Phyre2

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Description	P31435
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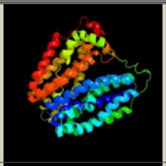
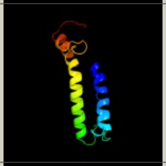
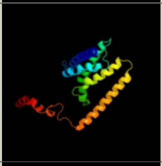
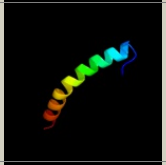
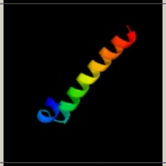
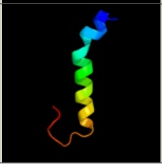
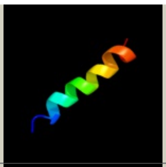
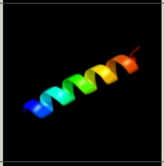
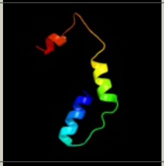
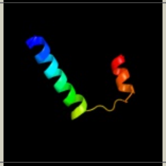
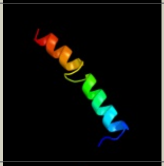
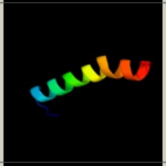
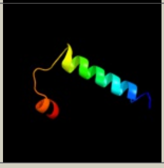
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pv7a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
2	d1pw4a_	Alignment		99.9	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
3	c2gfpA_	Alignment		99.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
4	c3o7pA_	Alignment		99.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2xutC_	Alignment		99.7	9	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3qnqD_	Alignment		79.1	11	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
7	c3hd6A_	Alignment		34.9	10	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
8	c3b9yA_	Alignment		29.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
9	d1y7ua1	Alignment		19.4	12	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
10	c2rdcA_	Alignment		15.3	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
11	d1jyma_	Alignment		15.3	16	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase

12	c1by0A_	Alignment		15.3	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
13	c1zxaB_	Alignment		15.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
14	c3mnfA_	Alignment		14.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pac2 family protein; **PDBTitle:** crystal structure of pac2 family protein from streptomyces avermitilis2 ma
15	c3d9sB_	Alignment		13.5	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
16	d2f23a1	Alignment		12.8	31	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
17	c2l2lB_	Alignment		11.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure of the coiled-coil complex between mbd2 and2 p66alpha
18	d1oqwa_	Alignment		11.0	13	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
19	d1grja1	Alignment		10.3	14	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
20	d1j4na_	Alignment		9.5	17	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
21	c1ymgA_	Alignment	not modelled	9.4	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
22	d1ymga1	Alignment	not modelled	9.4	11	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
23	d2pila_	Alignment	not modelled	9.4	7	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
24	c3bpqC_	Alignment	not modelled	8.7	13	**PDB header:**toxin **Chain:** C: **PDB Molecule:**antitoxin relb3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
25	c1zvuA_	Alignment	not modelled	8.3	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
26	d1f6ga_	Alignment	not modelled	7.8	13	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
27	d1yuwa1	Alignment	not modelled	7.4	13	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
28	c2yxyA_	Alignment	not modelled	7.3	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein, gk0453; **PDBTitle:** crystarl structure of hypothetical conserved protein, gk0453
						PDB header:cell cycle protein

29	c1m46B_	Alignment	not modelled	7.3	18	**Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
30	d1cg2a2	Alignment	not modelled	7.3	10	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
31	c2novD_	Alignment	not modelled	7.3	23	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
32	c3he4A_	Alignment	not modelled	7.1	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip6; **PDBTitle:** heterospecific coiled-coil pair synzip5:synzip6
33	c3qx3B_	Alignment	not modelled	7.0	19	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
34	c2wl2B_	Alignment	not modelled	7.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
35	d1ab4a_	Alignment	not modelled	7.0	16	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
36	c1a92B_	Alignment	not modelled	6.9	15	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
37	c2y6xA_	Alignment	not modelled	6.9	11	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kd protein; **PDBTitle:** structure of psb27 from thermosynechococcus elongatus
38	d1iruc_	Alignment	not modelled	6.9	4	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
39	d1iwpg_	Alignment	not modelled	6.7	14	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
40	d1eexg_	Alignment	not modelled	6.7	19	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Diol dehydratase, gamma subunit **Family:**Diol dehydratase, gamma subunit
41	c1uc5M_	Alignment	not modelled	6.7	19	**PDB header:**lyase **Chain:** M: **PDB Molecule:**diol dehydrase gamma subunit; **PDBTitle:** structure of diol dehydratase complexed with (r)-1,2-2 propanediol
42	c3sokB_	Alignment	not modelled	6.6	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
43	c2w6jG_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
44	d2f6qa1	Alignment	not modelled	6.5	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
45	c2w8aC_	Alignment	not modelled	6.4	7	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
46	d1bjta_	Alignment	not modelled	6.4	16	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
47	c1bjtA_	Alignment	not modelled	6.4	16	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
48	d2jdig1	Alignment	not modelled	6.3	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
49	c3eh0C_	Alignment	not modelled	6.3	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
50	c2hlwA_	Alignment	not modelled	6.3	15	**PDB header:**ligase, signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2 variant 1; **PDBTitle:** solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
51	c1dipA_	Alignment	not modelled	6.1	10	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
52	d1kqfc_	Alignment	not modelled	6.0	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Formate dehydrogenase N, cytochrome (gamma) subunit
53	d1u69a_	Alignment	not modelled	6.0	27	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
54	c1nohB_	Alignment	not modelled	5.9	8	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding

						protein2 gp7 after prohead assembly
55	c2inrA_	Alignment	not modelled	5.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
56	c2xokG_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
57	c2kncB_	Alignment	not modelled	5.8	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
58	c2f6qA_	Alignment	not modelled	5.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peroxisomal 3,2-trans-enoyl-coa isomerase; **PDBTitle:** the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
59	d1hr6a2	Alignment	not modelled	5.7	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
60	c2owyB_	Alignment	not modelled	5.7	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
61	d2fgea3	Alignment	not modelled	5.6	10	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
62	c2hjmB_	Alignment	not modelled	5.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
63	c1lq7A_	Alignment	not modelled	5.3	7	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**alpha3w; **PDBTitle:** de novo designed protein model of radical enzymes
64	c3ifzA_	Alignment	not modelled	5.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
65	c3l60A_	Alignment	not modelled	5.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**branched-chain alpha-keto acid dehydrogenase; **PDBTitle:** crystal structure of branched-chain alpha-keto acid2 dehydrogenase subunit e2 from mycobacterium tuberculosis
66	c2g9pA_	Alignment	not modelled	5.1	17	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
67	c2pnvA_	Alignment	not modelled	5.1	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
68	c1kilE_	Alignment	not modelled	5.1	10	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**complexin i snare-complex binding region; **PDBTitle:** three-dimensional structure of the complexin/snare complex
69	c2rkkA_	Alignment	not modelled	5.1	10	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein vta1; **PDBTitle:** crystal structure of s.cerevisiae vta1 n-terminal domain
70	c2xcqA_	Alignment	not modelled	5.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
71	d2cqea1	Alignment	not modelled	5.0	17	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger