Phyre^2

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Description	P0A6P1
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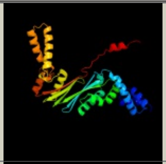
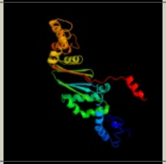
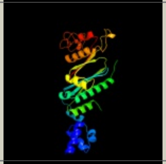
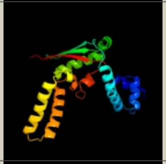
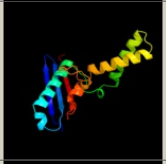
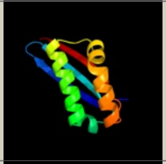
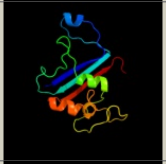
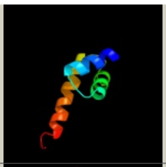
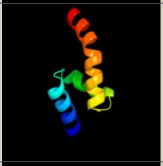
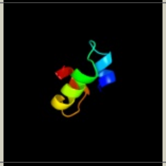
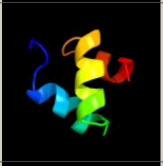
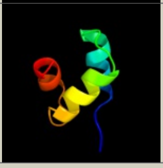
Unique Job ID	271ecbe5cb8124ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1efuB_	Alignment		100.0	100	**PDB header:**complex (two elongation factors) **Chain:** B: **PDB Molecule:**elongation factor ts; **PDBTitle:** elongation factor complex ef-tu/ef-ts from escherichia coli
2	c3agqA_	Alignment		100.0	100	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
3	c3mmpC_	Alignment		100.0	100	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
4	c1xb2B_	Alignment		100.0	29	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
5	c1aipG_	Alignment		100.0	53	**PDB header:**complex of two elongation factors **Chain:** G: **PDB Molecule:**elongation factor ts; **PDBTitle:** ef-tu ef-ts complex from thermus thermophilus
6	d1efub2	Alignment		100.0	100	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
7	d1tfea_	Alignment		100.0	53	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
8	d1efub4	Alignment		99.9	100	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
9	d1xb2b2	Alignment		99.9	24	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
10	d1xb2b3	Alignment		99.9	27	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
11	d1efub3	Alignment		99.8	100	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain

12	d1aipc1	Alignment		99.8	55	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
13	d1xb2b1	Alignment		99.8	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
14	d2cp9a1	Alignment		99.7	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
15	d1ifya_	Alignment		96.7	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
16	c1tr8A_	Alignment		96.6	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
17	d1wiva_	Alignment		96.3	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
18	d1vega_	Alignment		96.2	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
19	c2daiA_	Alignment		95.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
20	c2dakA_	Alignment		95.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
21	c2dagA_	Alignment	not modelled	94.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
22	c1wr1B_	Alignment	not modelled	94.7	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
23	c2jy5A_	Alignment	not modelled	94.4	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
24	d1veja1	Alignment	not modelled	94.3	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
25	c2dahA_	Alignment	not modelled	94.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
26	c2cpwA_	Alignment	not modelled	94.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant; **PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna
27	d1whca_	Alignment	not modelled	94.1	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
28	d1oqya1	Alignment	not modelled	94.1	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
						Fold: RuvA C-terminal domain-like

29	d2dnaa1	Alignment	not modelled	93.8	18	**Superfamily:**UBA-like **Family:**UBA domain
30	d1wj7a1	Alignment	not modelled	93.7	37	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
31	c2dnaA_	Alignment	not modelled	93.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
32	d2bwba1	Alignment	not modelled	93.7	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
33	d1veka_	Alignment	not modelled	93.5	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
34	c2cwbA_	Alignment	not modelled	93.3	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
35	d2daha1	Alignment	not modelled	93.2	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
36	d2cpwa1	Alignment	not modelled	92.9	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
37	d1vdla_	Alignment	not modelled	92.2	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
38	d2crna1	Alignment	not modelled	92.0	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
39	c2crnA_	Alignment	not modelled	91.6	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
40	d1v92a_	Alignment	not modelled	89.7	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
41	d2g3qa1	Alignment	not modelled	89.4	28	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
42	d1oaia_	Alignment	not modelled	88.2	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
43	c2jp7A_	Alignment	not modelled	85.8	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
44	c2damA_	Alignment	not modelled	85.4	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**etea protein; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
45	c2dalA_	Alignment	not modelled	85.3	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein kiaa0794; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
46	d1go5a_	Alignment	not modelled	85.1	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
47	c2do6A_	Alignment	not modelled	84.8	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
48	c2d9sA_	Alignment	not modelled	84.4	37	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
49	c3bq3A_	Alignment	not modelled	82.4	15	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
50	d1oqya2	Alignment	not modelled	80.1	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
51	c2jnhA_	Alignment	not modelled	79.1	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
52	d1dd3a2	Alignment	not modelled	75.9	32	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
53	d1ctfa_	Alignment	not modelled	71.0	23	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
54	d2zjq51	Alignment	not modelled	63.1	30	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Ribosomal protein L7/12, C-terminal domain
55	c2zjq5_	Alignment	not modelled	63.1	30	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** interaction of l7 with l11 induced by microccocin binding2 to the deinococcus radiodurans 50s subunit
						PDB header:ribosome

56	c1giyJ_	Alignment	not modelled	59.3	32	**Chain:** J: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
57	d1z96a1	Alignment	not modelled	53.8	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
58	d1wjia_	Alignment	not modelled	53.2	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
59	d1dv0a_	Alignment	not modelled	50.6	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
60	c3k6gA_	Alignment	not modelled	46.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**telomeric repeat-binding factor 2-interacting protein 1; **PDBTitle:** crystal structure of rap1 and trf2 complex
61	c2ftcF_	Alignment	not modelled	37.9	29	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**39s ribosomal protein l12, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
62	d1lgta2	Alignment	not modelled	30.5	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
63	d1wgla_	Alignment	not modelled	28.2	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
64	d2qswa1	Alignment	not modelled	25.3	46	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
65	c2gya3_	Alignment	not modelled	25.1	23	**PDB header:**ribosome **Chain:** 3: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
66	c1zswA_	Alignment	not modelled	23.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
67	d1fipa_	Alignment	not modelled	20.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
68	d1zq1a1	Alignment	not modelled	20.2	38	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
69	d3dhxa1	Alignment	not modelled	20.0	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
70	c2zi8A_	Alignment	not modelled	19.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable biphenyl-2,3-diol 1,2-dioxygenase bphc; **PDBTitle:** crystal structure of the hsac extradiol dioxygenase from m.2 tuberculosis in complex with 3,4-dihydroxy-9,10-3 seconandrost-1,3,5(10)-triene-9,17-dione (dhsa)
71	c3cz6A_	Alignment	not modelled	18.3	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna-binding protein rap1; **PDBTitle:** crystal structure of the rap1 c-terminus
72	c1knfA_	Alignment	not modelled	18.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,3-dihydroxybiphenyl 1,2-dioxygenase; **PDBTitle:** crystal structure of 2,3-dihydroxybiphenyl 1,2-dioxygenase complexed2 with 3-methyl catechol under anaerobic condition
73	c2dhyA_	Alignment	not modelled	17.9	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
74	d1kw3b2	Alignment	not modelled	16.5	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
75	c2xecD_	Alignment	not modelled	15.7	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
76	c2kjgA_	Alignment	not modelled	15.6	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**archaeal protein sso6904; **PDBTitle:** solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus
77	c2kc2A_	Alignment	not modelled	14.9	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the f1 domain (residues 86-202) of the2 talin
78	c3rmuD_	Alignment	not modelled	14.8	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial; **PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee
79	c3fmyA_	Alignment	not modelled	14.8	4	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)

80	d1zhva2	Alignment	not modelled	14.7	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
81	c3c4mD_	Alignment	not modelled	14.6	43	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
82	c3c4mC_	Alignment	not modelled	14.6	43	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
83	c1umqA_	Alignment	not modelled	14.0	0	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
84	d1umqa_	Alignment	not modelled	14.0	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
85	d2cosa1	Alignment	not modelled	13.6	37	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
86	c2ei2A_	Alignment	not modelled	13.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1,2-dihydroxynaphthalene dioxygenase; **PDBTitle:** crystal structure analysis of the 1,2-dihydroxynaphthalene dioxygenase2 from pseudomonas sp. stain c18
87	d2dsya1	Alignment	not modelled	13.0	33	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA0281-like
88	d1ysra1	Alignment	not modelled	12.9	13	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
89	c3nicA_	Alignment	not modelled	12.7	8	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
90	d2flia1	Alignment	not modelled	12.3	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
91	d2qrra1	Alignment	not modelled	12.0	38	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
92	d1etob_	Alignment	not modelled	11.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
93	c1zwgA_	Alignment	not modelled	11.7	43	**PDB header:**hormone **Chain:** A: **PDB Molecule:**parathyroid hormone; **PDBTitle:** succinyl human parathyroid hormone 4-37, nmr, 10 structures
94	d1mpya1	Alignment	not modelled	11.3	6	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
95	d1hsta_	Alignment	not modelled	11.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
96	c1xg2B_	Alignment	not modelled	11.2	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**pectinesterase inhibitor; **PDBTitle:** crystal structure of the complex between pectin2 methylesterase and its inhibitor protein
97	c1zhvA_	Alignment	not modelled	11.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
98	c3pkwA_	Alignment	not modelled	10.9	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla); **PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
99	c3ey7B_	Alignment	not modelled	10.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**biphenyl-2,3-diol 1,2-dioxygenase iii-related **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1