Phyre2

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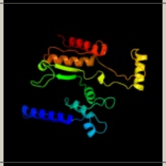
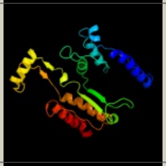
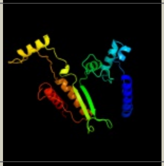
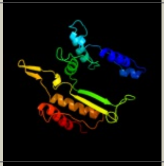
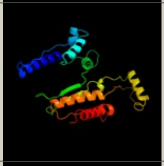
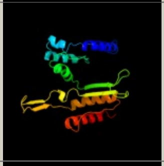
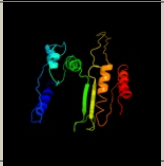
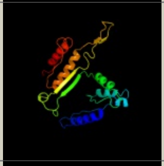
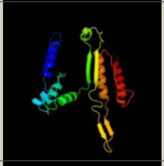
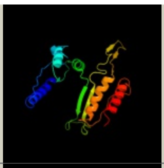
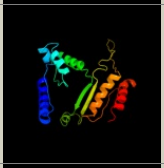
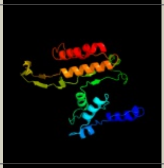
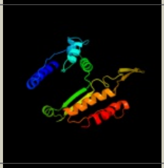
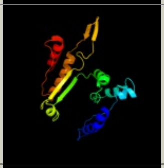
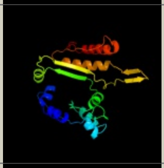
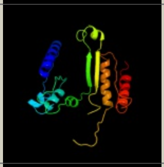
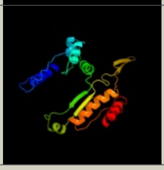
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pb1a_	Alignment		100.0	100	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
2	c2d4vD_	Alignment		100.0	69	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
3	d1hqsa_	Alignment		100.0	71	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
4	c2e0cA_	Alignment		100.0	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
5	c2d1cB_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
6	c1tyoA_	Alignment		100.0	54	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
7	d1w0da_	Alignment		100.0	31	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
8	c3fmxX_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**tartrate dehydrogenase/decarboxylase; **PDBTitle:** crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
9	d1cm7a_	Alignment		100.0	23	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
10	d1v53a1	Alignment		100.0	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
11	d1vlca_	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases

12	d1cnza_	Alignment		100.0	22	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
13	d1g2ua_	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
14	c1zorB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
15	c3r8wC_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2, chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
16	d1xaca_	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
17	d1wpwa_	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
18	c1x0lB_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
19	c3u1hA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
20	d1a05a_	Alignment		100.0	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
21	c2uxqB_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase native; **PDBTitle:** isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
22	c3blxL_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
23	c2qfyE_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
24	c3us8A_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
25	d1lwda_	Alignment	not modelled	100.0	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
26	d1t0la_	Alignment	not modelled	100.0	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
27	c3blxM_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
28	c2iv0A_	Alignment	not modelled	100.0	62	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2

						archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
29	d1hioa_	Alignment	not modelled	20.3	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
30	d1f66c_	Alignment	not modelled	17.1	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
31	c1f66C_	Alignment	not modelled	17.1	14	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
32	d1tzya_	Alignment	not modelled	16.8	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
33	c2f8nK_	Alignment	not modelled	16.8	13	**PDB header:**structural protein/dna **Chain:** K: **PDB Molecule:**histone h2a type 1; **PDBTitle:** 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
34	d1n1ja_	Alignment	not modelled	16.5	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
35	d2pbea1	Alignment	not modelled	15.9	5	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**AadK C-terminal domain-like
36	d2ffea1	Alignment	not modelled	15.9	17	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
37	d2jssa1	Alignment	not modelled	14.5	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
38	d1aoic_	Alignment	not modelled	13.6	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
39	d1n1jb_	Alignment	not modelled	13.5	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
40	d1u35c1	Alignment	not modelled	13.1	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
41	d1q77a_	Alignment	not modelled	13.0	4	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
42	c2dumD_	Alignment	not modelled	12.9	28	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
43	c2p0yA_	Alignment	not modelled	11.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780; **PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
44	c1yy3A_	Alignment	not modelled	10.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
45	d1kx3c_	Alignment	not modelled	10.6	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
46	d1a7wa_	Alignment	not modelled	10.6	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
47	c3hgmD_	Alignment	not modelled	10.3	4	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
48	c1v8cA_	Alignment	not modelled	10.2	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
49	d1ku5a_	Alignment	not modelled	10.1	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
50	c3dwmA_	Alignment	not modelled	9.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
51	c2jaxA_	Alignment	not modelled	9.3	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein tb31.7; **PDBTitle:** universal stress protein rv2623 from mycobaterium2 tuberculosis
52	d1zcza1	Alignment	not modelled	9.1	18	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
53	d1htaa_	Alignment	not modelled	8.7	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
54	d1k6ka_	Alignment	not modelled	8.4	19	**Fold:**Double Clp-N motif **Superfamily:**Double Clp-N motif **Family:**Double Clp-N motif
						Fold: Histone-fold

55	d1s32d_	Alignment	not modelled	8.4	24	**Superfamily:**Histone-fold **Family:**Nucleosome core histones
56	d1i7na1	Alignment	not modelled	8.3	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Synapsin domain
57	d2bykb1	Alignment	not modelled	8.1	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
58	c2bykB_	Alignment	not modelled	8.1	10	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**chrac-14; **PDBTitle:** histone fold heterodimer of the chromatin accessibility2 complex
59	c3qd7X_	Alignment	not modelled	8.1	22	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
60	d1tzyb_	Alignment	not modelled	8.0	29	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
61	c2pbeA_	Alignment	not modelled	7.7	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminoglycoside 6-adenylyltransferase; **PDBTitle:** crystal structure of an aminoglycoside 6-adenyltransferase2 from bacillus subtilis
62	d1kx5c_	Alignment	not modelled	7.7	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
63	d1eqzb_	Alignment	not modelled	7.5	24	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
64	d2z3va1	Alignment	not modelled	7.4	28	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
65	c2ppvA_	Alignment	not modelled	7.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
66	c2q7xA_	Alignment	not modelled	7.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
67	c3dloC_	Alignment	not modelled	6.9	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
68	d1id3c_	Alignment	not modelled	6.7	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
69	d1kx5d_	Alignment	not modelled	6.7	24	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
70	d2hzba1	Alignment	not modelled	6.6	39	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
71	d1jmva_	Alignment	not modelled	6.6	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
72	c2jssA_	Alignment	not modelled	6.6	13	**PDB header:**chaperone/nuclear protein **Chain:** A: **PDB Molecule:**chimera of histone h2b.1 and histone h2a.z; **PDBTitle:** nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
73	c2pfsA_	Alignment	not modelled	6.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
74	d2z8la1	Alignment	not modelled	6.3	18	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
75	d2huec1	Alignment	not modelled	6.1	23	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	d1eqza_	Alignment	not modelled	6.0	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
77	d1id3d_	Alignment	not modelled	5.7	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
78	c3idfA_	Alignment	not modelled	5.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
79	c3fh0A_	Alignment	not modelled	5.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative universal stress protein kpn_01444; **PDBTitle:** crystal structure of putative universal stress protein kpn_01444 -2 atpase
80	c1urqA_	Alignment	not modelled	5.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m-tomosyn isoform; **PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
						PDB header:structural genomics, unknown function

81	c3ca8B_	Alignment	not modelled	5.4	14	**Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
82	c3fh2A_	Alignment	not modelled	5.3	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent protease (heat shock protein); **PDBTitle:** the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
83	d2r61a1	Alignment	not modelled	5.2	20	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
84	c3fpvC_	Alignment	not modelled	5.1	28	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
85	d1bev1_	Alignment	not modelled	5.1	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)