

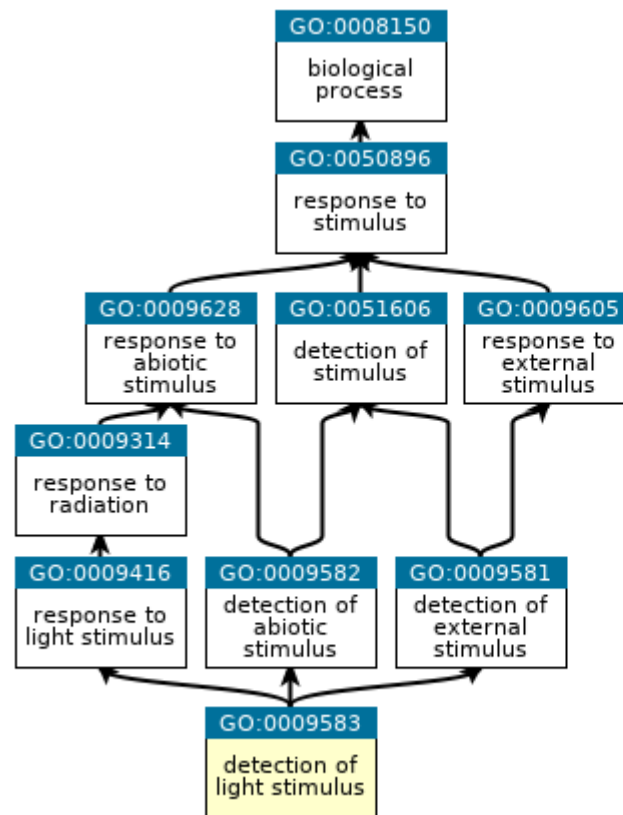
# Rice gene functional data

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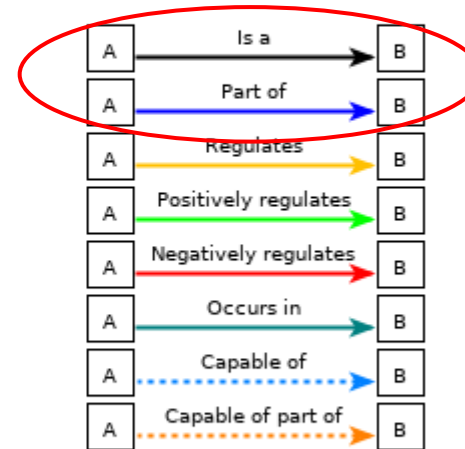
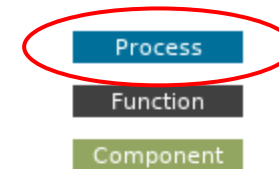
# Gene functions

**GO:0009583** detection of light stimulus

## Ancestor Chart



QuickGO - <https://www.ebi.ac.uk/QuickGO>



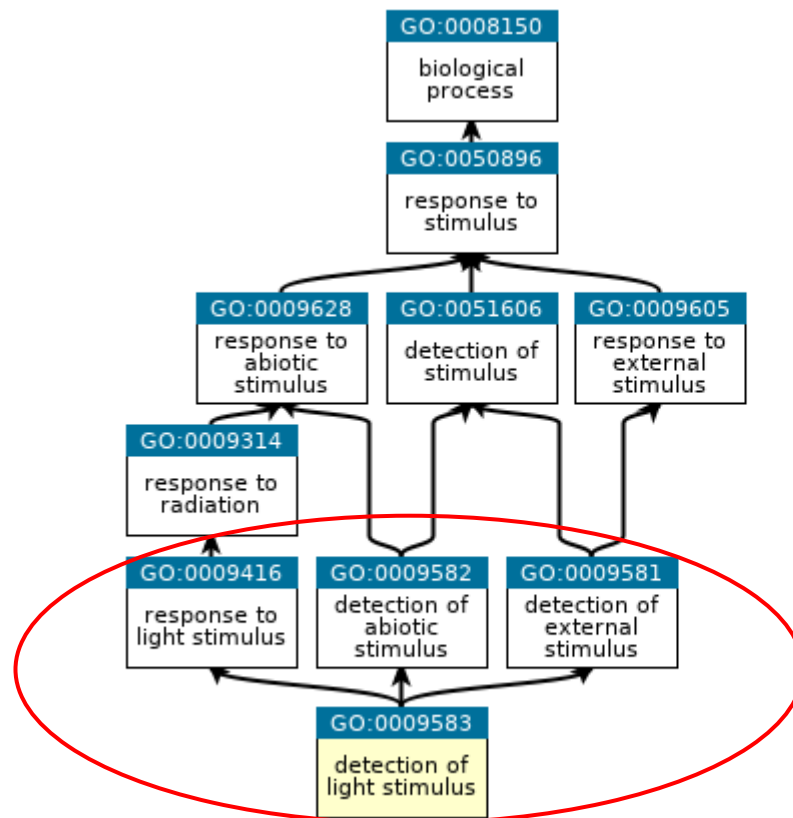
**Biological processes**

# Gene functions

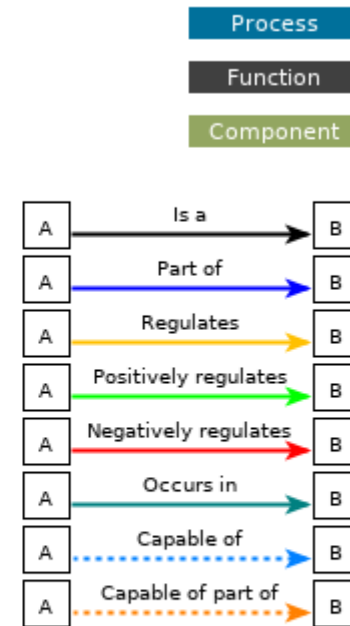
**GO:0009583** detection of light stimulus

## Ancestor Chart

**Function  
and its  
parents**



QuickGO - <https://www.ebi.ac.uk/QuickGO>

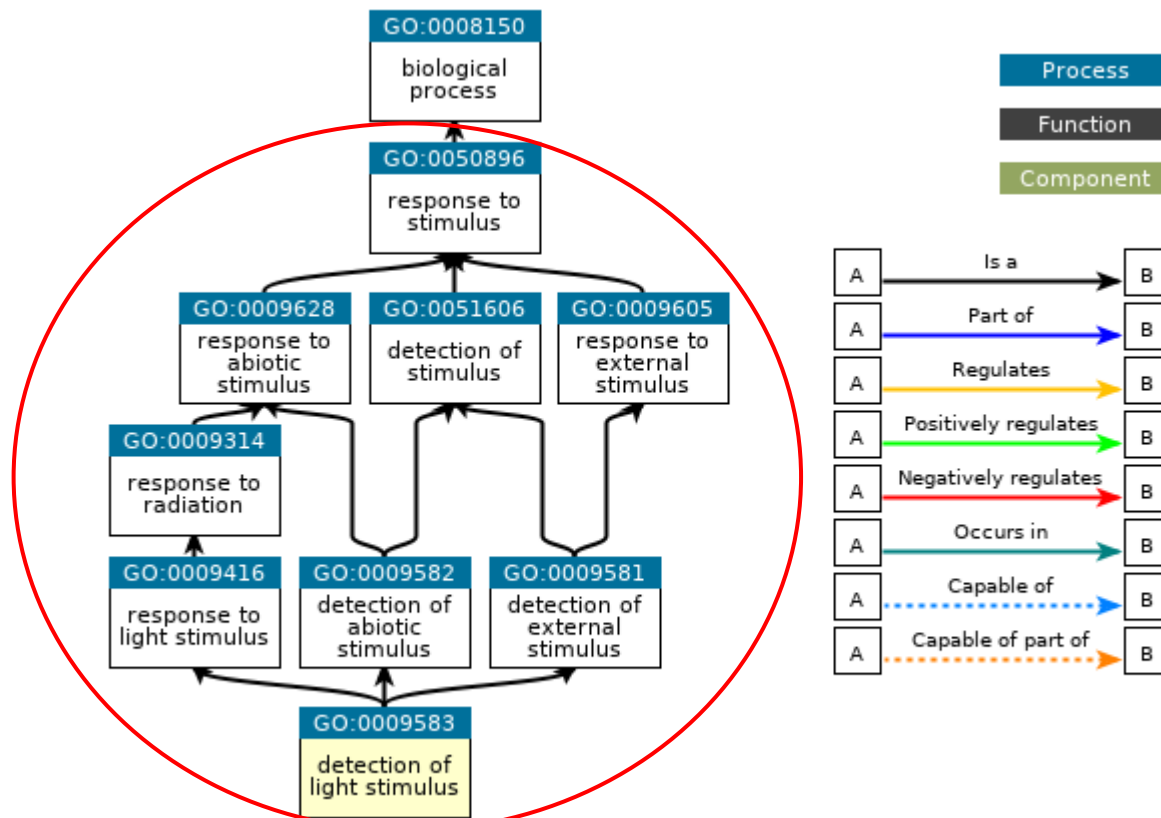


# Gene functions

**GO:0009583** detection of light stimulus

## Ancestor Chart

**Function**  
**and all its**  
**ancestors**



QuickGO - <https://www.ebi.ac.uk/QuickGO>

# Gene functions

## Hypothesis

If a gene is associated to a function (biological process) then it is associated to all ancestors of the function.

# RAPDB+Oryzabase+Gene2GO+QuickGO +Gene Ontology

<b>Gene-function associations</b>	13116	24855	24835
<b>Genes</b>	7478	9294	9294
<b>Functions</b>	617	2012	3743
<b>Ancestral relations</b>	442	2138	7186

# RAPDB+Oryzabase+Gene2GO+QuickGO +Gene Ontology

<b>Gene-function associations</b>	24835	220598
<b>Genes</b>	9294	9294
<b>Functions</b>	3743	3743
<b>Ancestral relations</b>	7186	50479

# Term hierarchies

<b>Filtered terms</b>	271	991	1797
<b>Terms to predict</b>	394	1397	1938
<b>Subhierarchies</b>	190	700	3670
<b>Terms in subhierarchies</b>	336	1336	6171



# Term hierarchies

<b>Average terms per hierarchy</b>	4.95	7.14	363
<b>Min</b>	2	2	2
<b>Max</b>	14	22	1996

# To do

- Run experiments with probabilistic model on Hydra (**ongoing**).
- Run experiments with machine learning model on Hydra.
  - Define attributes and datasets (**next**).
  - Run experiments for every dataset.
- Compare performance of the models.
- Write a paper! (**hopefully soon**).