

Processing and curation of the biological knowledge in UniProtKB/Swiss-Prot



Choice of the protein to be annotated

- Update request
- family annotation
- collaborations
- direct submission
- "hot" topics
- new publication, ...

manual annotation by an expert team of biologists

Choice of the most accurate sequence

Bibliography
Literature search (PubMed, Patent databases, ...)
Nomenclature, ...

External expertise
Contact "wet" labs to get additional information or clarifications

Bioinformatics tools
InterPro scan
BLAST
SignalP, TargetP
Predotar
TMHMM, ESKW, MEMSAT etc.

Every new entry is submitted to a "checking program" to make sure that our annotation and format rules are enforced, and then double checked by a second annotator before integration in UniProtKB/Swiss-Prot

Protein or gene names
EC Number, ordered locus name, ORF name(s).
All synonyms found in the literature are cited and we are using a coherent nomenclature based on the names proposed by international and/or community-specific nomenclature committee.

Relevant articles describing: mRNA, genomic or protein sequences, function, regulation, expression, tissue specificity, mutations, PTM, diseases, ...
The type of information extracted from a given article is indicated in the first line of the reference block (RP line).
Links to PubMed are provided.

24 different topics in the comment section:
Free text and/or controlled vocabularies.
Includes **experimental qualifiers** to indicate the level of confidence (cf. Sequence features » below).

Cross-references to about 100 other databases
EMBL/GenBank/DBJ, Gramene, TAIR, InterPro, PROSITE, PDB, MIM, SGD, MGI, FlyBase, WormPep, RGD, HGNC, ...

Controlled vocabulary
Based on function, structure and other criteria

Experimentally proven, predicted or propagated features.
Includes experimental qualifiers:
« **By similarity** »: Experimental confirmation available for an homologous protein.
« **Probable** »: Not indicated by the authors, but inferred from other sources.
« **Potential** »: Predicted by computer analysis

Manually checked protein sequence
Protein sequences derived from the same gene are merged, the most accurate sequence is displayed and differences are fully documented

UniProtKB/Swiss-Prot entry Q42578

Entry information
Entry name: PER53, ARATH
Primary accession number: Q42578
Secondary accession numbers: None
Integrated into Swiss-Prot: December 6, 2002
Sequence was last modified on: November 1, 1998 (Sequence version 1)
Annotations were last modified on: May 16, 2006 (Entry version 60)

Name and origin of the protein
Protein name: Peroxidase 53 [Peroxidase]
Synonyms: P53, Aterox P53, ATPA2
Gene name: Name: PER53
Synonyms: P53
Ordered locus names: A0506720
ORF names: NP115.8
From: Arabidopsis thaliana (Mouse-ear cress) [TaxID: 3702]
Taxonomy: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosid1; Brassicales; Brassicaceae; Arabidopsis

References
[1] NUCLEOTIDE SEQUENCE STRAIN: Colombia
DOI: 10.1093/oxfordjournals.oxfordjournals.a012446 PubMed: 877116 [NCBI, EMBL, EBI, Israel, Japan]
Osterberg L, Aboody A K, Mattsson O, Wajander K, S...
[2] Structure and organ specificity of an anionic peroxidase from FES1. Let. 395: 245-247 (1998)
[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN: Colombia
DOI: 10.1093/oxfordjournals.oxfordjournals.a012446 PubMed: 1130714 [NCBI, EMBL, EBI]
Tabata S, Kaneko T, Nakamura Y, Kato H, Kato T, Asanuma E, Miyajima N, Sasamoto S, Kimura T, Hosokawa T, Kawasumi K, Kohno M, Matsuno M, Matsuno A, Muraki A, Nakayama S, Nakazaki N, Nishio K, Okumura S, Wakiyama P, F...
[4] Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana. Nature 405: 923-929 (2000)

Comments
• **FUNCTION** Removal of H₂O₂, oxidation of toxic reductants, biosynthesis and degradation of lignin, subunit of lignin, catalyzes the oxidation of phenolic compounds to quinones, which are then oxidized to catechols, which are then oxidized to catecholamines and then to catecholamines.
• **FUNCTION** Closely related to lignin formation by showing a catalytic activity. Oxidation of H₂O₂ to oxygen and water.
• **COFACTOR** Binds 2 calcium ions per subunit.
• **COFACTOR** Binds 2 calcium ions per subunit.
• **SUBCELLULAR LOCATION** Secreted protein (By similarity).
• **TISSUE SPECIFICITY** Mainly expressed in roots.
• **MISCELLANEOUS** There are 73 peroxidase genes in Arabidopsis.
• **SIMILARITY** Belongs to the peroxidase family. Class III plant class II peroxidase subfamily.

Cross-references
EMBL: X09952, CAAB82121.1, mRNA [EMBL/GenBank/DBJ][CC-0 Sequence]
EMBL: AF020322, BAB0806.1, Genomic DNA [EMBL/GenBank/DBJ][CC-0 Sequence]
EMBL: AY058186, AAL07035.1, mRNA [EMBL/GenBank/DBJ][CC-0 Sequence]
EMBL: AY067113, AAM02347.1, mRNA [EMBL/GenBank/DBJ][CC-0 Sequence]
EMBL: AY076704, AAM02311.1, mRNA [EMBL/GenBank/DBJ][CC-0 Sequence]
UniGene: At03
3D structure databases: 1P42, X-ray, A=31, 1004, X-ray, A=31, Detailed list of links
PDB: Q42578
Protein-protein interaction databases: Q42578
Genome annotation databases: GeneReviews: BAB0806.1, AT5G06720
Other: UniProt: Q42578
Ligand: View cluster of proteins with at least 50% / 100% / 100% identity
Keywords: 3D-structure, Calcium, Glycoprotein, Heme, Hydrogen peroxide, Peroxidase, Pyridoxal carboxylic acid, Signal

Sequence features
Feature table viewer
Key From To Length Description PTM
1 30 30 1 Proximal, N-terminus
CHAIN 31 335 305 Peroxidase 53, PRO_000003719
ACT_SITE 72 72 1 Peptide acceptor
METAL 73 73 1 Calcium 1
METAL 76 76 1 Calcium 1 (via covalent oxygen)
METAL 78 78 1 Calcium 1 (via covalent oxygen)
METAL 80 80 1 Calcium 1
METAL 82 82 1 Calcium 1
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