

Evolution of Intrinsic Disorder in Protein Loops

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Table S2. List of ‘ordered’ loop prototypes mapped to SCOP FFs represented by their SCOP concise classification strings (*ccs*).

Loop prototype	SCOP <i>ccs</i>	Fold family (FF) description	Age (<i>nd</i>)	Molecular function	Function description	Venn group
DS.HG.2.1.35	e.18.1.1	Nickel-iron hydrogenase, large subunit	0.545	Metabolism	Other enzymes	AB
DS.HH.8.9.1	e.18.1.1	Nickel-iron hydrogenase, large subunit	0.545	Metabolism	Other enzymes	AB
DS.BK.5.93.1	d.41.1.1	CO dehydrogenase molybdo-protein N-domain-like	0.356	Metabolism	Electron transfer/transport	ABE
DS.BK.6.34.1	d.145.1.2	Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain	0.472	General	Small molecule binding	ABE
DS.BN.2.90.1	d.127.1.1	Creatinase/aminopeptidase	0.137	Intracellular processes	Proteases, peptidases, and their inhibitors	ABE
DS.BN.4.118.1	b.69.11.1	Putative isomerase YbhE	0.777	Metabolism	Other enzymes	ABE
DS.EH.2.19.5	c.1.12.7	Phosphoenolpyruvate mutase/Isocitrate lyase-like	0.335	Metabolism	Energy production and conversion	ABE
DS.EH.3.33.1	c.55.1.13	CoaX-like	0.3266	Metabolism	Other enzymes	ABE
DS.EH.4.88.1	c.36.1.6	TK-like Pyr module	0.193	General	Small molecule binding	ABE
DS.GH.0.1.119	d.90.1.1	NADH oxidase/flavin reductase	0.184	Metabolism	Electron transfer/transport	ABE
DS.HE.11.1.1	a.102.1.3	N-acylglucosamine (NAG) epimerase	0.472	Metabolism	Carbohydrate transport and metabolism	ABE
DS.HE.4.14.5	c.69.1.21	PepX catalytic domain-like	0.421	Metabolism	Other enzymes	ABE
DS.HE.5.27.3	c.1.9.15	PP1699/LP2961-like	0.356	Metabolism	Other enzymes	ABE
DS.HH.4.92.1	f.21.2.1	Fumarate reductase respiratory complex cytochrome b subunit, FrdC	0.502	Metabolism	Other enzymes	ABE
DS.HH.8.6.1	f.44.1.1	Ammonium transporter	0.270	Intracellular processes	Transport	ABE
DS.BK.4.16.1	e.1.1.1	Serpins	0.880	Intracellular processes	Proteases, peptidases, and their inhibitors	ABEV
DS.BK.6.65.1	d.144.1.6	APH phosphotransferases	0.210	Regulation	Kinases, phosphatases, and inhibitors	ABEV
DS.BK.7.1.2	c.10.2.7	Ngr ectodomain-like	0.987	General	General or several functions	ABEV
DS.BN.12.4.1	c.67.1.1	AAT-like	0.107	Metabolism	Transferases	ABEV
DS.BN.8.37.1	g.37.1.1	Classic zinc finger, C2H2	0.982	Regulation	DNA-binding (transcription factors)	ABEV
DS.EG.2.16.3	c.66.1.18	Mycolic acid cyclopropane synthase	0.326	Metabolism	Transferases	ABEV
DS.EG.2.16.4	c.66.1.49	BC2162-like	0.446	Metabolism	Transferases	ABEV
DS.EG.2.82.1	c.66.1.42	AD-003 protein-like	0.78969 957	Metabolism	Transferases	ABEV

DS.EH.0.1.88	c.68.1.7	1,3-glucuronyltransferase	0.876	Metabolism	Transferases	ABEV
DS.EH.1.27.1	c.7.1.2	R1 subunit of ribonucleotide reductase, C-terminal domain	0.481	Metabolism	Other enzymes	ABEV
DS.EH.2.9.10	c.3.1.6	Thi4-like	0.579	General	Small molecule binding	ABEV
DS.EH.3.77.1	c.53.2.1	beta-carbonic anhydrase, cab	0.283	Metabolism	Other enzymes	ABEV
DS.EH.4.73.1	c.69.1.1	Acetylcholinesterase-like	0.721	Metabolism	Other enzymes	ABEV
DS.GE.1.33.2	b.29.1.15	Trypanosoma sialidase, C-terminal domain	0.588	Metabolism	Secondary metabolites biosynthesis, transport, and catabolism	ABEV
DS.HE.2.23.2	b.50.1.2	Pepsin-like	0.841	Intracellular processes	Proteases, peptidases, and their inhibitors	ABEV
DS.HE.5.136.1	d.159.1.3	Protein serine/threonine phosphatase	0.343	Intracellular processes	Proteases, peptidases, and their inhibitors	ABEV
DS.HE.5.158.1	c.36.1.9	Pyruvate oxidase and decarboxylase PP module	0.253	General	Small molecule binding	ABEV
DS.HH.1.3.35	a.138.1.1	Cytochrome c3-like	0.532	Metabolism	Oxidation/reduction	ABEV
DS.HH.10.9.1	a.74.1.1	Cyclin	0.983	Regulation	DNA-binding (transcription factors)	ABEV
DS.HH.3.25.1	a.104.1.1	Cytochrome P450	0.974	Metabolism	Oxidation/reduction	ABEV
DS.HH.4.26.3	a.211.1.1	HD domain	0.094	Metabolism	Other enzymes	ABEV
DS.HH.4.50.1	a.25.1.2	Ribonucleotide reductase-like	0.485	Intracellular processes	Inorganic ion transport and metabolism	ABEV
DS.HH.4.70.1	a.211.1.2	PDEase	0.863	Metabolism	Other enzymes	ABEV
DS.HH.4.8.4	a.102.1.2	Cellulases catalytic domain	0.378	Metabolism	Carbohydrate transport and metabolism	ABEV
DS.GE.3.21.2	g.35.1.1	HIPIP (high-potential iron protein)	0.485	Metabolism	Electron transfer/transport	ABV
DS.EG.2.16.6	c.66.1.19	Histamine methyltransferase	0.588	Metabolism	Transferases	BE
DS.HH.5.10.3	a.123.1.1	Nuclear receptor ligand-binding domain	0.880	Regulation	Signal transduction	BE
DS.BK.3.56.2	b.22.1.1	TNF-like	0.858	Extracellular processes	Immune response	BEV
DS.EG.1.6.14	a.119.1.2	Animal lipoxygenases	0.678	Metabolism	Coenzyme metabolism	BEV
DS.EH.1.5.32	c.141.1.1	Glycerate kinase I	0.348	Metabolism	Other enzymes	BEV
DS.HH.9.11.1	d.42.1.1	BTB/POZ domain	0.970	General	Protein-protein interaction (dimerization domains)	BEV
DS.BK.4.96.1	b.2.5.7	DNA-binding domain from NDT80	0.704	Regulation	DNA-binding (transcription factors)	E
DS.HH.5.17.3	a.7.5.1	Tubulin chaperone cofactor A	0.678	Intracellular processes	Posttranslational modification, protein turnover, chaperones	E