

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**

The image shows a two-part screenshot of the FungiDB website. The top part displays the main gene record for MGG_02741, an RRM domain-containing protein from *Fusarium graminearum*. It includes metadata like Type (protein coding), Chromosome (7), Location, Species, Strain, and Status. A 'Shortcuts' section offers links to Synteny, BLAT Alignments, SNPs, Transcriptomics, and Protein Features. A 'Contents' sidebar on the left lists 14 sections, with '13 Protein features and properties' highlighted with a purple box. The main content area shows '1 Gene models' and a genomic track with a 'View in genome browser' button. A purple curved arrow points from the highlighted sidebar item to the bottom screenshot. The bottom screenshot shows the '13 Protein features and properties' section, which contains links to BLASTP, InterPro Domains, MitoProt, Proteins Properties and Features, and WoLFPSORT. The 'Contents' sidebar on the left remains visible, with '13 Protein features and properties' now selected.

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.

▼ **WoLFPSORT**

Select an organism type:

☐ Animal
☐ Plant
☒ Fungi

For more information about this tool [click here](#)

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:

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	site	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.	
FIPI_YEAST	nucl	415.621	14.1509% [Uniprot]	SWISS-PROT45:Nuclear. GO: 0005847 ; C:mRNA cleavage and polyadenylation specifi...; Evidence:IP	
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:IP	
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):

Alignment (PAM120) of query: queryProtein to nearest (by WoLF PSORT distance) neighbors

Alignment of query: queryProtein to sequence ROX3_YEAST (nucl)

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MAEEDFEIDIYGDANQEQGGDDNKHDSYEGGDHGDGHGANDNEQYRDDQQAEDSSHAKHDDSSHTESATPQ 75
MASR-----VDETTPSYYYVDPEITYT-----YQQPNPLQDLISVYGLDDISRQVARTNLD 53
**                               *      *      *      *      *      *      *      *

QSNPLKRKEGSDRAIDPGATSAILISELQWITDDDIRGWIREAGCEEELKDITFSEHKVNGKSKGQVYIELTS 150
GTKAVKLKRSYKNQIADLSGKFSTIPT-----RENGKGGQIAHILF-----QNNPDMMIQ-PP 105
      *      *      *      *      *      *      *      *      *      *      *

QQAATAVKHRLESSEGGEDGASQAGRKQQVIYSSPTMNPFRITLPKDQPRITGKDGQNRPTSAGAGYNNDRITGNMSGGG 225
QQG-----QNMSEQQWRERQLNRDIAL--F-----QP-----PNFDWDLCSVL--S 143
**                               *      *      *      *      *      *      *      *

NFRGGYNNRGRGGYNNMRGGMVNNMNQGGFNRFNNNAYNNNSMGFNNPMGGGNFPGGGGANFGGFRGGGMGMNS 300
QFERSY-----PSEFANQNQGG-----AQAPFDIDDLAF-----DLDTGKSQ-----SGSNSGNNNS 190
*      *      *      *      *      *      *      *      *      *      *      *

NMRGGAMRGRGGMMGGMMGGMPGMNMGNMGGGMGNMGNMGMAMGMGGMPMGAMGAMGGNMGMAMMMGGGM 375
KKR-----KNKSSG-----SSMATP----- 205
      *      *      *      *      *      *      *      *

PGFQGMQGGFNPQGFPGGVGGNNNNNAQGGGGNNEWQNPFGAKRPRPE 424
-----THSDSHED-----MKRRRLLE 220
                               *      *      *

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Useful links:

1. WoLF PSORT: <https://wolfpsort.hgc.jp>
2. About WoLF PSORT: https://wolfpsort.hgc.jp/aboutWoLF_PSORT.html.en
3. PSORT II localization features <https://wolfpsort.hgc.jp/WoLFPSORTdoc/psortFeatureDescriptions.html>
4. PSORT: <https://psort.hgc.jp>