



The Oomycete Gene Order Browser

OGOB: The Oomycete Gene Order Browser

The Oomycete Gene Order Browser (OGOB) is a curated database that hosts genomes, genes, proteins, orthology information, functional annotations and syntenic information for a number of Oomycete species. OGOB displays a selected Oomycete gene and the neighbouring genes in its genome, as well syntenic regions of other selected Oomycete genomes. OGOB also hosts a number of bioinformatics tools that allow further analysis of Oomycete genomes and genes. OGOB is built on software developed by Dr. Kevin Byrne in the [laboratory of Professor Ken Wolfe](#) and is similar in structure to YGOB. This document describes how to use OGOB.

OGOB is developed, curated and maintained by the Genome Evolution Laboratory in the Maynooth University Department of Biology. If you have any queries or suggestions regarding OGOB please contact Jamie McGowan (jamie.mcgowan@mu.ie) or Dr. David Fitzpatrick (david.fitzpatrick@mu.ie). OGOB is available at <https://ogob.ie>.

Control Panel

The panel at the bottom of the OGOB interface (**Figure 1**) allows a user to select which genes and genomes are visible.

- “Choose species” allows users to choose which genomes are displayed by checking and unchecking the checkboxes for each species.
- Users can choose how many genes/homology pillars are visible by changing the “Window size”. This varies from ± 4 genes up to ± 200 genes, the default is ± 6 .
- “Navigate to Gene ID” allows the user to enter a specific gene ID to focus the browser on.
- “Browse” focuses the browser on the chosen gene.
- “Search” opens OGOB’s search interface which allows users to search the OGOB database using text queries and also perform BLAST searches, see below.
- The “Help (?)” button opens this help document.



Figure 1 – The OGOB control panel

Browser Window:

Gene Box:

Genes are represented by coloured boxes that show its gene ID. Horizontal tracks correspond to chromosome / scaffold segments. Each genome has a colour palette that distinguishes different chromosomes or scaffolds. Genes that are in the same vertical column (homology pillar) are orthologs. Genes that are coloured grey are not syntenic. Hovering over a gene displays a popup with the gene ID, species name, scaffold name and any Pfam domain(s). Each gene box has an “e”, “b” and “i” box, described below.

Focused Gene:

A gold border highlights the gene currently in focus (PITG_00207 from *Phytophthora infestans* is the gene in focus in the example shown in **Figure 2**).

Connectors:

Connectors join nearby genes. A solid connector between two genes indicates that the two genes are adjacent in the genome, two small bars indicate that they are within 5 genes of each other and one small bar if they are within 20 genes. Connectors that are coloured orange denote an inversion. The connectors are continued over any intervening space between genes with grey extensions.

Arrows:

The arrows under each gene box denote the gene’s relative orientation (i.e. Watson or Crick strand).

Brackets:

A bracket around a gene box indicates the end of a chromosome or scaffold.

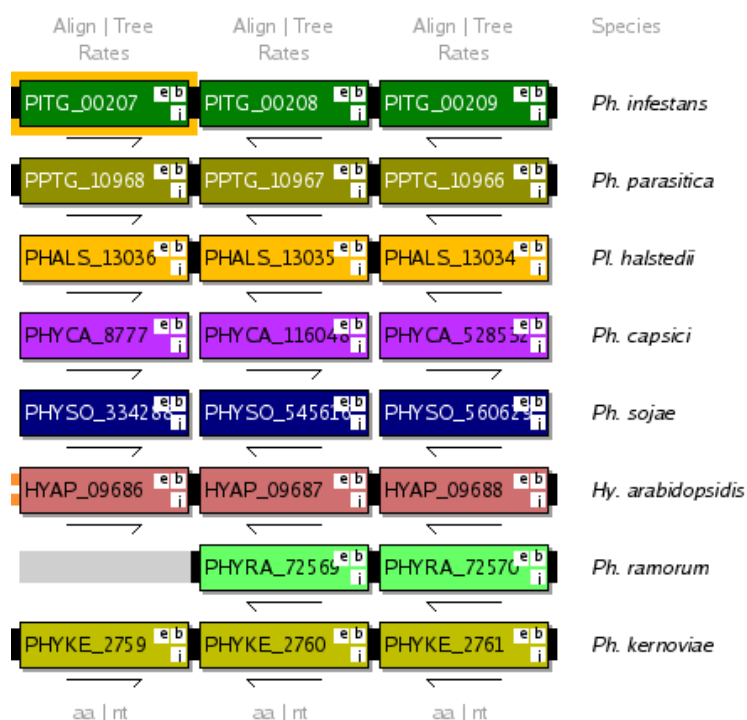


Figure 2 - The OGOB browser window

Buttons:

“e” Button:

The “e” button (not shown) allows curators to edit homology pillars to add/remove orthologs.

“i” Button:

The “i” button opens a webpage showing identified functional domains present in the chosen gene. All genomes were annotated using InterProScan and include Pfam, PANTHER, Gene Ontology (GO), SignalP and TMHMM annotations. Clicking on an annotation opens a link with additional information. For example, clicking an InterPro ID will open the InterPro record on the InterPro website, clicking on a Pfam ID will open up the Pfam record for that ID and clicking on a GO term will open up the term description on the QuickGO website where users can see additional information including a term ancestor chart. Gene and protein sequences are also shown on the gene information page. See **Figure 3** for an example.

“b” Button:

The “b” button runs a BLASTp search of that gene against the Oomycete genomes in OGOB. Hits are highlighted in pink if they are in the same column as the query gene, blue if they appear on the screen outside of its column and orange if they are a tandem copy of the gene. Clicking on a hit name will focus the browser on that hit. Full BLAST output alignments are found towards the bottom of the page. The “b” button is coloured orange if that gene belongs to a tandem cluster.

“Align” Button:

The “Align” button generates a multiple sequence alignment for the genes (based on amino acid sequences) in that pillar using MUSCLE. The alignment is presented in an interactive interface implemented using [MSAViewer](#) and shows the consensus sequence for that pillar. Also provided is the alignment in FASTA and Clustal format.

“Tree” Button:

The “Tree” button draws a phylogenetic tree for the genes in that pillar. The protein sequences are aligned using MUSCLE, GBLOCKS is run on the alignment, then PhyML is run to calculate a maximum likelihood phylogeny. The phylogeny is displayed in an interactive interface that allows users to manipulate and root trees, implemented using [phylotree.js](#).

“Rates” Button:

The “Rates” button calculates synonymous and non-synonymous substitution rates for the genes in that pillar using yn00. Ka, Ks and Omega values are shown in a sortable table. Omega values greater than or equal to 1 are highlighted green.

“aa” Button:

The “aa” button extracts the proteins sequences for genes in that pillar in FASTA format.

“nt” Button:

The “nt” button extracts the nucleotide sequences for genes in that pillar in FASTA format.

“Species” Button:

The “species” button (top right) displays a phylogenetic tree depicting the phylogenetic relationships among Oomycete species.

PITG_00005

Length 493 amino acids

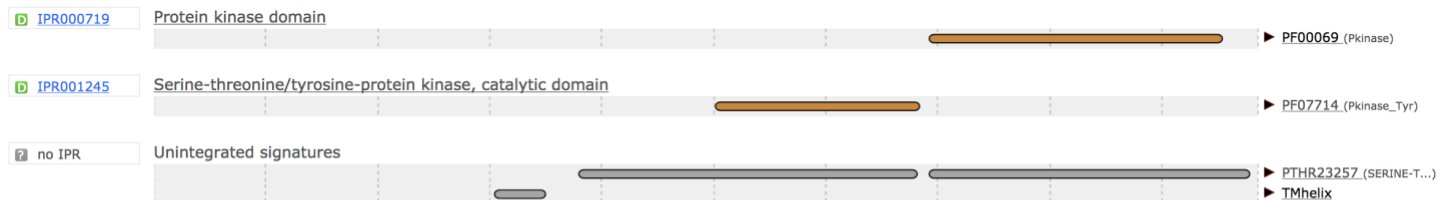
Protein family membership None predicted.

Homologous superfamilies none

Domains and repeats



Detailed signature matches



GO Term prediction

Biological process

[GO:0006468](#) protein phosphorylation

Molecular function

[GO:0004672](#) protein kinase activity
[GO:0005524](#) ATP binding



Cellular component

None predicted.

Figure 3 – Example of the OGOB gene information page. The annotation for PITG_00005, a protein kinase from *Phytophthora infestans*, is shown. Annotations are generated using InterProScan and include Pfam, PANTHER, Gene Ontology, SignalP and TMHMM annotations. Clicking on an annotated term links to further information.

Search Interface:

Text Query Search:

Clicking on the “Search” button in OGOB’s control panel opens the search interface where users can search the OGOB database using text terms. Supported queries include Gene IDs, scaffold names, Pfam domains, GO terms, etc. Results are shown in a sortable table (**Figure 4**). Clicking  loads the corresponding gene information page. Clicking  focuses the browser on that gene.

Search

BLAST

cutinase

	Protein ID	OGOB Pillar ▾	Scaffold	Pfam domains	GO terms
<div><div>i</div><div></div></div>	PYAP_14429	98252	scaffold_27	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PYAP_14421	98249	scaffold_27	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYRA_71624	69337	scaffold_32	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	HYAP_06962	64428	scaffold_57	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYSO_517658	59350	scaffold_7	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYSO_516798	59297	scaffold_7	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYSO_354923	53563	scaffold_6	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYRA_47458	53355	scaffold_32	Cutinase	GO:0008152 GO:0016787
<div><div>i</div><div></div></div>	PHYCA_555221	53355	scaffold_71	Cutinase	GO:0008152 GO:0016787

Figure 4 – The OGOB search interface. In this example, the OGOB database was searched for the Pfam term ‘cutinase’ and the results were sorted according by OGOB pillars.

Blast search:

It is also possible to search query sequences against the OGOB database using BLAST. BLAST searches can be performed by clicking the “BLAST” tab at the top of the search page (Figure 4). Amino acid and nucleotide queries are supported. Protein sequences are searched against OGOB proteins using BLASTp. Nucleotide sequences are searched against OGOB gene sequences using BLASTn. Query sequences must be in FASTA format. Only one sequence can be searched at a time. Results are shown in a table, clicking on a hit name will focus the browser on that hit. Full BLAST output alignments are found towards the bottom of the results page.

Genomes:***Phytophthora infestans*:**

Data for *Phytophthora infestans* was downloaded from NCBI. The version retrieved was T30-4, assembly ASM14294v1. Protein names begin with “PITG_” and correspond to NCBI and UniProt records.

***Phytophthora parasitica*:**

Data for *Phytophthora parasitica* was downloaded from NCBI. The version retrieved was INRA-310_V2. Protein names begin with “PPTG_” and correspond to NCBI and UniProt records.

***Plasmopara halstedii*:**

Data for *Plasmopara halstedii* was downloaded from ENSEMBL. Proteins are named after their locus-tag and begin with “PHALS_”. They correspond to NCBI records.

***Phytophthora capsici*:**

Data for *Phytophthora capsici* was downloaded from JGI. The version retrieved was LT1534 v11.0. Protein names correspond to JGI protein IDs but are prefixed with “PHYCA_”.

***Phytophthora sojae*:**

Data for *Phytophthora sojae* was downloaded from JGI. The version retrieved was v3.0. Protein names correspond to JGI protein IDs but are prefixed with “PHYSO_”.

***Hyaloperonospora arabidopsidis*:**

Data for *Hyaloperonospora arabidopsidis* was retrieved from ENSEMBL. The version retrieved was HyaAraEmoy2_2.0. Protein names correspond to ENSEMBL transcript IDs except they are prefixed with “HYAP_” instead of “HpaT8”.

***Phytophthora ramorum*:**

Data for *Phytophthora ramorum* was retrieved from JGI. The version retrieved was v1.1. Protein names correspond to JGI protein IDs but are prefixed with “PHYRA_”.

***Phytophthora kernoviae*:**

Data for *Phytophthora kernoviae* was retrieved from ENSEMBL. The version retrieved was PhyKer238_432v1. Protein names correspond to the final number in transcript IDs but are prefixed with “PHYKE_”.

***Phytophthora vexans*:**

Data for *Phytophthora vexans* was downloaded from ENSEMBL. The version retrieved was pve_scaffolds_v1. Protein names are prefixed with “PYVX_”.

Pythium irregulare:

Data for *Pythium irregulare* was downloaded from ENSEMBL. The version retrieved was pir_scaffolds_v1. Protein names correspond to ENSEMBL transcript IDs but are prefixed with "PYIR_" instead of "EPPrIT000000".

Pythium iwayamai:

Data for *Pythium iwayamai* was downloaded from ENSEMBL. The version retrieved was piw_scaffolds_v1. Protein names correspond to ENSEMBL transcript IDs but are prefixed with "PYIW_" instead of "EPPrWT000000".

Pythium ultimum var. ultimum:

Data for *Pythium ultimum var. ultimum* was downloaded from ENSEMBL. Protein names begin with "PYU1_G0" and correspond to ENSEMBL gene/protein IDs.

Pythium aphanidermatum:

Data for *Pythium aphanidermatum* was downloaded from ENSEMBL. The version retrieved was "pag1_scaffolds_v1". Protein names correspond to ENSEMBL transcript IDs but are prefixed with "PYAP_" instead of "EPPrAT000000".

Pythium arrhenomanes:

Data for *Pythium arrhenomanes* was downloaded from ENSEMBL. The version retrieved was "par_scaffolds_v1". Protein names correspond to ENSEMBL transcript IDs but are prefixed with "PYAR_" instead of "EPPrPT000000".

Albugo laibachii:

Data for *Albugo laibachii* was downloaded from ENSEMBL. The version retrieved was ENA1. Protein names begin with "CCA" and correspond to ENSEMBL, NCBI and UniProt records.

Albugo candida:

Data for *Albugo candida* was downloaded from ENSEMBL. The version retrieved was ASM107853v1. Protein names begin with "CCI" and correspond to ENSEMBL, NCBI and UniProt records.

Saprolegnia parasitica:

Data for *Saprolegnia parasitica* was downloaded from ENSEMBL. The version retrieved was ASM15154v2. Protein names begin with "SPRG_" and correspond to ENSEMBL, NCBI and UniProt records.

Saprolegnia diclina:

Data for *Saprolegnia diclina* was downloaded from ENSEMBL. The version retrieved was Sap_diclina_VS20_V1. Protein names begin with "SDRG_" and correspond to ENSEMBL, NCBI and UniProt records.

Aphanomyces astaci:

Data for *Aphanomyces astaci* was downloaded from ENSEMBL. The version retrieved was Apha_asta_APO3_V1. Protein names begin with "H257_" and correspond to ENSEMBL, NCBI and UniProt records.

Aphanomyces invadans:

Data for *Aphanomyces invadans* was downloaded from ENSEMBL. The version retrieved was Apha_inva_NJM9701_V1. Protein names begin with "H310_" and correspond to ENSEMBL, NCBI and UniProt records.

References:

Species	Source	Reference
<i>Phytophthora infestans</i>	NCBI	Haas et al. 2009
<i>Phytophthora parasitica</i>	NCBI	Broad Institute (INRA-310)
<i>Plasmopara halstedii</i>	ENSEMBL	Sharma et. al 2015
<i>Phytophthora capsici</i>	JGI	Lamour et al. 2012
<i>Hyaloperonospora arabidopsidis</i>	ENSEMBL	Baxter et al. 2010
<i>Phytophthora sojae</i>	JGI	Tyler et al. 2006
<i>Phytophthora ramorum</i>	JGI	Tyler et al. 2006
<i>Phytophthora kernoviae</i>	ENSEMBL	PhyKer238/432
<i>Phytophthora vexans</i>	ENSEMBL	Adhikari et al. 2013
<i>Pythium iwayamai</i>	ENSEMBL	Adhikari et al. 2013
<i>Pythium irregulare</i>	ENSEMBL	Adhikari et al. 2013
<i>Pythium ultimum</i> var. <i>ultimum</i>	ENSEMBL	Lévesque et al. 2010
<i>Pythium arrhenomanes</i>	ENSEMBL	Adhikari et al. 2013
<i>Pythium aphanidermatum</i>	ENSEMBL	Adhikari et al. 2013
<i>Albugo laibachii</i>	ENSEMBL	Kemen et al. 2011
<i>Albugo candida</i>	ENSEMBL	Links et al. 2011
<i>Saprolegnia diclina</i>	ENSEMBL	Broad Institute (VS20)
<i>Saprolegnia parasitica</i>	ENSEMBL	Jiang et al. 2013
<i>Aphanomyces invadans</i>	ENSEMBL	Broad Institute (9901)
<i>Aphanomyces astaci</i>	ENSEMBL	Broad Institute (APO3)