Phyre^2

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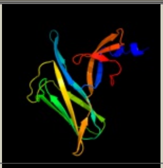
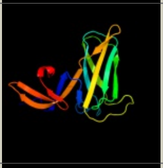
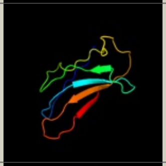
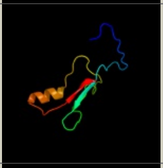
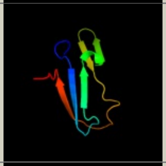
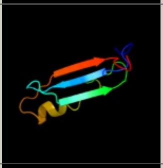
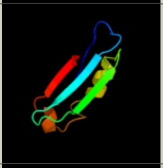
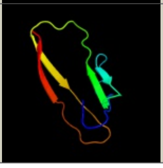
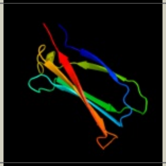
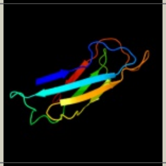
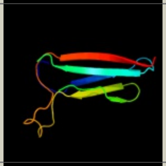
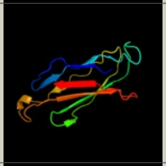
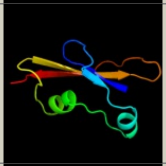
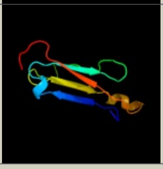
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c12A_	Alignment		100.0	30	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**flagellar protein; **PDBTitle:** crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
2	c3osvC_	Alignment		100.0	29	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**flagellar basal-body rod modification protein flgd; **PDBTitle:** the crytsal structure of flgd from p. aeruginosa
3	c1xf1A_	Alignment		96.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**c5a peptidase; **PDBTitle:** structure of c5a peptidase- a key virulence factor from2 streptococcus
4	c3d33B_	Alignment		95.3	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
5	c2p9rA_	Alignment		93.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin; **PDBTitle:** human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
6	c3isyA_	Alignment		91.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
7	c3payB_	Alignment		89.7	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative adhesin; **PDBTitle:** crystal structure of a putative adhesin (bacova_04077) from2 bacteroides ovatus at 2.50 a resolution
8	c3gf8A_	Alignment		89.2	25	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution
9	d2c9qa1	Alignment		85.7	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
10	c3sd2A_	Alignment		85.5	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative member of duf3244 protein family; **PDBTitle:** crystal structure of a putative member of duf3244 protein family2 (bt_3571) from bacteroides thetaiotaomicron vpi-5482 at 1.40 a3 resolution
11	d1ix2a_	Alignment		83.6	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)

12	c3pe9D_	Alignment		82.9	15	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
13	c2xwxB_	Alignment		82.1	15	**PDB header:**chitin-binding protein **Chain:** B: **PDB Molecule:**glcnac-binding protein a; **PDBTitle:** vibrio cholerae colonization factor gbpa crystal structure
14	c2pn5A_	Alignment		81.2	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**thioester-containing protein i; **PDBTitle:** crystal structure of tep1r
15	d1nqja_	Alignment		80.4	12	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
16	c3cu7A_	Alignment		79.7	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
17	c3pdgA_	Alignment		77.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
18	c3irpX_	Alignment		76.9	30	**PDB header:**cell adhesion **Chain:** X: **PDB Molecule:**uro-adherence factor a; **PDBTitle:** crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
19	c3pe9B_	Alignment		75.6	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
20	c3jqxA_	Alignment		74.0	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cademium
21	d1cwva3	Alignment	not modelled	68.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
22	d2d7na1	Alignment	not modelled	66.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
23	c2k7pA_	Alignment	not modelled	65.3	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
24	c3pe9A_	Alignment	not modelled	59.3	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
25	d1cwva1	Alignment	not modelled	53.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
26	c3mn8A_	Alignment	not modelled	49.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
27	c3ohnA_	Alignment	not modelled	46.3	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
28	c1uwyA_	Alignment	not modelled	46.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
29	d2d7pa1	Alignment	not modelled	44.1	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains

						Family: Filamin repeat (rod domain)
30	c2nsmA_	Alignment	not modelled	43.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
31	c2b39B_	Alignment	not modelled	39.7	14	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
32	d1zdxa1	Alignment	not modelled	39.4	43	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
33	d2q4ma1	Alignment	not modelled	38.1	20	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
34	c1zxuA_	Alignment	not modelled	38.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750
35	d1nqjb_	Alignment	not modelled	37.2	13	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
36	d2e9ia1	Alignment	not modelled	37.2	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
37	c2x5pA_	Alignment	not modelled	37.0	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
38	c2k7qA_	Alignment	not modelled	36.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 18-19
39	c3mkqA_	Alignment	not modelled	35.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
40	d1zdva1	Alignment	not modelled	35.0	43	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
41	d2diaa1	Alignment	not modelled	33.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
42	c2kutA_	Alignment	not modelled	32.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
43	d1bf2a1	Alignment	not modelled	31.7	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
44	c3pe9C_	Alignment	not modelled	30.8	11	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
45	c2l0dA_	Alignment	not modelled	30.1	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell surface protein; **PDBTitle:** solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
46	c3dsmA_	Alignment	not modelled	29.7	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bacuni_02894; **PDBTitle:** crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
47	d1uwya1	Alignment	not modelled	28.9	14	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
48	d1nkga1	Alignment	not modelled	27.8	20	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
49	d2hc5a1	Alignment	not modelled	27.5	17	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
50	d1clca2	Alignment	not modelled	27.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
51	c3kptA_	Alignment	not modelled	27.1	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagen adhesion protein; **PDBTitle:** crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
52	c2jojA_	Alignment	not modelled	26.8	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centrin protein; **PDBTitle:** nmr solution structure of n-terminal domain of euplotes2 octocarinatus centrin
53	d1l0qa1	Alignment	not modelled	26.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
54	c2e7mA_	Alignment	not modelled	26.3	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein kiaa0319; **PDBTitle:** solution structure of the pkd domain (329-428) from human2 kiaa0319
						PDB header:carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-

55	c1h8lA_	Alignment	not modelled	26.2	20	882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
56	d2dj4a1	Alignment	not modelled	25.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
57	d2d7ma1	Alignment	not modelled	25.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
58	d1v05a_	Alignment	not modelled	25.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
59	d2vzsa3	Alignment	not modelled	24.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
60	c2pz4A_	Alignment	not modelled	23.9	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein gbs052; **PDBTitle:** crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae
61	c2kzwA_	Alignment	not modelled	23.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
62	d1edqa1	Alignment	not modelled	23.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
63	d1b77a2	Alignment	not modelled	22.1	23	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
64	c3hrzA_	Alignment	not modelled	21.8	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b
65	d2dmba1	Alignment	not modelled	20.3	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
66	d2dmca1	Alignment	not modelled	20.3	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
67	d2ag4a1	Alignment	not modelled	19.9	27	**Fold:**Ganglioside M2 (gm2) activator **Superfamily:**Ganglioside M2 (gm2) activator **Family:**Ganglioside M2 (gm2) activator
68	d2di8a1	Alignment	not modelled	19.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
69	c2qkiA_	Alignment	not modelled	19.3	17	**PDB header:**immune system/hydrolase inhibitor **Chain:** A: **PDB Molecule:**complement c3; **PDBTitle:** human c3c in complex with the inhibitor compstatin
70	c3pddA_	Alignment	not modelled	19.3	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
71	d1cwva2	Alignment	not modelled	17.6	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
72	c3b9eA_	Alignment	not modelled	17.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
73	d2j3sa2	Alignment	not modelled	16.6	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
74	d2w0pa1	Alignment	not modelled	16.4	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
75	c3ottB_	Alignment	not modelled	16.1	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two-component system sensor histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
76	d1l0qa2	Alignment	not modelled	15.9	16	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
77	d1h8la1	Alignment	not modelled	15.7	20	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
78	d2hq2a1	Alignment	not modelled	15.6	17	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
79	d1uwfa1	Alignment	not modelled	15.0	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
80	d1wlga_	Alignment	not modelled	14.4	13	**Fold:**Flagellar hook protein flgE **Superfamily:**Flagellar hook protein flgE **Family:**Flagellar hook protein flgE
81	c3cnkB_	Alignment	not modelled	14.1	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
						PDB header:cell adhesion/transport/chaperone

82	c3rfzB_	Alignment	not modelled	13.9	15	**Chain:** B: **PDB Molecule:**outer membrane usher protein, type 1 fimbrial synthesis; **PDBTitle:** crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
83	c1qfhB_	Alignment	not modelled	13.8	20	**PDB header:**actin binding protein **Chain:** B: **PDB Molecule:**protein (gelation factor); **PDBTitle:** dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
84	c3iswA_	Alignment	not modelled	13.0	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
85	c1ponB_	Alignment	not modelled	12.9	13	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
86	c3rghA_	Alignment	not modelled	12.6	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
87	d1ccda_	Alignment	not modelled	12.2	11	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
88	c2yh5A_	Alignment	not modelled	12.0	11	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
89	d1qfha2	Alignment	not modelled	11.9	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
90	d1pzsa_	Alignment	not modelled	11.7	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
91	c1pzsA_	Alignment	not modelled	11.7	25	**PDB header:**oxidoreductase, metal binding protein **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** crystal structure of a cu-zn superoxide dismutase from mycobacterium2 tuberculosis at 1.63 resolution
92	d3bwud1	Alignment	not modelled	11.5	40	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
93	d1wpga2	Alignment	not modelled	11.4	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
94	d2cwza1	Alignment	not modelled	11.3	20	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
95	d1wgoa_	Alignment	not modelled	11.1	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
96	c2qt7B_	Alignment	not modelled	10.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**receptor-type tyrosine-protein phosphatase-like **PDBTitle:** crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
97	c3gzkA_	Alignment	not modelled	10.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** structure of a. acidocaldarius cellulase cela
98	c2go2A_	Alignment	not modelled	10.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kunitz-type serine protease inhibitor bbki; **PDBTitle:** crystal structure of bbki, a kunitz-type kallikrein inhibitor
99	c2kzxA_	Alignment	not modelled	10.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116