Phyre^2

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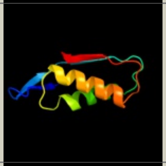
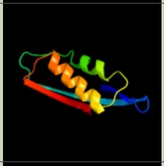
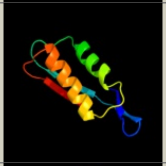
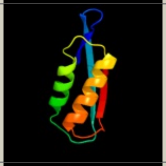
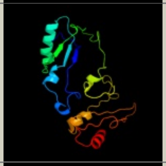
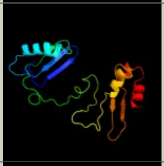
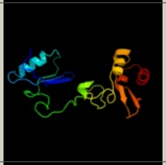
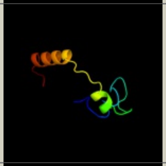
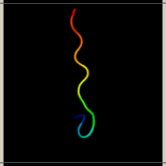
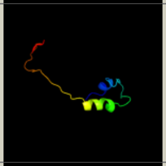
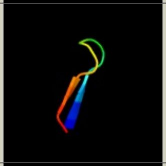
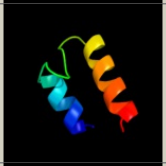
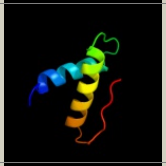
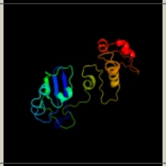
Description	Q46920
Date	Thu Jan 5 12:35:53 GMT 2012
Unique Job ID	da6b85928219f7a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bp1A_	Alignment		100.0	64	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-dependent 7-cyano-7-deazaguanine reductase; **PDBTitle:** crystal structure of putative 7-cyano-7-deazaguanine2 reductase quef from vibrio cholerae o1 biovar eltor
2	c1wm9D_	Alignment		97.8	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8
3	d1wura1	Alignment		97.8	19	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
4	c1is7F_	Alignment		95.5	20	**PDB header:**hydrolase/protein binding **Chain:** F: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex
5	d1wpla_	Alignment		95.5	20	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
6	d1a8ra_	Alignment		95.2	19	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
7	c1rg9D_	Alignment		77.9	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
8	c3imlB_	Alignment		60.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
9	c2obvA_	Alignment		52.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
10	c2f42A_	Alignment		49.5	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
11	c3hjhA_	Alignment		48.9	53	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair-coupling factor; **PDBTitle:** a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor

12	d3bz6a2	Alignment		32.7	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
13	c3pg6D_	Alignment		32.6	25	**PDB header:**ligase **Chain:** D: **PDB Molecule:**e3 ubiquitin-protein ligase dtx3l; **PDBTitle:** the carboxyl terminal domain of human deltex 3-like
14	d2b2na1	Alignment		31.1	54	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
15	d1j6ra_	Alignment		31.0	27	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Hypothetical protein TM0269
16	d2eyqa4	Alignment		30.7	54	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
17	d2o4ta1	Alignment		29.2	13	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
18	c3gzfD_	Alignment		28.7	18	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** structure of the c-terminal domain of nsp4 from feline coronavirus
19	c3rv2B_	Alignment		27.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
20	c3fpnB_	Alignment		26.2	31	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**geobacillus stearothermophilus uvrb interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
21	c3ty1B_	Alignment	not modelled	19.7	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**hypothetical aldose 1-epimerase; **PDBTitle:** crystal structure of a hypothetical aldose 1-epimerase (kpn_04629)2 from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.90 a3 resolution
22	d1nb9a_	Alignment	not modelled	16.4	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
23	d2pvaa_	Alignment	not modelled	15.6	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Penicillin V acylase
24	d1t5la1	Alignment	not modelled	15.5	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
25	c2hezB_	Alignment	not modelled	15.3	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bile salt hydrolase; **PDBTitle:** bifidobacterium longum bile salt hydrolase
26	c3bz6A_	Alignment	not modelled	15.1	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0502 protein pspto_2686; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
27	c3op1A_	Alignment	not modelled	14.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
28	d1n08a_	Alignment	not modelled	13.9	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like

29	c3bnwA_	Alignment	not modelled	12.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase, putative; **PDBTitle:** crystal structure of riboflavin kinase from trypanosoma brucei
30	d1tyja1	Alignment	not modelled	12.6	25	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
31	d1zv9a1	Alignment	not modelled	12.4	32	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
32	c3izcW_	Alignment	not modelled	12.2	22	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
33	c2eyqA_	Alignment	not modelled	11.8	54	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
34	c2im9A_	Alignment	not modelled	11.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
35	d2im9a1	Alignment	not modelled	11.2	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
36	c3h8mB_	Alignment	not modelled	11.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 7; **PDBTitle:** sam domain of human ephrin type-a receptor 7 (epha7)
37	c3lhiA_	Alignment	not modelled	10.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
38	c4a1dM_	Alignment	not modelled	10.3	26	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein l22; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
39	c3kkaD_	Alignment	not modelled	10.1	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** co-crystal structure of the sam domains of epha1 and epha2
40	c2b59A_	Alignment	not modelled	9.7	44	**PDB header:**hydrolase/structural protein **Chain:** A: **PDB Molecule:**cog1196: chromosome segregation atpases; **PDBTitle:** the type ii cohesin dockerin complex
41	d2c2la2	Alignment	not modelled	9.7	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
42	d2bm3a1	Alignment	not modelled	9.6	44	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
43	c2kreA_	Alignment	not modelled	9.6	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
44	c3o2kA_	Alignment	not modelled	9.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**brevianamide f prenyltransferase; **PDBTitle:** crystal structure of brevianamide f prenyltransferase complexed with2 brevianamide f and dimethylallyl s-thiolodiphosphate
45	c2x0kB_	Alignment	not modelled	9.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
46	c1m0kA_	Alignment	not modelled	9.3	50	**PDB header:**ion transport **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** bacteriorhodopsin k intermediate at 1.43 a resolution
47	d1m0ka_	Alignment	not modelled	9.3	50	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
48	c3fnkA_	Alignment	not modelled	9.2	56	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
49	c2y9xC_	Alignment	not modelled	9.1	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**polyphenol oxidase; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
50	c2xfmA_	Alignment	not modelled	8.6	33	**PDB header:**rna/protein **Chain:** A: **PDB Molecule:**piwi-like protein 1; **PDBTitle:** complex structure of the miwi paz domain bound to methylated single2 stranded rna
51	d1gwya_	Alignment	not modelled	8.2	12	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Anemone pore-forming cytolysin
52	d2phcb2	Alignment	not modelled	8.1	29	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
53	d1iyca_	Alignment	not modelled	8.0	50	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins

						Family: Antifungal peptide scarabaecin
54	c3ghpA_	Alignment	not modelled	7.9	56	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)
55	d1v2ya_	Alignment	not modelled	7.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
56	c3i4zA_	Alignment	not modelled	7.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tryptophan dimethylallyltransferase; **PDBTitle:** crystal structure of the dimethylallyl tryptophan synthase fgapt2 from2 aspergillus fumigatus
57	d2cqpa1	Alignment	not modelled	7.6	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
58	c1t6zB_	Alignment	not modelled	7.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
59	c2quoA_	Alignment	not modelled	7.4	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**heat-labile enterotoxin b chain; **PDBTitle:** crystal structure of c terminal fragment of clostridium2 perfringens enterotoxin
60	c3htkC_	Alignment	not modelled	7.3	17	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
61	d1p42a1	Alignment	not modelled	6.9	10	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
62	c3dclC_	Alignment	not modelled	6.8	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
63	d2gpia1	Alignment	not modelled	6.8	27	**Fold:**Shew3726-like **Superfamily:**Shew3726-like **Family:**Shew3726-like
64	c2dbhA_	Alignment	not modelled	6.6	56	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
65	d1mxaa2	Alignment	not modelled	6.5	33	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
66	d2hiya1	Alignment	not modelled	6.4	20	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
67	c1zc1A_	Alignment	not modelled	6.1	21	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
68	d2d9ra1	Alignment	not modelled	5.9	25	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
69	d1ogya1	Alignment	not modelled	5.8	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
70	d1c8sa_	Alignment	not modelled	5.8	50	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
71	c3vcbB_	Alignment	not modelled	5.8	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** c425s mutant of the c-terminal cytoplasmic domain of non-structural2 protein 4 from mouse hepatitis virus a59
72	d2baya1	Alignment	not modelled	5.8	40	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
73	d2p02a2	Alignment	not modelled	5.6	40	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
74	c1zbe1_	Alignment	not modelled	5.4	23	**PDB header:**virus **Chain:** 1: **PDB Molecule:**coat protein vp1; **PDBTitle:** foot-and mouth disease virus serotype a1061
75	d2dira1	Alignment	not modelled	5.4	15	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**Minimal THUMP
76	d1x6ma_	Alignment	not modelled	5.3	25	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
77	d1usua_	Alignment	not modelled	5.2	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Hsp90 middle domain
78	c2hz7A_	Alignment	not modelled	5.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
79	d1qm4a2	Alignment	not modelled	5.1	40	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase