Phyre2

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Description	Q46953
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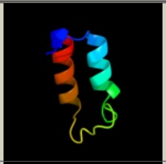
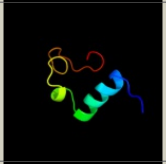
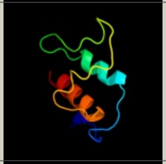
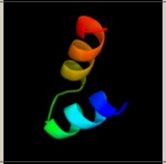
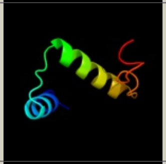
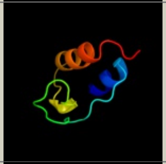
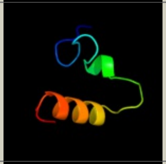
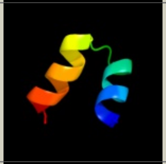
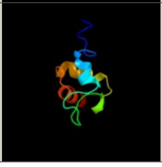
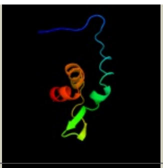
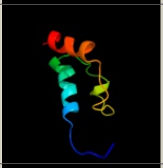
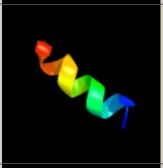
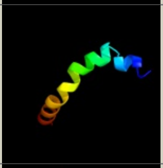
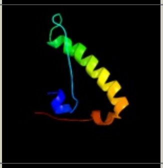
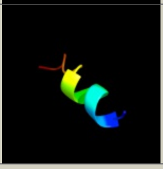
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fwtA_	Alignment		52.9	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
2	c2jvwA_	Alignment		43.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
3	d1zeea1	Alignment		22.1	34	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
4	c2bh7A_	Alignment		22.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
5	c2hl7A_	Alignment		21.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
6	c1yx3A_	Alignment		20.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
7	d1wj7a1	Alignment		19.3	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
8	c2dnwA_	Alignment		19.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
9	c3g2bA_	Alignment		18.8	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
10	c2kw0A_	Alignment		18.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
11	c1wr1B_	Alignment		16.6	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin

12	d1veja1	Alignment		13.5	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
13	c2d86A_	Alignment		12.8	21	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**vav-3 protein; **PDBTitle:** solution structure of the ch domain from human vav-3 protein
14	c2pbyB_	Alignment		11.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
15	c1ziiA_	Alignment		11.3	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
16	c1ziiB_	Alignment		11.3	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
17	c2pjwH_	Alignment		11.1	18	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
18	c2ae8C_	Alignment		11.1	28	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
19	d1sr9a1	Alignment		10.7	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
20	c1zijB_	Alignment		10.7	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
21	c1zijA_	Alignment	not modelled	10.7	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
22	c1zijC_	Alignment	not modelled	10.7	46	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
23	d1whra_	Alignment	not modelled	10.6	13	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
24	d1nq4a_	Alignment	not modelled	10.5	23	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
25	d1t8ka_	Alignment	not modelled	9.8	23	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
26	c2g2qB_	Alignment	not modelled	9.6	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the crystal structure of g4, the poxviral disulfide oxidoreductase2 essential for cytoplasmic disulfide bond formation
27	c2cnrA_	Alignment	not modelled	9.6	7	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
28	c2fq2A_	Alignment	not modelled	9.1	22	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
						Fold:SAM domain-like

29	d1szpa1	Alignment	not modelled	8.7	21	**Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
30	d1q9ja1	Alignment	not modelled	8.5	18	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
31	d1gjja2	Alignment	not modelled	8.3	14	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
32	c2kwlA_	Alignment	not modelled	8.2	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
33	c2kebA_	Alignment	not modelled	8.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
34	c2yfvC_	Alignment	not modelled	8.1	31	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
35	c3ce7A_	Alignment	not modelled	7.8	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
36	c3pcqX_	Alignment	not modelled	7.7	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
37	c1jb0X_	Alignment	not modelled	7.6	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
38	d1jb0x_	Alignment	not modelled	7.6	58	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
39	d2hlya1	Alignment	not modelled	7.2	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
40	d1n7va_	Alignment	not modelled	7.0	60	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
41	c2fvfA_	Alignment	not modelled	6.8	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
42	c2dakA_	Alignment	not modelled	6.7	18	**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)
43	d1vkua_	Alignment	not modelled	6.4	25	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
44	d1rkta2	Alignment	not modelled	6.1	21	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
45	d2af8a_	Alignment	not modelled	6.1	25	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
46	c3ejbC_	Alignment	not modelled	6.1	23	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
47	d1yo5c1	Alignment	not modelled	5.9	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ets domain
48	d1oqya2	Alignment	not modelled	5.8	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
49	c2lafA_	Alignment	not modelled	5.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
50	d1d0qa_	Alignment	not modelled	5.7	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
51	c3a58A_	Alignment	not modelled	5.7	30	**PDB header:**protein transport/exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** crystal structure of sec3p - rho1p complex from2 saccharomyces cerevisiae
52	c2l3gA_	Alignment	not modelled	5.6	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** solution nmr structure of ch domain of rho guanine nucleotide exchange2 factor 7 from homo sapiens, northeast structural genomics consortium3 target hr4495e
53	d1jjcb6	Alignment	not modelled	5.5	24	**Fold:**PheT/TilS domain **Superfamily:**PheT/TilS domain **Family:**B3/B4 domain of PheRS, PheT
54	d1wiva_	Alignment	not modelled	5.4	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
						PDB header:transferase **Chain:** A: **PDB Molecule:**acyl carrier protein;

55	c2l4bA_	Alignment	not modelled	5.3	17	**PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
56	d1zcba1	Alignment	not modelled	5.3	41	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
57	c2l9fA_	Alignment	not modelled	5.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
58	c2dagA_	Alignment	not modelled	5.1	23	**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)
59	d1sknp_	Alignment	not modelled	5.1	17	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
60	d1hfes_	Alignment	not modelled	5.0	30	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Fe-only hydrogenase smaller subunit **Family:**Fe-only hydrogenase smaller subunit