Phyre^2

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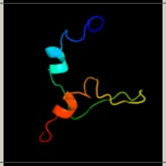
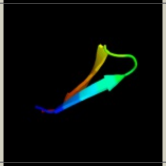
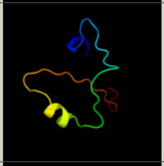
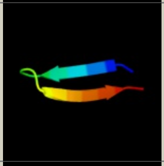
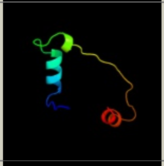
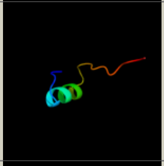
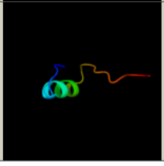
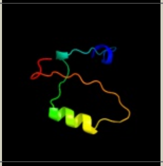
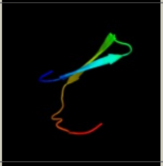
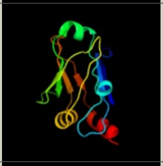
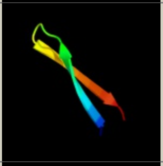
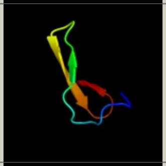
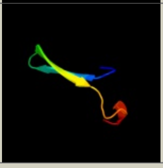
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ylxa1	Alignment		63.6	19	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
2	c2eg9B_	Alignment		26.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-ribosyl cyclase 1; **PDBTitle:** crystal structure of the truncated extracellular domain of2 mouse cd38
3	d1uzva_	Alignment		25.5	40	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
4	d1wmxb_	Alignment		21.6	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
5	c3eitB_	Alignment		20.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** the 2.6 angstrom crystal structure of chbp, the cif homologue from2 burkholderia pseudomallei
6	d2chha1	Alignment		18.9	33	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
7	c3hbkA_	Alignment		18.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase, was domain of2 unknown function (duf1080) (yp_001302580.1) from parabacteroides3 distasonis atcc 8503 at 2.36 a resolution
8	d1r4xa2	Alignment		17.4	16	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Coatomer appendage domain
9	c2khgA_	Alignment		16.8	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in tfe
10	c2anuA_	Alignment		16.6	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm0559; **PDBTitle:** crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
11	d2anua1	Alignment		16.6	8	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain

12	c2khfA_	Alignment		16.5	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in dpc-micelles
13	c3efyB_	Alignment		14.8	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
14	c2r0fA_	Alignment		14.0	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cgl3 lectin; **PDBTitle:** ligand free structure of fungal lectin cgl3
15	c2boiA_	Alignment		13.7	13	**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
16	c3dtdI_	Alignment		12.7	9	**PDB header:**structural genomics, unknown function **Chain:** I: **PDB Molecule:**invasion-associated protein b; **PDBTitle:** crystal structure of invasion associated protein b from bartonella2 henselae
17	c2zw7A_	Alignment		11.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bleomycin acetyltransferase; **PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
18	c3tdqB_	Alignment		11.7	43	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
19	c3n3fB_	Alignment		11.6	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
20	d2nn8a1	Alignment		11.5	26	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
21	d1wmxa_	Alignment	not modelled	10.5	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
22	d1q56a_	Alignment	not modelled	10.3	11	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
23	c3nv4A_	Alignment	not modelled	10.1	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin 9 short isoform variant; **PDBTitle:** crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose
24	d1isia_	Alignment	not modelled	9.8	19	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
25	d1fyxa_	Alignment	not modelled	9.1	25	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
26	d1e5ba_	Alignment	not modelled	8.8	24	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
27	d1d2sa_	Alignment	not modelled	8.1	11	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
28	c2eg5C_	Alignment	not modelled	8.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
29	c3hshA	Alignment	not modelled	7.9	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**collagen alpha-1(xviii) chain;

		Alignment				**PDBTitle:** crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
30	d1kkea2	Alignment	not modelled	7.9	13	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Reovirus attachment protein sigma 1 head domain
31	c2wjsA_	Alignment	not modelled	7.7	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**laminin subunit alpha-2; **PDBTitle:** crystal structure of the lg1-3 region of the laminin alpha22 chain
32	c3b9cB_	Alignment	not modelled	7.5	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hspc159; **PDBTitle:** crystal structure of human grp crd
33	d1fyva_	Alignment	not modelled	7.2	25	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
34	d1uypa1	Alignment	not modelled	7.1	24	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 32 C-terminal domain
35	c3kb8A_	Alignment	not modelled	6.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
36	d2ef1a1	Alignment	not modelled	6.9	17	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
37	c3mpbA_	Alignment	not modelled	6.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
38	c3b5iB_	Alignment	not modelled	6.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine:salicylic acid carboxyl **PDBTitle:** crystal structure of indole-3-acetic acid methyltransferase
39	d1wdja_	Alignment	not modelled	6.7	12	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
40	d2f20a1	Alignment	not modelled	6.6	11	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
41	c1vjqB_	Alignment	not modelled	6.6	21	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
42	c1kkeA_	Alignment	not modelled	6.5	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sigma 1 protein; **PDBTitle:** crystal structure of reovirus attachment protein sigma12 trimer
43	d2gala_	Alignment	not modelled	6.5	22	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
44	d1qhoa3	Alignment	not modelled	6.4	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
45	c3gqjA_	Alignment	not modelled	6.3	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cell inhibiting factor (cif); **PDBTitle:** crystal structure of cell inhibiting factor (cif) from photorhabdus2 luminescens
46	c2yroA_	Alignment	not modelled	6.2	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-8; **PDBTitle:** solution structure of the c-terminal gal-bind lectin2 protein from human galectin-8
47	d2aw2a1	Alignment	not modelled	6.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
48	c1qu0D_	Alignment	not modelled	6.2	9	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**laminin alpha2 chain; **PDBTitle:** crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
49	c1qu0A_	Alignment	not modelled	6.2	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**laminin alpha2 chain; **PDBTitle:** crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
50	d2axwa1	Alignment	not modelled	6.1	18	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
51	d2ftxb1	Alignment	not modelled	6.1	0	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc24-like
52	c2fv4B_	Alignment	not modelled	6.1	0	**PDB header:**structural protein, protein binding **Chain:** B: **PDB Molecule:**hypothetical 24.6 kda protein in ilv2-ade17 **PDBTitle:** nmr solution structure of the yeast kinetochore spc24/spc252 globular domain
53	d1xaua_	Alignment	not modelled	5.8	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
54	c1x50A_	Alignment	not modelled	5.5	22	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-4; **PDBTitle:** solution structure of the c-terminal gal-bind lectin domain2 from human galectin-4
						Fold: Composite domain of metallo-dependent hydrolases

55	d2uz9a1	Alignment	not modelled	5.4	29	**Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
56	d1c1la_	Alignment	not modelled	5.3	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
57	c2ealB_	Alignment	not modelled	5.2	25	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**galectin-9; **PDBTitle:** crystal structure of human galectin-9 n-terminal crd in complex with2 forssman pentasaccharide
58	d1wdjb_	Alignment	not modelled	5.2	12	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
59	d1fltx_	Alignment	not modelled	5.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains