

## Supplementary Information

**Table S1.** Total number and average length of protein sequences in the analyzed algae proteomes.

Species	Number of Sequences		Average Protein Sequence Length after Filtering
	Before Filtering	After Filtering	
<i>O. sp. RCC809</i>	7773	7670	378
<i>O. tauri</i>	7725	7606	383
<i>M. sp. RCC299</i>	10,103	9956	471
<i>M. pusilla</i>	10,660	10,542	440
<i>C. sp. C-169</i>	9629	9367	423
<i>C. vulgaris</i>	9994	9760	401
<i>V. carteri</i>	14,542	13,852	562
<i>C. reinhardtii</i>	16,706	15,624	493
<i>P. ramorum</i>	15,743	13,354	487
<i>P. sojae</i>	19,027	16,643	496
<i>P. infestans</i>	22,658	18,825	394
<i>P. capsici</i>	17,414	16,411	382
<i>P. tricornutum</i>	10,387	10,036	457
<i>F. cylindrus</i>	27,143	19,908	403
<i>T. pseudonana</i>	11,637	11,452	490
<i>A. anophagefferens</i>	11,501	10,754	507
<i>E. siliculosus</i>	16,533	15,318	516
<i>C. merolae</i>	5014	4855	503
<i>P. yezoensis</i>	10,327	9859	288
<i>P. purpureum</i>	8355	7955	463

Data filtering was performed as described in Experimental Section.

**Table S2.** Preferences of multiple PTMs for protein disorder in species-specific and common protein clusters of each algae proteomes.

Species		Disorder	S-pho	T-pho	Y-pho	O-gly	N-gly	Ubi
Green algae	<i>O. sp. RCC809</i>	specific	38%	3.1	2.1	0.8	1.2	1.2
		common	17%	0.4	0.3	0.5	0.6	0.5
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	0.222	<0.05
		ratio of s/c	2.2	7.1	8.0	1.6	2.0	2.2
	<i>O. tauri</i>	specific	36%	4.0	2.4	0.6	1.8	0.7
		common	18%	0.5	0.3	0.5	0.6	0.5
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	0.213	<0.05
		ratio of s/c	2.0	8.3	7.9	1.2	3.1	1.4
	<i>M. sp. RCC299</i>	specific	41%	3.4	1.9	0.8	1.9	1.2
		common	20%	0.6	0.4	0.5	0.8	0.6
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	0.095	<0.05
		ratio of s/c	2.0	5.4	5.0	1.6	2.5	2.0
	<i>M. pusilla</i>	specific	45%	3.2	1.7	0.7	2.1	1.0
		common	20%	0.5	0.3	0.5	0.8	0.6
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	0.309	<0.05
		ratio of s/c	2.2	6.2	6.1	1.4	2.6	1.8
	<i>C. sp. C-169</i>	specific	36%	2.0	0.9	0.6	1.6	1.1
		common	19%	0.5	0.3	0.5	0.8	0.6
		<i>p</i> -value	<0.05	<0.05	0.143	<0.05	<0.05	<0.05
		ratio of s/c	1.9	4.3	3.1	1.2	2.1	2.0
	<i>C. vulgaris</i>	specific	42%	2.3	1.0	0.6	1.7	1.1
		common	20%	0.5	0.3	0.5	0.8	0.6
		<i>p</i> -value	<0.05	0.054	0.111	<0.05	<0.05	<0.05
		ratio of s/c	2.2	4.6	3.2	1.2	2.1	2.0

Table S2. Cont.

Species		Disorder	S-pho	T-pho	Y-pho	O-gly	N-gly	Ubi	
Green algae	<i>V. carteri</i>	specific	38%	2.3	1.1	0.7	1.9	2.3	0.7
		common	22%	0.6	0.3	0.5	0.9	1.2	0.5
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	1.7	4.0	3.3	1.5	2.0	1.9	1.3
	<i>C. reinhardtii</i>	specific	40%	2.3	1.1	0.7	2.1	1.9	0.6
		common	23%	0.6	0.3	0.5	1.0	1.1	0.5
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	0.053	0.059
		ratio of s/c	1.7	4.2	3.4	1.4	2.1	1.7	1.1
Oomycetes	<i>P. ramorum</i>	specific	31%	1.7	1.0	0.6	1.1	1.9	1.1
		common	19%	0.6	0.3	0.5	0.7	1.6	0.7
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	1.6	2.7	2.9	1.4	1.5	1.2	1.7
	<i>P. sojae</i>	specific	31%	1.9	1.0	0.6	1.2	2.2	1.0
		common	20%	0.7	0.4	0.5	0.8	1.2	0.7
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	0.201	<0.05
		ratio of s/c	1.5	2.7	2.9	1.4	1.6	1.9	1.5
	<i>P. infestans</i>	specific	23%	1.1	0.6	0.6	0.8	1.6	0.7
		common	20%	0.7	0.4	0.5	0.7	2.2	0.7
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	0.363	0.298
		ratio of s/c	1.2	1.6	1.6	1.4	1.2	0.7	1.0
	<i>P. capsici</i>	specific	23%	1.2	0.6	0.5	0.9	1.9	0.9
		common	18%	0.5	0.3	0.4	0.7	2.1	0.6
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	0.069	<0.05
		ratio of s/c	1.2	2.6	2.5	1.5	1.3	0.9	1.4

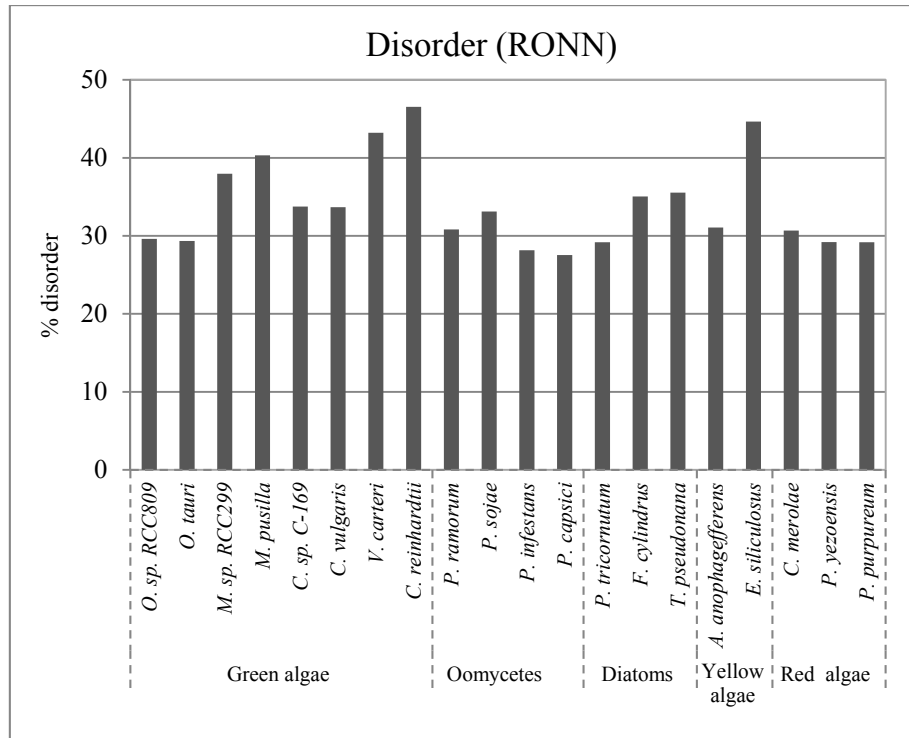
Table S2. Cont.

Species		Disorder	S-pho	T-pho	Y-pho	O-gly	N-gly	Ubi	
Diatoms	<i>P. tricornutum</i>	specific	30%	2.2	1.1	0.7	1.4	2.5	1.5
		common	17%	0.5	0.2	0.5	0.6	1.0	0.6
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	1.8	4.7	5.1	1.5	2.4	2.4	2.6
	<i>F. cylindrus</i>	specific	34%	1.8	0.9	0.7	0.9	3.1	1.7
		common	17%	0.4	0.2	0.4	0.5	1.3	0.8
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	2.2	5.7	5.4	1.8	2.3	2.4	3.1
	<i>T. pseudonana</i>	specific	37%	2.5	1.1	0.9	1.3	2.5	2.0
		common	17%	0.4	0.2	0.5	0.5	1.1	0.6
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	2.2	5.7	5.4	1.8	2.3	2.3	3.1
Yellow algae	<i>A. anophagefferens</i>	specific	27%	1.6	0.7	0.7	1.8	1.5	0.6
		common	16%	0.4	0.2	0.5	1.0	0.7	0.3
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	0.063	<0.05
		ratio of s/c	1.7	3.8	3.3	1.4	1.8	2.2	1.6
	<i>E. siliculosus</i>	specific	42%	3.1	1.5	0.6	1.4	1.2	1.2
		common	25%	1.2	0.5	0.5	0.9	0.9	0.7
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	1.7	2.7	2.9	1.3	1.7	1.3	2.4

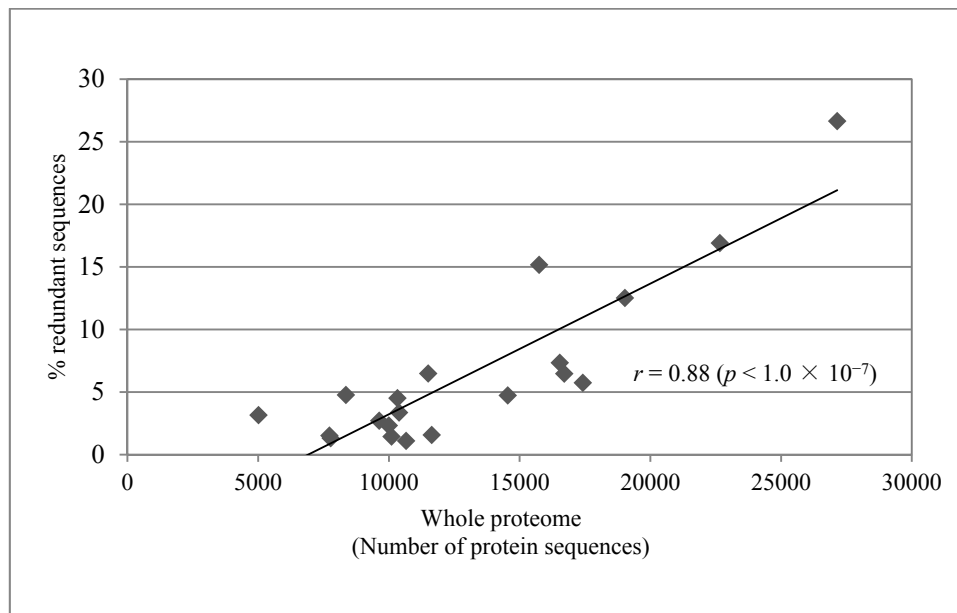
Table S2. *Cont.*

Species		Disorder	S-pho	T-pho	Y-pho	O-gly	N-gly	Ubi	
Red algae	<i>C. merolae</i>	specific	29%	1.9	1.1	0.6	1.4	2.9	0.8
		common	22%	0.9	0.5	0.5	0.9	2.0	0.5
		<i>p</i> -value	<0.05	0.084	<0.05	<0.05	<0.05	0.301	<0.05
		ratio of s/c	1.3	2.1	2.2	1.3	1.6	1.4	1.5
	<i>P. yezoensis</i>	specific	21%	1.3	0.8	0.6	1.6	1.2	0.4
		common	19%	0.8	0.5	0.5	1.3	1.1	0.3
		<i>p</i> -value	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05	<0.05
		ratio of s/c	1.1	1.6	1.5	1.2	1.2	1.1	1.6
	<i>P. purpureum</i>	specific	29%	1.9	0.8	0.6	1.1	2.0	1.3
		common	22%	0.7	0.3	0.5	0.7	1.1	0.7
		<i>p</i> -value	<0.05	0.342	0.053	<0.05	<0.05	0.081	<0.05
		ratio of s/c	1.3	2.6	2.5	1.1	1.4	1.8	1.8

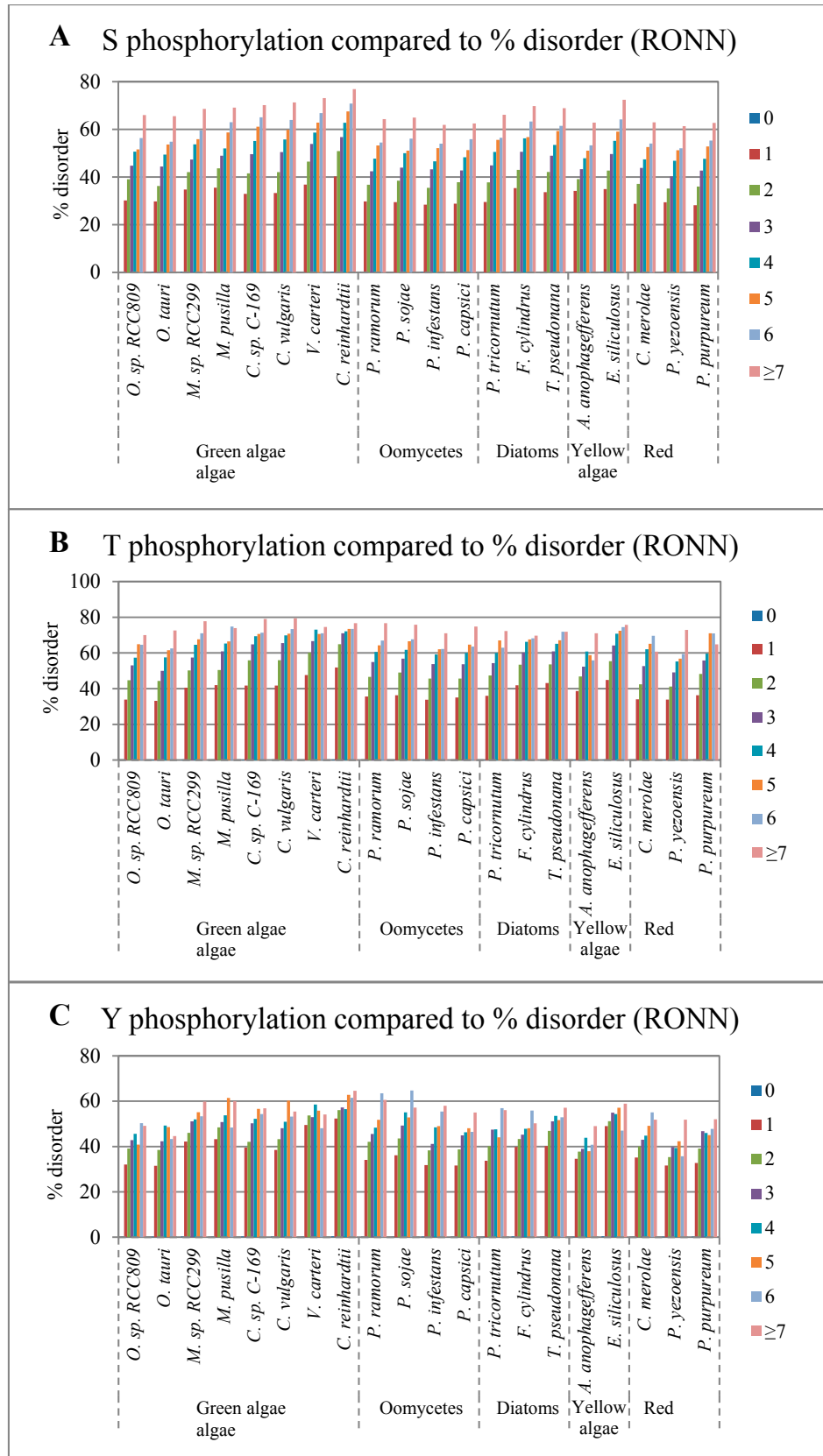
Total values of each parameter, *p*-value from t-test and Ratio of s/c (the value of specific/the value of common) are indicated.



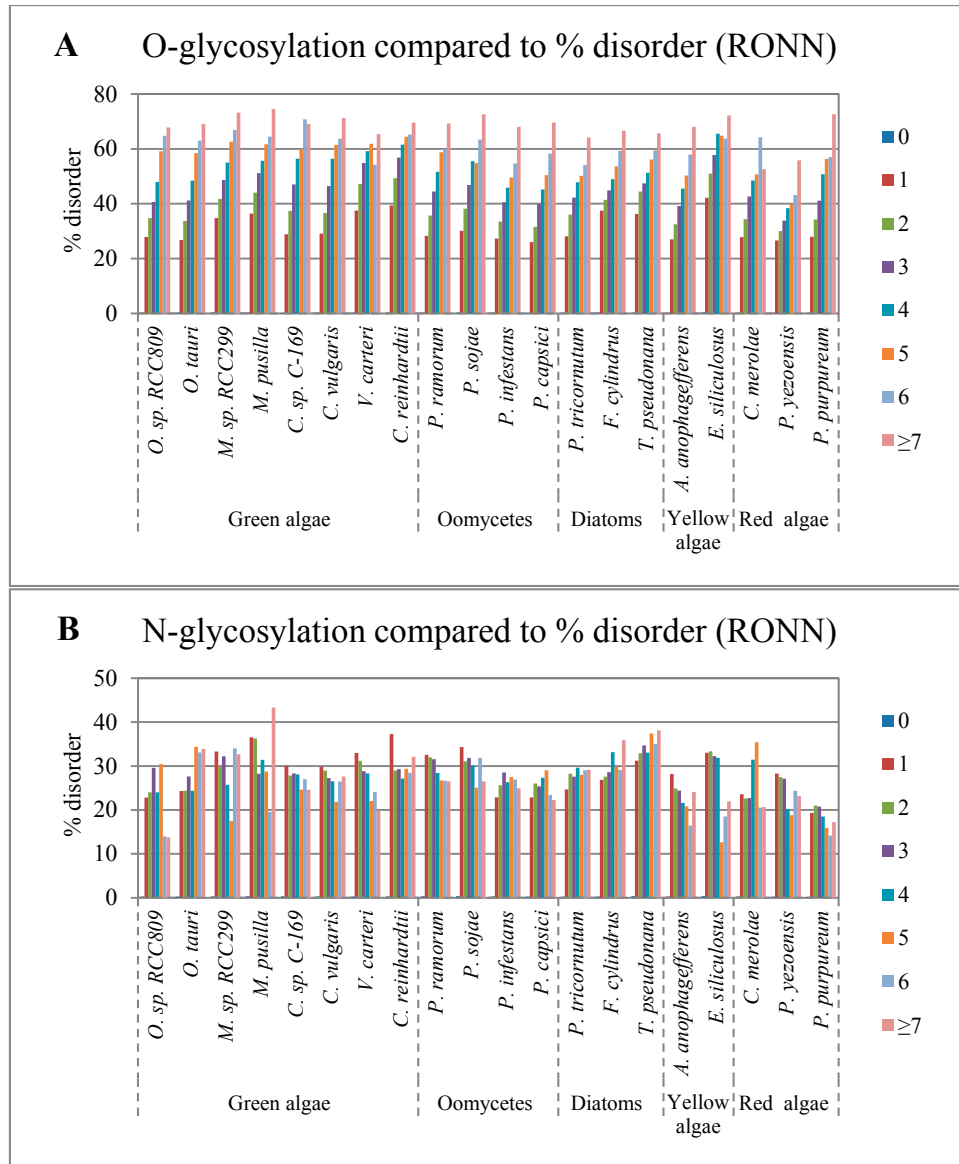
**Figure S1.** Predictive disordered protein content using the RONN tool in the studied algae proteomes.



**Figure S2.** Correlation between protein redundancy and proteome size. The percentage of redundant sequences of each algal species was calculated as the number of removed sequences divided by the number of sequences before filtering sequence redundancy. The numbers of sequences before and after filtering sequence redundancy are shown in Table S1. The correlation coefficient and one-tailed probability values are indicated.

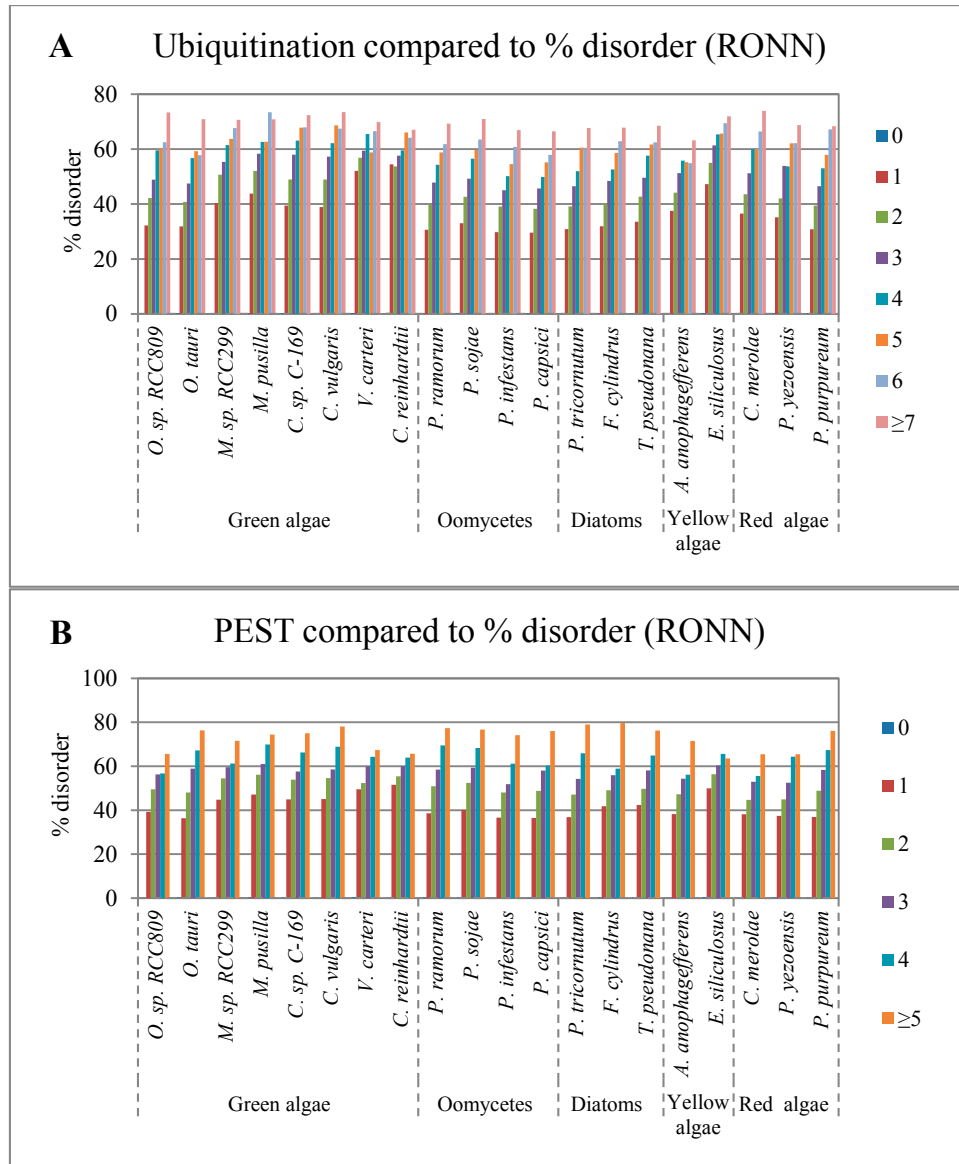


**Figure S3.** Correlation between disordered protein content and S/T/Y phosphorylation sites. Relative percentages of protein disorder calculated with the RONN tool with different numbers of predicted S, T, and Y phosphorylation sites, are presented in (A–C) respectively.

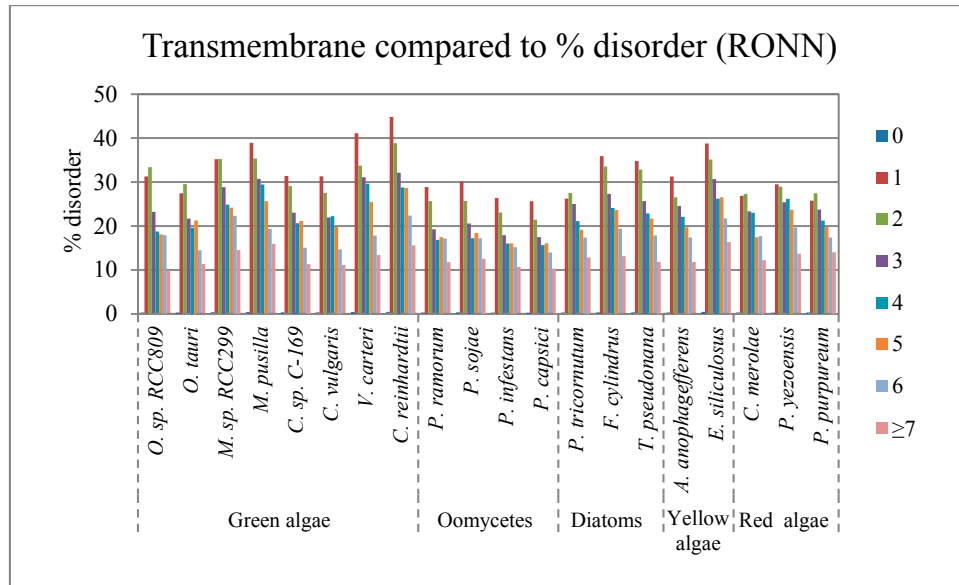


**Figure S4.** Correlation between disordered protein content and glycosylation. Relative percentages of protein disorder calculated with RONN tool with different numbers of predicted sites of O- and N-glycosylation, are presented in (A,B), respectively.





**Figure S5.** Correlations between disordered protein content and ubiquitination or PEST. Relative percentages of protein disorder calculated with RONN tool with different numbers of predicted sites of ubiquitination and predicted regions of PEST, are presented in (A,B), respectively.



**Figure S6.** Correlations between disordered protein content and transmembrane helices. Relative percentages of protein disorder calculated with RONN tool with different numbers of predicted regions transmembrane helices, are presented.