Phyre2

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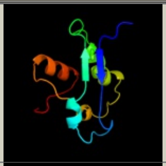
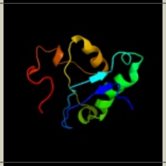
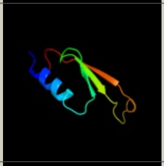
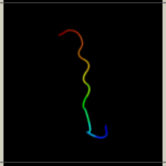
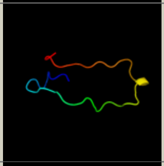
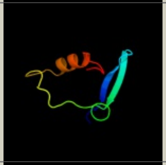
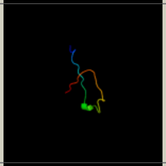
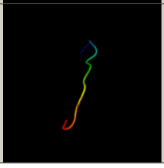
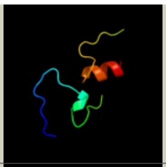
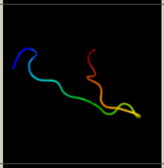
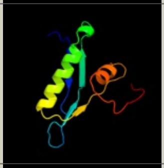
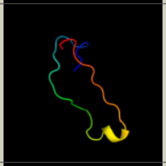
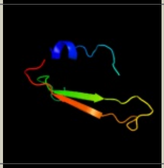
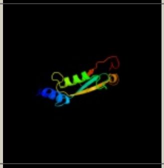
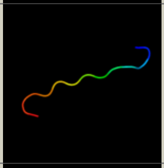
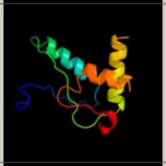
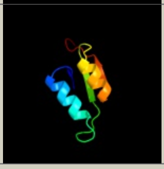
Description	P39308
Date	Thu Jan 5 11:59:11 GMT 2012
Unique Job ID	9dccec09a4b5ac89

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2atra1	Alignment		40.4	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
2	c3s6fA_	Alignment		31.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical acetyltransferase; **PDBTitle:** crystal structure of a hypotetical acetyltransferase (dr_1678) from2 deinococcus radiodurans at 1.19 a resolution
3	d2q9oa2	Alignment		26.0	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
4	d1yf9a1	Alignment		23.9	23	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
5	d1yx0a1	Alignment		20.7	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
6	c2xr4A_	Alignment		19.7	46	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
7	c1m2oA_	Alignment		19.3	22	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
8	d2choa2	Alignment		18.5	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
9	d1fjra_	Alignment		17.7	23	**Fold:**Methuselah ectodomain **Superfamily:**Methuselah ectodomain **Family:**Methuselah ectodomain
10	d1j58a_	Alignment		17.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
11	c2vnvC_	Alignment		15.6	31	**PDB header:**sugar-binding protein **Chain:** C: **PDB Molecule:**bcla; **PDBTitle:** crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution

12	c3ijrF_	Alignment		15.0	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
13	d1ekga_	Alignment		14.9	20	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
14	d1y9wa1	Alignment		14.7	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
15	d2cbia2	Alignment		14.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
16	d1c4zd_	Alignment		13.3	19	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
17	c3nvaB_	Alignment		13.1	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
18	c2boiA_	Alignment		12.4	15	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2l in2 complex with alpha-methyl-fucoside
19	d1qd1a2	Alignment		12.4	14	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
20	c3gemC_	Alignment		12.3	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of short-chain dehydrogenase from pseudomonas2 syringae
21	d2nvuc1	Alignment	not modelled	12.0	16	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
22	d2chha1	Alignment	not modelled	11.8	23	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
23	d1uzva_	Alignment	not modelled	11.4	23	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
24	c2xlfA_	Alignment	not modelled	10.7	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
25	d1h2ka_	Alignment	not modelled	10.4	24	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
26	d1k2wa_	Alignment	not modelled	10.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
27	d2ga5a1	Alignment	not modelled	10.2	32	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
28	d1xeba_	Alignment	not modelled	9.7	26	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
29	c2xsbA_	Alignment	not modelled	9.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase;

						PDBTitle: ogoga pugnac complex
30	c3o2uB_	Alignment	not modelled	9.5	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nedd8-conjugating enzyme ubc12; **PDBTitle:** s. cerevisiae ubc12
31	c2l7lB_	Alignment	not modelled	9.2	70	**PDB header:**metal binding protein/transferase **Chain:** B: **PDB Molecule:**calcium/calmodulin-dependent protein kinase type 1; **PDBTitle:** solution structure of ca2+/calmodulin complexed with a peptide2 representing the calmodulin-binding domain of calmodulin kinase i
32	c2jtmA_	Alignment	not modelled	8.9	34	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of sso6901 from sulfolobus solfataricus2 p2
33	c2vxkA_	Alignment	not modelled	8.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate acetyltransferase; **PDBTitle:** structural comparison between aspergillus fumigatus and2 human gna1
34	c2npiD_	Alignment	not modelled	8.8	50	**PDB header:**transcription **Chain:** D: **PDB Molecule:**protein pcf11; **PDBTitle:** clp1-atp-pcf11 complex
35	c1mxeE_	Alignment	not modelled	8.8	70	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**target sequence of rat calmodulin-dependent **PDBTitle:** structure of the complex of calmodulin with the target2 sequence of camki
36	c1mxeF_	Alignment	not modelled	8.8	70	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**target sequence of rat calmodulin-dependent **PDBTitle:** structure of the complex of calmodulin with the target2 sequence of camki
37	c3gzaB_	Alignment	not modelled	8.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
38	c2du7C_	Alignment	not modelled	8.8	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
39	d1hywa_	Alignment	not modelled	8.2	42	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
40	d1su3a1	Alignment	not modelled	7.9	44	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
41	c2cbjA_	Alignment	not modelled	7.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase; **PDBTitle:** structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnacase in3 complex with pugnac
42	d2ae6a1	Alignment	not modelled	7.5	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
43	c2qj8B_	Alignment	not modelled	7.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
44	d1o8ba1	Alignment	not modelled	7.2	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
45	d1fasa_	Alignment	not modelled	7.0	60	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
46	d1ed7a_	Alignment	not modelled	7.0	42	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
47	d2jdca1	Alignment	not modelled	6.7	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
48	c3pvlA_	Alignment	not modelled	6.7	20	**PDB header:**motor protein/protein transport **Chain:** A: **PDB Molecule:**myosin viia isoform 1; **PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
49	d2fiwa1	Alignment	not modelled	6.5	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
50	d1slma1	Alignment	not modelled	6.3	57	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
51	d1wzva1	Alignment	not modelled	6.2	20	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
52	d2fd6u1	Alignment	not modelled	6.1	14	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
53	d1ejda_	Alignment	not modelled	6.1	16	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
						Fold:NIF3 (NGG1p interacting factor 3)-like

54	d2gx8a1	Alignment	not modelled	6.1	23	**Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
55	d1xs8a_	Alignment	not modelled	6.0	23	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
56	d2qtva3	Alignment	not modelled	6.0	21	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
57	d1ew4a_	Alignment	not modelled	6.0	15	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
58	d1yvoa1	Alignment	not modelled	5.7	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
59	d1bwva2	Alignment	not modelled	5.6	18	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
60	d2r7ca2	Alignment	not modelled	5.5	33	**Fold:**Rotavirus NSP2 fragment, N-terminal domain **Superfamily:**Rotavirus NSP2 fragment, N-terminal domain **Family:**Rotavirus NSP2 fragment, N-terminal domain
61	c3iuwA_	Alignment	not modelled	5.5	46	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
62	c2pdoG_	Alignment	not modelled	5.2	21	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
63	c1iclA_	Alignment	not modelled	5.2	40	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
64	d1o8bb1	Alignment	not modelled	5.1	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
65	d1j7db_	Alignment	not modelled	5.1	29	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
66	c2w7tA_	Alignment	not modelled	5.1	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
67	d1yq2a2	Alignment	not modelled	5.1	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
68	d1n10a2	Alignment	not modelled	5.1	43	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Pollen allergen PHL P 1 N-terminal domain