Phyre2

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Description	P0A6N4
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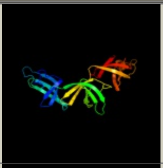
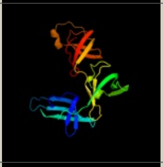
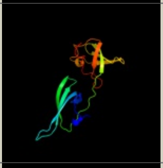
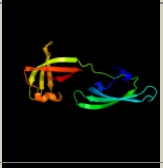
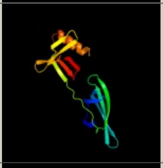
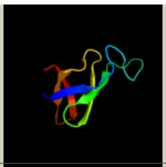
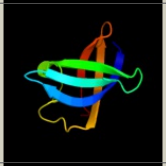
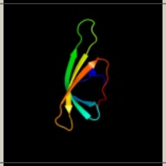
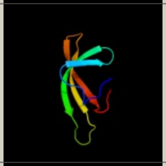
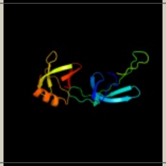
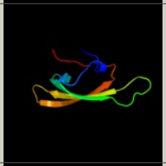
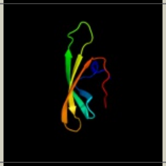
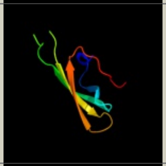
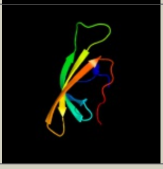
Unique Job ID	8982b95073c60958

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oyyA_	Alignment		100.0	35	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
2	c1uebB_	Alignment		100.0	46	**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	45	**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	54	**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	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
7	c2eifA_	Alignment		100.0	22	**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	15	**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	20	**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	22	**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	14	**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	72	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d1ueba2	Alignment		99.8	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	d1ueba1	Alignment		99.8	32	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
15	c3a5zF_	Alignment		99.8	100	**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	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
17	d1iz6a1	Alignment		99.1	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
18	d1bkba1	Alignment		99.1	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
19	d2eifa1	Alignment		99.1	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
20	d1x6oa1	Alignment		98.7	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
21	d1khia1	Alignment	not modelled	98.0	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
22	d1bkba2	Alignment	not modelled	97.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	d1iz6a2	Alignment	not modelled	97.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	d2eifa2	Alignment	not modelled	97.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	c3fp9E_	Alignment	not modelled	52.4	33	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
26	d1eu1a1	Alignment	not modelled	51.1	24	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
27	d1vlfm1	Alignment	not modelled	51.0	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
28	d1ogya1	Alignment	not modelled	50.4	29	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
						Fold: Double psi beta-barrel

29	d1dmra1	Alignment	not modelled	50.0	29	**Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
30	d1g8ka1	Alignment	not modelled	49.1	24	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d2iv2x1	Alignment	not modelled	49.0	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1kqfa1	Alignment	not modelled	45.6	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	c2z14A_	Alignment	not modelled	45.6	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
34	d1pmpa_	Alignment	not modelled	45.3	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
35	d1mdca_	Alignment	not modelled	43.9	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
36	d1bwya_	Alignment	not modelled	43.5	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
37	d1y5ia1	Alignment	not modelled	42.8	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
38	d1tmoa1	Alignment	not modelled	41.7	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d2jioa1	Alignment	not modelled	41.5	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c2ki8A_	Alignment	not modelled	40.6	43	**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
41	c1tmoA_	Alignment	not modelled	39.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
42	d1ftpa_	Alignment	not modelled	39.8	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
43	c2kcmA_	Alignment	not modelled	38.8	11	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**cold shock domain family protein; **PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
44	d1h0ha1	Alignment	not modelled	37.1	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
45	c1h5nC_	Alignment	not modelled	36.8	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
46	d1slqa_	Alignment	not modelled	35.5	14	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
47	d1yiva1	Alignment	not modelled	35.1	10	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
48	d1hmsa_	Alignment	not modelled	33.4	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
49	c3iyuY_	Alignment	not modelled	32.4	14	**PDB header:**virus **Chain:** Y: **PDB Molecule:**outer capsid protein vp4; **PDBTitle:** atomic model of an infectious rotavirus particle
50	c1h0hA_	Alignment	not modelled	31.7	10	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
51	d2cqaa1	Alignment	not modelled	31.2	39	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
52	c2kxjA_	Alignment	not modelled	31.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubx domain-containing protein 4; **PDBTitle:** solution structure of ubx domain of human ubxd2 protein
53	c1eu1A_	Alignment	not modelled	31.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
54	d2cr5a1	Alignment	not modelled	29.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like

						Family:UBX domain
55	c2ivfA_	Alignment	not modelled	29.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
56	c1g8jC_	Alignment	not modelled	27.9	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
57	c1vlfQ_	Alignment	not modelled	26.4	14	**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
58	d2pu9b1	Alignment	not modelled	25.4	42	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
59	d1b56a_	Alignment	not modelled	25.1	5	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
60	c1kqgA_	Alignment	not modelled	24.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
61	d2hnxa1	Alignment	not modelled	24.3	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
62	c1y5iA_	Alignment	not modelled	24.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
63	d2gp4a1	Alignment	not modelled	23.6	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
64	c3hslX_	Alignment	not modelled	23.6	14	**PDB header:**replication **Chain:** X: **PDB Molecule:**orf59; **PDBTitle:** the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
65	c1ogyA_	Alignment	not modelled	22.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
66	d1sa8a_	Alignment	not modelled	22.0	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
67	c3m9bK_	Alignment	not modelled	21.7	30	**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
68	c2iv2X_	Alignment	not modelled	21.6	19	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
69	d1q42a_	Alignment	not modelled	21.1	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
70	d1ifca_	Alignment	not modelled	20.7	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
71	d1i42a_	Alignment	not modelled	19.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
72	d1ed7a_	Alignment	not modelled	19.0	21	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
73	c2v45A_	Alignment	not modelled	18.9	19	**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
74	d1g7na_	Alignment	not modelled	17.8	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
75	d2es2a1	Alignment	not modelled	17.5	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
76	c2nyaF_	Alignment	not modelled	16.4	38	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
77	c2wkdA_	Alignment	not modelled	16.4	38	**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
78	c2e7zA_	Alignment	not modelled	16.2	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
79	d1go3e2	Alignment	not modelled	16.0	31	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE)

						Family:N-terminal, heterodimerisation domain of RBP7 (RpoE)
80	d1hfua1	Alignment	not modelled	15.3	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
81	c2ey4A_	Alignment	not modelled	15.0	29	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
82	d2as0a1	Alignment	not modelled	15.0	28	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
83	d1p6pa_	Alignment	not modelled	15.0	5	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
84	d2f9ha1	Alignment	not modelled	14.8	10	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
85	d2ftba1	Alignment	not modelled	14.2	8	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
86	d2cu8a2	Alignment	not modelled	14.1	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
87	c1q40C_	Alignment	not modelled	13.8	16	**PDB header:**translation **Chain:** C: **PDB Molecule:**mrna transport regulator mtr2; **PDBTitle:** crystal structure of the c. albicans mtr2-mex67 m domain complex
88	d1cyoa_	Alignment	not modelled	13.6	15	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
89	c2vq5B_	Alignment	not modelled	13.5	19	**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
90	d1euea_	Alignment	not modelled	13.3	18	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
91	d1jt8a_	Alignment	not modelled	12.9	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	c2gp4A_	Alignment	not modelled	12.6	50	**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
93	d1kv7a2	Alignment	not modelled	12.5	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
94	d1x3ha2	Alignment	not modelled	12.5	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
95	d1uhta_	Alignment	not modelled	12.3	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
96	d2piea1	Alignment	not modelled	12.2	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
97	d1kqwa_	Alignment	not modelled	12.2	14	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
98	d1k0ha_	Alignment	not modelled	12.1	26	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
99	d1fdqa_	Alignment	not modelled	12.0	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like