Phyre²

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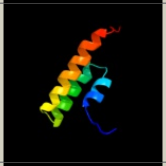
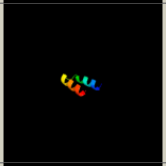
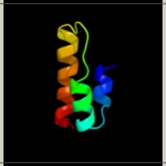
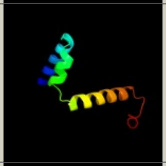
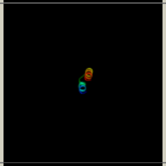
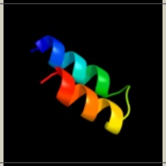
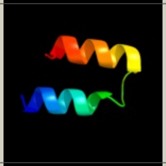
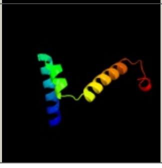
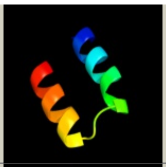
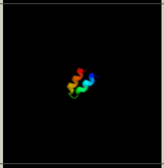
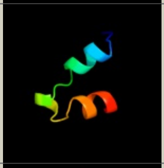
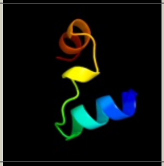
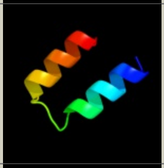
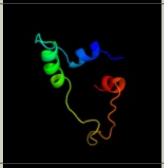
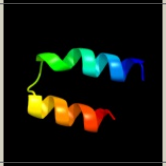
Description	P0ACE3
Date	Thu Jan 5 11:18:00 GMT 2012
Unique Job ID	e5fdeedaf18a5fb7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jw2a_	Alignment		100.0	100	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Hemolysin expression modulating protein HHA **Family:**Hemolysin expression modulating protein HHA
2	c2jqtA_	Alignment		99.6	40	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**h-ns/stpa-binding protein 2; **PDBTitle:** structure of the bacterial replication origin-associated2 protein cnu
3	d1t1ua1	Alignment		25.8	7	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
4	d1xl7a1	Alignment		25.3	14	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
5	c2jpnA_	Alignment		25.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** solution structure of t4 bacteriophage helicase uvsw.1
6	d1trra_	Alignment		22.8	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
7	d1nm8a1	Alignment		21.7	18	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
8	c2fyoA_	Alignment		20.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine o-palmitoyltransferase ii, **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
9	d1ndba1	Alignment		18.3	18	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
10	c1q6xA_	Alignment		17.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** crystal structure of rat choline acetyltransferase
11	d1jhga_	Alignment		17.9	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR

12	c2h4tB_	Alignment		16.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
13	c3cm8A_	Alignment		15.4	39	**PDB header:**rna binding protein/transferase **Chain:** A: **PDB Molecule:**polymerase acidic protein; **PDBTitle:** a rna polymerase subunit structure from virus
14	c1xl8B_	Alignment		15.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
15	d1i27a_	Alignment		14.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
16	d1ej2a_	Alignment		13.7	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
17	c1t7qA_	Alignment		13.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine acetyltransferase; **PDBTitle:** crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
18	d2bsza1	Alignment		13.2	27	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
19	c2fy2A_	Alignment		12.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** structures of ligand bound human choline acetyltransferase2 provide insight into regulation of acetylcholine synthesis
20	c3s6n2_	Alignment		12.3	31	**PDB header:**splicing **Chain:** 2: **PDB Molecule:**survival of motor neuron protein-interacting protein 1; **PDB Fragment:**gemin2-binding domain; **PDBTitle:** crystal structure of the gemin2-binding domain of smn, gemin2 in2 complex with smd1/d2/f/e/g from human
21	c3nd5D_	Alignment	not modelled	12.1	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
22	d2oa4a1	Alignment	not modelled	11.6	41	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
23	c3htxA_	Alignment	not modelled	11.4	22	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
24	d1vlha_	Alignment	not modelled	11.1	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
25	c3frwF_	Alignment	not modelled	10.8	13	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
26	d1tfua_	Alignment	not modelled	10.3	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
27	d1od6a_	Alignment	not modelled	9.7	7	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
28	c3h0gP_	Alignment	not modelled	9.7	14	**PDB header:**transcription **Chain:** P: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb4; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
						PDB header:structural genomics, unknown function

29	c2rbgB_	Alignment	not modelled	9.5	23	**Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493; **PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
30	d1t07a_	Alignment	not modelled	9.3	14	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
31	d1ckma1	Alignment	not modelled	9.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
32	c2l3lA_	Alignment	not modelled	8.7	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**tubulin-specific chaperone c; **PDBTitle:** the solution structure of the n-terminal domain of human tubulin2 binding cofactor c reveals a platform for the interaction with ab-3 tubulin
33	d1qjca_	Alignment	not modelled	8.6	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
34	c2l5aA_	Alignment	not modelled	8.2	40	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
35	c3f3mA_	Alignment	not modelled	8.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
36	d1kq8a_	Alignment	not modelled	8.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
37	c1kq8A_	Alignment	not modelled	8.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
38	d1kama_	Alignment	not modelled	7.5	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
39	d1o6ba_	Alignment	not modelled	7.5	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
40	c2gutA_	Alignment	not modelled	7.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2 glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
41	c3kevA_	Alignment	not modelled	7.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**galieria sulfuraria dcun1 domain-containing protein; **PDBTitle:** x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria
42	c3ocfB_	Alignment	not modelled	7.1	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate lyase:delta crystallin; **PDBTitle:** crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
43	d1xs8a_	Alignment	not modelled	7.0	21	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
44	c3krbB_	Alignment	not modelled	6.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
45	d1xsza1	Alignment	not modelled	6.4	19	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
46	c2jrtA_	Alignment	not modelled	6.2	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
47	d1re0b_	Alignment	not modelled	6.0	28	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
48	c1plpA_	Alignment	not modelled	6.0	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**phospholamban; **PDBTitle:** solution structure of the cytoplasmic domain of2 phospholamban
49	d1ku1a_	Alignment	not modelled	5.8	24	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
50	c3lyvF_	Alignment	not modelled	5.8	13	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
51	d1wpga4	Alignment	not modelled	5.7	17	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
52	c2jvnA_	Alignment	not modelled	5.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
53	d1ppjj_	Alignment	not modelled	5.5	26	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)

54	d1rj9a1	Alignment	not modelled	5.4	26	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
55	c1wwuA_	Alignment	not modelled	5.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
56	d2r09a1	Alignment	not modelled	5.4	19	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
57	d1ud0a_	Alignment	not modelled	5.3	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
58	d1r8se_	Alignment	not modelled	5.3	7	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
59	c3d9wA_	Alignment	not modelled	5.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
60	d1ppjw_	Alignment	not modelled	5.1	26	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
61	d1jyoe_	Alignment	not modelled	5.1	20	**Fold:**Non-globular alpha+beta subunits of globular proteins **Superfamily:**Non-globular alpha+beta subunits of globular proteins **Family:**Virulence effector SptP domain
62	d1uhra_	Alignment	not modelled	5.0	27	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain