

## GBROWSE

### Reference genome:

- *Nannochloropsis\_oceanica\_CCMP1779\_v1*: Genome assembly and annotation as referred to in the genome publication

### Specific tracks and explanations:

- **gene**: This track displays all gene models as annotated by both maker pipeline runs. Benning/Shiu lab annotations have the prefix **NannoCCMP1779\_** followed by consecutive numbers, Yandell lab annotations have the prefix **Nanno1\_** followed by consecutive numbers.
- **maker\***: Shows the final annotation output from the annotation pipeline, genes are named as above.
- **augustus\_masked\***: Intermediate ab initio gene annotations using the augustus gene annotation algorithm.
- **snap\_masked\***: Intermediate ab initio gene annotations using the SNAP gene annotation algorithm.
- **blastn**: Expressed Sequence Tags (ESTs) from Nitrogen replete and deplete conditions aligned to the genomic assembly using blastn
- **EST2genome**: ESTs from Nitrogen replete and deplete conditions aligned to the genomic assembly using the est2genome option for Exonerate.
- **protein2genome\***: Translated protein sequences from other heterokonts aligned to the genomic assembly using the protein2genome option for Exonerate.
- **blastx\***: Translated protein sequences from other heterokont organisms aligned to the genomic assembly using blastx.
- **repeatmasker\***: Shows genomic regions that have been masked before genome annotation because of low complexity or the occurrence of simple repeats as identified by repeatmasker.

\*Tracks are also available with the prefix 'Yandell'. These tracks were generated from an additional maker pipeline annotation with an updated version and slightly modified settings (see Vieler et al. 2012 (in preparation); Cantarel et al., [Genome Res.](#) 2008 Jan;18(1):188-96)

Other tracks (CDS, exon, 3-frame translations etc.) are generic gbrowse tracks.

## BLAST Databases

- **Nanno\_oceanica\_CCMP1779v1**: nucleotide database corresponding to the published genome assembly
- **Nanno\_oceanica\_CCMP1779v1\_protein**: protein database corresponding to the published genome annotation
- **Yandell\_proteins**: protein database as predicted by the Yandell lab genome annotation
- **Yandell\_transcripts**: nucleotide database with predicted transcripts from the Yandell lab genome annotation