Aldo-keto reductase

The **aldo-keto reductase family** is a family of proteins that are subdivided into 16 categories; these include a number of related monomeric NADPH-dependent oxidoreductases, such as aldehyde reductase, aldose reductase, prostaglandin F synthase, xylose reductase, rho crystallin, and many others. [1]

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Structure

All possess a similar structure, with a beta-alpha-beta fold characteristic of nucleotide binding proteins. [2] The fold comprises a parallel beta-8/alpha-8-barrel, which contains a novel NADP-binding motif. The binding site is located in a large, deep, elliptical pocket in the C-terminal end of the beta sheet, the substrate being bound in an extended conformation. The hydrophobic nature of the pocket favours aromatic and apolar substrates over highly polar ones.[13]

Binding of the NADPH coenzyme causes a massive conformational change, reorienting a loop, effectively locking the coenzyme in place. This binding is more similar to FAD- than to NAD(P)-binding oxidoreductases.[4]

Examples

Some proteins of this family contain a potassium channel beta chain regulatory domain; these are reported to have oxidoreductase activity. [15]

See also

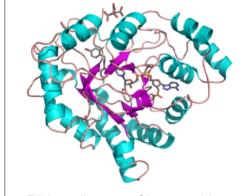
- AKR1
- Steroidogenic enzyme

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Aldo/keto reductase family



Ribbon diagram of human aldose reductase in complex with NADP+, citrate, and IDD594, a small molecule inhibitor. From PDB: 1us0 (https://ww w.rcsb.org/structure/1us0).

Identifiers Symbol Aldo_ket_red

Pfam PF00248 (http://pfam.xfa m.org/family?acc=PF0024

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InterPro IPR001395 (https://www.e bi.ac.uk/interpro/entry/IPR 001395)

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1ads (http://scop2.mrc-lm b.cam.ac.uk/search?t=txt; q=1ads) / SCOPe (https:// scop.berkeley.edu/pdb/cod e=1ads) / SUPFAM (http:// supfam.org/SUPERFAMIL Y/cgi-bin/search.cgi?searc h_field=1ads)

CDD cd06660 (https://www.ncb i.nlm.nih.gov/Structure/cd d/cddsrv.cgi?uid=cd06660)

Available protein structures:

structures (http://pfam.xfam.or Pfam g/family/PF00248?tab=pdbBl ock) / ECOD (http://prodata.s wmed.edu/ecod/complete/sea rch?kw=PF00248)

> RCSB PDB (https://www.rcsb. org/search?q=rcsb_polymer entity_annotation.annotation_i d:PF00248%20AND%20rcsb _polymer_entity_annotation.ty pe:Pfam); PDBe (https://www. ebi.ac.uk/pdbe/entry/search/in dex?pfam accession:PF0024 8); PDBj (https://pdbj.org/sear chFor?query=PF00248)

PDBsum structure summary (https://ww w.ebi.ac.uk/thornton-srv/datab ases/cgi-bin/pdbsum/GetPfam Str.pl?pfam_id=PF00248)

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