Phyre^2

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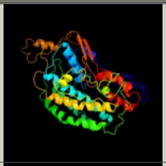
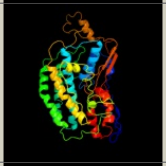
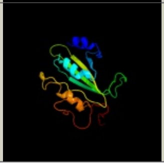
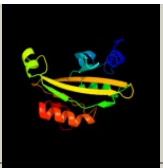
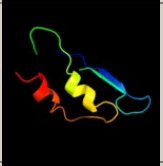
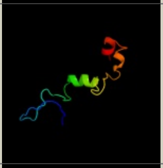
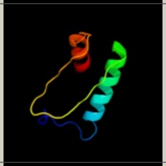
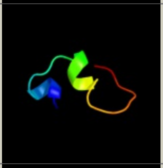
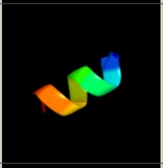
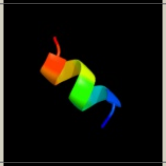
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug41	Alignment		100.0	42	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
2	c2fug4_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
3	d1frfl_	Alignment		100.0	15	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
4	d1e3db_	Alignment		100.0	16	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
5	d1yq9h1	Alignment		100.0	15	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
6	c1h2aL_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
7	c2wpnB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
8	d1cc1l_	Alignment		100.0	17	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
9	c3myrB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
10	d1wui l1	Alignment		100.0	15	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
11	d2fug51	Alignment		100.0	34	**Fold:**Nqo5-like **Superfamily:**Nqo5-like **Family:**Nqo5-like

12	c3mcrA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh dehydrogenase, subunit c; **PDBTitle:** crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
13	d1v97a4	Alignment		45.2	2	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
14	c2ibpB_	Alignment		29.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from pyrobaculum aerophilum
15	d1ghha_	Alignment		25.7	15	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
16	d1ffvc1	Alignment		24.6	10	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
17	d2ntka1	Alignment		23.4	23	**Fold:**Ntn hydrolase-like **Superfamily:**Archaeal IMP cyclohydrolase PurO **Family:**Archaeal IMP cyclohydrolase PurO
18	c1ufiD_	Alignment		23.3	40	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of the dimerization domain of human cenp-b
19	d1ufia_	Alignment		23.0	40	**Fold:**ROP-like **Superfamily:**Dimerisation domain of CENP-B **Family:**Dimerisation domain of CENP-B
20	d2qswa1	Alignment		21.4	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
21	d2zpya3	Alignment	not modelled	20.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
22	d1ni2a3	Alignment	not modelled	19.6	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
23	d2qrra1	Alignment	not modelled	19.4	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
24	d1ef1a3	Alignment	not modelled	19.0	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
25	c2w3zA_	Alignment	not modelled	18.6	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
26	d2c5sa2	Alignment	not modelled	18.4	10	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
27	d1vqza1	Alignment	not modelled	16.8	17	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
28	c2dgyA_	Alignment	not modelled	16.6	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
29	c3kfwX	Alignment	not modelled	16.0	36	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**uncharacterized protein;

29	c3kfwX_	Alignment	not modelled	16.0	30	**PDBTitle:** uncharacterized protein rv0674 from mycobacterium tuberculosis
30	c2f3oB_	Alignment	not modelled	15.9	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
31	c2g40A_	Alignment	not modelled	15.4	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
32	d2g40a1	Alignment	not modelled	15.4	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**YkgG-like
33	d1u07a_	Alignment	not modelled	15.4	7	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
34	c3kwlA_	Alignment	not modelled	15.3	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
35	d1gg3a3	Alignment	not modelled	15.2	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
36	c2cveA_	Alignment	not modelled	14.4	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
37	c3hrdC_	Alignment	not modelled	14.1	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
38	c2dnwA_	Alignment	not modelled	12.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
39	c2oqkA_	Alignment	not modelled	12.8	6	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
40	c1wvtA_	Alignment	not modelled	12.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
41	c2grxC_	Alignment	not modelled	12.0	4	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
42	d3dhxa1	Alignment	not modelled	11.8	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
43	c1bl1A_	Alignment	not modelled	11.7	38	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**parathyroid hormone receptor; **PDBTitle:** pth receptor n-terminus fragment, nmr, 1 structure
44	c2c5sA_	Alignment	not modelled	11.5	10	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
45	c3echC_	Alignment	not modelled	11.1	55	**PDB header:**transcription, transcription regulation **Chain:** C: **PDB Molecule:**25-mer fragment of protein armr; **PDBTitle:** the marr-family repressor mexr in complex with its antirepressor armr
46	d1rtya_	Alignment	not modelled	10.7	10	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
47	d1r9da_	Alignment	not modelled	10.6	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
48	d2gskb1	Alignment	not modelled	10.4	4	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
49	c2jynA_	Alignment	not modelled	10.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0368 protein ypl225w; **PDBTitle:** a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
50	d1es6a2	Alignment	not modelled	10.0	55	**Fold:**EV matrix protein **Superfamily:**EV matrix protein **Family:**EV matrix protein
51	c1es6A_	Alignment	not modelled	9.8	55	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein vp40; **PDBTitle:** crystal structure of the matrix protein of ebola virus
52	c1xx3A_	Alignment	not modelled	9.7	3	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
53	d1gxma_	Alignment	not modelled	9.5	25	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
54	d1n62c1	Alignment	not modelled	9.0	9	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like

55	c3k1dA_	Alignment	not modelled	8.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
56	d1d7qa_	Alignment	not modelled	8.6	5	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
57	d1x2ga1	Alignment	not modelled	8.5	19	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
58	d1yeya2	Alignment	not modelled	8.1	14	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
59	d1jt8a_	Alignment	not modelled	7.3	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	c2fq2A_	Alignment	not modelled	7.3	12	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
61	d2oeza1	Alignment	not modelled	7.3	8	**Fold:**YacF-like **Superfamily:**YacF-like **Family:**YacF-like
62	d1h4ra3	Alignment	not modelled	7.2	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
63	c2kw0A_	Alignment	not modelled	7.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
64	d3ceda1	Alignment	not modelled	7.0	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
65	c2zhzC_	Alignment	not modelled	7.0	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
66	c2l9fA_	Alignment	not modelled	7.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
67	d1vi7a2	Alignment	not modelled	6.9	12	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
68	c1vi7A_	Alignment	not modelled	6.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein
69	c2hl7A_	Alignment	not modelled	6.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
70	d1jroa3	Alignment	not modelled	6.5	17	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
71	c2p4vA_	Alignment	not modelled	6.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
72	c2fq8A_	Alignment	not modelled	6.4	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**2f; **PDBTitle:** nmr structure of 2f associated with lipid disc
73	c2fq5A_	Alignment	not modelled	6.4	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**peptide 2f; **PDBTitle:** nmr structure of 2f associated with lipid disc
74	d7mdha2	Alignment	not modelled	6.3	0	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
75	c1hucC_	Alignment	not modelled	6.3	18	**PDB header:**thiol protease **Chain:** C: **PDB Molecule:**cathepsin b; **PDBTitle:** the refined 2.15 angstroms x-ray crystal structure of human2 liver cathepsin b: the structural basis for its specificity
76	c3sc0A_	Alignment	not modelled	6.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methylmalonic aciduria and homocystinuria type c protein; **PDBTitle:** crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
77	d1v8ca2	Alignment	not modelled	6.2	20	**Fold:**TBP-like **Superfamily:**MoaD-related protein, C-terminal domain **Family:**MoaD-related protein, C-terminal domain
78	d2up1a2	Alignment	not modelled	6.1	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
79	c2ochA_	Alignment	not modelled	6.1	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
80	c2vgpD_	Alignment	not modelled	6.1	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**inner centromere protein a; **PDBTitle:** crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor

81	d1uptd_	Alignment	not modelled	6.1	31	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
82	d2jeka1	Alignment	not modelled	6.0	19	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
83	d2r4qa1	Alignment	not modelled	6.0	12	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
84	c2e5aA_	Alignment	not modelled	5.9	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
85	d1t3qc1	Alignment	not modelled	5.9	8	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
86	c2l4bA_	Alignment	not modelled	5.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
87	c2kciA_	Alignment	not modelled	5.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
88	d2q22a1	Alignment	not modelled	5.8	13	**Fold:**Ava3019-like **Superfamily:**Ava3019-like **Family:**Ava3019-like
89	c2pt7G_	Alignment	not modelled	5.7	13	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
90	d1vcta1	Alignment	not modelled	5.7	10	**Fold:**Spectrin repeat-like **Superfamily:**PhoU-like **Family:**PhoU-like
91	d2qlvb1	Alignment	not modelled	5.7	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
92	d1r6ta2	Alignment	not modelled	5.6	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
93	c2k9kA_	Alignment	not modelled	5.6	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
94	d2f15a1	Alignment	not modelled	5.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
95	c3g59A_	Alignment	not modelled	5.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
96	c2or0B_	Alignment	not modelled	5.5	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxylase; **PDBTitle:** structural genomics, the crystal structure of a putative hydroxylase2 from rhodococcus sp. rha1
97	c2dn9A_	Alignment	not modelled	5.5	21	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
98	c3oakC_	Alignment	not modelled	5.5	57	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of a spn1 (iws1)-spt6 complex
99	c3fq9A_	Alignment	not modelled	5.4	5	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin; **PDBTitle:** design of an insulin analog with enhanced receptor-binding2 selectivity. rationale, structure, and therapeutic3 implications