Phyre^2

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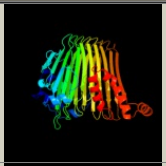
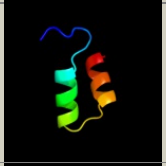
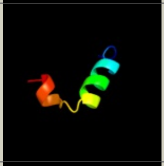
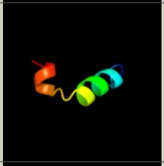
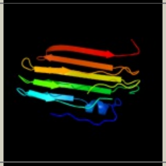
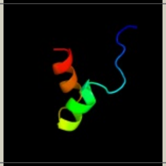
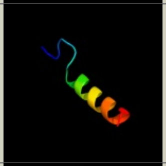
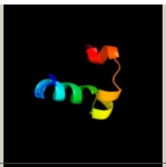
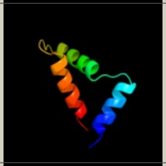
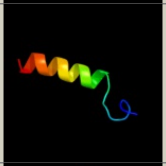
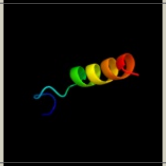
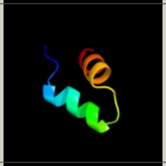
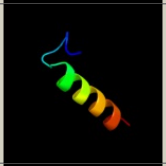
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vh4a_	Alignment		100.0	100	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD
2	c2dagA_	Alignment		74.2	17	**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)
3	d1whca_	Alignment		67.3	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
4	c1dd9A_	Alignment		63.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
5	d1dd9a_	Alignment		63.0	17	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
6	c2daiA_	Alignment		62.2	19	**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)
7	c3sf5D_	Alignment		58.4	13	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**urease accessory protein ureh; **PDBTitle:** crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
8	d1veka_	Alignment		54.2	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
9	c2crnA_	Alignment		54.0	10	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
10	d1p32a_	Alignment		53.8	26	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
11	d1nuia1	Alignment		52.5	33	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein

12	d2csba4	Alignment		50.8	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
13	d1rfza_	Alignment		48.3	17	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
14	d1yqfa1	Alignment		47.7	35	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
15	c3qv0A_	Alignment		44.4	39	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mitochondrial acidic protein mam33; **PDBTitle:** crystal structure of saccharomyces cerevisiae mam33
16	c3jv1A_	Alignment		41.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**p22 protein; **PDBTitle:** crystal structure of the trypanosoma brucei p22 protein
17	c1q57G_	Alignment		41.5	36	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
18	d1wiva_	Alignment		39.7	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
19	c3ic3C_	Alignment		39.1	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative pyruvate dehydrogenase; **PDBTitle:** structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodopseudomonas palustrus cga009
20	d2crna1	Alignment		38.6	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
21	c2qh9B_	Alignment	not modelled	37.2	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0215 protein af_1433; **PDBTitle:** the crystal structure of a protein of unknown function from2 archaeoglobus fulgidus dsm 4304
22	c3fp5A_	Alignment	not modelled	36.4	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa binding protein; **PDBTitle:** crystal structure of acbp from moniliophthora perniciosa
23	c2f46A_	Alignment	not modelled	36.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
24	d2cpwa1	Alignment	not modelled	34.1	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
25	c2cpwA_	Alignment	not modelled	33.3	21	**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
26	d1n9pa_	Alignment	not modelled	33.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Cytoplasmic domain of inward rectifier potassium channel
27	d1yqga1	Alignment	not modelled	31.3	24	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
28	c2au3A_	Alignment	not modelled	29.1	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
						PDB header:transferase

29	c2o2kA_	Alignment	not modelled	28.9	22	**Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
30	c2zc1A_	Alignment	not modelled	28.8	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
31	c2dakA_	Alignment	not modelled	28.3	10	**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)
32	d2e1za2	Alignment	not modelled	27.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
33	c2wknE_	Alignment	not modelled	26.8	25	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
34	d1g99a2	Alignment	not modelled	26.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
35	d1mska_	Alignment	not modelled	24.8	22	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Methionine synthase SAM-binding domain
36	d2ahra1	Alignment	not modelled	20.6	10	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
37	c1nuiA_	Alignment	not modelled	20.5	33	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
38	d2ddha2	Alignment	not modelled	20.2	13	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
39	d1vega_	Alignment	not modelled	20.0	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
40	d1ivza_	Alignment	not modelled	19.9	25	**Fold:**Ferredoxin-like **Superfamily:**SEA domain **Family:**SEA domain
41	c1tuuA_	Alignment	not modelled	18.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
42	c3e3vA_	Alignment	not modelled	18.4	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
43	c3my3A_	Alignment	not modelled	18.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mterf domain-containing protein 1, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial transcription termination2 factor 3
44	c2d9sA_	Alignment	not modelled	18.2	33	**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
45	c3khyA_	Alignment	not modelled	18.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
46	d1ifya_	Alignment	not modelled	16.7	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
47	c1sazA_	Alignment	not modelled	16.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable butyrate kinase 2; **PDBTitle:** membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
48	c3zq4C_	Alignment	not modelled	16.2	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease j 1; **PDBTitle:** unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
49	d1wfda_	Alignment	not modelled	16.0	7	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
50	c1x3nA_	Alignment	not modelled	15.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
51	d2gcla1	Alignment	not modelled	15.3	42	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**SSRP1-like
52	c3qyeA_	Alignment	not modelled	15.2	17	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**tbc1 domain family member 1; **PDBTitle:** crystal structure of human tbc1d1 rabgap domain
53	d1saza2	Alignment	not modelled	15.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
54	d2g3qa1	Alignment	not modelled	14.5	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
55	d1kx5d_	Alignment	not modelled	14.4	21	**Fold:**Histone-fold **Superfamily:**Histone-fold

						Family: Nucleosome core histones
56	d1v3aa_	Alignment	not modelled	14.0	34	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
57	c2e4fA_	Alignment	not modelled	13.8	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**g protein-activated inward rectifier potassium channel 2; **PDBTitle:** crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2
58	c3rhgA_	Alignment	not modelled	13.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
59	d1oqya1	Alignment	not modelled	13.4	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
60	c3ff5B_	Alignment	not modelled	13.3	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
61	c1tlqA_	Alignment	not modelled	12.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ypjq; **PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64
62	d1tlqa_	Alignment	not modelled	12.6	17	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
63	c2iirJ_	Alignment	not modelled	12.6	22	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
64	d2gu3a1	Alignment	not modelled	12.5	36	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
65	c3gypA_	Alignment	not modelled	12.4	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**histone chaperone rtt106; **PDBTitle:** rtt106p
66	c2gu3A_	Alignment	not modelled	12.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ypmb protein; **PDBTitle:** ypmb protein from bacillus subtilis
67	c2do6A_	Alignment	not modelled	12.2	19	**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
68	c3gztF_	Alignment	not modelled	11.9	23	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
69	c2kerA_	Alignment	not modelled	11.9	43	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**alpha-amylase inhibitor z-2685; **PDBTitle:** alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
70	d1eqzb_	Alignment	not modelled	11.8	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
71	d1ok0a_	Alignment	not modelled	11.8	29	**Fold:**alpha-Amylase inhibitor tendamistat **Superfamily:**alpha-Amylase inhibitor tendamistat **Family:**alpha-Amylase inhibitor tendamistat
72	c3p4iA_	Alignment	not modelled	11.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
73	d1wjia_	Alignment	not modelled	11.5	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
74	d1s32d_	Alignment	not modelled	11.2	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
75	c3mhvC_	Alignment	not modelled	11.0	12	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of vps4 and vta1
76	c2w85A_	Alignment	not modelled	10.6	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
77	c3m66A_	Alignment	not modelled	10.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mterf domain-containing protein 1, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial transcription termination2 factor 3
78	c1jrjA_	Alignment	not modelled	10.4	17	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
79	c3hy5A_	Alignment	not modelled	10.4	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**retinaldehyde-binding protein 1; **PDBTitle:** crystal structure of cralbp
80	d1oiza1	Alignment	not modelled	10.1	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
81	d1y9ia_	Alignment	not modelled	9.7	15	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like

82	c3dfgA_	Alignment	not modelled	9.5	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
83	c3f4cA_	Alignment	not modelled	9.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
84	c1ye9E_	Alignment	not modelled	9.3	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli
85	d1auaa1	Alignment	not modelled	9.2	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
86	c2akhZ_	Alignment	not modelled	9.0	18	**PDB header:**protein transport **Chain:** Z: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a non-2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
87	c3d5lA_	Alignment	not modelled	8.6	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of regulatory protein recx
88	c3rj1P_	Alignment	not modelled	8.6	16	**PDB header:**transcription **Chain:** P: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 17; **PDBTitle:** architecture of the mediator head module
89	d1abaa_	Alignment	not modelled	8.5	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	c3k2gA_	Alignment	not modelled	8.5	13	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
91	c2hjmB_	Alignment	not modelled	8.1	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
92	d1tzyb_	Alignment	not modelled	8.1	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
93	d1bf6a_	Alignment	not modelled	8.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
94	c2jnhA_	Alignment	not modelled	7.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
95	c2i7aA_	Alignment	not modelled	7.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calpain 13; **PDBTitle:** domain iv of human calpain 13
96	c3okzB_	Alignment	not modelled	7.8	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein gbs0355; **PDBTitle:** crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
97	d1y02a1	Alignment	not modelled	7.8	23	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
98	c2fhgC_	Alignment	not modelled	7.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome, beta subunit; **PDBTitle:** crystal structure of mycobacterial tuberculosis proteasome
99	c2vc7A_	Alignment	not modelled	7.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities