Phyre^{2}

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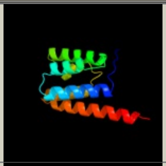
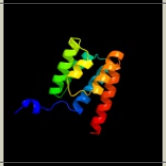
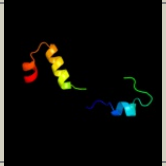
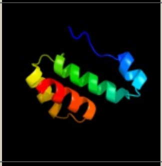
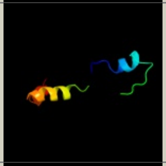
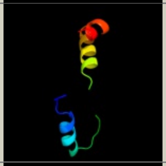
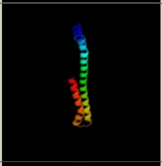
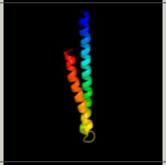
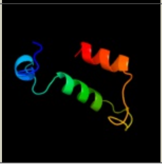
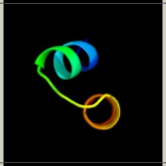
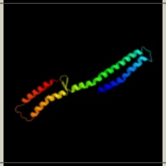
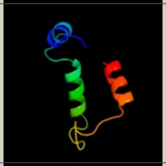
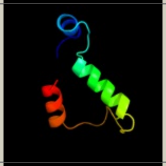
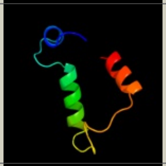
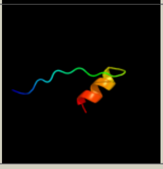
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c1qA_	Alignment		99.9	51	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general secretion pathway protein f; **PDBTitle:** the three-dimensional structure of the cytoplasmic domains of epsf2 from the type 2 secretion system of vibrio cholerae
2	c2whnA_	Alignment		99.9	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**pilus assembly protein pilc; **PDBTitle:** n-terminal domain from the pilc type iv pilus biogenesis2 protein
3	c3c8mA_	Alignment		42.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
4	d3cuma1	Alignment		38.1	8	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
5	c3i3aC_	Alignment		36.5	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
6	c3ingA_	Alignment		34.4	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
7	c2ejwB_	Alignment		34.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8
8	c2d1lA_	Alignment		33.4	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**metastasis suppressor protein 1; **PDBTitle:** structure of f-actin binding domain imd of mim (missing in metastasis)
9	c3ok8A_	Alignment		31.0	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein **PDBTitle:** i-bar of pinkbar
10	d1y2oa1	Alignment		29.7	15	**Fold:**BAR/IMD domain-like **Superfamily:**BAR/IMD domain-like **Family:**IMD domain
11	c3iugA_	Alignment		20.0	17	**PDB header:**splicing **Chain:** A: **PDB Molecule:**rho/cdc42/rac gtpase-activating protein rics; **PDBTitle:** crystal structure of the rhogap domain of rics

12	d2jf2a1	Alignment		17.0	11	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
13	c3k4iC_	Alignment		15.1	25	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
14	c3r1fO_	Alignment		14.5	15	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
15	c2c5qE_	Alignment		14.1	19	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
16	c2bbjB_	Alignment		13.0	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
17	d1xa6a1	Alignment		12.8	13	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
18	c3kuqA_	Alignment		12.8	15	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 7; **PDBTitle:** crystal structure of the dlc1 rhogap domain
19	c3byiA_	Alignment		12.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho gtpase activating protein 15; **PDBTitle:** crystal structure of human rho gtpase activating protein 15 (arhgap15)
20	d1vq3a_	Alignment		11.9	13	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
21	d2ezla_	Alignment	not modelled	11.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
22	c2f4qA_	Alignment	not modelled	10.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
23	c3ibqA_	Alignment	not modelled	10.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
24	c3r0sA_	Alignment	not modelled	10.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
25	c3do5A_	Alignment	not modelled	10.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
26	c2hx1D_	Alignment	not modelled	10.4	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
27	d1j2za_	Alignment	not modelled	9.3	12	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
28	d1gtda_	Alignment	not modelled	9.3	4	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase

29	c2zw2B_	Alignment	not modelled	9.2	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
30	c1xa6A_	Alignment	not modelled	8.9	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**beta2-chimaerin; **PDBTitle:** crystal structure of the human beta2-chimaerin
31	c3neuA_	Alignment	not modelled	8.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
32	c2pmzN_	Alignment	not modelled	8.4	13	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
33	d1hara_	Alignment	not modelled	8.3	5	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
34	d2f06a1	Alignment	not modelled	7.8	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
35	d1e8ob_	Alignment	not modelled	7.6	23	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
36	c3mtjA_	Alignment	not modelled	7.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
37	d2c4na1	Alignment	not modelled	6.8	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
38	d2gyqa1	Alignment	not modelled	6.3	18	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
39	c3gdeA_	Alignment	not modelled	5.7	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** the closed conformation of atp-dependent dna ligase from2 archaeoglobus fulgidus
40	d1ijwc_	Alignment	not modelled	5.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
41	c1n54A_	Alignment	not modelled	5.6	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**80 kda nuclear cap binding protein; **PDBTitle:** cap binding complex m7gpppg free
42	c1zk6A_	Alignment	not modelled	5.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
43	d1jnsa_	Alignment	not modelled	5.6	8	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
44	d1zhva2	Alignment	not modelled	5.5	29	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
45	c2i7aA_	Alignment	not modelled	5.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calpain 13; **PDBTitle:** domain iv of human calpain 13
46	c2kk6A_	Alignment	not modelled	5.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fer; **PDBTitle:** solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d
47	d1914a2	Alignment	not modelled	5.3	23	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
48	d2gs4a1	Alignment	not modelled	5.1	20	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
49	c2kncB_	Alignment	not modelled	5.1	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
50	c1ebuA_	Alignment	not modelled	5.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine
51	c2kncA_	Alignment	not modelled	5.1	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
52	c1sneB_	Alignment	not modelled	5.1	31	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein
53	c1sneA_	Alignment	not modelled	5.1	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein

54	d1hcra_	Alignment	not modelled	5.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
55	c3nmeA_	Alignment	not modelled	5.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase