Phyre^2

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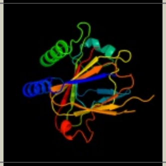
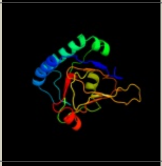
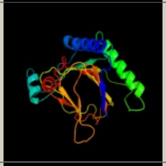
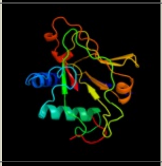
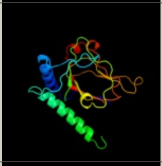
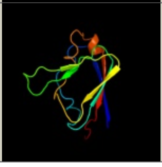
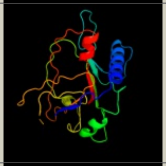
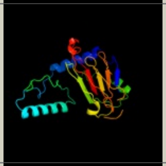
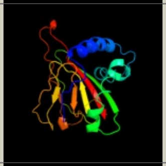
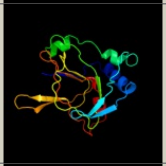
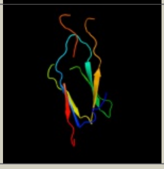
Description	P05050
Date	Thu Jan 5 10:58:38 GMT 2012
Unique Job ID	651b94aedeafc13f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fdia1	Alignment		100.0	100	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**AlkB-like
2	c3thtB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkylated dna repair protein alkb homolog 8; **PDBTitle:** crystal structure and rna binding properties of the rrm/alkb domains2 in human abh8, an enzyme catalyzing trna hypermodification, northeast3 structural genomics consortium target hr5601b
3	d2iuwa1	Alignment		100.0	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**AlkB-like
4	c2iuwA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkylated repair protein alkb homolog 3; **PDBTitle:** crystal structure of human abh3 in complex with iron ion2 and 2-oxoglutarate
5	c3btzA_	Alignment		100.0	22	**PDB header:**oxidoreductase/dna **Chain:** A: **PDB Molecule:**alpha-ketoglutarate-dependent dioxygenase alkb homolog 2; **PDBTitle:** crystal structure of human abh2 cross-linked to dsdna
6	c3dkqB_	Alignment		98.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
7	c2g19A_	Alignment		98.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** cellular oxygen sensing: crystal structure of hypoxia-2 inducible factor prolyl hydroxylase (phd2)
8	c3itqB_	Alignment		97.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit domain protein; **PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
9	c3ouiA_	Alignment		97.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**egl nine homolog 1; **PDBTitle:** phd2-r717 with 40787422
10	c2jijA_	Alignment		97.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl-4 hydroxylase; **PDBTitle:** crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
11	c3lfmA_	Alignment		96.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein fto; **PDBTitle:** crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity

12	c3gjbA_	Alignment		95.8	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
13	d2a1xa1	Alignment		92.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
14	c2opwA_	Alignment		92.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
15	c2rdsA_	Alignment		92.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- **PDBTitle:** crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
16	c3emrA_	Alignment		89.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
17	d2fcta1	Alignment		88.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
18	c3nnlB_	Alignment		88.7	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
19	c3kt4A_	Alignment		83.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pkhd-type hydroxylase tpa1; **PDBTitle:** crystal structure of tpa1 from saccharomyces cerevisiae, a2 component of the messenger ribonucleoprotein complex
20	c3pl0B_	Alignment		79.6	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
21	d1w9ya1	Alignment	not modelled	78.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
22	d1vrba1	Alignment	not modelled	75.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
23	d1dcsa_	Alignment	not modelled	74.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
24	c3bvcA_	Alignment	not modelled	65.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ism_01780; **PDBTitle:** crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
25	d1vr3a1	Alignment	not modelled	38.9	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
26	c3ooxA_	Alignment	not modelled	35.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
27	d1gp6a_	Alignment	not modelled	32.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
28	c3on7C_	Alignment	not modelled	23.6	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution

29	d1odma_	Alignment	not modelled	16.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
30	c2q30C_	Alignment	not modelled	13.3	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
31	d1htwa_	Alignment	not modelled	13.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
32	d2oqea1	Alignment	not modelled	13.0	25	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
33	c3uyjA_	Alignment	not modelled	12.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
34	c3al6A_	Alignment	not modelled	12.7	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
35	c2uvpB_	Alignment	not modelled	12.5	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hoba; **PDBTitle:** crystal structure of hoba (hp1230)from helicobacter pylori
36	c2rohA_	Alignment	not modelled	10.6	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**telomere binding protein-1; **PDBTitle:** the dna binding domain of rtbp1
37	d1h2ka_	Alignment	not modelled	9.0	25	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
38	d1e5ra_	Alignment	not modelled	8.4	7	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Type II Proline 3-hydroxylase (proline oxidase)
39	c1ljzB_	Alignment	not modelled	8.1	33	**PDB header:**receptor, toxin **Chain:** B: **PDB Molecule:**acetylcholine receptor protein; **PDBTitle:** nmr structure of an achr-peptide (torpedo californica,2 alpha-subunit residues 182-202) in complex with alpha-3 bungarotoxin
40	d1sroa_	Alignment	not modelled	7.6	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d1w6ga1	Alignment	not modelled	7.6	13	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
42	d1w2za1	Alignment	not modelled	6.8	14	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
43	d1u1sa1	Alignment	not modelled	6.7	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
44	d1zrra1	Alignment	not modelled	6.7	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
45	d2ckxa1	Alignment	not modelled	6.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
46	d1zvfa1	Alignment	not modelled	6.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
47	d1yfua1	Alignment	not modelled	6.5	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
48	d1hk9a_	Alignment	not modelled	5.7	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
49	d1slqa_	Alignment	not modelled	5.6	19	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
50	d1ud9a2	Alignment	not modelled	5.4	17	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
51	d1sfna_	Alignment	not modelled	5.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like