



Short communication

ATDB 2.0: A database integrated toxin-ion channel interaction data

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ABSTRACT

We have developed an updated version of the Animal Toxin Database (ATDB 2.0) that provides a new bioinformatics resource for analyzing toxin-channel (T-C) interactions. Data on more than 54,000 T-C interactions, including 9193 high-confidence interactions, has been extracted, formatted and mapped to toxin and ion channel databases. The interaction data can be accessed easily through a new network browser on the website at <http://protchem.hunnu.edu.cn/toxin>. This resource may be useful for sequence pattern recognition and prediction of the function of new toxins.

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The Animal Toxin Database (ATDB) (He et al., 2008) is an integrative database of animal toxins. In recent two years, we have updated the database continually and taken great efforts to build an integrated platform for the toxin–target interaction data. It now contains more than 54,000 T-C interactions between 817 toxins and 1013 ion channels, including 9193 high-confidence interactions with active site information, as core dataset. These data are categorized carefully by species, toxin/ion channel types as well as interaction types (e.g., inhibition or activation). To facilitate the easy accessibility to these data, we built a new network browser. Other advanced features, such as an upgraded search engine, on-line 3D structural views and new sequence analysis tools are also available for more accurate analysis and less time consuming.

1. Data construct of ATDB 2.0

ATDB 2.0 consists of three parts of data: toxin, ion channel and toxin–channel interaction (Fig. 1A). The

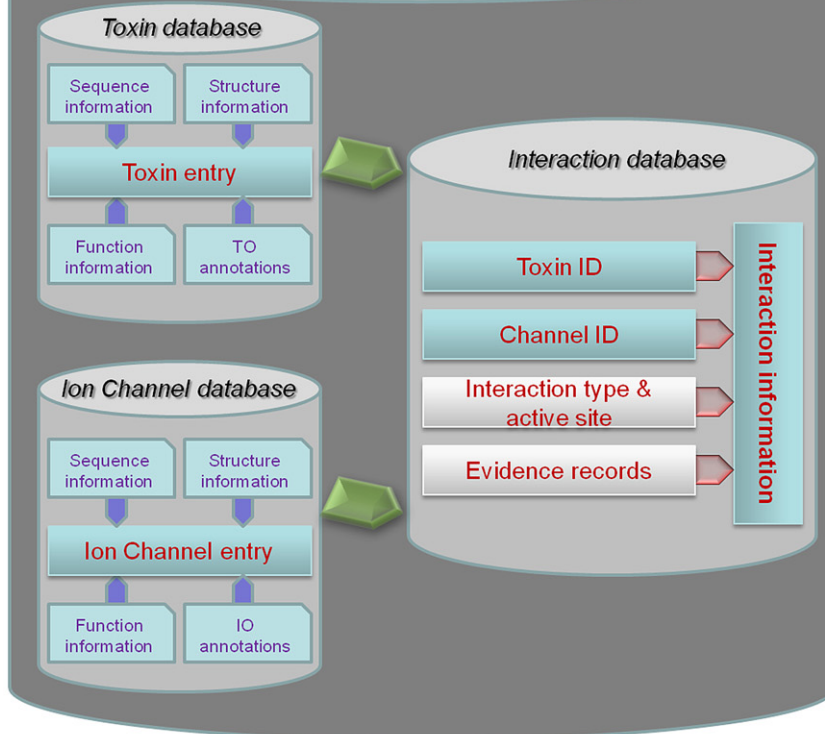
protein and nucleic acid sequences of ion channel were extracted from UniProtKB/Swiss-Prot, TrEMBL (Boeckmann et al., 2003), NCBI-nucleotide (Pruitt et al., 2007). Domain architectures of ion channel were determined by HMMER software based on the deposit of HMM models of PFAM (Finn et al., 2006) database version 23 with default parameters. 3D structure models were downloaded from PDB database (Berman et al., 2000). Pictures of more than 200 animal species were collected from internet. At last, 5097 protein sequences, 8396 nucleic acid sequences and 525 structure models of ion channels from 299 species were deposited in the dataset.

Because ion channels have complex features, it is necessary to create a hierarchic controlled term system (ion channel ontology) (Camerino et al., 2007; Catterall et al., 2005a,b; Clapham and Garbers, 2005; Clapham et al., 2005; Goldstein et al., 2005; Gutman et al., 2005; Hofmann et al., 2005; Kubo et al., 2005; Wei et al., 2005; Yu et al., 2005; Wood et al., 2009) to annotate and classify them.

The ion channel ontology (IO) contains 507 unique terms and was designed to answer six biological questions about ion channels (detailed information in <http://protchem.hunnu.edu.cn/toxin/Ontology/Introduction.jsp>).

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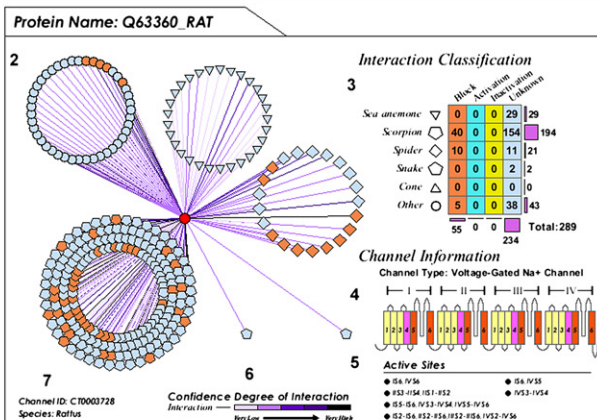
ATDB 2.0



Interaction detail view

Interaction | Detail view

1	Protein Name	Q63960_RAT	Taxon ID	10116	Species	Rattus norvegicus (Rat.)
	Function	SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein (By similarity).				
	Sequence	LFLVVFIFIS IFPMNSFAYV KHEAGIDGMV NFETGNSMI CLQITISAG WDGILLPIIL RPPDCSLDKE HPGSGFKGDK GNPVSQFFIF VSYVLIISFL VYRMVYIAL ENFSVATES ADLSEDDFE PDIITWEKFD PDAQTGFYEQ KLAFDAFLEE HPLRVKRFPP IELIADMLPM VSGDRIDKGL ILFATIKVVL GDSGEIIDL QMVERFASV NPSKVSYPEI TILTRAKGEE VSAVLQLRAY RGLMARAGFI CKKTTSMKLE NGQTHAKKEK STPTASLPS YDSVTKPEKE KQRAEEGR ERARKQGLR FSKC				



Confidence degree	Protein ID	Protein Name	Enzyme	Very High
	ALT1_PART1	Altitoxin.	IDA:PMID 15151	High
	BCTX1_BACCT	Babycurus-toxin 1	IDA:PubMed	Normal
	BEST_PART1	Bestoxin.	IDA:PMID 15151	Low
	BIRT_PART1	Birtoxin.	IDA:PMID 15151	Very Low
	CXDE4_CONA1	Delta-conotoxin Am 2766.	IDA:PMID 12423335	
	CXDE4_CONA1	Delta-conotoxin AVIA	IDA:PMID 14550575	
	CXDE4_CONA1	Delta-conotoxin AVIA	IDA:PMID 11683628	

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