

Supplementary data 4. *List of SCOP families involving cis – trans conversions, identified in this study.*

- a.2.11.1 - Fe,Mn superoxide dismutase (SOD), N-terminal domain
- a.3.1.8 Di-heme cytochrome c SoxA
- a.39.1.7 - EF-hand modules in multidomain proteins
- a.43.1.3 - CopG-like
- a.45.1.1 - Glutathione S-transferase (GST), C-terminal domain
- a.52.1.1 - Plant lipid-transfer and hydrophobic proteins
- a.61.1.6 - MMLV matrix protein-like
- a.102.2.1 - Class I alpha-1;2-mannosidase, catalytic domain
- a.104.1.1 - Cytochrome P450
- a.118.8.6 6 - SusD-like
- a.123.1.1 - Nuclear receptor ligand-binding domain
- a.133.1.2 - Vertebrate phospholipase A2
- b.1.18.2 - E-set domains of sugar-utilizing enzymes
- b.1.8.1 Cu,Zn superoxide dismutase-like
- b.2.2.2 Cellulose-binding domain family III
- b.3.1.3 - PUD-like
- b.3.4.1 Transthyretin (synonym: prealbumin)
- b.6.1.1 Plastocyanin/azurin-like
- b.7.1.2 Synaptotagmin-like (S variant)
- b.11.1.1 - Crystallins/Ca-binding development proteins
- b.18.1.10 - Family 6 carbohydrate binding module, CBM6
- b.18.1.18 - Family 27 carbohydrate binding module, CBM27
- b.18.1.33 3 - NPCBM-like
- b.29.1.1 - Legume lectins
- b.29.1.13 - Lectin leg-like
- b.29.1.2 - Glycosyl hydrolases family 16
- b.29.1.14 - vp4 sialic acid binding domain
- b.29.1.11 - Xylanase/endo-glucanase 11/12
- b.30.2.1 - Amine oxidase catalytic domain
- b.34.2.1 - SH3-domain
- b.34.9.1 - Tudor domain
- b.36.1.1 - PDZ domain
- b.40.4.5 - Cold shock DNA-binding domain-like
- b.40.5.1 - Inorganic pyrophosphatase
- b.42.1.2 - Interleukin-1 (IL-1)
- b.44.2.1 - Aminomethyltransferase beta-barrel domain
- b.50.1.2 - Pepsin-like
- b.52.1.1 - Eng V-like
- b.55.1.1 - Pleckstrin-homology domain (PH domain)
- b.55.1.2 - Phosphotyrosine-binding domain (PTB)
- b.67.2.1 - alpha-L-arabinanase-like
- b.68.1.1 - Sialidases (neuraminidases)
- b.68.6.1 - SGL-like
- b.70.1.1 - Quinoprotein alcohol dehydrogenase-like
- b.71.1.1 - alpha-Amylases, C-terminal beta-sheet domain
- b.72.2.1 - Carbohydrate binding domain
- b.74.1.1 - Carbonic anhydrase
- b.80.1.1 - Pectate lyase-like

b.80.1.3 - Galacturonase
b.81.1.5 - gamma-carbonic anhydrase-like
b.82.1.1 - dTDP-sugar isomerase
c.1.2.4 Tryptophan biosynthesis enzymes
c.1.4.1 FMN-linked oxidoreductases
c.1.6.1 Alanine racemase-like, N-terminal domain
c.1.8.4 Family 1 of glycosyl hydrolase
c.1.8.5 Type II chitinase
c.1.8.10 - alpha-D-glucuronidase/Hyaluronidase catalytic domain
c.1.10.1 - Class I aldolase
c.1.11.1 - Enolase
c.1.11.2 - D-glucarate dehydratase-like
c.1.16.1 - Bacterial luciferase (alkanal monooxygenase)
c.2.1.3 Glycerinaldehyde-3-phosphate dehydrogenase-like, N-terminal domain
c.2.1.5 LDH N-terminal domain-like
c.3.1.2 FAD-linked reductases, N-terminal domain
c.4.1.2 D-aminoacid oxidase, N-terminal domain
c.6.1.1 Glycosyl hydrolases family 6, cellulases
c.6.2.3 NodB-like polysaccharide deacetylase
c.10.2.1 - Internalin LRR domain
c.14.1.3 - Crotonase-like
c.18.1.1 - Uracil-DNA glycosylase
c.23.5.3 - Quinone reductase
c.23.16.2 - DJ-1/PfpI
c.26.2.3 - ETFP subunits
c.27.1.1 - Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
c.30.1.1 - BC N-terminal domain-like
c.108.1.1 - HAD-related
c.108.1.4 - Phosphoserine phosphatase
c.36.1.5 - Pyruvate oxidase and decarboxylase Pyr module
c.37.1.1 - Nucleotide and nucleoside kinases
c.37.1.8 - G proteins
c.37.1.10 - Nitrogenase iron protein-like
c.37.1.20 - Extended AAA-ATPase domain
c.41.1.1 - Subtilases
c.41.1.2 - Serine-carboxyl proteinase, SCP
c.42.1.1 - Arginase-like amidino hydrolases
c.47.1.1 - Thioltransferase
c.47.1.5 - Glutathione S-transferase (GST), N-terminal domain
c.47.1.10 - Glutathione peroxidase-like
c.47.1.12 - ArsC-like
c.51.2.1 - TolB, N-terminal domain
c.51.4.1 - ITPase (Ham1)
c.55.1.8 - Ppx/GppA phosphatase
c.55.3.5 - DnaQ-like 3'-5' exonuclease
c.56.2.1 - Purine and uridine phosphorylases
c.60.1.1 - Cofactor-dependent phosphoglycerate mutase
c.61.1.1 - Phosphoribosyltransferases (PRTases)
c.62.1.1 - Integrin A (or I) domain
c.66.1.3 - Fibrillarlin homologue
c.67.1.1 - AAT-like
c.67.1.3 - Cystathionine synthase-like

c.67.1.4 - GABA-aminotransferase-like
c.68.1.13 - Cytidilytransferase
c.69.1.1 - Acetylcholinesterase-like
c.69.1.2 - Carboxylesterase
c.69.1.3 - Mycobacterial antigens
c.69.1.27 7 - Hypothetical protein TT1662
c.69.1.8 - Haloalkane dehalogenase
c.69.1.10 - Carbon-carbon bond hydrolase
c.69.1.17 - Fungal lipases
c.71.1.1 - Dihydrofolate reductases
c.79.1.1 - Tryptophan synthase beta subunit-like PLP-dependent enzymes
c.80.1.1 - double-SIS domain
c.86.1.1 - Phosphoglycerate kinase
c.92.2.3 - Nitrogenase iron-molybdenum protein
c.93.1.1 - L-arabinose binding protein-like
c.94.1.2 - Transferrin
c.95.1.2 - Chalcone synthase-like
c.96.1.1 - Fe-only hydrogenase
c.123.1.1 - CoA-transferase family III (CaiB/BaiF)
d.1.1.2 Bacterial ribonucleases
d.3.1.1 Papain-like
d.14.1.2 - RNase P protein
d.15.2.2 - PBI domain
d.16.1.1 - GMC oxidoreductases
d.16.1.3 - D-aminoacid oxidase-like
d.16.1.6 - GDI-like
d.17.1.5 - Latexin-like
d.17.2.1 - Amine oxidase N-terminal region
d.19.1.1 - MHC antigen-recognition domain
d.20.1.1 - UBC-related
d.347.1.1 1 - Acetoacetate decarboxylase-like
d.21.1.1 - Diaminopimelate epimerase
d.24.1.1 - Pilin
d.24.1.2 - TcpA-like pilin
d.26.1.1 - FKBP immunophilin/proline isomerase
d.26.3.1 - Chitinase insertion domain
d.32.1.3 - Extradiol dioxygenases
d.37.1.1 - CBS-domain pair
d.52.3.1 - Prokaryotic type KH domain (KH-domain type II)
d.189.1.1 - PX domain
d.58.7.1 - Canonical RBD
d.250.1.1 1 - Aminomethyltransferase folate-binding domain
d.310.1.1 1 - VC0467-like
d.68.2.2 - Enolpyruvate transferase, EPT
d.212.1.2 - TonB
d.74.1.1 - PCD-like
d.79.4.1 - PurM N-terminal domain-like
d.273.1.1 1 - YjbQ-like
d.92.1.12 - Fungal zinc peptidase
d.92.1.2 - Thermolysin-like
d.92.1.9 - Reprolysin-like
d.92.1.11 - Matrix metalloproteases, catalytic domain
d.96.1.4 - Urate oxidase (uricase)
d.108.1.1 - N-acetyl transferase, NAT

d.110.1.1 - Profilin (actin-binding protein)
d.110.3.2 - Heme-binding PAS domain
d.111.1.1 - PR-1-like
d.122.1.1 - Heat shock protein 90, HSP90, N-terminal domain
d.124.1.1 - Ribonuclease Rh-like
d.127.1.1 - Creatinase/aminopeptidase
d.133.1.1 - Molybdenum cofactor-binding domain
d.134.1.1 - Nitrite and sulphite reductase 4Fe-4S domain-like
d.136.1.2 - Phospholipase D
d.227.1.1 - Ohr/OsmC resistance proteins
d.142.1.2 - BC ATP-binding domain-like
d.144.1.7 - Protein kinases, catalytic subunit
d.145.1.1 - FAD-linked oxidases, N-terminal domain
d.145.1.4 4 - CorC/HlyC domain-like
d.156.1.2 2 - Bacterial S-adenosylmethionine decarboxylase
d.157.1.2 - Glyoxalase II (hydroxyacylglutathione hydrolase)
d.160.1.2 - Carbamilase
d.165.1.1 - Plant cytotoxins
d.167.1.1 - Peptide deformylase
d.168.1.1 - Succinate dehydrogenase/fumarate reductase flavoprotein,
catalytic domain
d.169.1.1 - C-type lectin domain
e.5.1.1 Heme-dependent catalases
e.7.1.1 Inositol monophosphatase/fructose-1,6-bisphosphatase-like
e.22.1.2 - Iron-containing alcohol dehydrogenase
g.7.1.1 Snake venom toxins
g.68.1.1 - Ovomuroid domain III-like
h.1.1.1 Triple coiled coil domain of C-type lectins