Phyre2

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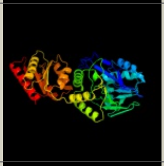
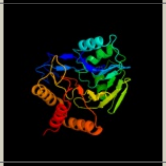
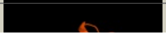
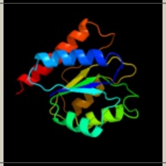
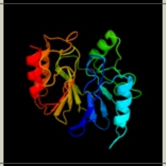
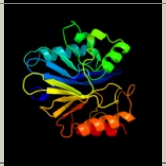
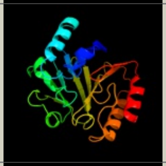
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ychD_	Alignment		100.0	41	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
2	c2q9uB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
3	c1vmeB_	Alignment		100.0	24	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
4	c1e5dA_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
5	c2ohiB_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
6	c3hnnD_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative diflavin flavoprotein a 5; **PDBTitle:** crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
7	d1ycga2	Alignment		100.0	45	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
8	d1e5da2	Alignment		100.0	36	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
9	d1vmea2	Alignment		100.0	29	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
10	d2q0ia1	Alignment		100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
11	d1m2xa_	Alignment		100.0	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
						

12	c3fniA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
13	c2zo4A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
14	c3hlyA_	Alignment		100.0	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
15	d1ko3a_	Alignment		100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
16	d2gmna1	Alignment		100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
17	d1mqoa_	Alignment		100.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
18	c2cfuA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
19	d1ycga1	Alignment		100.0	36	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	d2cfua2	Alignment		100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
21	d1znba_	Alignment	not modelled	100.0	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
22	d1jjta_	Alignment	not modelled	100.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
23	d1e5da1	Alignment	not modelled	100.0	31	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
24	c3lvzA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr6230 protein; **PDBTitle:** new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
25	d1vmea1	Alignment	not modelled	100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
26	c3rkjA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
27	c3l6nA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
28	c2yz3B_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
29	c3spuB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1;

						PDBTitle: apo ndm-1 crystal structure
30	d2aioa1	Alignment	not modelled	100.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
31	d1x8ha_	Alignment	not modelled	100.0	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
32	c2fhxB_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
33	d1k07a_	Alignment	not modelled	100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
34	c3sd9B_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
35	d2arka1	Alignment	not modelled	99.9	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
36	d1xm8a_	Alignment	not modelled	99.9	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
37	c3adrA_	Alignment	not modelled	99.9	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1585; **PDBTitle:** the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfolobus tokodaii
38	c3tp9B_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
39	c3d7nA_	Alignment	not modelled	99.9	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
40	c3r2uC_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
41	d2qeda1	Alignment	not modelled	99.9	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
42	d2a5la1	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
43	c2gcuD_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
44	d2fz5a1	Alignment	not modelled	99.9	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
45	d1qh5a_	Alignment	not modelled	99.9	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
46	d5nula_	Alignment	not modelled	99.9	28	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
47	c3b6iB_	Alignment	not modelled	99.9	22	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
48	c3aj3A_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
49	d2p97a1	Alignment	not modelled	99.9	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
50	c2xf4A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
51	c2zkiH_	Alignment	not modelled	99.9	21	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
52	c2p18A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
53	c3f6sI_	Alignment	not modelled	99.9	18	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
54	d1ydga_	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily

55	c2zwrA_	Alignment	not modelled	99.8	21	protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
56	c2r2dC_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
57	c3eshB_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
58	d1f4pa_	Alignment	not modelled	99.8	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
59	c3zq4C_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease j 1; **PDBTitle:** unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
60	c3klbA_	Alignment	not modelled	99.8	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
61	c2hnbA_	Alignment	not modelled	99.8	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
62	c2p4zA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal-dependent hydrolases of the beta-lactamase **PDBTitle:** a ferredoxin-like metallo-beta-lactamase superfamily protein from2 thermoanaerobacter tengcongensis
63	d1ztca1	Alignment	not modelled	99.8	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
64	c2br6A_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
65	c3bk2A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
66	c1p9eA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
67	d1p9ea_	Alignment	not modelled	99.8	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
68	d1b1ca_	Alignment	not modelled	99.7	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
69	d1ykga1	Alignment	not modelled	99.7	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
70	d1oboa_	Alignment	not modelled	99.7	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
71	c2xr1A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
72	d1ag9a_	Alignment	not modelled	99.7	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
73	c3edoA_	Alignment	not modelled	99.7	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
74	d1czna_	Alignment	not modelled	99.6	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
75	d1sqsa_	Alignment	not modelled	99.6	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
76	d2i7ta1	Alignment	not modelled	99.6	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
77	d1yoba1	Alignment	not modelled	99.6	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
78	c2xr1B_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
79	c3af5A_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404

						from2 pyrococcus horikoshii
80	d2i7xa1	Alignment	not modelled	99.6	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
81	c2i7xA_	Alignment	not modelled	99.6	12	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
82	c2ycbA_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
83	d1bvyf_	Alignment	not modelled	99.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
84	c1bvyF_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
85	d1ja1a2	Alignment	not modelled	99.6	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
86	d2dkfa1	Alignment	not modelled	99.6	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
87	c1zkpD_	Alignment	not modelled	99.6	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ba1088; **PDBTitle:** 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homolgue of bacillus anthracis, a putative3 ribonuclease
88	c3hr4C_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
89	c2az4A_	Alignment	not modelled	99.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ef2904; **PDBTitle:** crystal structure of a protein of unknown function from enterococcus2 faecalis v583
90	d2fcra_	Alignment	not modelled	99.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
91	c2wc1A_	Alignment	not modelled	99.5	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
92	c2hpvA_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
93	d1tlla2	Alignment	not modelled	99.4	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
94	c3h3eA_	Alignment	not modelled	99.4	21	**PDB header:**structural genomics, metal binding prote **Chain:** A: **PDB Molecule:**uncharacterized protein tm1679; **PDBTitle:** crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
95	d1t5ba_	Alignment	not modelled	99.4	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
96	c3p0rA_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
97	d1fuea_	Alignment	not modelled	99.4	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
98	d1zkpa1	Alignment	not modelled	99.4	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
99	c2q62A_	Alignment	not modelled	99.4	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
100	c2v9cA_	Alignment	not modelled	99.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1; **PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
101	d2z98a1	Alignment	not modelled	99.3	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
102	c3fvwA_	Alignment	not modelled	99.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
103	c3k1yE_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
104	c2vzhA_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex

105	d1rlia_	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
106	c3f2vA_	Alignment	not modelled	99.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
107	d2qwxa1	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
108	c3kl7A_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
109	d1t0ia_	Alignment	not modelled	99.3	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
110	c2fzvC_	Alignment	not modelled	99.3	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
111	c3lcmB_	Alignment	not modelled	99.2	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
112	d1y44a1	Alignment	not modelled	99.2	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
113	c3g1pA_	Alignment	not modelled	99.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12
114	c3zwfA_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
115	c1tllA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
116	d1nni1_	Alignment	not modelled	99.1	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
117	d1rtta_	Alignment	not modelled	99.1	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
118	c2bibA_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
119	c3rpeA_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
120	c3md7A_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase-like; **PDBTitle:** crystal structure of a beta-lactamase-like protein bound to gmp from2 brucella melitensis