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.[3]

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.[5]

See also

- AKR1
- Steroidogenic enzyme

References

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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://www.rcsb.org/structure/1us0).

Identifiers	
Symbol	Aldo_ket_red
Pfam	PF00248 (http://pfam.xfam.org/family?acc=PF00248)
InterPro	IPR001395 (https://www.ebi.ac.uk/interpro/entry/IPR001395)
PROSITE	PDOC00061 (https://prosite.expasy.org/PDOC00061)
SCOP2	1ads (http://scop2.mrc-lmb.cam.ac.uk/search?t=txt;q=1ads) / SCOPe (https://scop.berkeley.edu/pdb/code=1ads) / SUPFAM (http://supfam.org/SUPERFAMILY/cgi-bin/search.cgi?search_field=1ads)
CDD	cd06660 (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=cd06660)
Available protein structures:	
Pfam	structures (http://pfam.xfam.org/family/PF00248?tab=pdbBlock) / ECOD (http://prodata.swmed.edu/ecod/complete/search?kw=PF00248)
PDB	RCSB PDB (https://www.rcsb.org/search?q=rcsb_polymer_entity_annotation.annotation_id:PF00248%20AND%20rcsb_polymer_entity_annotation.type:Pfam); PDBe (https://www.ebi.ac.uk/pdbe/entry/search/index?pfam_accession:PF00248); PDBj (https://pdbj.org/searchFor?query=PF00248)
PDBsum	structure summary (https://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPfamStr.pl?pfam_id=PF00248)
PDB	1a80 (https://www.rcsb.org/structure/1a80), 1abn (https://www.rcsb.org/structure/1abn), 1ads (https://www.rcsb.org/structure/1ads), 1ae4 (https://www.rcsb.org/structure/1ae4), 1afs (https://www.rcsb.org/structure/1afs), 1ah0 (https://www.rcsb.org/structure/1ah0), 1ah3 (https://www.rcsb.org/structure/1ah3), 1ah4 (https://w

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