_{320}$RQG*S*$_{324}$T$_{325}$KVAVAPPSRPGS$_{337}$GK	3	111.781445	S(6): 11.8; S(10): 88.4; T(11): 99.8; S(19): 1.8; S(23): 98.2
	QG*S*$_{324}$*T*$_{325}$KVAVAPPSRPGSGK	1	133.099006	S(3): 91.3; T(4): 8.7; S(12): 0.0; S(16): 0.0
	QG*S*$_{324}$TKVAVAPPS$_{333}$RPGS$_{337}$GK	3	44.5661717	S(3): 87.6; T(4): 12.5; S(12): 99.9; S(16): 100.0
	QG*S*$_{324}$*T*$_{325}$KVAVAPPS$_{333}$RPGS$_{337}$GKVAVAPAAPAR	3	88.4543771	S(3): 50.1; T(4): 50.1; S(12): 99.8; S(16): 100.0
	VAVAPPS$_{333}$RPGSGKVAVAPAAPAR	1	191.460996	S(7): 99.3; S(11): 0.7
	VAVAPPS$_{333}$RPGs$_{337}$GKVAVAPAAPAR	2	170.550444	S(7): 100.0; S(11): 100.0
	VAVAPPSRPGS$_{337}$GK	1	208.761831	S(7): 0.0; S(11): 100.0
	VAVAPPS$_{333}$RPGS$_{337}$GK	2	141.364916	S(7): 100.0; S(11): 100.0
	VAVAPAAPARS$_{350}$AS$_{352}$VR	2	131.504347	S(11): 100.0; S(13): 100.0
Cre20.g759250 (PF07059)	***Ac*-SGDDPETS$_{9}$FHFQAVQQPR**	1	136.027337	S(1): 0.0; T(7): 0.8; S(8): 99.2
	Ac-S$_{2}$GDDPE*T*$_{8}$*S*$_{9}$FHFQAVQQPR	2	98.4391931	S(1): 100.0; T(7): 9.2; S(8): 90.8
	WT$_{21}$RAES$_{25}$LGDAANLVLEGK	2	162.557741	T(2): 100.0; S(6): 100.0
	AES$_{25}$LGDAANLVLEGK	1	193.160292	S(3): 100.0
	S$_{216}$NSMAAPFANTAAAAAAAGSASTR	1	168.011681	S(1): 99.1; S(3): 0.9; T(11): 0.0; S(20): 0.0; S(22): 0.0; T(23): 0.0
	SNSM(ox)AAPFANT$_{226}$AAAAAAAGSASTR	1	116.001038	S(1): 0.0; S(3): 0.0; T(11): 99.8; S(20): 0.2; S(22): 0.0; T(23): 0.0
	VGs$_{595}$ETTAATAAAAATIAR	1	217.620392	S(3): 100.0; T(5): 0.0; T(6): 0.0; T(9): 0.0; T(15): 0.0
Cre06.g261750.t1.1	**SVS$_{359}$PQPDVAK**	1	180.823896	S(1): 0.0; S(3): 100.0
	S$_{357}$VS$_{359}$PQPDVAK	2	131.708728	S(1): 100.0; S(3): 100.0

(Bestrophin)	**AGVGAVAPGAPLM(ox)PQAPVRSPSPT$_{400}$R**	1	177.723555	S(20): 0.0; S(22): 0.0; T(24): 100.0
	SPS$_{398}$PTRS$_{402}$VS$_{404}$PSFPR	3	95.4008966	S(1): 0.5; S(3): 98.9; T(5): 1.1; S(7): 99.4; S(9): 99.4; S(11): 0.6
	SPSPT$_{400}$RS$_{402}$VSPSFPR	2	113.176274	S(1): 0.0; S(3): 0.0; T(5): 99.6; S(7): 99.6; S(9): 0.7; S(11): 0.0
	SVS$_{404}$PSFPR	1	133.275124	S(1): 0.0; S(3): 100.0; S(5): 0.0
	S$_{585}$**R*S*$_{587}$GNGGGGSSDTELSEANRPR**	1	187.002052	S(1): 93.1; S(3): 6.9; S(10): 0.0; S(11): 0.0; T(13): 0.0; S(16): 0.0
	SGNGGGGS$_{594}$SDTELSEANRPR	1	129.579849	S(1): 0.7; S(8): 98.5; S(9): 0.7; T(11): 0.0; S(14): 0.0
	S$_{585}$RS$_{587}$GNGGGGSSDTELSEANRPR	2	74.7590117	S(1): 100.0; S(3): 99.3; S(10): 0.3; S(11): 0.3; T(13): 0.1; S(16): 0.0
	S$_{587}$GNGGGGSSDTELSEANRPR	1	130.496507	S(1): 100.0; S(8): 0.0; S(9): 0.0; T(11): 0.0; S(14): 0.0
CDS1	**AQNGEGMDPPSGEP*S*$_{101}$*S*$_{102}$K*S*$_{104}$GSALDLR**	2	148.997659	S(11): 0.0; S(15): 91.1; S(16): 91.2; S(18): 15.6; S(20): 2.1
	AQNGEGM(ox)DPPSGEP *S*$_{101}$*S*$_{102}$K*S*$_{104}$GSALDLR	2	157.545892	S(11): 0.0; S(15): 90.9; S(16): 90.9; S(18): 15.9; S(20): 2.2
HSP70B	RMS$_{117}$EVGSESTQVPYR	1	163.44525	S(3): 100.0; S(7): 0.0; S(9): 0.0; T(10): 0.0; Y(14): 0.0
Cre17.g737450.t1.2	**ISAGAQAS$_{2481}$PTVS$_{2485}$QGPAR**	2	99.1102601	S(2): 0.0; S(8): 98.9; T(10): 1.2; S(12): 99.9
	ISAGAQA*S*$_{2481}$P*T*$_{2486}$VSQGPAR	1	162.381103	S(2): 0.0; S(8): 48.4; T(10): 48.4; S(12): 3.2
Cre06.g284100.t1.1	**S$_{483}$HHNQSVSVGQLNPIR**	1	186.107204	S(1): 99.6; S(6): 0.4; S(8): 0.0
	SHHNQS$_{488}$VSVGQLNPIR	1	141.380957	S(1): 0.5; S(6): 99.5; S(8): 0.0
	SHHNQSVS$_{490}$VGQLNPIR	1	209.083848	S(1): 0.0; S(6): 0.0; S(8): 100.0
	SHHNQS$_{488}$VS$_{490}$VGQLNPIR	2	160.23552	S(1): 0.0; S(6): 100.0; S(8): 100.0