

Kumar R R, Jency S M, Bhavatarini G, Devapriya M J P. CO₂ sequestration: microalgae genome analysis and its application of effective green source technology . Plant Science Today (Early Access). <https://doi.org/10.14719/pst.1365>

Supplementary Table 1. CRISPR/Cas9 tools.

Sl. No	Species available	Family	Tools/Software	Description	References
1	<i>Thalassiosira pseudonana</i> (JGI),	<u>Thalassiosiraceae</u>	Cas-OFFinder CRISPER RGEN tools	Cas-OFFinder searches for potential off-target sites in a given sequence. It is not limited by the number of mismatches and allows variations in protospacer-adjacent motif sequences recognized by cas9	(171)
2	<i>Nannochloropsis oceanic</i>	<u>Monodopsidaceae</u>			
3	<i>Volvox carteri</i> (v2.1),	Volvocaceae			
4	<i>Chlorella variabilis</i> NC64A,	Chlorellaceae			
5	<i>Chlorella vulgaris</i> UTEX395 (ASM102112v1), CCMP1779 (from JGI v2.0),				
6	<i>Chlamydomonas reinhardtii</i> (Chlre4),				
7	<i>Chlamydomonas reinhardtii</i> (v5.0),				
8	<i>Fragilariopsis cylindrus</i> CCMP 1102 (JGI),	<u>Bacillariaceae</u>			
9	<i>Phaeodactylum tricornutum</i> (phatr2),	<u>Phaeodactylaceae</u>			
10	<i>Volvox carteri</i> (v2.1),	Volvocaceae	Microhomology — CRISPER RGEN tools	Microhomology-Predictor helps to simply	
11	<i>Thalassiosira pseudonana</i> (JGI),	<u>Thalassiosiraceae</u>			

12	<i>Chlorella variabilis</i> NC64A,	Chlorellaceae		predict the mutation patterns caused by microhomology-mediated end joining (MMEJ) pathway. MMEJ is a double-strand break repairing pathway in DNA. It also estimates how frequently unwanted in-frame deletions would be happened	
13	<i>Chlorella vulgaris</i> UTEX395 (ASM102112v1),	<u>Monodopsidaceae</u>			
14	<i>Nannochloropsis oceanica</i> CCMP1779 (from JGI v2.0),				
15	<i>Chlamydomonas reinhardtii</i> (Chlre4),	<u>Chlamydomonadaceae</u>			
16	<i>Chlamydomonas reinhardtii</i> (v5.0),				
17	<i>Fragilariopsis cylindrus</i> CCMP 1102 (JGI),	<u>Bacillariaceae</u>			
18	<i>Phaeodactylum tricornutum</i> (phatr2),	<u>Phaeodactylaceae</u>			
19	<i>Emiliana huxleyi</i> (GCA_000372725.1)	<u>Noelaerhabdaceae</u>			
20	<i>Chlamydomonas reinhardtii</i> (v5.5),	<u>Chlamydomonadaceae</u>	CRISPR-P		CRISPR-P 2.0 provides web services for computer-aided design of highly efficient sgRNA with minimal off-target effects
21	<i>Cyanidioschyzon merolae</i> (9120v1)				
22	<i>Volvox cateri</i> (v2.1),	Volvocaceae	Cas-designer— CRISPR GEN tools	Cas- Designer helps the users in choosing appropriate target sites in a gene of	
23	<i>Thalassiosira pseudonana</i> (JGI),	<u>Thalassiosiraceae</u>			
24	<i>Chlorella variabilis</i>				

25	NC64A, <i>Chlorella vulgaris</i> UTEX395 (ASM102112v1),	Chlorellaceae		interest for type II CRISPR/Cas-derived RNA-guided endonucleases. The program rapidly provides the list of all possible guide RNA sequences in a given input DNA sequence and their potential off-target sites including bulge-type sites in a genome of choice. In addition, it assigns an outof-frame score to each target site to help users choose appropriate sites for gene knockout	(175)
26	<i>Nannochloropsis oceanica</i> CCMP1779 (from JGI v2.0),	<u>Monodopsidaceae</u>			
27	<i>Chlamydomonas reinhardtii</i> (Chlre4),	<u>Chlamydomonadaceae</u>			
29	<i>Chlamydomonas reinhardtii</i> (v5.0),				
30	<i>Fragilariopsis cylindrus</i> CCMP 1102 (JGI),	<u>Bacillariaceae</u>			
31	<i>Phaeodactylum tricornutum</i> (phatr2)	<u>Phaeodactylaceae</u>			
32	<i>Chlamydomonas reinhardtii</i> (v3.1),	<u>Chlamydomonadaceae</u>	CCTop— CRISPR/Cas9 target online predictor	CCTop is a web tool for the rapid and efficient identification of high quality target sites. It identifies and ranks all candidate	(176)
33	<i>Nannochloropsis gaditana</i> (B-31)	<u>Monodopsidaceae</u>			

				sgRNA target sites according to their off-target quality	
34	<i>Chlorella sorokiniana</i> (CSI2_1230),	Chlorellaceae	CHOPCHOP	CHOPCHOP is a web tool for selecting target sites for CRISPR/Cas9 , CRISPR/Cpf1 or TALEN-directed mutagenesis in the given sequence, gene name	(177, 178)
35	<i>Phaeodactylum tricornutum</i> (ASM15095v2),	<u>Phaeodactylaceae</u>			
36	<i>Chlamydomonas reinhardtii</i>	<u>Chlamydomonadaceae</u>	SgRNA design tool—broad institute	This tool ranks and picks candidate sgRNA sequences for the targets provided while attempting to maximize on-target activity and minimizing off-target activity	(179)
37	<i>Thalassiosira pseudonana</i> (ASM14940v2),	<u>Thalassiosiraceae</u>	Digenome-seq—CRISPER RGEN tools	Digenome-seq (digested genome sequencing), is an in vitro nuclease-	
38	<i>Phaeodactylum tricornutum</i> (ASM15095v2_bd)	<u>Phaeodactylaceae</u>			

				<p>digested whole-genome sequencing to profile genome-wide nuclease off-target effects in cells. Digenome-seq points the exact location of double-strand break (DSB) sites by recognizing specific patterns of aligned reads. This in vitro digest yields sequence reads with the same 5' ends at cleavage sites that can be computationally identified by Digenome-seq program</p>	(180, 181)
39	<i>Volvox carteri</i> (v2.1),	Volvocaceae	Cas-analyzer—CRISPR GEN tools		

40	<i>Thalassiosira pseudonana</i> (JGI),	<u>Thalassiosiraceae</u>	Base editing— CRISPR RGEN tools	It is a guide- RNA designer for CRISPR base editing enable the direct conversion of DNA bases (C to T/A/G) without inducing doublestran d breaks of DNA by the fusion of cytidine deaminase with deactivated Cas9 (dCas9) or Cas9 nickase	http://www.rgenome.net/be-designer/
41	<i>Chlorella variabilis</i> NC64A,	Chlorellaceae			
42	<i>Chlorella vulgaris</i> UTEX395 (ASM102112v1),				
43	<i>Nannochloropsis oceanica</i> CCMP1779 (from JGI v2.0),	<u>Monodopsidaceae</u>			
44	<i>Chlamydomonas reinhardtii</i> (Chlre4),	<u>Chlamydomonadaceae</u>			
45	<i>Chlamydomonas reinhardtii</i> (v5.0),				
46	<i>Fragilariopsis cylindrus</i> CCMP 1102 (JGI),	<u>Bacillariaceae</u>			
47	<i>Phaeodactylum tricornutum</i> (phatr2)	<u>Phaeodactylaceae</u>			