Phyre^2

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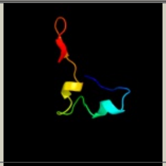
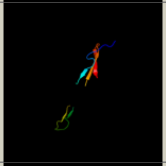
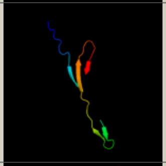
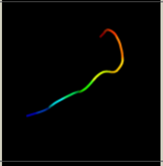
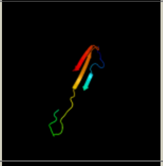
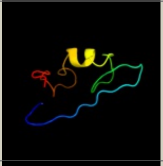
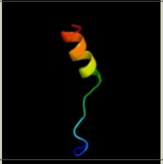
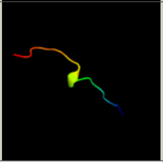
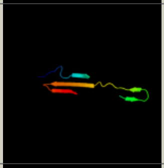
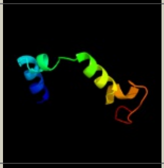
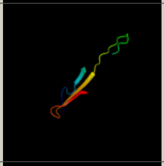
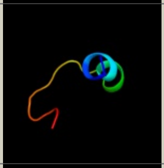
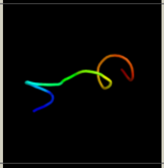
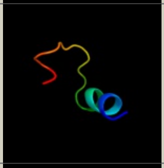
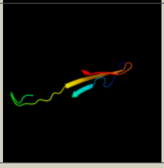
Description	P71296
Date	Thu Jan 5 12:12:41 GMT 2012
Unique Job ID	99327265e9614ee0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ebkA_	Alignment		48.0	33	**PDB header:**allergen **Chain:** A: **PDB Molecule:**allergen bla g 4; **PDBTitle:** crystal structure of major allergens, bla g 4 from2 cockroaches
2	c1ksiA_	Alignment		34.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
3	c3loyB_	Alignment		28.0	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
4	d2cs0a1	Alignment		24.6	7	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
5	c2cwoD_	Alignment		19.1	25	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**rna silencing suppressor; **PDBTitle:** crystal structure of rna silencing suppressor p21 from beet yellows2 virus
6	d2azea1	Alignment		18.3	20	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**DP dimerization segment
7	c1d6uB_	Alignment		18.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
8	c3hizB_	Alignment		17.1	21	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
9	c1x37A_	Alignment		16.1	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** structure of bacillus subtilis lon protease ssd domain
10	d1kcfa1	Alignment		16.0	30	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
11	c3rpjA_	Alignment		15.8	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**curlin genes transcriptional regulator; **PDBTitle:** structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.

12	d2al6a2	Alignment		15.6	50	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
13	d1qzma_	Alignment		14.6	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
14	c1w7cA_	Alignment		13.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** pplo at 1.23 angstroms
15	d1qmga1	Alignment		12.6	31	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
16	d2oqea1	Alignment		11.9	13	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
17	c3cuqD_	Alignment		11.5	19	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
18	c1gngX_	Alignment		11.0	54	**PDB header:**transferase **Chain:** X: **PDB Molecule:**frattide; **PDBTitle:** glycogen synthase kinase-3 beta (gsk3) complex with frattide2 peptide
19	c2zmeD_	Alignment		10.8	19	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
20	c3nbbC_	Alignment		10.7	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxisomal primary amine oxidase; **PDBTitle:** crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
21	d2e1fa1	Alignment	not modelled	10.2	29	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
22	d2odka1	Alignment	not modelled	9.6	31	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
23	d1ylxa1	Alignment	not modelled	9.1	35	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
24	d1w2za1	Alignment	not modelled	8.6	20	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
25	c2owyB_	Alignment	not modelled	8.5	6	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
26	d1pprm2	Alignment	not modelled	8.2	18	**Fold:**Peridinin-chlorophyll protein **Superfamily:**Peridinin-chlorophyll protein **Family:**Peridinin-chlorophyll protein
27	d1q9ja2	Alignment	not modelled	8.1	16	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
28	c1yveK_	Alignment	not modelled	7.5	31	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**acetohydroxy acid isomeroreductase; **PDBTitle:** acetohydroxy acid isomeroreductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropyloxamate)
						PDB header:transport protein

29	c3jqoV_	Alignment	not modelled	7.3	27	**Chain:** V: **PDB Molecule:**traf protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
30	c3u5cH_	Alignment	not modelled	7.2	27	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**40s ribosomal protein s7-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
31	c1eakA_	Alignment	not modelled	7.0	9	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
32	c2jerG_	Alignment	not modelled	6.8	15	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
33	d2jera1	Alignment	not modelled	6.7	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
34	c3higB_	Alignment	not modelled	6.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amiloride-sensitive amine oxidase; **PDBTitle:** crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
35	d1w6ga1	Alignment	not modelled	6.5	16	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
36	d2ewoa1	Alignment	not modelled	6.4	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
37	c2odkD_	Alignment	not modelled	6.4	31	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
38	d1pprm1	Alignment	not modelled	6.2	8	**Fold:**Peridinin-chlorophyll protein **Superfamily:**Peridinin-chlorophyll protein **Family:**Peridinin-chlorophyll protein
39	c2bj3D_	Alignment	not modelled	6.2	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
40	d1uptd_	Alignment	not modelled	6.0	36	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
41	c3zrkY_	Alignment	not modelled	6.0	54	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
42	c3mazA_	Alignment	not modelled	5.8	4	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 1; **PDBTitle:** crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal ptyr136 peptide
43	d1vkpa_	Alignment	not modelled	5.7	10	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
44	c2owlA_	Alignment	not modelled	5.7	9	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** crystal structure of e. coli rdgc
45	d2cmua1	Alignment	not modelled	5.6	8	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
46	c2o01J_	Alignment	not modelled	5.6	19	**PDB header:**photosynthesis **Chain:** J: **PDB Molecule:**photosystem i reaction center subunit ix; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
47	d2hzaa1	Alignment	not modelled	5.6	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
48	c3e7nB_	Alignment	not modelled	5.6	50	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**d-ribose high-affinity transport system; **PDBTitle:** crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
49	c3pamB_	Alignment	not modelled	5.5	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transmembrane protein; **PDBTitle:** crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
50	d1nexa2	Alignment	not modelled	5.3	19	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
51	c2p9rA_	Alignment	not modelled	5.3	0	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin; **PDBTitle:** human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
52	c1q5vB_	Alignment	not modelled	5.3	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
53	c3zvkG_	Alignment	not modelled	5.2	24	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
54	d1xkna_	Alignment	not modelled	5.2	23	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
55	c2ca9B_	Alignment	not modelled	5.1	17	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator;

55	c2ca9B_	Alignment	not modelled	5.1	17	**PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation