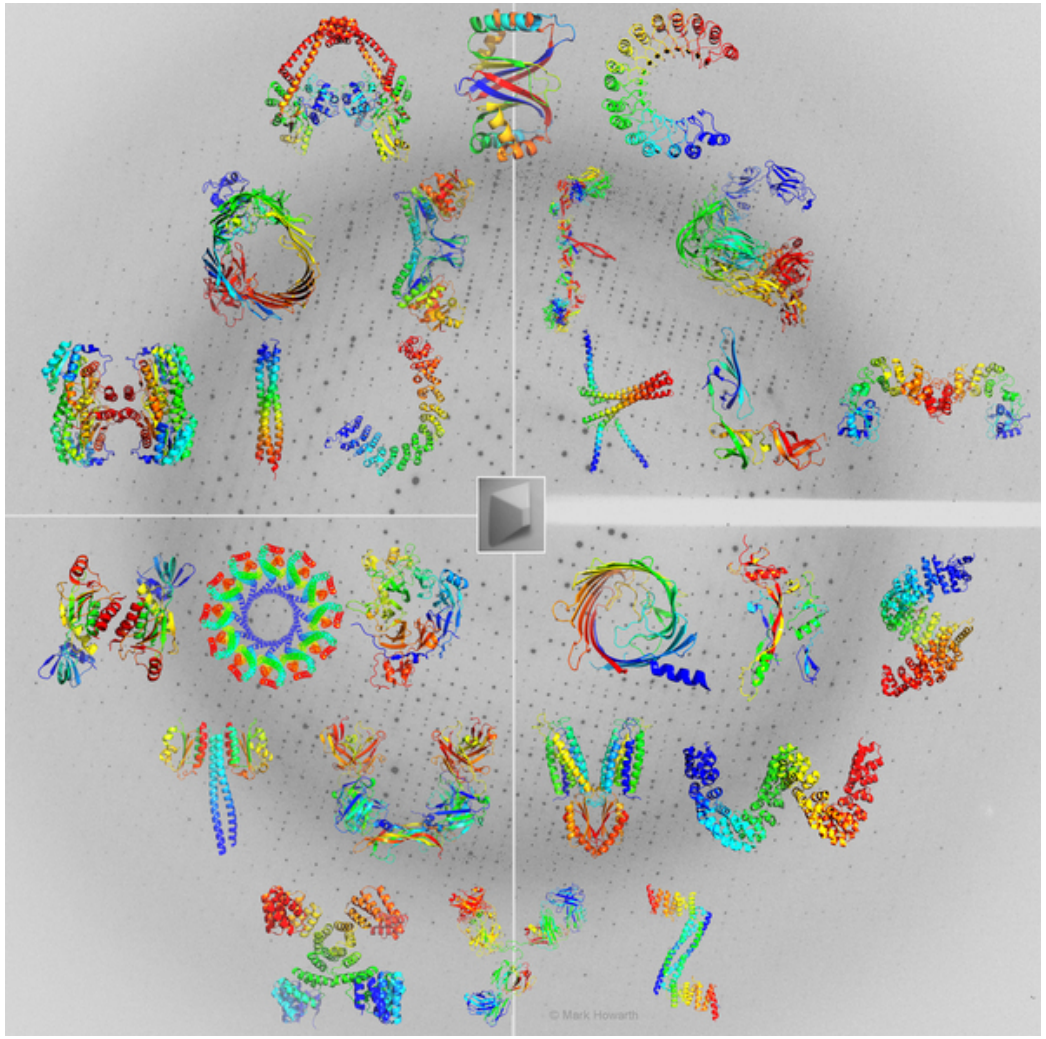
Databases and online tools for protein structure

Shaikh Nausad Hossain

Proteins



Why Protein structure?

- ❑ Understand the function
- ❑ Protein ligand interaction for drug discovery

Protein: Dihydropholate reductase
Drug: Trimethoprim

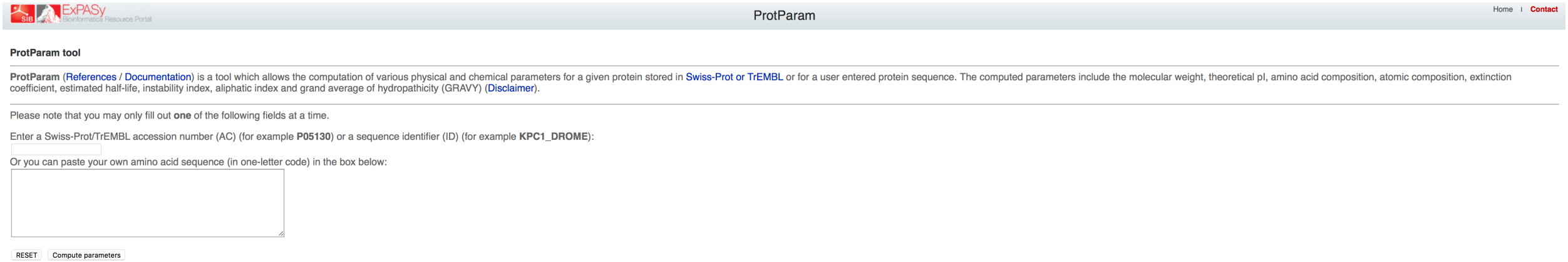
Protein Data Bank (PDB)

- ❑ 120057 structures deposited
- ❑ 111438 protein structures
- ❑ 2518 Membrane proteins

Protein sequence

- Prediction of domains
- Secondary structure prediction

Online tools for protein



- ❑ Molecular weight
- ❑ Isoelectic point
- ❑ Amino acid composition
- ❑ Atomic composition
- ❑ Extinction coefficient

- ❑ Half life
- ❑ Instability index
- ❑ Hydrophobicity

Domain prediction

ScanProsite Results Viewer

Ouput format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [help].

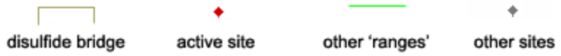
Hits for all PROSITE (release 20.127) motifs on sequence USERSEQ1 :

found: 4 hits in 1 sequence

USERSEQ1 (608 aa)

```
MKWLKQLQSLHTKLVIVYVLLIIIGMQIIGLYFTNNLEKELLDNFKKNITQYAKQLEISIEKVYDE
KGSVNAQKDIQNLLSEYANRQEIGEIRFIDKDQIIIATTKQSNRSLINQKANDSSVQKALSLGQSN
DHLILKDYGGGKDRVWVYNIPVKVDKKVIGNIYIESKINDVYNQLNNINQIFIVGTAISLLITVIL
GFFIARTITKPITDMRNQTVEMSKGNYTQRVKIYGNDEIGELALAFNNLSKRVQEAQANTESEKCR
LDSVITHMSDGIIATDRRGRIRIVNDMALKMLGMAKEDIIGYYMLSVLSLEDEFKLEEIQENNDSF
LLDLNEEEGLIARVNFSTIVQETGFVTGYIAVLHDVTEQQQVERERREFVANVSHELRTPLTSMNS
YIEALEEGAWKDEELAPQFLSVTREETERMIRLVNDLLQLSKMDNESDQINKEIIDFNMFINKIIN
RHEMSTKDTTFIRDIPKKTIFTEFDPDKMTQVFDNVITNAMKYSRGDKRVEFHVKQNPLYNRMTIR
IKDNGIGIPINKVDKIFDRFYRVDKARTRKMGGTGLGLAISKEIVEAHNGRIWANSVEGQGTSIFI
TLPCEVIEDGDWDE
```

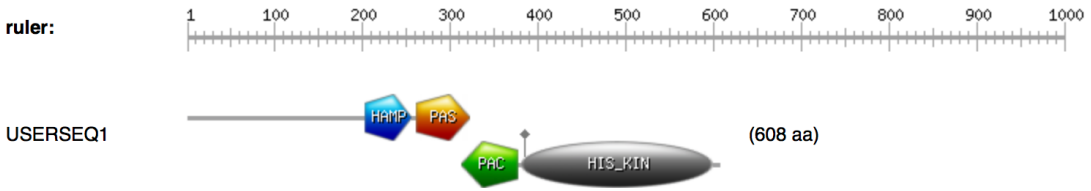
Legend:



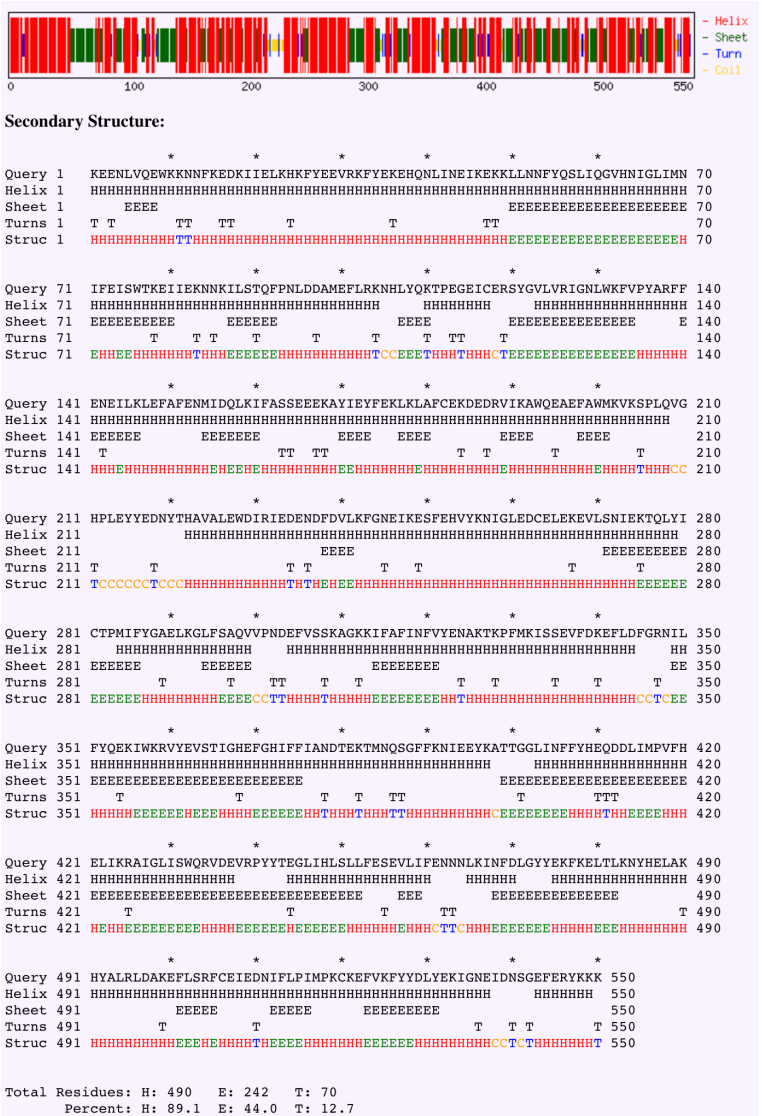
Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to http://prosite.expasy.org/mydomains/.

hits by profiles: [4 hits (by 4 distinct profiles) on 1 sequence]

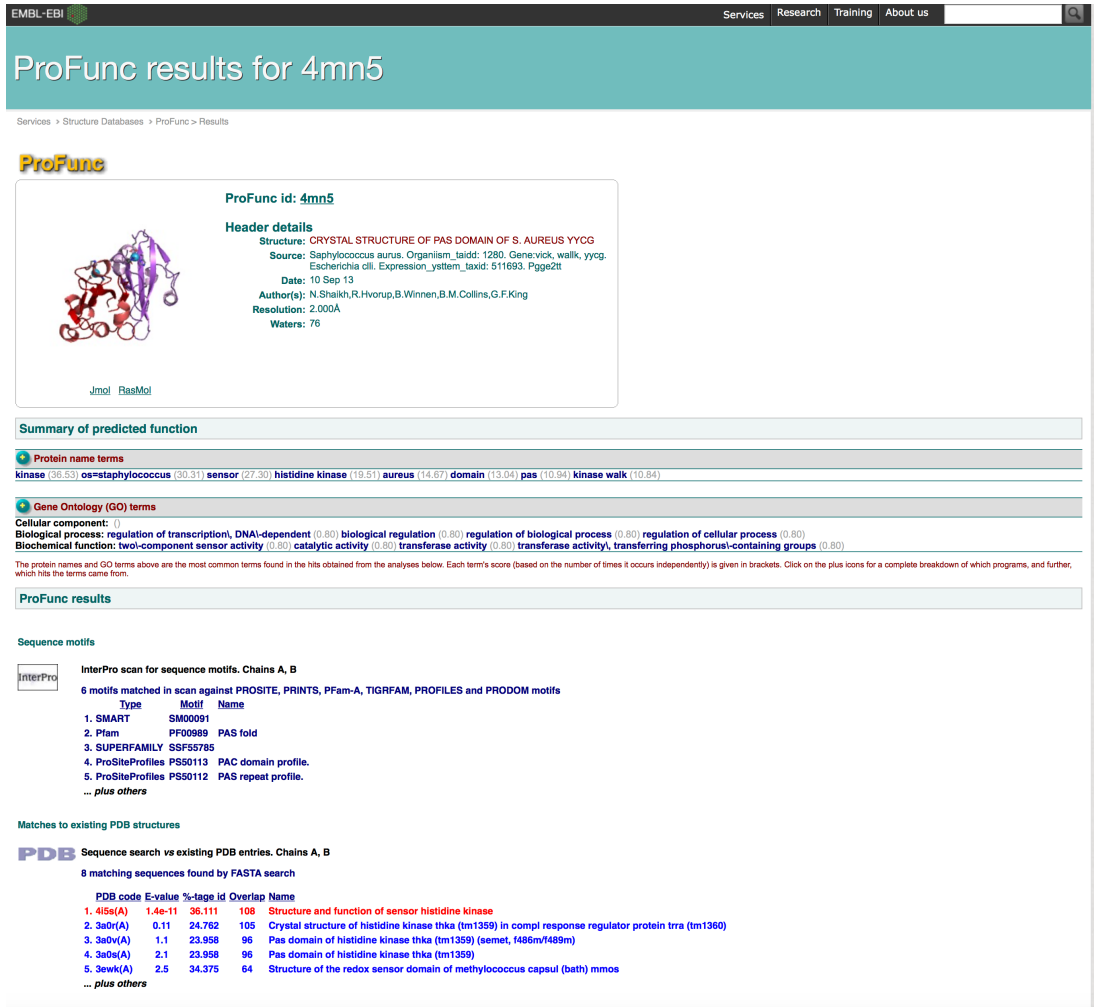
Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.



Secondary structure prediction



Functional analysis from structure



EMBL-EBI Services Research Training About us

ProFunc results for 4mn5

Services > Structure Databases > ProFunc > Results

ProFunc

ProFunc id: 4mn5

Header details

Structure: CRYSTAL STRUCTURE OF PAS DOMAIN OF S. AUREUS YYCG
Source: Saphylococcus aurus. Organiism_taidd: 1280. Gene:vick, wallk, yycg. Escherichia clli. Expression_ysttem_taxid: 511693. Pgge2tt
Date: 10 Sep 13
Author(s): N.Shaikh,R.Hvorup,B.Winnen,B.M.Collins,G.F.King
Resolution: 2.000Å
Waters: 76

Jmol RasMol

Summary of predicted function

Protein name terms

kinase (36.53) os=staphylococcus (30.31) sensor (27.30) histidine kinase (19.51) aureus (14.67) domain (13.04) pas (10.94) kinase walk (10.84)

Gene Ontology (GO) terms

Cellular component: ()
Biological process: regulation of transcription\, DNA\-dependent (0.80) biological regulation (0.80) regulation of biological process (0.80) regulation of cellular process (0.80)
Biochemical function: two\-component sensor activity (0.80) catalytic activity (0.80) transferase activity (0.80) transferase activity\, transferring phosphorus\-containing groups (0.80)

The protein names and GO terms above are the most common terms found in the hits obtained from the analyses below. Each term's score (based on the number of times it occurs independently) is given in brackets. Click on the plus icons for a complete breakdown of which programs, and further, which hits the terms came from.

ProFunc results

Sequence motifs

InterPro scan for sequence motifs. Chains A, B

6 motifs matched in scan against PROSITE, PRINTS, PFam-A, TIGRFAM, PROFILES and PRODOM motifs

	Type	Motif	Name
1.	SMART	SM00091	
2.	Pfam	PF00989	PAS fold
3.	SUPERFAMILY	SSF55785	
4.	ProSiteProfiles	PS50113	PAC domain profile.
5.	ProSiteProfiles	PS50112	PAS repeat profile.

... *plus others*

Matches to existing PDB structures

Sequence search *vs* existing PDB entries. Chains A, B

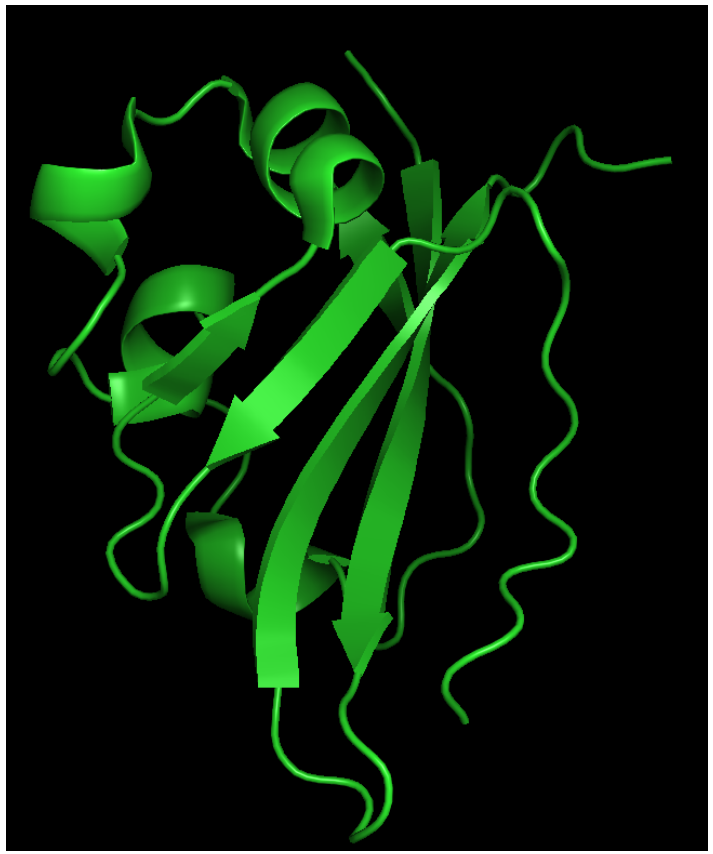
8 matching sequences found by FASTA search

	PDB code	E-value	%-tage id	Overlap	Name
1.	4i5s(A)	1.4e-11	36.111	108	Structure and function of sensor histidine kinase
2.	3a0r(A)	0.11	24.762	105	Crystal structure of histidine kinase thka (tm1359) in compl response regulator protein trra (tm1360)
3.	3a0v(A)	1.1	23.958	96	Pas domain of histidine kinase thka (tm1359) (semet, f486m/f489m)
4.	3a0s(A)	2.1	23.958	96	Pas domain of histidine kinase thka (tm1359)
5.	3ewk(A)	2.5	34.375	64	Structure of the redox sensor domain of methylococcus capsul (bath) mmos

... *plus others*

Input: PDB code

Structure matching



4MN5

4I5S

Sequence search

BLAST search *vs* Uniprot. Chains A, B

50 matching sequences found by BLAST search

Ref. no.	E-value	%-tage id	Overlap	Name
1. Q1ZZY3_STAAU	2e-55	96.262	107	Q1ZZY3 VicK (Fragment) OS=Staphylococcus aureus GN=vicK PE=4
2. WALK_STAAE	3e-51	95.327	107	A6QD58 Sensor protein kinase WalK OS=Staphylococcus aureus (strain
3. A0A0E1ACC5_STAAU	4e-51	96.226	106	A0A0E1ACC5 Two-component sensor kinase WalK OS=Staphylococcus
4. A0A133S0T2_9FIRM	7e-50	85.047	107	A0A133S0T2 PAS domain S-box protein (Fragment) OS=Veillonella
5. A0A0W3BNW6_STAHA	1e-48	87.850	107	A0A0W3BNW6 PAS domain-containing sensor histidine kinase OS=Staphylococcus

... plus others

Residue conservation analysis

Conservation mapped onto 3D structure.

Matching folds detected by PDBeFold

Matching folds. Chains A, B

24296 significant structural matches

Q-score	Rmsd	No. SSE	Z-score	PDB	Name
1. 0.860	0.74Å	9	13.5	4mn6	Crystal structure of truncated pas domain from s. Aureus yyc
2. 0.432	1.77Å	6	8.3	1g28	Structure of a flavin-binding domain, lov2, from the chimeric phytochrome/phototropin photoreceptor phy3
3. 0.428	2.10Å	5	8.1	1odv	Photoactive yellow protein 1-25 deletion mutant
4. 0.424	2.17Å	6	7.5	5iu1	N-terminal pas domain homodimer of ppanr map3k from physcomi patens.
5. 0.422	1.99Å	5	7.7	4hqa	Crystal structure of pas domain from the human erg (herg) po channel

... plus others

Nest analysis

Nest analysis. Chains A, B

4 nests located in the structure

Score	No. resid.	Ave. access-ibility	Cleft	Ave. conser-vation	Residues
1. 1.964	3	0.00	3	0.964	Arg282(A), Gly283(A), Arg284(A)
2. 1.634	3	0.00	4	0.634	Leu296(A), Gly297(A), Mse298(A)
3. 1.000	3	0.00	-	1.000	Thr353(A), Gly354(A), Phe355(A)
4. 0.905	4	0.00	-	0.905	Leu312(A), Ser313(A), Leu314(A), Glu315(A)

Cleft analysis

Surface clefts.

3D functional template searches

Enzyme active site templates.

No hits obtained from any of the 584 enzyme active site templates.

Ligand-binding templates.

1 significant hit out of 94055 ligand-binding templates.

Score	Template	PDB	Name
1. 174.117	PXGb0001	1b9i	Crystal structure of 3-amino-5-hydroxybenzoic acid (ahba) sy Het Group PXG

DNA-binding templates.

No hits obtained from any of the 5320 DNA-binding templates.

Nest analysis results for 4mn5 (chain A)

Services > Structure Databases > ProFunc > Results

ProFunc

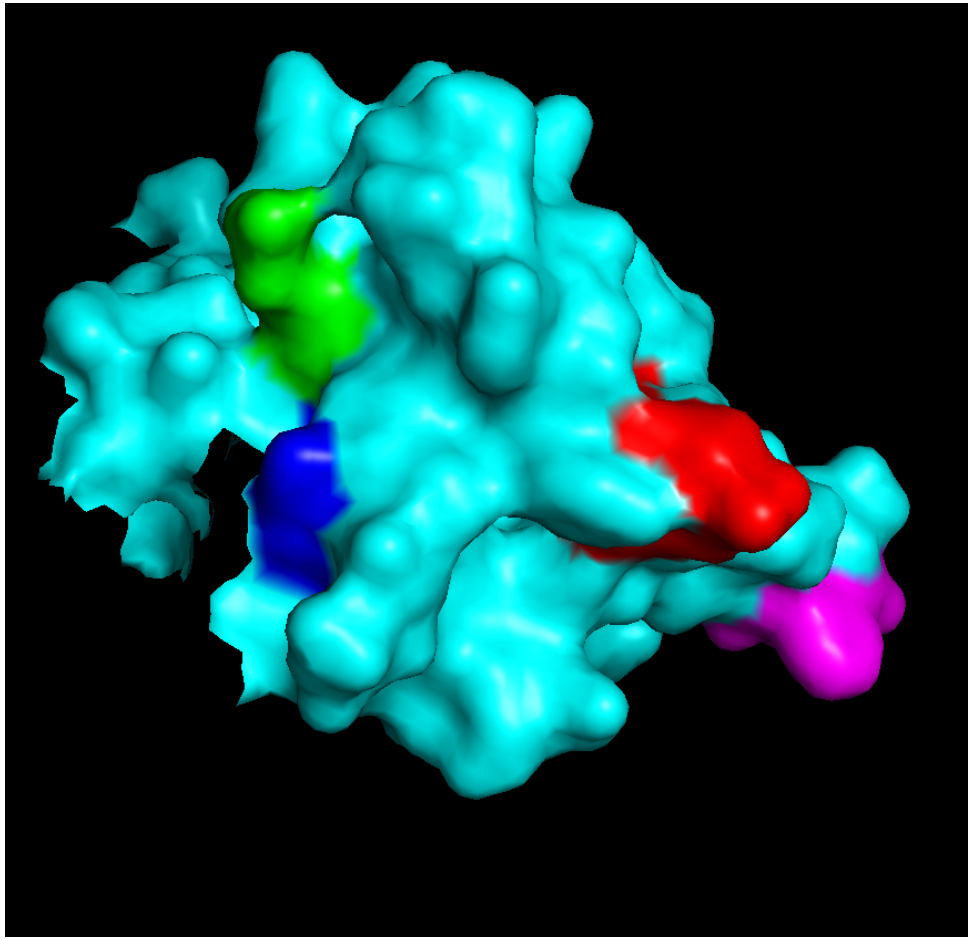
Nests are structural motifs that are often found in functionally important regions of protein structures.

4 nests were located in this chain, as shown below.

Nest	Score	Residue range	View in RasMol	Residue	Ramachandran region	Solvent accessibility	Cleft	Depth in cleft	Residue conservation
1.	1.96	Arg282(A)-Arg284(A)		Arg282(A)	RIGHT	0.00%	3	-	0.89
				Gly283(A)	LEFT	0.00%	-	-	1.00
				Arg284(A)	-	0.00%	-	-	1.00
2.	1.63	Leu296(A)-Mse298(A)		Leu296(A)	RIGHT	0.00%	-	-	0.90
				Gly297(A)	LEFT	0.00%	4	4.96	1.00
				Mse298(A)	-	0.00%	-	-	0.00
3.	1.00	Thr353(A)-Phe355(A)		Thr353(A)	RIGHT	0.00%	-	-	1.00
				Gly354(A)	LEFT	0.00%	-	-	1.00
				Phe355(A)	-	0.00%	-	-	1.00
4.	0.90	Leu312(A)-Glu315(A)		Leu312(A)	RIGHT	0.00%	-	-	1.00
				Ser313(A)	LEFT	0.00%	-	-	0.62
				Leu314(A)	RIGHT	0.00%	-	-	1.00
				Glu315(A)	RIGHT	0.00%	-	-	1.00

Key to table entries

Nest analysis



Possible ligand binding sites

Welcome to ArachnoServer

ArachnoServer is a manually curated database containing information on the sequence, three-dimensional structure, and biological activity of protein toxins derived from spider venom. Spiders are the largest group of venomous animals and they are predicted to contain by far the largest number of pharmacologically active peptide toxins (Escoubas et al., 2006). ArachnoServer has been custom-built so that a wide range of biological scientists, including neuroscientists, pharmacologists, and toxinologists, can readily access key data relevant to their discipline without being overwhelmed by extraneous information.

All spider toxin entries are sourced from UniProtKB/Swiss-Prot then manually curated by our expert team using available literature and patent information. Spider taxonomy is based on the latest version of the authoritative World Spider Catalog. A key feature of ArachnoServer is the use of a molecular target ontology based on the channel and receptor subtype definitions recommended by IUPHAR. Moreover, in addition to any legacy synonyms, all peptide toxins in the database have been assigned names according to the recently described rational nomenclature for spider toxins (King et al., 2008).

ArachnoServer allows advanced searches of toxin information, browsing, as well as similarity searches using BLAST. Each toxin record is displayed in a single page and, where available, a toxin's structure can be dynamically visualised.

You can get started by using the search box at the top of each page to search toxin names, synonyms, spider common names, and spider taxonomy. For advanced searches, click either the 'search' tab or the 'advanced' link below the search box. Help snippets are available at the top right corner of the 'search', 'browse' and 'blast' pages. You can download the user manual using the link at the top of each page.

Please find an example of curated toxin card here

Database Information

Toxins (total)	1525
Toxins (curated)	1407
Species	97

Please visit the download page to download data from ArachnoServer.

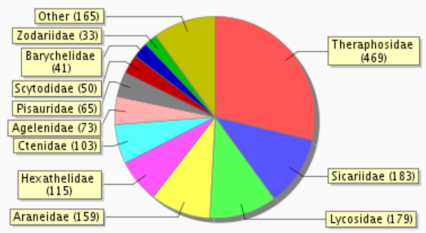
UPDATE: Please try out **Tox|Note**, our new pipeline to significantly fast track the analysis of spider venom-gland transcriptomes, by isolating all toxin/ toxin-like sequences generated by large Next Generation (NG) sequencing projects.

Tested with:

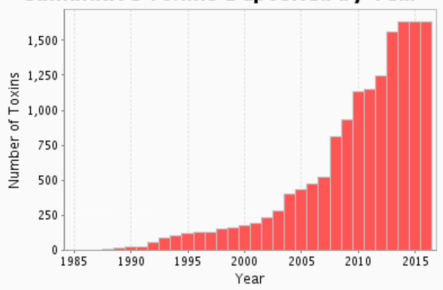
v7.0 v3.0 v3.2 v1.0 v9.6

But please enable javascript

Toxin Distribution by Family



Cumulative Toxins Deposited by Year



If you used ArachnoServer for your research and found it useful, please cite the manuscript:

Volker Herzig, David L. A. Wood, Felicity Newell, Pierre-Alain Chaumeil, Quentin Kaas, Greta J. Binford; Graham M. Nicholson; Dominique Gorse; Glenn F. King (2011) **ArachnoServer 2.0, an updated online resource for spider toxin sequences and structures.** *Nucleic Acids Research* **39**, D653-D657 | PubMed | Journal |

QFAB BIOINFORMATICS EMBL Australia Bioinformatics Resource The University Of Queensland AUSTRALIA IMB