Phyre2

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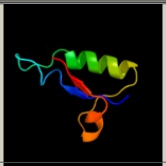
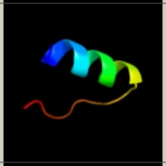
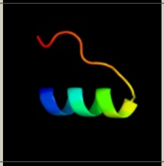
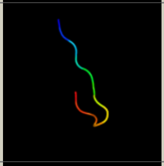
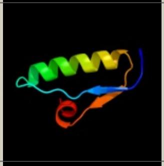
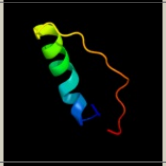
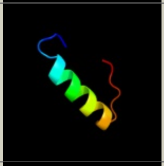
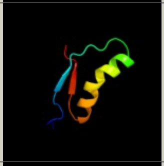
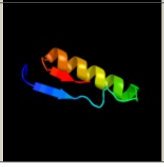
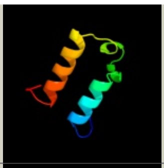
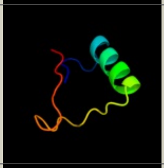
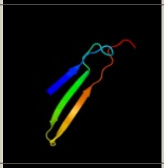
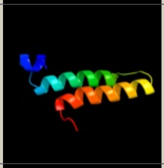
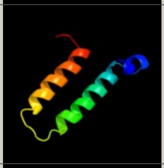
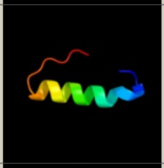
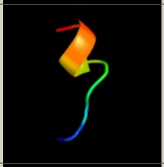
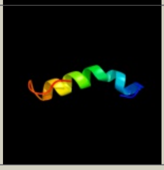
Description	P13979
Date	Thu Jan 5 11:33:52 GMT 2012
Unique Job ID	552c5a64ad17fc76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bf2A_	Alignment		81.1	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of the a1ksw9_neimf protein from2 neisseria meningitidis. northeast structural genomics3 consortium target mr36a
2	c2jxpA_	Alignment		63.2	13	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
3	d2okfa1	Alignment		48.0	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like
4	d2inba1	Alignment		47.3	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like
5	d1j1ta_	Alignment		34.3	33	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Alginate lyase
6	d1a9xa2	Alignment		31.7	15	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
7	d1nn4a_	Alignment		29.2	25	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
8	c3he8A_	Alignment		28.9	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
9	d2ayxa2	Alignment		26.2	27	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**RcsC linker domain-like
10	d1o1xa_	Alignment		23.2	28	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
11	c3s5pA_	Alignment		22.6	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia

12	c1ciiA_	Alignment		22.0	23	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
13	c2o6lA_	Alignment		21.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7; **PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
14	c2r76A_	Alignment		20.3	8	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**rare lipoprotein b; **PDBTitle:** crystal structure of the rare lipoprotein b (so_1173) from shewanella2 oneidensis, northeast structural genomics consortium target sor91a
15	d1v7wa2	Alignment		18.4	19	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
16	d1cola_	Alignment		18.2	19	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
17	c3fewX_	Alignment		18.2	19	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
18	d2vvpa1	Alignment		15.9	20	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
19	d1qoja_	Alignment		15.4	60	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
20	c3k7pA_	Alignment		13.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
21	c3m1pA_	Alignment	not modelled	13.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
22	c1uwvA_	Alignment	not modelled	12.2	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
23	c1rh1A_	Alignment	not modelled	11.9	16	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**colicin b; **PDBTitle:** crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
24	c1v7wA_	Alignment	not modelled	10.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
25	c2lllA_	Alignment	not modelled	9.4	38	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
26	d1ufga_	Alignment	not modelled	9.3	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
27	c3jt0B_	Alignment	not modelled	8.3	32	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
						Fold: Common fold of diphtheria toxin/transcription

28	d1x9la_	Alignment	not modelled	8.1	30	factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
29	c2cqtA_	Alignment	not modelled	7.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
30	c1w17A_	Alignment	not modelled	7.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
31	d1i4ma_	Alignment	not modelled	7.3	32	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
32	d1rh1a2	Alignment	not modelled	7.2	15	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
33	c2yvqA_	Alignment	not modelled	7.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
34	d2as0a2	Alignment	not modelled	6.9	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
35	c3sz3A_	Alignment	not modelled	6.8	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
36	c1vraB_	Alignment	not modelled	6.4	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
37	c2vzkD_	Alignment	not modelled	6.4	44	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
38	c2vfyA_	Alignment	not modelled	6.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
39	c3bghB_	Alignment	not modelled	5.7	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative neuraminyllactose-binding hemagglutinin homolog; **PDBTitle:** crystal structure of putative neuraminyllactose-binding hemagglutinin2 homolog from helicobacter pylori
40	d1uwva2	Alignment	not modelled	5.6	32	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
41	c3it4B_	Alignment	not modelled	5.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
42	c2k6zA_	Alignment	not modelled	5.4	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
43	d1ul7a_	Alignment	not modelled	5.3	26	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
44	c1qy9B_	Alignment	not modelled	5.3	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ydde; **PDBTitle:** crystal structure of e. coli se-met protein ydde
45	d1x6va3	Alignment	not modelled	5.3	5	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
46	d1qwia_	Alignment	not modelled	5.1	15	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
47	d1ifra_	Alignment	not modelled	5.1	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
48	c2lbgA_	Alignment	not modelled	5.0	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles