

Welcome to MPID ~ ~ ~

A database of predicted protein-protein interaction network in rice blast fungus

Protein-protein interactions tend to be evolutionary conserved cross species. Therefore we can predict protein-protein interactions in Magnaporthe grisea using model organism protein interaction datasets. Based on this method, we have built a network of 11674 predicted physical interactions among 3017 M.grisea proteins. More details about the generation of the network are available from the [Help page](#). To search the predicted interaction network for your protein of interest, please use the [Query page](#). You can download all the predicted PPI data [here](#). For questions and comments, please contact [Fei HE](#). The website was last updated in October 2008.

Quick search: (Example: MGG_10268)

[Advanced Search](#)

A

Your input protein MGG_10268 can interact with 11 proteins

[View interactions among these 11 proteins \(?\)](#)[View the interaction map \(?\)](#)

Degree	Protein name	GO annotation	Score	Homolog in Swissprot (E-value)	P value based on GO terms	P value based on PCC
1	MGG_06844	No GO annotation in our database	2.4560	Q9FIT4 (1e-08)	-	0.40214
1	MGG_08772	No GO annotation in our database	2.4560	Q9SXZ2 (3e-08)	-	0.04456
5	MGG_01843	No GO annotation in our database	2.4560	P31729 (4e-15)	0.57259	0.19176
5	MGG_05207	molecular_function: catalytic activity (GO:0003824) molecular_function: protein serine/threonine phosphatase activity (GO:0004722) biological_process: protein amino acid dephosphorylation (GO:0006470) cellular_component: protein serine/threonine phosphatase complex (GO:0008287)	2.7850	P40371 (9e-72)	0.7345	0.80951

B