Phyre^2

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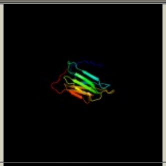
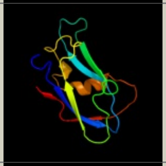
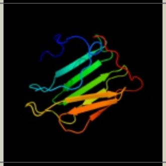
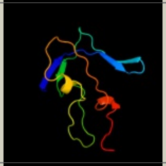
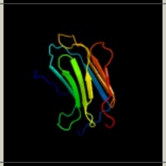
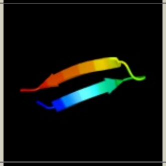
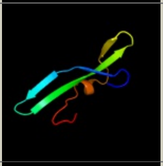
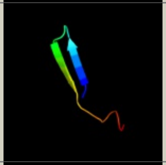
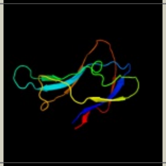
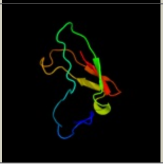
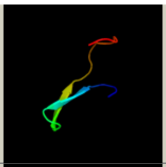
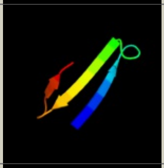
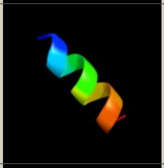
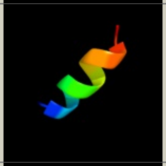
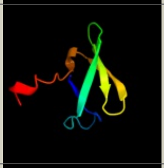
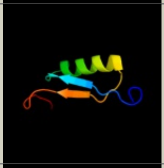
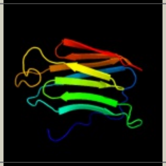
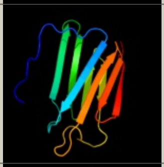
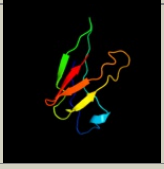
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q56a_	Alignment		46.5	11	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
2	d1wmxa_	Alignment		40.4	20	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
3	c3pveA_	Alignment		27.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**agrin, agrn protein; **PDBTitle:** crystal structure of the g2 domain of agrin from mus musculus
4	d1uzva_	Alignment		27.0	27	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
5	c2kfwA_	Alignment		25.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
6	d1pz7a_	Alignment		22.9	10	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
7	d2chha1	Alignment		22.0	20	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
8	d1ylxa1	Alignment		20.0	21	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
9	c2boiA_	Alignment		17.9	10	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2lin2 complex with alpha-methyl-fucoside
10	d1wmxb_	Alignment		16.6	23	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
11	d2d3na1	Alignment		16.4	16	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

12	c2r0fA_	Alignment		16.0	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cgl3 lectin; **PDBTitle:** ligand free structure of fungal lectin cgl3
13	d2bosa_	Alignment		15.7	24	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
14	c2khgA_	Alignment		15.1	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in tfe
15	c2khfA_	Alignment		14.9	42	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in dpc-micelles
16	c1w9iA_	Alignment		14.0	15	**PDB header:**myosin **Chain:** A: **PDB Molecule:**myosin ii heavy chain; **PDBTitle:** myosin ii dictyostelium discoideum motor domain s456y bound2 with mgadp-befx
17	c2eg5C_	Alignment		13.7	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
18	c1qu0A_	Alignment		13.5	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
19	c1qu0D_	Alignment		13.5	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
20	d1ud2a1	Alignment		13.4	11	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
21	d1ulea_	Alignment	not modelled	13.4	15	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
22	d2anua1	Alignment	not modelled	13.3	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
23	c2anuA_	Alignment	not modelled	13.3	16	**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
24	d2aw2a1	Alignment	not modelled	13.3	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
25	d1hvxa1	Alignment	not modelled	12.9	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
26	c2wjsA_	Alignment	not modelled	12.8	13	**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
27	c2fvnA_	Alignment	not modelled	12.8	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
28	c3hqxA_	Alignment	not modelled	12.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1

29	d1fyxa_	Alignment	not modelled	12.6	25	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
30	c3eo6B_	Alignment	not modelled	12.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
31	c2zw7A_	Alignment	not modelled	12.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bleomycin acetyltransferase; **PDBTitle:** crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
32	d2gjpa1	Alignment	not modelled	12.3	16	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
33	d1r4pb_	Alignment	not modelled	11.7	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
34	d1c4qa_	Alignment	not modelled	11.7	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
35	d2nn8a1	Alignment	not modelled	11.7	26	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
36	d1dyka2	Alignment	not modelled	11.5	10	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
37	c3nv4A_	Alignment	not modelled	11.3	20	**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
38	c3efyB_	Alignment	not modelled	10.4	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
39	d2axwa1	Alignment	not modelled	9.4	19	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
40	c3eitB_	Alignment	not modelled	9.3	12	**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
41	d1fyva_	Alignment	not modelled	8.9	25	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
42	d2oyza1	Alignment	not modelled	8.9	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
43	c3b5iB_	Alignment	not modelled	8.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine:salicylic acid carboxyl **PDBTitle:** crystal structure of indole-3-acetic acid methyltransferase
44	c2eg9B_	Alignment	not modelled	8.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-ribosyl cyclase 1; **PDBTitle:** crystal structure of the truncated extracellular domain of2 mouse cd38
45	d1wdja_	Alignment	not modelled	8.7	15	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
46	d1e43a1	Alignment	not modelled	8.0	11	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
47	c1qu0C_	Alignment	not modelled	7.6	9	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**laminin alpha2 chain; **PDBTitle:** crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
48	d2ftxb1	Alignment	not modelled	7.4	13	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc24-like
49	c3b9cB_	Alignment	not modelled	7.4	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hspc159; **PDBTitle:** crystal structure of human grp crd
50	c2fv4B_	Alignment	not modelled	7.3	13	**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
51	d2gala_	Alignment	not modelled	6.5	25	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
52	c2yroA_	Alignment	not modelled	6.5	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
53	d2uz9a1	Alignment	not modelled	6.4	36	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
54	c3sh5A_	Alignment	not modelled	6.1	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lg3 peptide; **PDBTitle:** calcium-bound laminin g like domain 3 from human perlecan

55	c2c5dA_	Alignment	not modelled	6.1	9	**PDB header:**signaling protein/receptor **Chain:** A: **PDB Molecule:**growth-arrest-specific protein 6 precursor; **PDBTitle:** structure of a minimal gas6-axl complex
56	d1wdjb_	Alignment	not modelled	6.0	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
57	d2zgwa2	Alignment	not modelled	5.9	36	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
58	c2eayB_	Alignment	not modelled	5.9	45	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
59	c3dtdl_	Alignment	not modelled	5.8	13	**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
60	c2xr4A_	Alignment	not modelled	5.8	30	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
61	d2h3ka1	Alignment	not modelled	5.6	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**NEAT domain-like **Family:**NEAT domain
62	d1xaua_	Alignment	not modelled	5.5	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains