Pseudokinases in UniProtKB
a curator point-of-view

- Protein kinases form one of the largest protein families and are found in all species, from viruses to humans.
- They catalyze the reversible phosphorylation of proteins, often modifying their activity and localization.
- They are implicated in virtually all cellular processes and are one of the most intensively studied protein families.
- They are key therapeutic targets in drug development as natural mutations affecting kinase genes are the cause of a number of diseases.

- The vast amount of data contained in the primary literature and across a variety of biological data collections highlights the need for a repository where this information is stored in a concise and easily accessible manner.

UniProtKB provides the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

How are kinases annotated in UniProtKB?

How we assess if a kinase is active?
- Sequence analysis: presence of conserved aspartic acid in active site and ATP binding sites
- Experimental evidence
- Orthologs

Propagation between species always valid?

Annotation status
(2016_06 release)

418 kinases (ePK)

C.elegans kinome in UniProtKB

Catalytic activity status

Inactive kinases

How to identify and annotate other pseudoenzymes?
- Sequence analysis
- Experimental evidence
- Annotation: for the moment the lack of catalytic activity is reported in "Function" and EC number/catalytic activity are not added.

How to make this information searchable?

The advanced search allows users to refine the query for specific enzyme characteristics.

In addition to providing information related to enzymatic activity we also provide information on function, expression, subcellular location, protein interaction etc...

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