Phyre^2

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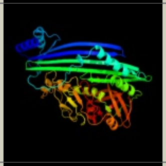
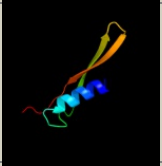
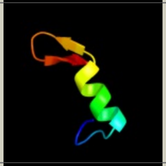
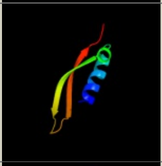
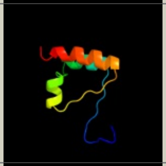
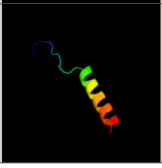
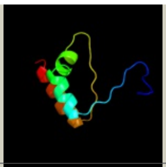
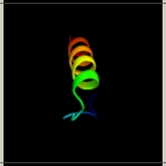
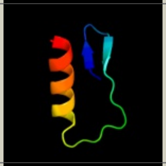
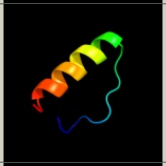
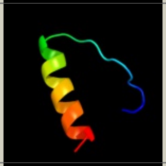
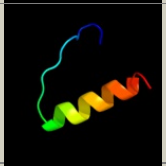
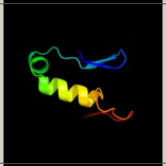
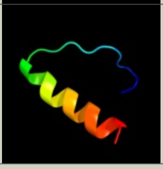
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qtdC_	Alignment		100.0	50	**PDB header:**gene regulation **Chain:** C: **PDB Molecule:**pmba protein; **PDBTitle:** crystal structure of putative modulator of gyrase (pmba) from2 pseudomonas aeruginosa pao1
2	d1vpba_	Alignment		100.0	28	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
3	d1vl4a_	Alignment		100.0	28	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
4	c3onrI_	Alignment		25.1	12	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
5	d1o12a1	Alignment		24.5	29	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
6	d2ux9a1	Alignment		23.2	16	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
7	c2vxaL_	Alignment		23.0	16	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
8	c3oqtP_	Alignment		22.6	14	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
9	c3gknA_	Alignment		11.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
10	d1xaca_	Alignment		11.5	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
11	d2pjua1	Alignment		9.2	21	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like

12	c2d1cB_	Alignment		8.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
13	d1pb1a_	Alignment		8.0	15	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
14	c3ixrA_	Alignment		7.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
15	c2iv0A_	Alignment		7.2	19	**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
16	d1w0da_	Alignment		6.8	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
17	d1hqsa_	Alignment		6.7	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
18	d1jjga_	Alignment		6.7	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	d1n8ja_	Alignment		6.4	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	c3blxM_	Alignment		6.4	15	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
21	c3f7xA_	Alignment	not modelled	6.2	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
22	c2kilA_	Alignment	not modelled	6.2	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
23	c3r8wC_	Alignment	not modelled	6.1	15	**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
24	c3e8vA_	Alignment	not modelled	6.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
25	d1a05a_	Alignment	not modelled	6.1	8	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
26	c1bknA_	Alignment	not modelled	5.9	15	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
27	d1ydua1	Alignment	not modelled	5.9	9	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
28	d1cm7a_	Alignment	not modelled	5.9	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases

29	c3mhsE_	Alignment	not modelled	5.9	15	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
30	d3ckma1	Alignment	not modelled	5.8	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
31	d1luza_	Alignment	not modelled	5.8	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
32	d1ylea1	Alignment	not modelled	5.7	6	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
33	c1tyoA_	Alignment	not modelled	5.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
34	d1wpwa_	Alignment	not modelled	5.5	23	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
35	d1b25a1	Alignment	not modelled	5.5	15	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
36	c2kk4A_	Alignment	not modelled	5.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_2094; **PDBTitle:** solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consotium (nesg)3 target gt2
37	c2op8A_	Alignment	not modelled	5.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
38	d1m1ha1	Alignment	not modelled	5.4	46	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
39	c1htrP_	Alignment	not modelled	5.4	29	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
40	d1dl6a_	Alignment	not modelled	5.3	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
41	d1ka1a_	Alignment	not modelled	5.3	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
42	d2q0ia1	Alignment	not modelled	5.2	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
43	d1cnza_	Alignment	not modelled	5.2	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
44	d1yrra2	Alignment	not modelled	5.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
45	c3dbaB_	Alignment	not modelled	5.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
46	d2h6ca2	Alignment	not modelled	5.1	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
47	d1aora1	Alignment	not modelled	5.1	8	**Fold:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Superfamily:**Aldehyde ferredoxin oxidoreductase, C-terminal domains **Family:**Aldehyde ferredoxin oxidoreductase, C-terminal domains
48	d1g2ua_	Alignment	not modelled	5.1	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
49	c3hz4A_	Alignment	not modelled	5.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
50	d1u55a_	Alignment	not modelled	5.1	6	**Fold:**Ligand-binding domain in the NO signalling and Golgi transport **Superfamily:**Ligand-binding domain in the NO signalling and Golgi transport **Family:**H-NOX domain
51	c2ideE_	Alignment	not modelled	5.1	25	**PDB header:**biosynthetic protein **Chain:** E: **PDB Molecule:**molybdenum cofactor biosynthesis protein c; **PDBTitle:** crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus theromophilus hb8