Phyre^2

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Description	P31660
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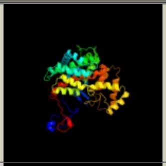
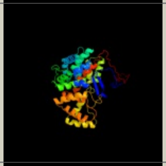
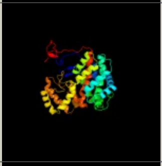
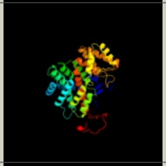
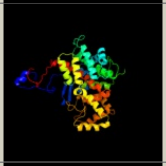
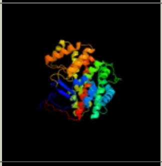
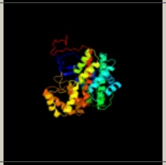
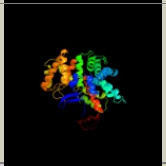
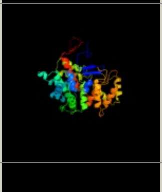
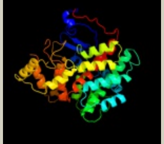
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h12C_	Alignment		100.0	31	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
2	d1k3pa_	Alignment		100.0	30	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
3	d1ioma_	Alignment		100.0	36	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
4	c2ibpB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from pyrobaculum aerophilum
5	d1aj8a_	Alignment		100.0	36	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
6	c3o8jH_	Alignment		100.0	97	**PDB header:**transferase **Chain:** H: **PDB Molecule:**2-methylcitrate synthase; **PDBTitle:** crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
7	c3msuA_	Alignment		100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
8	d1a59a_	Alignment		100.0	41	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
9	c3hwkE_	Alignment		100.0	38	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methylcitrate synthase; **PDBTitle:** crystal structure of methylcitrate synthase from2 mycobacterium tuberculosis
10	c3tqgA_	Alignment		100.0	52	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-methylcitrate synthase; **PDBTitle:** structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
11	c1vgpA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**373aa long hypothetical citrate synthase; **PDBTitle:** crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7

12	c2r26C_	Alignment		100.0	35	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
13	c1vgmB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**378aa long hypothetical citrate synthase; **PDBTitle:** crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
14	c2p2wA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from thermotoga maritima msb8
15	c2c6xA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase 1; **PDBTitle:** structure of bacillus subtilis citrate synthase
16	d1csha_	Alignment		100.0	23	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
17	d2ctsa_	Alignment		100.0	23	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
18	d1o7xa_	Alignment		100.0	33	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
19	d1csca_	Alignment		100.0	23	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
20	c2xzmS_	Alignment		48.8	36	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rps15e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
21	d2huec1	Alignment	not modelled	27.0	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
22	d1poib_	Alignment	not modelled	24.8	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
23	d1khda2	Alignment	not modelled	22.2	21	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
24	d1kx5b_	Alignment	not modelled	20.7	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
25	d1id3b_	Alignment	not modelled	17.6	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
26	c2iouC_	Alignment	not modelled	14.7	30	**PDB header:**viral protein/membrane protein **Chain:** C: **PDB Molecule:**major tropism determinant p1; **PDBTitle:** major tropism determinant p1 (mtd-p1) variant complexed with2 bordetella brochiseptica virulence factor pertactin extracellular3 domain (prn-e).
27	d1r3sa_	Alignment	not modelled	12.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
28	c2kebA_	Alignment	not modelled	11.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit

29	d1yu0a2	Alignment	not modelled	11.7	30	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Mtd variable domain
30	d1keaa_	Alignment	not modelled	11.0	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
31	d1hiod_	Alignment	not modelled	10.6	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
32	d1orna_	Alignment	not modelled	10.4	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
33	c3ajvD_	Alignment	not modelled	9.8	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** splicing endonuclease from aeropyrum pernix
34	d1b8za_	Alignment	not modelled	9.4	29	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
35	d1mula_	Alignment	not modelled	8.3	23	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
36	c3c65A_	Alignment	not modelled	8.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
37	d2o97b1	Alignment	not modelled	7.8	29	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
38	c1fctA_	Alignment	not modelled	7.7	71	**PDB header:**transit peptide **Chain:** A: **PDB Molecule:**ferredoxin chloroplastic transit peptide **PDBTitle:** nmr structures of ferredoxin chloroplastic transit peptide2 from chlamydomonas reinhardtii promoted by3 trifluoroethanol in aqueous solution
39	d1yu3a2	Alignment	not modelled	7.7	30	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Mtd variable domain
40	c2l5aA_	Alignment	not modelled	7.7	15	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
41	d2abka_	Alignment	not modelled	7.1	12	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
42	d1fhea1	Alignment	not modelled	6.8	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
43	c2q6vA_	Alignment	not modelled	6.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp
44	c1jpkA_	Alignment	not modelled	6.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
45	c3kgkA_	Alignment	not modelled	6.2	46	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
46	c3ktbD_	Alignment	not modelled	6.1	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
47	c3ts3D_	Alignment	not modelled	5.9	24	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
48	d1o17a1	Alignment	not modelled	5.8	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
49	d1brwa2	Alignment	not modelled	5.7	13	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
50	d1m6ya1	Alignment	not modelled	5.7	19	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
51	c1j9zB_	Alignment	not modelled	5.7	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
52	d1wg8a1	Alignment	not modelled	5.6	17	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
53	c2nv4A_	Alignment	not modelled	5.6	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0066 protein af_0241; **PDBTitle:** crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
						PDB header:structural genomics, unknown function

54	c2l0cA_	Alignment	not modelled	5.4	30	**Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
55	c2fheA_	Alignment	not modelled	5.3	12	**PDB header:**transferase/substrate **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** fasciola hepatica glutathione s-transferase isoform 1 in complex with2 glutathione
56	c3gndC_	Alignment	not modelled	5.2	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
57	d2bv3a3	Alignment	not modelled	5.1	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
58	c3ieyA_	Alignment	not modelled	5.1	36	**PDB header:**hydrolase/rna binding protein **Chain:** A: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** crystal structure of the functional nanoarchaeum equitans trna2 splicing endonuclease
59	d2elca2	Alignment	not modelled	5.1	25	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
60	c2xzmV_	Alignment	not modelled	5.0	24	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**rps17e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1