Phyre2

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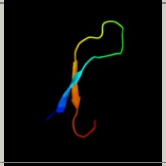
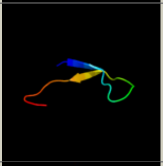
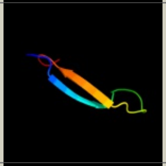
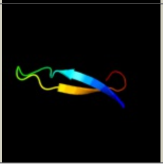
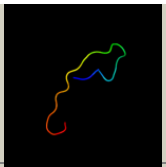
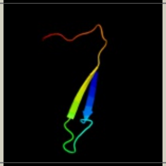
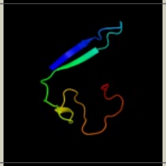
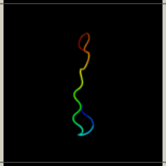
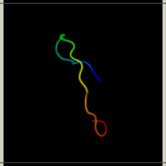
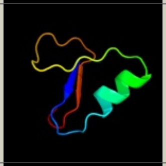
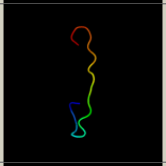
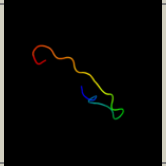
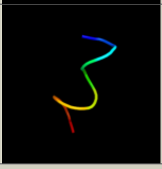
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1aorB_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde ferredoxin oxidoreductase; **PDBTitle:** structure of a hyperthermophilic tungstopterin enzyme,2 aldehyde ferredoxin oxidoreductase
2	c1b4nD_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formaldehyde ferredoxin oxidoreductase; **PDBTitle:** formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
3	d1aora1	Alignment		100.0	23	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
4	d1b25a1	Alignment		100.0	23	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
5	d1b25a2	Alignment		100.0	40	**Fold:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Superfamily:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Family:**Aldehyde ferredoxin oxidoreductase, N-terminal domain
6	d1aora2	Alignment		100.0	44	**Fold:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Superfamily:**Aldehyde ferredoxin oxidoreductase, N-terminal domain **Family:**Aldehyde ferredoxin oxidoreductase, N-terminal domain
7	d2fug32	Alignment		55.6	15	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
8	c2e7zA_	Alignment		51.8	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
9	c2vpyE_	Alignment		48.4	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
10	c2nyaF_	Alignment		47.6	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
11	d1ogya2	Alignment		45.9	12	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3

12	c1ogyA_	Alignment		39.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
13	d1g8ka2	Alignment		32.3	20	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
14	c1g8jC_	Alignment		32.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
15	c2iv2X_	Alignment		30.2	22	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
16	d2iv2x2	Alignment		29.9	19	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
17	c3dfuB_	Alignment		29.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein from 6-phosphogluconate **PDBTitle:** crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
18	d2jioa2	Alignment		29.7	22	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
19	c2v45A_	Alignment		29.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
20	c1du9A_	Alignment		28.7	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**bmp02 neurotoxin; **PDBTitle:** solution structure of bmp02, a natural scorpion toxin which2 blocks apamin-sensitive calcium-activated potassium3 channels, 25 structures
21	c1h0hA_	Alignment	not modelled	28.5	15	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
22	c2ktcA_	Alignment	not modelled	25.6	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**potassium channel toxin alpha-ktx 9.4; **PDBTitle:** solution structure of a novel hkv1.1 inhibiting scorpion toxin from2 mesibuthus tamulus
23	c2g5cD_	Alignment	not modelled	25.5	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
24	c2h2wA_	Alignment	not modelled	24.8	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
25	d1yj5a2	Alignment	not modelled	24.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
26	d2ghra1	Alignment	not modelled	23.4	29	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
27	c3lx4B_	Alignment	not modelled	23.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fe-hydrogenase; **PDBTitle:** stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
28	c2pv7B_	Alignment	not modelled	22.7	31	**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
29	d1u5ta1	Alignment	not modelled	22.0	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
30	c3gmbB_	Alignment	not modelled	20.2	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic2 acid oxygenase
31	c3iufA_	Alignment	not modelled	20.0	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of2 human ubi-d4
32	c2f1kD_	Alignment	not modelled	19.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
33	c3cgxA_	Alignment	not modelled	19.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
34	c2l6aA_	Alignment	not modelled	18.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nacht, lrr and pyd domains-containing protein 12; **PDBTitle:** three-dimensional structure of the n-terminal effector pyrin domain of2 nlrp12
35	d2pv7a2	Alignment	not modelled	18.4	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
36	c2vq3B_	Alignment	not modelled	18.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
37	c2fugC_	Alignment	not modelled	18.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
38	c3d1lB_	Alignment	not modelled	17.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
39	c1np3B_	Alignment	not modelled	17.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
40	d2psba1	Alignment	not modelled	17.0	22	**Fold:**YerB-like **Superfamily:**YerB-like **Family:**YerB-like
41	c2psbA_	Alignment	not modelled	17.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yerb protein; **PDBTitle:** crystal structure of yerb protein from bacillus subtilis.2 northeast structural genomics target sr586
42	d1h0ha2	Alignment	not modelled	16.6	17	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
43	d2ahra2	Alignment	not modelled	16.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
44	d2f1ka2	Alignment	not modelled	15.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d2pgda2	Alignment	not modelled	15.7	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
46	d1yqga2	Alignment	not modelled	15.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
47	d1g99a2	Alignment	not modelled	14.8	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
48	c3dzbA_	Alignment	not modelled	14.7	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
49	c2rafC_	Alignment	not modelled	14.6	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase; **PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
50	d2g5ca2	Alignment	not modelled	14.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
51	d2oiea1	Alignment	not modelled	14.1	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
52	c3qhaB_	Alignment	not modelled	14.1	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from

						mycobacterium2 avium 104
53	d1f0ya2	Alignment	not modelled	13.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
54	c1z82A_	Alignment	not modelled	13.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
55	c3ktdC_	Alignment	not modelled	13.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
56	d1kqfa2	Alignment	not modelled	12.9	22	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
57	d1vpda2	Alignment	not modelled	12.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
58	c1wxpA_	Alignment	not modelled	12.2	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
59	c3o0yC_	Alignment	not modelled	12.1	6	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
60	c2ofpB_	Alignment	not modelled	12.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
61	d1i36a2	Alignment	not modelled	12.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c3b1fA_	Alignment	not modelled	12.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
63	d1a9xa1	Alignment	not modelled	11.9	15	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
64	c1ks9A_	Alignment	not modelled	11.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
65	c2axoA_	Alignment	not modelled	11.3	83	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu2684; **PDBTitle:** x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
66	c1i36A_	Alignment	not modelled	11.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747; **PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
67	d2axoa1	Alignment	not modelled	11.2	83	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
68	c2fpgA_	Alignment	not modelled	10.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
69	c1wcnA_	Alignment	not modelled	10.9	35	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
70	c2uyyD_	Alignment	not modelled	10.9	15	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
71	c3k3qB_	Alignment	not modelled	10.8	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**botulinum neurotoxin type a; **PDBTitle:** crystal structure of a llama antibody complexed with the c.2 botulinum neurotoxin serotype a catalytic domain
72	c3g17H_	Alignment	not modelled	10.5	12	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-reductase; **PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
73	d2jeka1	Alignment	not modelled	10.3	32	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
74	c2howB_	Alignment	not modelled	10.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**356aa long hypothetical dipeptidase; **PDBTitle:** dipeptidase (ph0974) from pyrococcus horikoshii ot3
75	c3idwA_	Alignment	not modelled	10.3	39	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
76	c3qf2B_	Alignment	not modelled	10.1	15	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**nacht, lrr and pyd domains-containing protein 3; **PDBTitle:** crystal structure of nalp3 pyd

77	d1bg6a2	Alignment	not modelled	10.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
78	c1kqgA_	Alignment	not modelled	9.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
79	c2eapA_	Alignment	not modelled	9.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
80	c2yx6C_	Alignment	not modelled	9.6	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
81	d1af7a1	Alignment	not modelled	9.5	16	**Fold:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Superfamily:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Family:**Chemotaxis receptor methyltransferase CheR, N-terminal domain
82	c1e1hC_	Alignment	not modelled	9.4	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**botulinum neurotoxin type a light chain; **PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
83	c3ju3A_	Alignment	not modelled	9.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; **PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
84	c3i83B_	Alignment	not modelled	9.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus
85	d1wdka3	Alignment	not modelled	9.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c3bd1B_	Alignment	not modelled	9.2	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
87	c2q4pA_	Alignment	not modelled	9.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
88	d2a3qa1	Alignment	not modelled	9.0	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
89	c2kn6A_	Alignment	not modelled	9.0	28	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis-associated speck-like protein containing a card; **PDBTitle:** structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card)
90	d1trba1	Alignment	not modelled	9.0	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
91	c3k96B_	Alignment	not modelled	8.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
92	c3ewiB_	Alignment	not modelled	8.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
93	c3iukB_	Alignment	not modelled	8.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
94	d3c8ya1	Alignment	not modelled	8.8	14	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
95	c2vouA_	Alignment	not modelled	8.8	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,6-dihydroxypyridine hydroxylase; **PDBTitle:** structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
96	c3h0mE_	Alignment	not modelled	8.7	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
97	d1nvma1	Alignment	not modelled	8.6	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
98	d1y5ia2	Alignment	not modelled	8.6	10	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
99	c2p2vA_	Alignment	not modelled	8.5	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-2,3-sialyltransferase; **PDBTitle:** crystal structure analysis of monofunctional alpha-2,3-2 sialyltransferase cst-i from campylobacter jejuni