Phyre2

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Description	P76445
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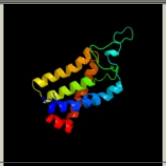
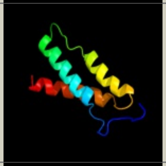
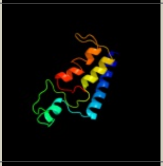
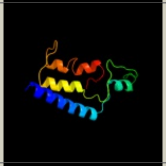
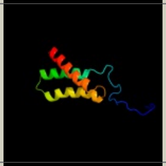
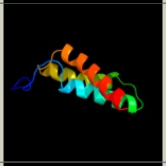
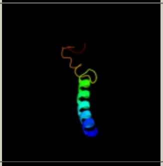
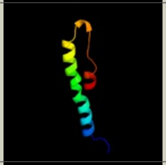
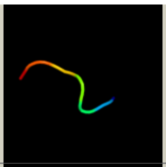
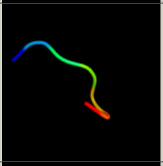
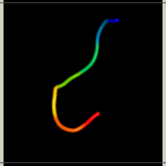
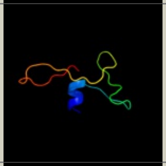
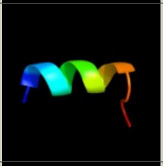
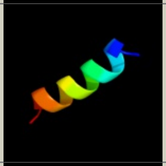
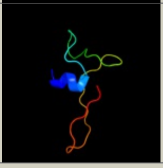
Unique Job ID	6429ddb82649195e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1d2ta_	Alignment		99.6	11	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Type 2 phosphatidic acid phosphatase, PAP2
2	c2akcC_	Alignment		99.5	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**class a nonspecific acid phosphatase phon; **PDBTitle:** crystal structure of tungstate complex of the phon protein2 from s. typhimurium
3	d1qi9a_	Alignment		97.9	27	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
4	d1vnsa_	Alignment		97.7	16	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Chloroperoxidase
5	c1vngA_	Alignment		97.6	16	**PDB header:**haloperoxidase **Chain:** A: **PDB Molecule:**vanadium chloroperoxidase; **PDBTitle:** chloroperoxidase from the fungus curvularia inaequalis:2 mutant h404a
6	d1qhba_	Alignment		97.0	16	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
7	d1up8a_	Alignment		96.9	16	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
8	c2kncA_	Alignment		27.4	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
9	c3fseB_	Alignment		22.5	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
10	c2ys9A_	Alignment		17.9	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox and leucine zipper protein homez; **PDBTitle:** structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez
11	d2a65a1	Alignment		17.5	14	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like

12	d1eh9a2	Alignment		14.5	57	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
13	d1dsva_	Alignment		14.3	43	**Fold:**Retrovirus zinc finger-like domains **Superfamily:**Retrovirus zinc finger-like domains **Family:**Retrovirus zinc finger-like domains
14	c1cl4A_	Alignment		12.7	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (gag polyprotein); **PDBTitle:** nucleocapsid protein from mason-pfizer monkey virus (mpmv)
15	c2oniA_	Alignment		10.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4-like protein; **PDBTitle:** catalytic domain of the human nedd4-like e3 ligase
16	c3gr1A_	Alignment		10.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
17	d2i3da1	Alignment		10.4	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
18	c2i3dA_	Alignment		10.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu1826; **PDBTitle:** crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
19	c3ksrA_	Alignment		10.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative serine hydrolase; **PDBTitle:** crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
20	c3olmA_	Alignment		9.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rsp5; **PDBTitle:** structure and function of a ubiquitin binding site within the2 catalytic domain of a hect ubiquitin ligase
21	c1zvdA_	Alignment	not modelled	9.4	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** regulation of smurf2 ubiquitin ligase activity by anchoring the e2 to2 the hect domain
22	d2r4qa1	Alignment	not modelled	9.2	22	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
23	d1puna_	Alignment	not modelled	8.6	40	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
24	c2k1aA_	Alignment	not modelled	8.4	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
25	c2y69Q_	Alignment	not modelled	7.8	9	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
26	c2k1kA_	Alignment	not modelled	7.4	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
27	c2k1lA_	Alignment	not modelled	7.4	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
28	c2k1kB_	Alignment	not modelled	7.4	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3

29	c2k1lB_	Alignment	not modelled	7.4	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
30	d1v54d_	Alignment	not modelled	7.3	9	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
31	c3a0hX_	Alignment	not modelled	7.2	24	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
32	c3a0bX_	Alignment	not modelled	7.2	24	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
33	c3a0bx_	Alignment	not modelled	7.2	24	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
34	c3a0hx_	Alignment	not modelled	7.2	24	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
35	c2b0tA_	Alignment	not modelled	7.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
36	d2ciwa2	Alignment	not modelled	7.1	13	**Fold:**EF Hand-like **Superfamily:**Cloroperoxidase **Family:**Cloroperoxidase
37	d1nd7a_	Alignment	not modelled	6.9	13	**Fold:**Hect, E3 ligase catalytic domain **Superfamily:**Hect, E3 ligase catalytic domain **Family:**Hect, E3 ligase catalytic domain
38	c3q4iA_	Alignment	not modelled	6.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
39	d1c4za_	Alignment	not modelled	6.8	13	**Fold:**Hect, E3 ligase catalytic domain **Superfamily:**Hect, E3 ligase catalytic domain **Family:**Hect, E3 ligase catalytic domain
40	d2j7ja2	Alignment	not modelled	6.8	16	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
41	d1itwa_	Alignment	not modelled	6.6	31	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
42	c1s5lx_	Alignment	not modelled	6.5	24	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
43	c3esiD_	Alignment	not modelled	6.5	22	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 erwinia carotovora subsp. atroseptica. northeast3 structural genomics target ewr179
44	d1njqa_	Alignment	not modelled	6.4	8	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Plant C2H2 finger (QALGGH zinc finger)
45	c2jvbA_	Alignment	not modelled	6.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
46	c3g1nA_	Alignment	not modelled	6.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase huwe1; **PDBTitle:** catalytic domain of the human e3 ubiquitin-protein ligase2 huwe1
47	c3hd6A_	Alignment	not modelled	6.3	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
48	c3aa6C_	Alignment	not modelled	6.2	50	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**23mer peptide from cd2-associated protein; **PDBTitle:** crystal structure of actin capping protein in complex with the cp-2 binding motif derived from cd2ap
49	c1bzkA_	Alignment	not modelled	6.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein (band 3 anion transport protein); **PDBTitle:** structural studies on the effects of the deletion in the2 red cell anion exchanger (band3, ae1) associated with3 south east asian ovalocytosis.
50	d1x6fa1	Alignment	not modelled	6.1	27	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
51	c3id9B_	Alignment	not modelled	5.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
52	c1xaxA_	Alignment	not modelled	5.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
53	d1ju3a2	Alignment	not modelled	5.7	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
54	d1l7aa_	Alignment	not modelled	5.7	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
						Fold: SopE-like GEF domain

55	d1gzsb_	Alignment	not modelled	5.7	57	**Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
56	d1oxwa_	Alignment	not modelled	5.6	29	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Patatin
57	c3hvyC_	Alignment	not modelled	5.6	6	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase family protein, ynbb b.subtilis **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
58	d1xm5a_	Alignment	not modelled	5.6	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
59	d1tvia_	Alignment	not modelled	5.6	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
60	c2qguA_	Alignment	not modelled	5.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
61	d1r7ma1	Alignment	not modelled	5.6	11	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
62	c2e6kB_	Alignment	not modelled	5.6	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** x-ray structure of thermus thermopilus hb8 tt0505
63	c1l7qA_	Alignment	not modelled	5.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
64	c2fhwA_	Alignment	not modelled	5.5	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**relaxin 3 (prorelaxin h3) (insulin-like peptide **PDBTitle:** solution structure of human relaxin-3
65	d2hu7a2	Alignment	not modelled	5.5	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
66	d2joka1	Alignment	not modelled	5.4	57	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
67	d1r6ea_	Alignment	not modelled	5.4	57	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
68	d3buxb2	Alignment	not modelled	5.3	40	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
69	c2w2hD_	Alignment	not modelled	5.3	50	**PDB header:**rna-binding protein **Chain:** D: **PDB Molecule:**protein tat; **PDBTitle:** structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiav
70	c3uk1A_	Alignment	not modelled	5.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of a transketolase from burkholderia thailandensis2 with an oxidized cysteinesulfonic acid in the active site
71	d1vk6a2	Alignment	not modelled	5.3	0	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
72	c3ib3A_	Alignment	not modelled	5.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
73	c1ql1A_	Alignment	not modelled	5.2	26	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
74	c2vlaA_	Alignment	not modelled	5.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease r.bpuji; **PDBTitle:** crystal structure of restriction endonuclease bpuji2 recognition domain in complex with cognate dna
75	c2ww9B_	Alignment	not modelled	5.1	9	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
76	c1fdfA_	Alignment	not modelled	5.1	57	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhodopsin; **PDBTitle:** helix 7 bovine rhodopsin
77	d1ifya_	Alignment	not modelled	5.0	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain