Phyre^2

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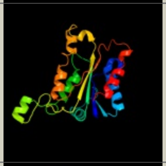
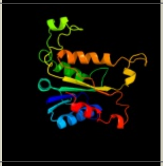
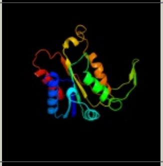
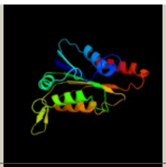
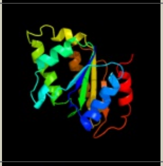
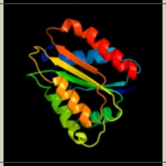
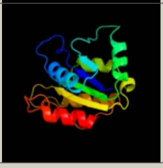
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rpeA_	Alignment		100.0	67	**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.
2	c2amjD_	Alignment		100.0	98	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
3	d1qrda_	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
4	d1d4aa_	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
5	d1dxqa_	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
6	c3eywA_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
7	c3ha2B_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
8	d2qwxa1	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
9	c3f2vA_	Alignment		100.0	24	**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.
10	c3lcmB_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
11	d1t5ba_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase

12	c2hpvA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
13	c3p0rA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
14	d2z98a1	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
15	c2v9cA_	Alignment		100.0	16	**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.
16	d1rlia_	Alignment		99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
17	d1rtta_	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
18	c3fvwA_	Alignment		99.9	18	**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.
19	d1sqsa_	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
20	d1nni1_	Alignment		99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
21	c3k1yE_	Alignment	not modelled	99.9	12	**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
22	d1t0ia_	Alignment	not modelled	99.8	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
23	c2vzhA_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
24	c2q62A_	Alignment	not modelled	99.8	25	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
25	d1ydga_	Alignment	not modelled	99.8	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
26	c2fzvC_	Alignment	not modelled	99.7	21	**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
27	d2fzva1	Alignment	not modelled	99.7	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
28	c3b6iB_	Alignment	not modelled	99.7	16	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure

29	d2a5la1	Alignment	not modelled	99.7	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
30	c2zkiH_	Alignment	not modelled	99.6	20	**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)
31	d1e5da1	Alignment	not modelled	99.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	c3d7nA_	Alignment	not modelled	99.6	14	**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
33	d1ycga1	Alignment	not modelled	99.6	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
34	d1vmea1	Alignment	not modelled	99.5	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
35	c2ohiB_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
36	c1ychD_	Alignment	not modelled	99.5	19	**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
37	d2arka1	Alignment	not modelled	99.3	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
38	c2q9uB_	Alignment	not modelled	99.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
39	c3klbA_	Alignment	not modelled	99.3	20	**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
40	c1e5dA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
41	c1vmeB_	Alignment	not modelled	99.2	8	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
42	c3fniA_	Alignment	not modelled	99.1	12	**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
43	c3hlyA_	Alignment	not modelled	99.0	15	**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.
44	c3edoA_	Alignment	not modelled	99.0	18	**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
45	d2fz5a1	Alignment	not modelled	98.7	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
46	d5nula_	Alignment	not modelled	98.5	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
47	d1oboa_	Alignment	not modelled	98.3	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
48	c3f6sI_	Alignment	not modelled	98.2	16	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
49	d1b1ca_	Alignment	not modelled	98.2	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
50	d1czna_	Alignment	not modelled	98.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	c2hnbA_	Alignment	not modelled	98.1	11	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
52	d1ag9a_	Alignment	not modelled	98.1	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
53	d1bvyf_	Alignment	not modelled	98.0	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
						PDB header:oxidoreductase

54	c1bvyF_	Alignment	not modelled	98.0	14	**Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
55	c2wc1A_	Alignment	not modelled	97.9	15	**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
56	d1ykga1	Alignment	not modelled	97.8	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
57	d1tlla2	Alignment	not modelled	97.7	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
58	d1ja1a2	Alignment	not modelled	97.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
59	d1f4pa_	Alignment	not modelled	97.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	d2fcra_	Alignment	not modelled	97.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
61	c3hr4C_	Alignment	not modelled	97.6	13	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
62	d1yoba1	Alignment	not modelled	97.3	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
63	d1fuea_	Alignment	not modelled	96.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
64	c1j9zB_	Alignment	not modelled	95.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
65	c1tllA_	Alignment	not modelled	93.8	9	**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.
66	c3u80A_	Alignment	not modelled	92.7	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii; **PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
67	c2bpoA_	Alignment	not modelled	88.0	14	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
68	d1uqra_	Alignment	not modelled	86.6	19	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
69	d2r4qa1	Alignment	not modelled	71.6	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
70	d1uana_	Alignment	not modelled	66.7	14	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
71	d2a9va1	Alignment	not modelled	65.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
72	c3l4eA_	Alignment	not modelled	63.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
73	c2kyrA_	Alignment	not modelled	61.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
74	c2x2oA_	Alignment	not modelled	61.4	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
75	c3s40C_	Alignment	not modelled	59.9	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
76	d1qdlb_	Alignment	not modelled	56.0	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
77	c3czcA_	Alignment	not modelled	52.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
78	d2p1ra1	Alignment	not modelled	50.6	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
79	c1tvmA_	Alignment	not modelled	47.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2

						phosphoenolpyruvate-dependent phosphotransferase system
80	c3crnA_	Alignment	not modelled	46.9	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like; **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
81	c2r60A_	Alignment	not modelled	42.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
82	d2dlda2	Alignment	not modelled	42.0	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
83	d2hrca1	Alignment	not modelled	40.6	13	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
84	d1iiba_	Alignment	not modelled	39.5	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
85	c2g76A_	Alignment	not modelled	38.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
86	c3nbmA_	Alignment	not modelled	38.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
87	c3dhnA_	Alignment	not modelled	38.3	17	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
88	d2r48a1	Alignment	not modelled	38.2	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
89	c3kklA_	Alignment	not modelled	35.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
90	d2naca2	Alignment	not modelled	34.5	26	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
91	c2l2qA_	Alignment	not modelled	34.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
92	d1dxya2	Alignment	not modelled	34.4	18	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
93	c3o1hB_	Alignment	not modelled	34.1	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
94	c3lwzC_	Alignment	not modelled	33.1	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
95	c3i42A_	Alignment	not modelled	32.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
96	d1t4za_	Alignment	not modelled	32.1	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
97	d1iowa1	Alignment	not modelled	31.5	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
98	c3jteA_	Alignment	not modelled	30.4	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
99	d1fyea_	Alignment	not modelled	29.5	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
100	c2gcgB_	Alignment	not modelled	29.4	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
101	d1gtza_	Alignment	not modelled	29.2	13	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
102	c3ia7A_	Alignment	not modelled	28.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
						PDB header:viral protein,transferase

103	c3oy2A_	Alignment	not modelled	27.5	14	**Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
104	c2pv7B_	Alignment	not modelled	26.7	27	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
105	d2hy5b1	Alignment	not modelled	26.5	17	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
106	c2i5bC_	Alignment	not modelled	26.2	40	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
107	d1n1ea2	Alignment	not modelled	25.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
108	d2d1pa1	Alignment	not modelled	25.1	23	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
109	c2f59B_	Alignment	not modelled	24.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
110	c1jr2A_	Alignment	not modelled	24.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
111	d1jr2a_	Alignment	not modelled	24.7	14	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
112	c1tjnA_	Alignment	not modelled	24.6	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
113	d1tjna_	Alignment	not modelled	24.6	8	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
114	c2qsjB_	Alignment	not modelled	23.0	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
115	c2jrlA_	Alignment	not modelled	22.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer