Phyre2

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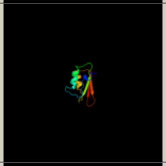
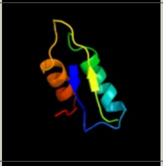
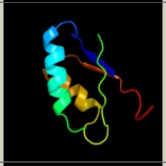
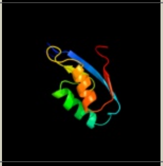
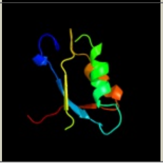
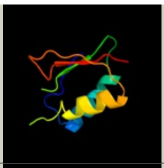
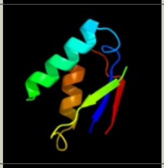
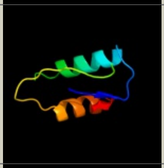
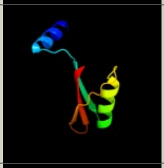
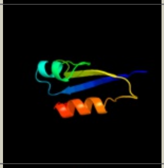
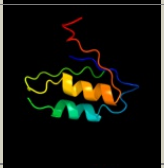
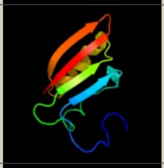
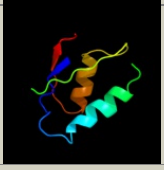
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dcja_	Alignment		99.9	100	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
2	d1je3a_	Alignment		99.9	30	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
3	d1pava_	Alignment		99.8	27	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
4	d1jdqa_	Alignment		99.8	30	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
5	c3hz7A_	Alignment		99.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
6	c1yg0A_	Alignment		90.5	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
7	c1y3kA_	Alignment		86.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
8	d1p6ta1	Alignment		82.0	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
9	d1p6ta2	Alignment		79.7	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	d1kvja_	Alignment		78.4	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
11	c2gcfA_	Alignment		74.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form

12	d2d9ia1	Alignment		73.0	12	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
13	d1cc8a_	Alignment		72.9	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
14	c2kt2A_	Alignment		71.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
15	c3qwuA_	Alignment		70.3	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
16	d2aw0a_	Alignment		70.3	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
17	d1q8la_	Alignment		70.2	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
18	c3grzA_	Alignment		68.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
19	c2vkcA_	Alignment		64.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
20	d2ggpb1	Alignment		64.8	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
21	d1s6ua_	Alignment	not modelled	64.3	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	c2l3mA_	Alignment	not modelled	61.4	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
23	c1yjrA_	Alignment	not modelled	60.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
24	d2qifa1	Alignment	not modelled	55.5	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
25	d1mwza_	Alignment	not modelled	54.2	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c2ldiA_	Alignment	not modelled	51.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
27	c2kyzA_	Alignment	not modelled	51.3	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
28	d1cpza_	Alignment	not modelled	48.4	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
29	c3dxsX_	Alignment	not modelled	48.2	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1;

29	[illegible]	Alignment	not modelled	46.2	14	**PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
30	c2aivA_	Alignment	not modelled	47.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**fragment of nucleoporin nup116/nsp116; **PDBTitle:** multiple conformations in the ligand-binding site of the2 yeast nuclear pore targeting domain of nup116p
31	d1osda_	Alignment	not modelled	46.1	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
32	d2nxca1	Alignment	not modelled	40.8	7	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
33	c2ofhX_	Alignment	not modelled	38.0	11	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
34	c3nf5A_	Alignment	not modelled	37.9	6	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup116; **PDBTitle:** crystal structure of the c-terminal domain of nuclear pore complex2 component nup116 from candida glabrata
35	d1afia_	Alignment	not modelled	36.9	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
36	d1sb6a_	Alignment	not modelled	35.2	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
37	c1ko6A_	Alignment	not modelled	34.9	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of c-terminal autoproteolytic domain of2 nucleoporin nup98
38	c2q5xA_	Alignment	not modelled	32.8	0	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** crystal structure of the c-terminal domain of hnup98
39	c2kkhA_	Alignment	not modelled	32.4	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
40	c3cg6A_	Alignment	not modelled	30.6	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible 45 gamma; **PDBTitle:** crystal structure of gadd45 gamma
41	c3kepA_	Alignment	not modelled	29.7	6	**PDB header:**protein transport, rna binding protein **Chain:** A: **PDB Molecule:**nucleoporin nup145; **PDBTitle:** crystal structure of the autoproteolytic domain from the2 nuclear pore complex component nup145 from saccharomyces3 cerevisiae
42	c3qd7X_	Alignment	not modelled	29.3	21	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
43	c2zqeA_	Alignment	not modelled	27.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
44	c2k2pA_	Alignment	not modelled	25.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
45	d1dusa_	Alignment	not modelled	24.9	4	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
46	d1fe0a_	Alignment	not modelled	24.7	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
47	c3ntaA_	Alignment	not modelled	24.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
48	d1y8ca_	Alignment	not modelled	23.9	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
49	d1uv7a_	Alignment	not modelled	22.9	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
50	c1uv7A_	Alignment	not modelled	22.9	15	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
51	d1wj4a_	Alignment	not modelled	22.8	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
52	c2kngA_	Alignment	not modelled	22.7	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
53	d1h8ca_	Alignment	not modelled	20.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
54	c2rmlA_	Alignment	not modelled	17.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa

55	d2cr5a1	Alignment	not modelled	17.1	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
56	d1jvaa3	Alignment	not modelled	17.1	9	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
57	c2rogA_	Alignment	not modelled	16.2	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
58	c3fpnB_	Alignment	not modelled	16.1	3	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
59	c2ziuA_	Alignment	not modelled	15.8	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
60	d2cc0a1	Alignment	not modelled	15.1	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
61	d1i42a_	Alignment	not modelled	13.2	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
62	c3qq5A_	Alignment	not modelled	12.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
63	c3icrA_	Alignment	not modelled	11.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
64	c3dlcA_	Alignment	not modelled	11.3	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosyl-l-methionine-dependent **PDBTitle:** crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
65	d1j23a_	Alignment	not modelled	11.1	14	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
66	c3ndjA_	Alignment	not modelled	11.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
67	d1l3ia_	Alignment	not modelled	11.0	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
68	c2jraB_	Alignment	not modelled	10.9	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein rpa2121; **PDBTitle:** a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
69	c2ga7A_	Alignment	not modelled	10.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
70	d2naca2	Alignment	not modelled	10.8	15	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
71	c3lteH_	Alignment	not modelled	10.8	14	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
72	d2obba1	Alignment	not modelled	10.3	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
73	c2pwyB_	Alignment	not modelled	10.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (adenine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a m1a58 trna methyltransferase
74	c2kxjA_	Alignment	not modelled	9.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubx domain-containing protein 4; **PDBTitle:** solution structure of ubx domain of human ubxd2 protein
75	c3fryB_	Alignment	not modelled	9.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a; **PDBTitle:** crystal structure of the copa c-terminal metal binding domain
76	c2zpmA_	Alignment	not modelled	9.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
77	c3d00A_	Alignment	not modelled	9.1	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit e; **PDBTitle:** crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
78	c2eseA_	Alignment	not modelled	8.9	22	**PDB header:**protein/rna complex **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** structure of the sam domain of vts1p in complex with rna
79	c2b6gA_	Alignment	not modelled	8.8	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** rna recognition by the vts1 sam domain

80	d1s3sg_	Alignment	not modelled	8.5	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
81	c2ropA_	Alignment	not modelled	8.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
82	c3evzA_	Alignment	not modelled	8.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
83	d2bgwa2	Alignment	not modelled	8.0	13	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
84	c3iz6A_	Alignment	not modelled	7.8	8	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
85	d2b2na1	Alignment	not modelled	7.6	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
86	c3hm2G_	Alignment	not modelled	7.5	7	**PDB header:**transferase **Chain:** G: **PDB Molecule:**precorrin-6y c5,15-methyltransferase; **PDBTitle:** crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
87	c3njrB_	Alignment	not modelled	7.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-6y methylase; **PDBTitle:** crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
88	c3c5yD_	Alignment	not modelled	7.0	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
89	d1o54a_	Alignment	not modelled	6.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
90	d1qupa2	Alignment	not modelled	6.4	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
91	c2dzkA_	Alignment	not modelled	6.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubx domain-containing protein 2; **PDBTitle:** structure of the ubx domain in mouse ubx domain-containing2 protein 2
92	c3hjhA_	Alignment	not modelled	6.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair-coupling factor; **PDBTitle:** a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
93	c3mruB_	Alignment	not modelled	6.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
94	c3fpnA_	Alignment	not modelled	5.9	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**geobacillus stearothermophilus uvra interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
95	c2aj1A_	Alignment	not modelled	5.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
96	d2b25a1	Alignment	not modelled	5.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
97	d1u0sy_	Alignment	not modelled	5.7	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	c2rpiA_	Alignment	not modelled	5.7	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
99	d2ciwa1	Alignment	not modelled	5.6	38	**Fold:**EF Hand-like **Superfamily:**Cloroperoxidase **Family:**Cloroperoxidase