A screenshot of a computer

Description automatically generated with medium confidence

Additional transporter pfam Notes   
- InterPro: big database that combines member databases into one

Member DB sources (https://www.ebi.ac.uk/interpro/) :

* CATH-Gene3D : protein fams + domain architectures in complete genomes; based at University College, London, UK
* CDD: collection of multiple annotated sequence alignment models for ancient domains and full-length proteins; includes NCBI mod4els, and domain models from several external source databases
* HAMAP: profiles manually created by expert curators; based at Swiss institute of bioinformatics (SIB)
* NCBIfam: collection of protein families including multiple sequence alignment, HMMS, and annotation; includes TIGRFAM models; maintained at NCBI (national center for bioinfo)
* PANTHER: protein fam collection subdivided into functionally related subfamilies; using human experts; HMMs built for each fam + subfam; based at USC
* Pfam: large collection of multiple sequence allignments + HMMS covering many common protein domains; at EMBL-EBI, UK
* PIRSF: protein classification system w multiple sequence diversity levels form super to sub-families; at Protein Information Resource, Georgetown University med center
* Prints: compendium of protein fingerprints, U of Manchester
* PROSITE profiles & patterns: db of protein families and domainsthat help reliably identify a new sequence to a known protein family; at SIB
* SFLD: hierarchical classification of enzymes that relates specific sequence-structure features to specific chemical capabilities
* SMART: allows identification & annotation of genetically mobile domains and analysis of domain architecture; at EMBL Germany
* SUPERFAMILY: library of profile hidem HMMS representing proteins of known structure, library based on SCOP classification; based on university if Bristol

Possible issues:

* Each db seems to have a diff protein classification nomenclature
* Tcdoms standard not applicable here