Phyre2

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Description	P0A6N8
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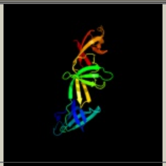
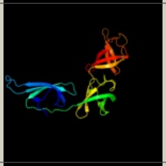
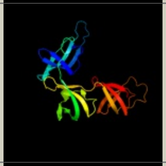
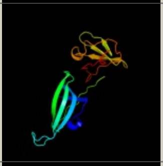
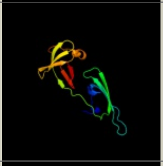
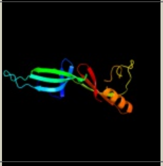
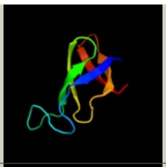
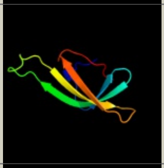
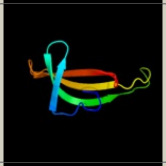
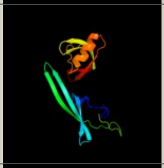
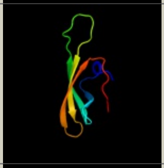
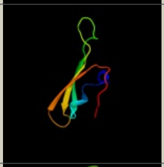
Unique Job ID	5c324d099f2fd13f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oyyA_	Alignment		100.0	30	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
2	c1uebB_	Alignment		100.0	31	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of translation elongation factor p from2 thermus thermophilus hb8
3	c1ybyB_	Alignment		100.0	29	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium2 thermocellum
4	c3treA_	Alignment		100.0	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
5	c1iz6B_	Alignment		100.0	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**initiation factor 5a; **PDBTitle:** crystal structure of translation initiation factor 5a from pyrococcus2 horikoshii
6	c1bkbA_	Alignment		100.0	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
7	c2eifA_	Alignment		100.0	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
8	c3hksB_	Alignment		100.0	17	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
9	c3er0A_	Alignment		100.0	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of the full length eif5a from2 saccharomyces cerevisiae
10	c1xtdA_	Alignment		99.9	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic initiation factor 5a; **PDBTitle:** structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
11	c3cpfB_	Alignment		99.9	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-1; **PDBTitle:** crystal structure of human eukaryotic translation initiation factor2 eif5a

12	d1ueba3	Alignment		99.9	47	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d1ueba1	Alignment		99.9	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
14	d1ueba2	Alignment		99.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	c3a5zF_	Alignment		99.8	24	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p
16	c1khiA_	Alignment		99.3	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
17	d1bkba1	Alignment		99.0	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
18	d1iz6a1	Alignment		99.0	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
19	d2eifa1	Alignment		99.0	17	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
20	d1x6oa1	Alignment		98.4	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
21	d1khia1	Alignment	not modelled	97.9	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
22	d1bkba2	Alignment	not modelled	97.1	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	d1iz6a2	Alignment	not modelled	96.8	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	d2eifa2	Alignment	not modelled	96.2	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	d1yiva1	Alignment	not modelled	55.4	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
26	c3fp9E_	Alignment	not modelled	47.0	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
27	d1eu1a1	Alignment	not modelled	44.1	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
28	d1vlfm1	Alignment	not modelled	43.4	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
29	d1g8ka1	Alignment	not modelled	42.5	5	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like

29	d1g8ka1	Alignment	not modelled	42.5	5	**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1dmra1	Alignment	not modelled	41.7	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d2hnxa1	Alignment	not modelled	41.5	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
32	d1ogya1	Alignment	not modelled	41.2	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1ftpa_	Alignment	not modelled	39.6	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
34	d2iv2x1	Alignment	not modelled	39.2	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
35	d2cr5a1	Alignment	not modelled	37.8	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
36	d1pmpa_	Alignment	not modelled	37.5	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
37	d1kqfa1	Alignment	not modelled	36.3	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d2pu9b1	Alignment	not modelled	34.8	26	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
39	d1wlfa1	Alignment	not modelled	33.6	15	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
40	d1y5ia1	Alignment	not modelled	32.7	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d2cqaa1	Alignment	not modelled	32.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
42	d1slqa_	Alignment	not modelled	30.8	14	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
43	c1wlfA_	Alignment	not modelled	30.0	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
44	c2z14A_	Alignment	not modelled	29.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ef-hand domain-containing family member c2; **PDBTitle:** crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein
45	d2jioa1	Alignment	not modelled	28.7	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
46	d1h0ha1	Alignment	not modelled	28.0	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
47	c2ki8A_	Alignment	not modelled	27.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
48	d1tmoa1	Alignment	not modelled	25.8	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
49	c1tmoA_	Alignment	not modelled	25.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
50	c1h5nC_	Alignment	not modelled	25.4	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
51	c2dzkA_	Alignment	not modelled	22.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubx domain-containing protein 2; **PDBTitle:** structure of the ubx domain in mouse ubx domain-containing2 protein 2
52	d1ifca_	Alignment	not modelled	22.7	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
53	c3iyuY_	Alignment	not modelled	22.4	14	**PDB header:**virus **Chain:** Y: **PDB Molecule:**outer capsid protein vp4; **PDBTitle:** atomic model of an infectious rotavirus particle
54	c1h0hA_	Alignment	not modelled	22.0	15	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
						PDB header:oxidoreductase

55	c1eu1A_	Alignment	not modelled	20.2	15	**Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
56	d1hmsa_	Alignment	not modelled	20.2	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
57	d2gp4a1	Alignment	not modelled	20.2	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
58	c1g8jC_	Alignment	not modelled	20.0	5	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
59	c2kxjA_	Alignment	not modelled	18.2	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubx domain-containing protein 4; **PDBTitle:** solution structure of ubx domain of human ubxd2 protein
60	d1i42a_	Alignment	not modelled	16.4	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
61	d2as0a1	Alignment	not modelled	15.7	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
62	d1ed7a_	Alignment	not modelled	15.4	21	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
63	c3m9bK_	Alignment	not modelled	15.1	22	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
64	c2ey4A_	Alignment	not modelled	14.9	18	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
65	d1mj4a_	Alignment	not modelled	14.9	11	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
66	c1ogyA_	Alignment	not modelled	14.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
67	d2f9ha1	Alignment	not modelled	14.5	8	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
68	c2iv2X_	Alignment	not modelled	14.5	15	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
69	c1vlfQ_	Alignment	not modelled	14.5	20	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
70	d1sa8a_	Alignment	not modelled	14.3	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
71	c2wkdA_	Alignment	not modelled	14.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
72	d1mdca_	Alignment	not modelled	14.2	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
73	d1g7na_	Alignment	not modelled	13.9	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
74	c1kqgA_	Alignment	not modelled	13.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
75	c1y5iA_	Alignment	not modelled	13.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
76	c2ivfA_	Alignment	not modelled	13.1	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
77	d1hkoa_	Alignment	not modelled	13.0	16	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
78	c2rrfA_	Alignment	not modelled	12.9	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21; **PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
79	d1opaa_	Alignment	not modelled	12.9	18	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
80	d1fdqa_	Alignment	not modelled	12.9	20	**Fold:**Lipocalins **Superfamily:**Lipocalins

						Family: Fatty acid binding protein-like
81	d2cu8a2	Alignment	not modelled	12.5	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
82	d1kv7a2	Alignment	not modelled	12.5	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
83	d1hfua1	Alignment	not modelled	12.4	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
84	d1kqwa_	Alignment	not modelled	11.8	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
85	c2v45A_	Alignment	not modelled	11.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
86	d1iccc_	Alignment	not modelled	11.6	8	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
87	c1cr5B_	Alignment	not modelled	11.4	8	**PDB header:**endocytosis/exocytosis **Chain:** B: **PDB Molecule:**sec18p (residues 22 - 210); **PDBTitle:** n-terminal domain of sec18p
88	c2vq5B_	Alignment	not modelled	11.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**s-norcoclaurine synthase; **PDBTitle:** x-ray structure of norcoclaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
89	d1m2ia_	Alignment	not modelled	11.0	16	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
90	c2nyaF_	Alignment	not modelled	10.7	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
91	d1x9la_	Alignment	not modelled	10.6	20	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
92	d1h8ca_	Alignment	not modelled	10.5	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
93	c2gp4A_	Alignment	not modelled	10.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
94	d1vioa2	Alignment	not modelled	10.3	15	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
95	c3e0jG_	Alignment	not modelled	10.1	10	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
96	d1bwya_	Alignment	not modelled	10.0	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
97	d2ix0a3	Alignment	not modelled	10.0	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
98	c2apoA_	Alignment	not modelled	9.8	14	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
99	c2ibjA_	Alignment	not modelled	9.7	12	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome b5; **PDBTitle:** structure of house fly cytochrome b5