Multicopper oxidase

In molecular biology, **multicopper oxidases** are <u>enzymes</u> which <u>oxidise</u> their substrate by accepting electrons at a mononuclear <u>copper centre</u> and transferring them to a trinuclear copper centre; <u>dioxygen binds</u> to the trinuclear centre and, following the transfer of four <u>electrons</u>, is <u>reduced</u> to two <u>molecules</u> of <u>water.[1]</u> There are three <u>spectroscopically</u> different <u>copper centres</u> found in multicopper oxidases: type 1 (or blue), type 2 (or normal) and type 3 (or coupled binuclear).[2][3] Multicopper oxidases consist of 2, 3 or 6 of these <u>homologous</u> domains, which also share homology with the cupredoxins <u>azurin</u> and <u>plastocyanin</u>. Structurally, these <u>domains</u> consist of a cupredoxin-like fold, a <u>beta-sandwich</u> consisting of 7 strands in 2 beta-sheets, arranged in a Greek-key beta-barrel.[4] Multicopper oxidases include:

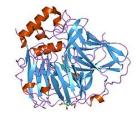
- Ceruloplasmin EC 1.16.3.1 (https://enzyme.expasy.org/EC/1.16.3.1) (ferroxidase), a 6-domain enzyme found in the serum of mammals and birds that oxidizes different inorganic and organic substances; exhibits internal sequence homology that appears to have evolved from the triplication of a Cu-binding domain similar to that of laccase and ascorbate oxidase.
- <u>Laccase EC 1.10.3.2</u> (https://enzyme.expasy.org/EC/1.10.3.2) (urishiol oxidase), a 3-domain enzyme found in <u>fungi</u> and plants, which oxidizes different <u>phenols</u> and <u>diamines</u>. CueO is a laccase found in <u>Escherichia coli</u> that is involved in copper-resistance. [4]
- Ascorbate oxidase <u>EC</u> 1.10.3.3 (https://enzyme.expasy.org/EC/1.10.3.3), a 3-domain enzyme found in higher plants.
- Nitrite reductase EC 1.7.2.1 (https://enzyme.expasy.org/EC/1.7.2.1), a 2-domain enzyme containing type-1 and type-2 copper centres. [5][6]

In addition to the above <u>enzymes</u> there are a number of other <u>proteins</u> that are similar to the multi-copper oxidases in terms of <u>structure</u> and sequence, some of which have lost the ability to bind copper. These include: copper resistance protein A (copA) from a <u>plasmid</u> in <u>Pseudomonas syringae</u>; domain A of (non-copper binding) <u>blood coagulation factors V (Fa V) and VIII (Fa VIII); [7] yeast Fet3p (FET3) required for ferrous iron uptake; [8] yeast hypothetical protein YFLO41w; and the fission yeast homologue SpAC1F7.08.</u>

References

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Multicopper oxidase (type 1)



crystal structures of e. coli laccase cueo under different copper binding situations

Identifiers		
Symbol	Cu-oxidase	
<u>Pfam</u>	PF00394 (http://pfam. xfam.org/family?acc= PF00394)	
Pfam clan	CL0026 (http://pfam.x fam.org/clan/CL0026)	
InterPro	IPR001117 (https://w ww.ebi.ac.uk/interpro/ entry/IPR001117)	
PROSITE	PDOC00076 (https://prosite.expasy.org/PDOC00076)	
SCOP2	1aoz (http://scop2.mr c-lmb.cam.ac.uk/sear ch?t=txt;q=1aoz) / SCOPe (https://scop. berkeley.edu/pdb/cod e=1aoz) / SUPFAM (h ttp://supfam.org/SUP ERFAMILY/cgi-bin/se arch.cgi?search_field =1aoz)	
Membranome	253 (http://membrano me.org/protein_superf amilies/253)	

Available protein structures:

Pfam	structures (http://pfam.xfam.or	
	g/family/PF00394?tab=pdbBl	
	ock) / ECOD (http://prodata.s	
	wmed.edu/ecod/complete/sea	
	rch?kw=PF00394)	
PDB	RCSB PDB (https://www.rcsb.	

RCSB PDB (https://www.rcsb. org/search?q=rcsb_polymer_ entity_annotation.annotation_i d:PF00394%20AND%20rcsb _polymer_entity_annotation.ty pe:Pfam); PDBe (https://www. ebi.ac.uk/pdbe/entry/search/in dex?pfam_accession:PF0039 4); PDBj (https://pdbj.org/sear chFor?query=PF00394) Lett. 553 (3): 239-44. doi:10.1016/S0014-5793(03)01000-7 (https://doi.org/10.10 16%2FS0014-5793%2803%2901000-7). PMID 14572631 (https://pubmed.ncbi.n lm.nih.gov/14572631). S2CID 85060706 (https://api.semanticscholar.org/CorpusI D:85060706).

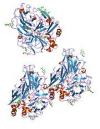
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PDBsum | structure summary (https://ww w.ebi.ac.uk/thornton-srv/datab ases/cgi-bin/pdbsum/GetPfam Str.pl?pfam_id=PF00394)

Multicopper oxidase (type 2)





active laccase from trametes versionler complexed with 2 E wyliding

versicolor complexed with 2,5-xylidine		
Identifiers		
Symbol	Cu-oxidase_2	
Pfam	PF07731 (http://pfam.xfam. org/family?acc=PF07731)	
Pfam clan	CL0026 (http://pfam.xfam.or g/clan/CL0026)	
InterPro	IPR011706 (https://www.eb i.ac.uk/interpro/entry/IPR01 1706)	
SCOP2	1aoz (http://scop2.mrc-lmb. cam.ac.uk/search?t=txt;q=1 aoz) / SCOPe (https://scop.	

Available protein structures:

oz)

berkeley.edu/pdb/code=1ao z) / SUPFAM (http://supfam. org/SUPERFAMILY/cgi-bin/ search.cgi?search_field=1a

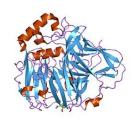
Pfam structures (http://pfam.xfam.or g/family/PF07731?tab=pdbBl ock) / ECOD (http://prodata.s wmed.edu/ecod/complete/sea rch?kw=PF07731) **PDB**

RCSB PDB (https://www.rcsb. org/search?q=rcsb_polymer entity annotation.annotation i d:PF07731%20AND%20rcsb polymer entity annotation.ty pe:Pfam); PDBe (https://www. ebi.ac.uk/pdbe/entry/search/in dex?pfam accession:PF0773 1); PDBj (https://pdbj.org/sear chFor?query=PF07731)

structure summary (https://ww w.ebi.ac.uk/thornton-srv/datab ases/cgi-bin/pdbsum/GetPfam Str.pl?pfam_id=PF07731)

Multicopper oxidase (type 3)

PDBsum



crystal structures of e. coli laccase cueo under different copper binding situations

Identifiers

Symbol Cu-oxidase 3

Pfam PF07732 (http://pfam.xfam. org/family?acc=PF07732)

Pfam CL0026 (http://pfam.xfam.or clan g/clan/CL0026)

InterPro IPR011707 (https://www.eb

i.ac.uk/interpro/entry/IPR01

1707)

SCOP2 1aoz (http://scop2.mrc-lmb.

> cam.ac.uk/search?t=txt;q=1 aoz) / SCOPe (https://scop. berkeley.edu/pdb/code=1ao z) / SUPFAM (http://supfam. org/SUPERFAMILY/cgi-bin/ search.cgi?search_field=1a

oz)

Available protein structures:

Pfam

structures (http://pfam.xfam.or g/family/PF07732?tab=pdbBl ock) / ECOD (http://prodata.s wmed.edu/ecod/complete/sea rch?kw=PF07732)

PDB RCSB PDB (https://www.rcsb.

org/search?q=rcsb_polymer entity annotation.annotation i d:PF07732%20AND%20rcsb _polymer_entity_annotation.ty pe:Pfam); PDBe (https://www. ebi.ac.uk/pdbe/entry/search/in dex?pfam_accession:PF0773 2); PDBj (https://pdbj.org/sear chFor?query=PF07732)

PDBsum structure summary (https://ww w.ebi.ac.uk/thornton-srv/datab ases/cgi-bin/pdbsum/GetPfam Str.pl?pfam_id=PF07732)

CMulti-copper polyphenol oxidoreductase laccase



crystal structure of protein cc_0490 from caulobacter crescentus, pfam duf152			
	Identifiers		
Symbol	Cu-oxidase_4		
Pfam	PF02578 (http://pfam.xfam. org/family?acc=PF02578)		
InterPro	IPR003730 (https://www.eb i.ac.uk/interpro/entry/IPR00 3730)		
Available protein structures:			
Pfam	structures (http://pfam.xfam.or g/family/PF02578?tab=pdbBl ock) / ECOD (http://prodata.s wmed.edu/ecod/complete/sea rch?kw=PF02578)		
PDB	RCSB PDB (https://www.rcsb.org/search?q=rcsb_polymer_entity_annotation.annotation_id:PF02578%20AND%20rcsb_polymer_entity_annotation.type:Pfam); PDBe (https://www.ebi.ac.uk/pdbe/entry/search/index?pfam_accession:PF02578); PDBj (https://pdbj.org/searchFor?query=PF02578)		
PDBsum	structure summary (https://ww w.ebi.ac.uk/thornton-srv/datab ases/cgi-bin/pdbsum/GetPfam Str.pl?pfam_id=PF02578)		

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