

AKAPDB: A-Kinase Anchoring Proteins Database

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Abstract

A-kinase-anchoring proteins (AKAPs) are scaffold proteins which compartmentalize protein kinase A (PKA, cAMP-dependent protein kinase) and other enzymes to specific subcellular sites. The spatiotemporal control of these enzymes by AKAPs is important for cellular function like cell growth and development etc. Hence, it is important to understand the basic function of AKAPs and their functional domains. However, diverse names, function, cellular localizations and many members of AKAPs increase difficulties when researchers search appropriate AKAPs for their experimental purpose. Nevertheless, there was no previous AKAPs-related database regardless of their important cellular functions and difficulty of finding appropriate AKAPs. So, we developed AKAPs database (AKAPDB), which contains their sequence information, functions and other information derived from prediction programs and other databases. Therefore, we propose that AKAPDB can be an important tool to researchers in the related fields. AKAPDB is available via the internet at <http://plaza3.snu.ac.kr/akapdb/>

Keywords: a-kinase anchoring protein, database

Introduction

Cellular regulation is controlled by the opposing actions

of protein kinases and phosphatases (Scott and Pawson, 2000). The spatiotemporal control of these enzymes by AKAPs is important to metabolism, gene transcription, ion channel conductivity, cell growth, cell division and actin cytoskeleton rearrangements (Francis *et al.*, 1994; Scott, 1991). AKAPs are functionally similar, but structurally diverse protein family which can be classified on the basis of their ability to bind to PKA holoenzyme inside cells (Colledge *et al.*, 1999; Rubin, 1994). In spite of their structural diversity, AKAPs exist in many eukaryotic species, including humans, mice, rats, zebrafish, *C.elegans* and even yeast. All AKAPs share three common features: first, they have a PKA-anchoring domain; second, they have unique subcellular localization domains that target them to specific sites; third, they bind other signaling molecules to form multi-protein complexes (Wong *et al.*, 2004).

Moreover, AKAPs have been reported to have diverse names, function, cellular localizations and many members of wide range of species. Accordingly, it is rapidly increasing in difficulties to search each appropriate AKAP for specific purpose. However, there is not AKAPs-related database regardless of their important cellular function and difficulty of finding appropriate AKAPs.

Therefore, we developed AKAPDB as secondary database which focuses on a specific topic using from the primary database and other literature sources (Bishop, 1999). AKAPDB provides sequence information and diverse function of AKAPs in all reported eukaryotic species. It contains putative phosphorylation sites, functionally important domains and cellular localizations derived from prediction programs and other databases. In addition, it provides predicted zebrafish AKAP partial sequences which can be used for morpholino-induced zebrafish reverse genetics. Morpholinos, chemically modified antisense oligonucleotides (~25 bases) which bind and block their specific target mRNA, are an easy and efficient technology of zebrafish target-selected functional study (Nasevicius *et al.*, 2000). So, AKAPDB provides biologists with information which can be used to the efficient setup of experiments. AKAPDB can be useful to researchers by providing AKAPs information and integrated understanding of these diverse proteins.

Methods

Data acquisition

Raw data and information for AKAPDB were collected from a primary database such as NCBI. And the pub-

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lished scientific literatures resulted from queries with the terms 'A-kinase-anchoring proteins' and 'AKAP' were collected from PubMed (Wheeler *et al.*, 2003) and Google Scholar. Articles that have been identified to contain information suitable for the database were used to serve as the primary source for data in AKAPDB.

Basic information, such as 'Official symbol', 'Preferred Names', 'Other names', 'Organism', 'Function', 'mRNA', and 'Protein', were collected from NCBI. Cellular localization of AKAPs was collected from LOCATE (Fink *et al.*, 2006) and eSLDB (Pierleoni *et al.*, 2006). And GPS 2.1 (Xue *et al.*, 2008; Xue and Ren, 2009) served phosphorylation site which is important for function of AKAPs. SMART (Letunic *et al.*, 2008) provides the prediction of domain. In addition, the predicted zebrafish AKAP partial sequences were derived from MegaBLAST (Wheeler *et al.*, 2006). AKAPDB focuses on the diverse protein function and cellular location.

Queries and visualization

The records of AKAPDB consisted of diverse AKAPs. Each of them contained 16 fields, including information on name, cellular localization, function, species, mRNA sequence, protein sequence, putative phosphorylation site and predicted zebrafish AKAP partial sequences. Therefore, users can retrieve the data corresponding with names, Gene IDs, Protein IDs and species.

Data fields

Structure of data is made up 'Isoforms', 'Gene ID',

'Official symbol', 'Function', 'Preferred Names', 'Other names', 'Cellular localizations', 'Organism', 'mRNA ID', 'mRNA sequence', 'mRNA length', 'Protein ID', 'Protein sequence', 'Protein length' and 'Putative zebrafish AKAP'. The 'Cellular localizations' field represents the functional location of AKAPs in a cell. The 'Putative phosphorylation site' field serves the functionally important domains of AKAPs. And the 'Domain prediction' field represents a possible functional region. Also the 'Putative zebrafish AKAP' field provides potential zebrafish AKAP sequences. These fields are linked to NCBI for any additional information.

Table 1. Number of AKAPs of each species in the AKAPDB

Species	No. of AKAPs
Homo sapiens	41
Danio rerio	38
Rattus norvegicus	30
Mus musculus	29
Pan troglodytes	18
Bos taurus	17
Drosophila melanogaster	15
Macaca mulatta	15
Gallus gallus	12
Equus caballus	11
Ornithorhynchus anatinus	10
etc.	264
Total	500

AKAP DB HOME AKAP? SEARCH LINK HELP CONTACT US

A-Kinase anchoring protein: Database

AKAP8L Search

e) Official symbol, Gene IDs, Protein IDs, Species

Organism	Official symbol	Preferred Names	Gene ID	mRNA ID	Protein ID
Homo sapiens	AKAP8L	A kinase (PRKA) anchor protein 8-like	26993	NM_014371	NP_055186
Mus musculus	Akap8l	A kinase (PRKA) anchor protein 8-like	54194	NM_017476	NP_059504
Rattus norvegicus	Akap8l	A kinase (PRKA) anchor protein 8-like	299569	NM_001013946	NP_001013968
Canis lupus familiaris	AKAP8L	A kinase (PRKA) anchor protein 8-like	612946	XM_847928	XP_853021
Macaca mulatta	AKAP8L	A kinase (PRKA) anchor protein 8-like	719202	XM_001113053	XP_001113053
Bos taurus	AKAP8L	A kinase (PRKA) anchor protein 8-like	539700	XM_864732	XP_869825
Pan troglodytes	AKAP8L	A kinase (PRKA) anchor protein 8-like	455795	XM_512453	XP_512453
Gallus gallus	AKAP8L	A kinase (PRKA) anchor protein 8-like	776856		XP_001236353
Danio rerio	akap8l	A kinase (PRKA) anchor protein 8-like	406500	NM_213219	NP_998384

Fig. 1. Screenshot of a search result of AKAPDB. It shows 'Organism', 'Official symbol', 'Preferred Names', 'Gene ID', 'mRNA ID' and 'Protein ID'. The 'Putative zebrafish AKAP' below the table means potential zebrafish AKAP sequences. Users can search for the data based on names, Gene IDs, Protein IDs and species.

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