Phyre2

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Description	P69913
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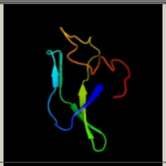
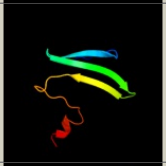
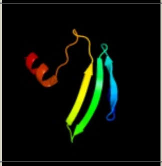
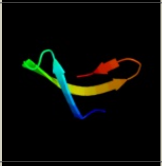
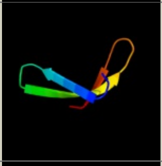
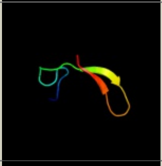
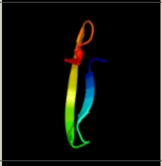
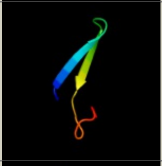
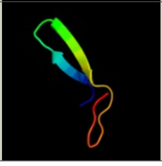
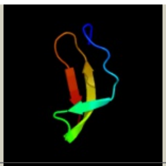
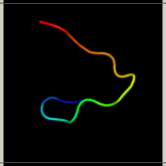
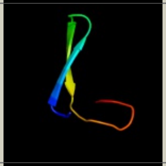
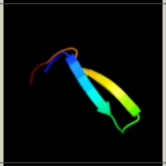
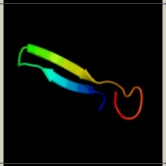
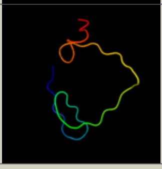
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3oA_	Alignment		99.9	41	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**carbon storage regulator; **PDBTitle:** solution structure of csra, a bacterial carbon storage2 regulatory protein
2	c2jppB_	Alignment		99.9	75	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**translational repressor; **PDBTitle:** structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
3	d1vpza_	Alignment		99.9	89	**Fold:**CsrA-like **Superfamily:**CsrA-like **Family:**CsrA-like
4	c1vpzB_	Alignment		99.9	89	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**carbon storage regulator homolog; **PDBTitle:** crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
5	d1e0ta1	Alignment		63.3	31	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
6	d2g50a1	Alignment		62.7	17	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
7	d1pkma1	Alignment		60.6	18	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
8	d1liua1	Alignment		59.6	21	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
9	c1e0tD_	Alignment		38.5	32	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
10	d2o3ga1	Alignment		35.6	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
11	c3eoeC_	Alignment		34.2	32	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007

12	d1vhka1	Alignment		34.0	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
13	c3ilaG_	Alignment		31.3	31	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
14	c1t5aB_	Alignment		30.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
15	d2o1ra1	Alignment		30.3	29	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
16	c1aqfB_	Alignment		29.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
17	d1a3xa1	Alignment		28.7	23	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
18	c1go3E_	Alignment		28.2	24	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex
19	d1pkla1	Alignment		27.8	25	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
20	d1pmia_	Alignment		27.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
21	c2eqsA_	Alignment	not modelled	26.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dhx8; **PDBTitle:** solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
22	c3llbA_	Alignment	not modelled	22.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
23	c3ma8A_	Alignment	not modelled	21.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
24	d2r2za1	Alignment	not modelled	20.0	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
25	c3ec1A_	Alignment	not modelled	19.6	24	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**yqeh gtpase; **PDBTitle:** structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
26	c3dedB_	Alignment	not modelled	19.6	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
27	c3h0gS_	Alignment	not modelled	18.3	16	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
28	d2z0sa1	Alignment	not modelled	18.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						PDB header:unknown function

29	c2xrhA_	Alignment	not modelled	16.5	29	**Chain:** A: **PDB Molecule:**protein hp0721; **PDBTitle:** crystal structure of the truncated form of hp0721
30	d3deda1	Alignment	not modelled	15.7	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
31	c2khiA_	Alignment	not modelled	14.8	24	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
32	c1pklB_	Alignment	not modelled	14.6	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
33	d1y14b1	Alignment	not modelled	14.4	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	d2p13a1	Alignment	not modelled	13.7	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
35	d2nqwa1	Alignment	not modelled	13.2	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
36	c2khjA_	Alignment	not modelled	12.9	32	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
37	d1go3e1	Alignment	not modelled	12.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
38	d2f23a2	Alignment	not modelled	12.7	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
39	c2b8kG_	Alignment	not modelled	12.5	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
40	d2oaia1	Alignment	not modelled	12.0	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
41	d1hh2p1	Alignment	not modelled	11.9	37	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c3e0vB_	Alignment	not modelled	11.7	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
43	d2plsa1	Alignment	not modelled	11.6	8	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
44	d1nxza1	Alignment	not modelled	11.3	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
45	d1xnea_	Alignment	not modelled	10.9	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
46	c3h2yA_	Alignment	not modelled	10.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtpase family protein; **PDBTitle:** crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound
47	d1c0fa1	Alignment	not modelled	10.2	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
48	d2plia1	Alignment	not modelled	10.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
49	d2c35b1	Alignment	not modelled	9.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
50	c2xoaA_	Alignment	not modelled	9.7	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
51	c3qr5B_	Alignment	not modelled	9.6	31	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**cardiac ca2+ release channel; **PDBTitle:** structure of the first domain of a cardiac ryanodine receptor mutant2 with exon 3 deleted
52	d2rk5a1	Alignment	not modelled	9.5	20	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
53	d2etna2	Alignment	not modelled	9.4	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
54	c2cqoA_	Alignment	not modelled	9.0	23	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**nucleolar protein of 40 kda; **PDBTitle:** solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
55	c1xzzA_	Alignment	not modelled	8.9	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inositol 1,4,5-trisphosphate receptor type 1; **PDBTitle:** crystal structure of the ligand binding suppressor domain of type 12 inositol 1,4,5-trisphosphate receptor
						Fold: Immunoglobulin-like beta-sandwich

56	d2q3za2	Alignment	not modelled	8.2	25	**Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
57	c1yz6A_	Alignment	not modelled	8.2	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha **PDBTitle:** crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
58	d1q46a2	Alignment	not modelled	8.1	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
59	c2z51A_	Alignment	not modelled	7.8	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
60	d1hqia_	Alignment	not modelled	7.2	22	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
61	d1wi5a_	Alignment	not modelled	7.2	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
62	d2asba1	Alignment	not modelled	6.6	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2k52A_	Alignment	not modelled	6.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
64	d1kl9a2	Alignment	not modelled	6.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	c3t8sA_	Alignment	not modelled	5.7	38	**PDB header:**transport protein, membrane protein **Chain:** A: **PDB Molecule:**inositol 1,4,5-trisphosphate receptor type 1; **PDBTitle:** apo and insp3-bound crystal structures of the ligand-binding domain of2 an insp3 receptor
66	c2c35F_	Alignment	not modelled	5.7	16	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
67	d2bf5a1	Alignment	not modelled	5.6	17	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
68	d1gdta1	Alignment	not modelled	5.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
69	d1jmxa3	Alignment	not modelled	5.5	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
70	d2bf2a1	Alignment	not modelled	5.5	17	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
71	c3l6tB_	Alignment	not modelled	5.3	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobilization protein trai; **PDBTitle:** crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
72	d1ttna1	Alignment	not modelled	5.2	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
73	c1ttnA_	Alignment	not modelled	5.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dendritic cell-derived ubiquitin-like protein; **PDBTitle:** solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
74	c2mobA_	Alignment	not modelled	5.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (methane monooxygenase regulatory **PDBTitle:** methane monooxygenase component b
75	d2moba_	Alignment	not modelled	5.1	11	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein