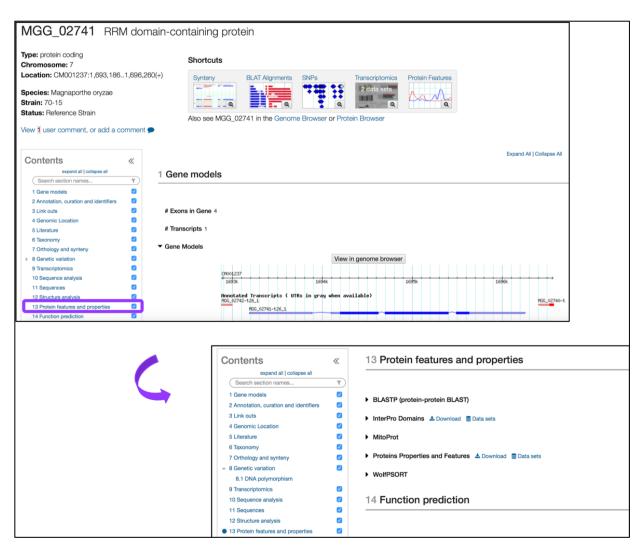
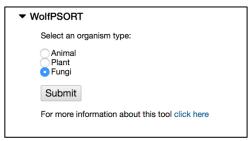
## Running WoLF PSORT from gene record pages.

WoLF PSORT predicts the subcellular localization sites of proteins based on their amino acid sequences. The results are displayed as a one-line output with information about detected sorting signals.

- 1. Navigate to a gene record page of your choice (e.g. MGG 02741
- 2. gene of *Fusarium graminearum* PH-1: http://fungidb.org/fungidb/app/record/gene/MGG 02741)
- 3. Use the Contents menu to navigate to the Protein features and properties menu



- 4. WoLF PSORT offers several organism types (Animal, Plant, and Fungi), for which it can predict the subcellular localization sites of proteins
  - a. Choose *Fungi* and click on the *Submit* button.



5. A new tab will be opened automatically, and you will be redirected to the WoLF PSORT results page:

```
queryProtein details nucl: 17.5, cyto_nucl: 13.833, cyto: 5, cyto_pero: 3.665, mito: 2, plas: 2
```

a. Click on the *details* link to learn more about nearest neighbours identified by WoLF PSORT algorithm:

cuspulDestrin Wal EDCOPT analistica analy 17.5 cets analy 12.922 cets 5 cets area 2.665 mits 2 miss 2					
queryProtein WoLFPSORT prediction nucl: 17.5, cyto_nucl: 13.833, cyto: 5, cyto_pero: 3.665, mito: 2, plas: 2					
PSORT features and traditional PSORTII prediction					
	27 Nearest Neighbors				
id		distance	identity	comments	
ROX3_YEAST	nucl	344.414	11.5566%	[Uniprot] SWISS-PROT45:Nuclear. GO:0005634; C:nucleus; Evidence:IDA	
PHP5_SCHPO	nucl	363.219	10.8235%	[Uniprot] SWISS-PROT45:Nuclear.	
WC1_NEUCR	nucl	374.651	9.16881%	[Uniprot] SWISS-PROT45:Nuclear.	
HAP5_YEAST	nucl	413.792	10.6132%	[Uniprot] SWISS-PROT45:Nuclear.	
FIP1_YEAST	nucl	415.621	14.1509%	[Uniprot] SWISS-PROT45:Nuclear. GO:0005847; C:mRNA cleavage and polyadenylation specifici; Evidence:IPI	
CCR4_YEAST	cyto_nucl	428.31	9.55795%	[Uniprot] SWISS-PROT45:Cytoplasmic and nuclear. GO:0005737; C:cytoplasm; Evidence:IDA	
NAB3_YEAST	nucl	438.079	11.8454%	[Uniprot] SWISS-PROT45:Nuclear; nucleoplasm. GO:0005654; C:nucleoplasm; Evidence:IDA	
IXR1_YEAST	nucl	445.397	10.2178%	[Uniprot] SWISS-PROT45:Nuclear. GO:0000228; C:nuclear chromosome; Evidence:IPI	
PUB1_YEAST	cyto_nucl	459.895	13.4066%	[Uniprot] SWISS-PROT45:Nuclear and cytoplasmic. GO: 0030530; C:heterogeneous nuclear ribonucleoprotein com; Evidence:IDA	
ST12_YEAST	nucl	464.718	11.0465%	[Uniprot] SWISS-PROT45:Nuclear.	
RPA2_NEUCR	nucl	465.585	8.58995%	[Uniprot] SWISS-PROT45:Nuclear.	
CCHL_CANAL	mito	470.462	11.7925%	[Uniprot] SWISS-PROT45:Mitochondrial inner membrane.	
YQKA_SCHPO	cyto_nucl	470.872	10.0622%	[Uniprot] SWISS-PROT45:Cytoplasmic and nuclear.	
WC2_NEUCR	nucl	475.304	13.371%	[Uniprot] SWISS-PROT45:Nuclear.	
FLO8_YEAST	nucl	484.533	12.6408%	[Uniprot] SWISS-PROT45:Nuclear. GO:0005634; C:nucleus; Evidence:IDA	
PSB4_YEAST	cyto_nucl	490.622	10.1415%	[Uniprot] SWISS-PROT45:Cytoplasmic and nuclear.	
DIG1_YEAST	nucl	496.014	12.8319%	[Uniprot] SWISS-PROT45:Nuclear.	
CK12_YEAST	plas	504.669	11.5385%	[Uniprot] SWISS-PROT45:Plasma membrane-bound. GO:0005886; C:plasma membrane; Evidence:IDA	
ERV1_YEAST	mito	511.505	11.5566%	[Uniprot] SWISS-PROT45:Mitochondrial. GO:0005758; C:mitochondrial intermembrane space; Evidence:IDA	
NOP3_YEAST	nucl	512.006	15.1869%	[Uniprot] SWISS-PROT45:Nuclear; nucleolar. GO: 0005634; C:nucleus; Evidence:IDA	
TAF1_YEAST	nucl	522.641	9.7561%	[Uniprot] SWISS-PROT45:Nuclear.	
PEXJ_YEAST	cyto_pero	524.059	12.0283%	[Uniprot] SWISS-PROT45:Peroxisomal and cytoplasmic. GO:0005829; C:cytosol; Evidence:IDA	

To learn more about abbreviations and Localization features, follow this link: https://wolfpsort.hgc.jp/WoLFPSORTdoc/psortFeatureDescriptions.html

b. Click on the *identity* link to visualize alignment of query strings to close (nearest) matches (neighbours):

## 

## **Useful links:**

- 1. WoLF PSORT: https://wolfpsort.hgc.jp
- 2. About WoLF PSORT: https://wolfpsort.hgc.jp/aboutWoLF PSORT.html.en
- PSORT II localization featureshttps://wolfpsort.hgc.jp/WolFPSORTdoc/psortFeatureDescriptions.html
- 4. PSORT: https://psort.hgc.jp