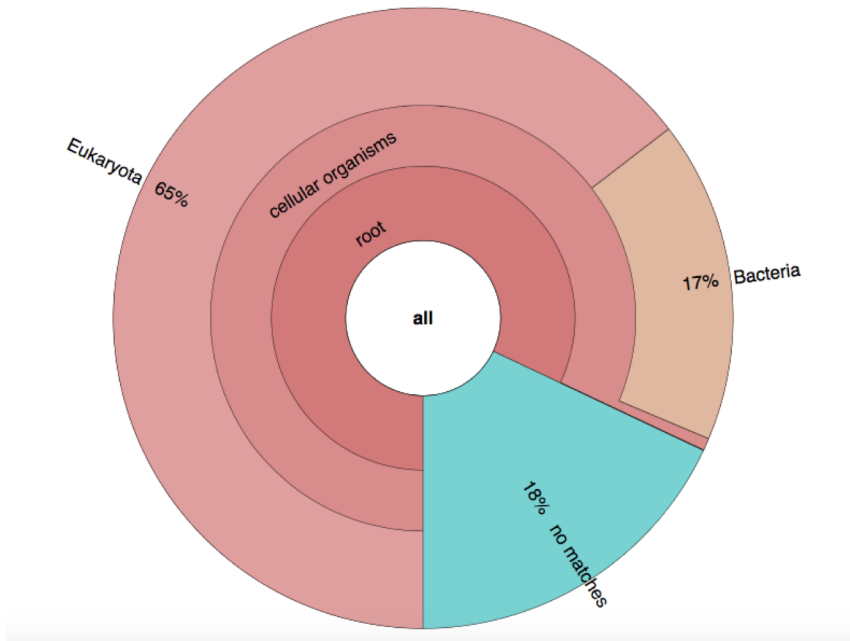
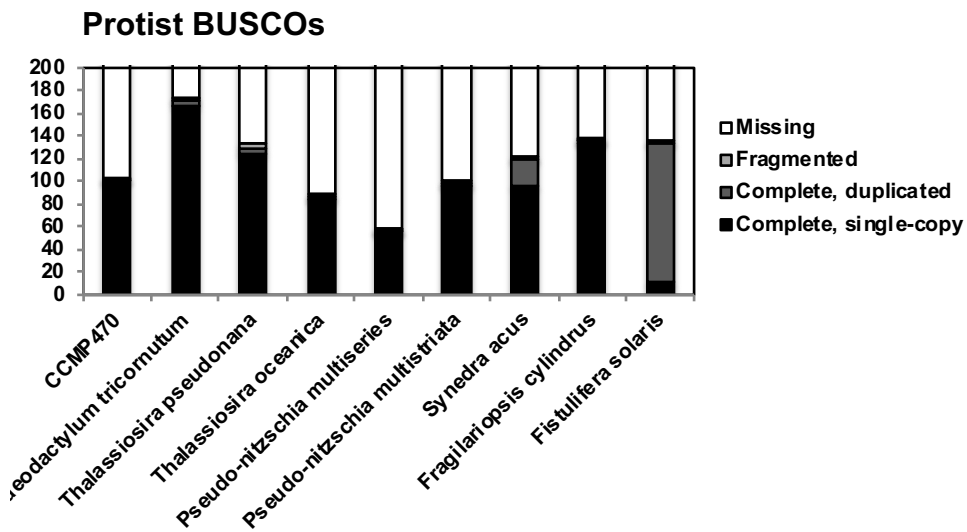
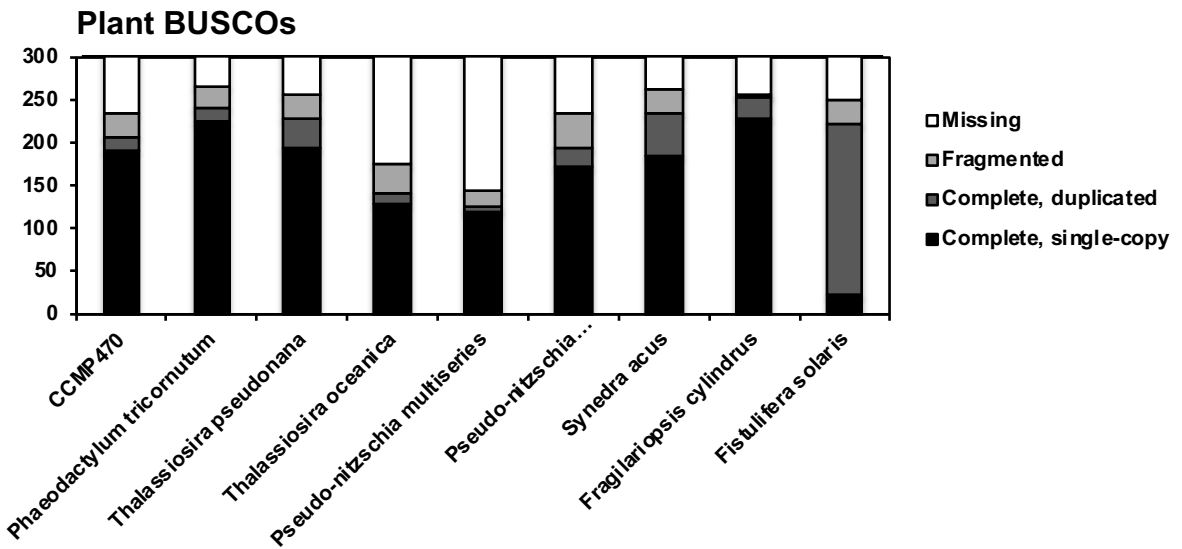


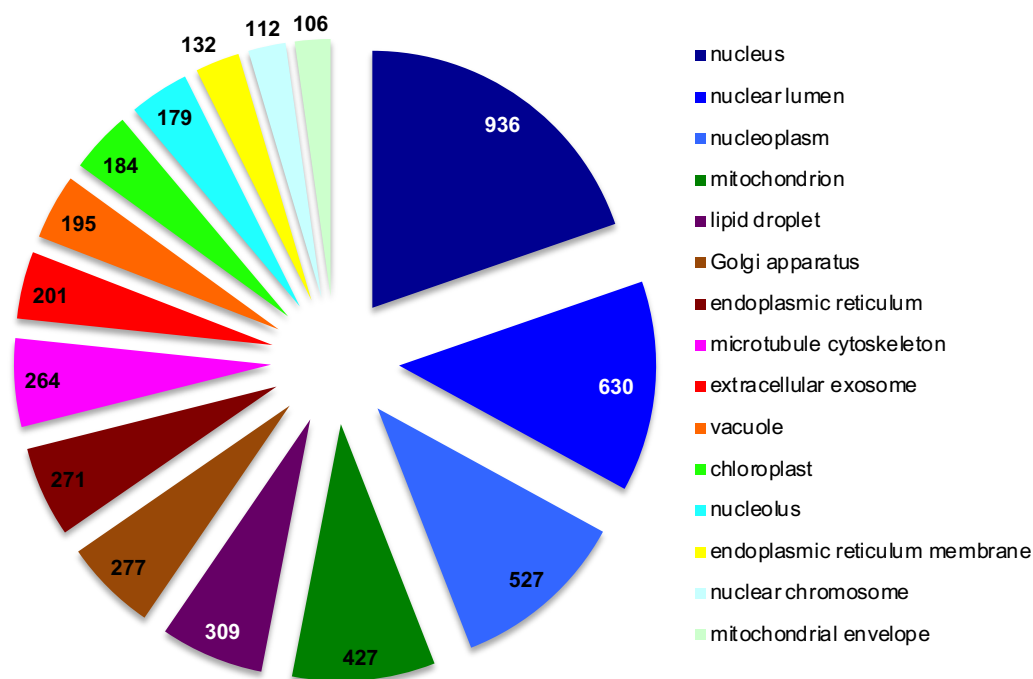
A)



B)



A)



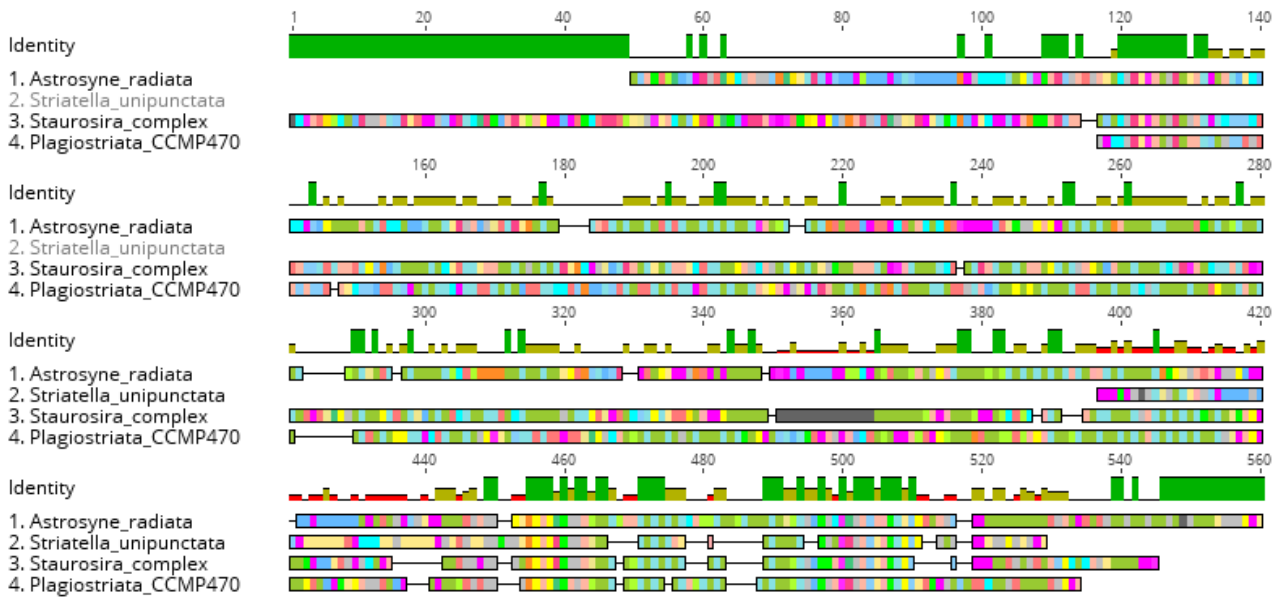
B)

Species	Fc	Pt	To	Tp	CCMP470	Key
PF00373	.	.	.	.	FERM domain	52
PF01306	.	.	.	.	LacY proton/sugar symporter	23
PF01345	.	.	.	.	Domain of unknown function DUF11	10
PF02434	.	.	.	.	Glucosaminyltransferase/ NOTCH	7
PF02653	.	.	.	.	Branched-chain amino acid transport system / permease component	5
PF03825	.	.	.	.	Nucleoside H <sup>+</sup> symporter	0
PF05753	.	.	.	.	Translocon-associated protein beta (TRAPB)	
PF07926	.	.	.	.	TPR/MLP1/MLP2-like protein	
PF09037	.	.	.	.	Stf0 sulfotransferase	
PF10712	.	.	.	.	NAD-specific glutamate dehydrogenase	
PF11496	.	.	.	.	Class II histone deacetylase complex subunits 2 and 3	
PF13304	.	.	.	.	AAA proteins	
PF13360	.	.	.	.	Methanol dehydrogenase PQQ-type domain	
PF13429	.	.	.	.	Tetratricopeptide repeat	
PF13604	.	.	.	.	AAA proteins	
PF00107	■	■	■	■	Zinc-binding alcohol dehydrogenase	
PF00132	■	■	■	■	Bacterial transferase hexapeptide	
PF00233	■	■	■	■	3'-5'-cyclic nucleotide phosphodiesterase	
PF00612	■	■	■	■	IQ calmodulin-binding motif	
PF01398	■	■	■	■	JAB1/Mov34/MPN/PAD-1 ubiquitin protease	
PF01535	■	■	■	■	Pentatricopeptide repeat	
PF02146	■	■	■	■	Sirtuin	
PF02493	■	■	■	■	MORN repeat	
PF02798	■	■	■	■	Glutathione S-transferase, N-terminal domain	
PF02826	■	■	■	■	D-isomer specific 2-hydroxyacid dehydrogenase	
PF04408	■	■	■	■	Helicase associated domain	

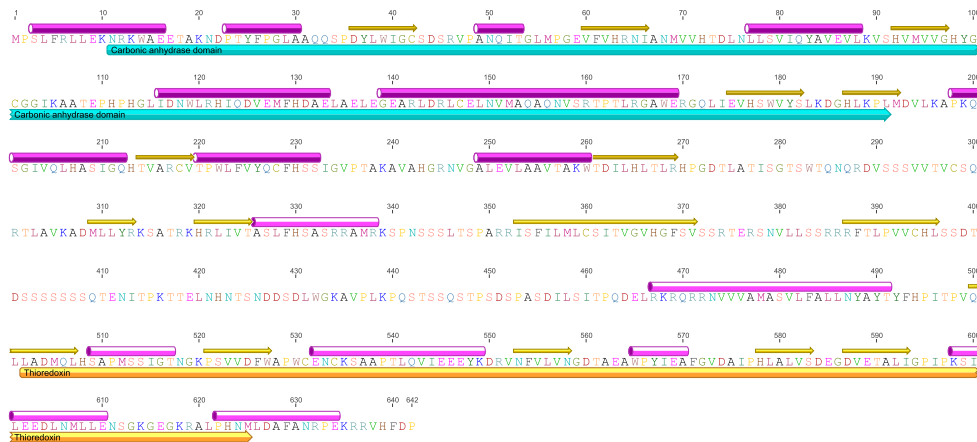
A)

Gene	<i>Staurosira</i> complex	<i>Grammatophora oceanica</i>	<i>Synedra</i> RCC2510	<i>Astrosyne radiata</i>	<i>Striatella unipunctata</i>
g8671	1				
g8195	3				
g7750	1	1			
g7216			1		
g4562	1			1	1

B)



A)



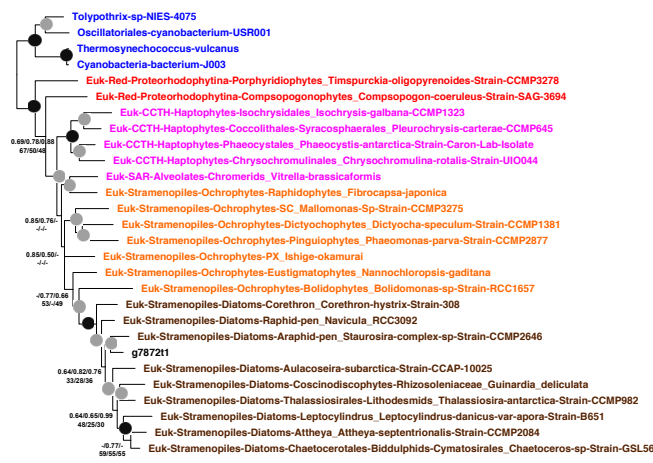
Jpred structure:

α-helix   
 β-sheet

B)

NTD

CTD



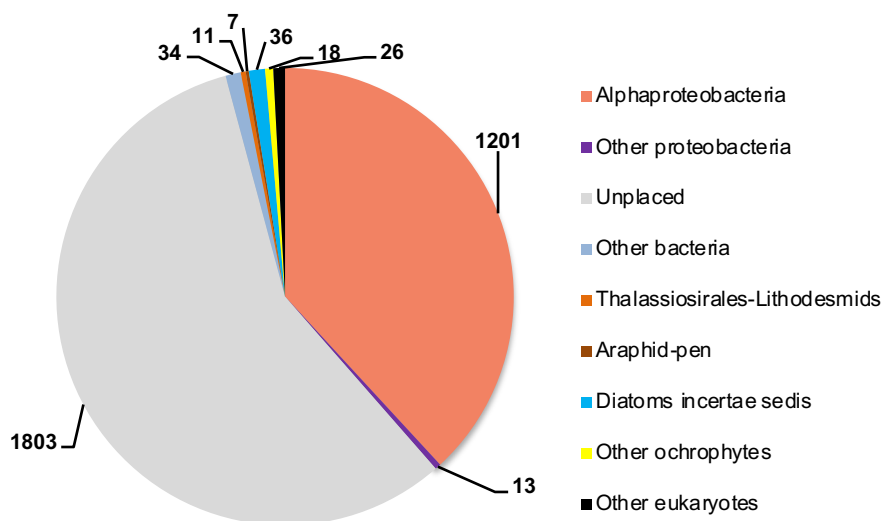
**Key**

- CCMP470
- Prokaryotes
- Diatoms
- Other ochrophytes
- Other algae with plastids of secondary red origin
- Algae with plastids of secondary green origin
- Aplastidic SAR clade members
- Red algae
- Green algae

0.2

0.3

A)



B)

