Phyre^2

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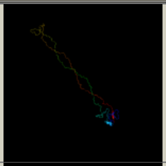
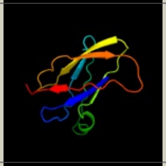
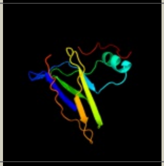
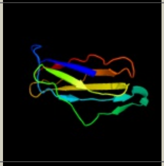
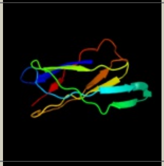
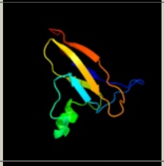
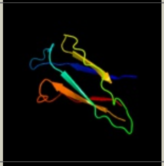
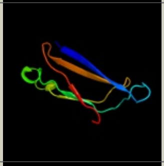
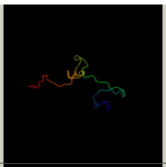
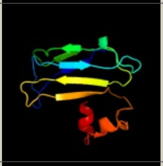
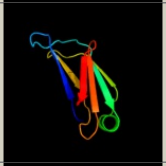
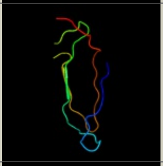
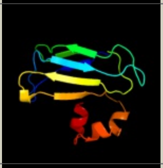
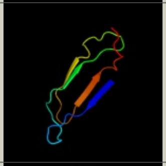
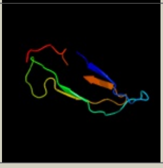
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xgfA_	 Alignment		98.6	70	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**long tail fiber protein p37; **PDBTitle:** structure of the bacteriophage t4 long tail fibre needle-2 shaped receptor-binding tip
2	c3mn8A_	 Alignment		98.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
3	d1h8la1	 Alignment		98.2	25	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
4	d1uwya1	 Alignment		98.2	19	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
5	c2nsmA_	 Alignment		98.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
6	c1h8lA_	 Alignment		97.9	28	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
7	c1uwyA_	 Alignment		97.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
8	d1nkga1	 Alignment		97.3	12	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
9	d1cwva2	 Alignment		96.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
10	c1cwvA_	 Alignment		95.6	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**invasin; **PDBTitle:** crystal structure of invasin: a bacterial integrin-binding protein
11	d1f00i1	 Alignment		95.2	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments

12	d1ocya_	Alignment		95.1	13	**Fold:**Receptor-binding domain of short tail fibre protein gp12 **Superfamily:**Receptor-binding domain of short tail fibre protein gp12 **Family:**Receptor-binding domain of short tail fibre protein gp12
13	d3pccm_	Alignment		94.9	17	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
14	d1s9aa_	Alignment		94.8	16	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
15	d1cwva1	Alignment		94.7	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
16	c2azqA_	Alignment		94.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
17	d2burb1	Alignment		94.3	16	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
18	d1dmha_	Alignment		94.2	22	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
19	c3irpX_	Alignment		93.8	24	**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
20	c3n9tA_	Alignment		93.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
21	d3pcca_	Alignment	not modelled	93.4	17	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
22	c2xsuA_	Alignment	not modelled	93.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2 dioxygenase; **PDBTitle:** crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
23	c1tmxA_	Alignment	not modelled	92.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
24	d2bura1	Alignment	not modelled	92.3	17	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
25	c1pdiQ_	Alignment	not modelled	92.3	13	**PDB header:**structural protein **Chain:** Q: **PDB Molecule:**short tail fiber protein; **PDBTitle:** fitting of the c-terminal part of the short tail fibers2 into the cryo-em reconstruction of t4 baseplate
26	d1cwva3	Alignment	not modelled	92.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
27	c3hj8A_	Alignment	not modelled	90.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
28	c2boyC_	Alignment	not modelled	90.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp

29	c3kptA_	Alignment	not modelled	89.6	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagen adhesion protein; **PDBTitle:** crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
30	c1nkgA_	Alignment	not modelled	81.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
31	c3qvaB_	Alignment	not modelled	72.6	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
32	c2pz4A_	Alignment	not modelled	66.4	13	**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
33	c2gpzC_	Alignment	not modelled	54.7	30	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
34	c2ww8A_	Alignment	not modelled	48.0	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
35	c2x5pA_	Alignment	not modelled	46.3	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
36	d1tfpa_	Alignment	not modelled	46.1	22	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
37	c1yq6A_	Alignment	not modelled	40.5	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**minor capsid protein; **PDBTitle:** prd1 vertex protein p5
38	c2h1xB_	Alignment	not modelled	40.4	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
39	d1kgia_	Alignment	not modelled	36.2	23	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
40	c1wlhA_	Alignment	not modelled	34.6	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**gelation factor; **PDBTitle:** molecular structure of the rod domain of dictyostelium2 filamin
41	c2xicB_	Alignment	not modelled	34.0	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**ancillary protein 1; **PDBTitle:** pilus-presented adhesin, spy0125 (cpa), p212121 form (esrf data)
42	d1ttaa_	Alignment	not modelled	33.6	25	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
43	d1oo2a_	Alignment	not modelled	31.4	19	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
44	c2pn5A_	Alignment	not modelled	29.5	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**thioester-containing protein i; **PDBTitle:** crystal structure of tep1r
45	d1f86a_	Alignment	not modelled	27.4	25	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
46	c1yq8A_	Alignment	not modelled	23.8	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**minor capsid protein; **PDBTitle:** prd1 vertex protein p5
47	d1eqwa_	Alignment	not modelled	23.1	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
48	c2e9jA_	Alignment	not modelled	22.5	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
49	d2o14a1	Alignment	not modelled	22.5	20	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**YxiM N-terminal domain-like
50	d2diba1	Alignment	not modelled	21.9	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
51	c2k7pA_	Alignment	not modelled	20.0	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
52	c2k7qA_	Alignment	not modelled	19.8	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 18-19
53	d1zdva1	Alignment	not modelled	19.6	12	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
54	c2p9rA_	Alignment	not modelled	18.0	16	**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
55	c2ds4A_	Alignment	not modelled	17.8	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45;

						PDBTitle: solution structure of the filamin domain from human2 tripartite motif protein 45
56	d1o6ea_	Alignment	not modelled	17.5	27	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
57	c1qfhB_	Alignment	not modelled	17.0	14	**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
58	d2dj4a1	Alignment	not modelled	17.0	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
59	c2h0eA_	Alignment	not modelled	16.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transthyretin-like protein pucm; **PDBTitle:** crystal structure of pucm in the absence of substrate
60	d2pbka1	Alignment	not modelled	16.8	25	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
61	c1ti2F_	Alignment	not modelled	16.8	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
62	d1vzva_	Alignment	not modelled	14.3	23	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
63	d1at3a_	Alignment	not modelled	14.2	29	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
64	c3njqB_	Alignment	not modelled	14.2	26	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
65	d1zdxa1	Alignment	not modelled	13.8	12	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
66	d2ozga1	Alignment	not modelled	13.8	17	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
67	d2d7ma1	Alignment	not modelled	13.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
68	d2vn6a1	Alignment	not modelled	12.9	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
69	c3rghA_	Alignment	not modelled	12.1	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
70	d1qfha1	Alignment	not modelled	12.0	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
71	d3bwud1	Alignment	not modelled	11.9	13	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
72	d1wlha1	Alignment	not modelled	11.8	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
73	d1mhhe_	Alignment	not modelled	11.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
74	c2ee6A_	Alignment	not modelled	11.5	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 21th filamin domain from human2 filamin-b
75	d2paja1	Alignment	not modelled	11.5	23	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
76	d2e9ia1	Alignment	not modelled	11.3	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
77	d2di9a1	Alignment	not modelled	11.2	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
78	d1k52a_	Alignment	not modelled	10.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
79	c1xctL_	Alignment	not modelled	10.7	22	**PDB header:**immune system **Chain:** L: **PDB Molecule:**protein l; **PDBTitle:** complex hcv core-fab 19d9d6-protein l mutant (d55a, l57h, y64w) in2 space group p21212
80	d1t6la2	Alignment	not modelled	10.6	19	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
81	d1qfha2	Alignment	not modelled	10.5	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
						Fold: Prealbumin-like

82	d2b59b2	Alignment	not modelled	10.5	17	**Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Pre-dockerin domain
83	d2ptla_	Alignment	not modelled	10.3	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
84	d2j3sa2	Alignment	not modelled	10.2	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
85	d1iega_	Alignment	not modelled	9.8	28	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
86	d1xkia_	Alignment	not modelled	9.7	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
87	c3la9A_	Alignment	not modelled	9.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**haemagluttinin family protein; **PDBTitle:** crystal structure of the trimeric autotransporter adhesin head domain2 bpaa from burkholderia pseudomallei, iodide phased
88	d2di8a1	Alignment	not modelled	9.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
89	c2aqmA_	Alignment	not modelled	9.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** cu/zn superoxide dismutase from brucella abortus
90	d1hz6a_	Alignment	not modelled	9.5	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
91	c2vnvC_	Alignment	not modelled	9.1	20	**PDB header:**sugar-binding protein **Chain:** C: **PDB Molecule:**bcla; **PDBTitle:** crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution
92	d1jkea_	Alignment	not modelled	9.0	15	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
93	d1pmya_	Alignment	not modelled	8.9	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
94	c3rpkA_	Alignment	not modelled	8.6	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**backbone pilus subunit; **PDBTitle:** structure of the full-length major pilin rrgb from streptococcus2 pneumoniae
95	c3pvmB_	Alignment	not modelled	8.5	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** structure of complement c5 in complex with cvf
96	c3iswA_	Alignment	not modelled	8.4	18	**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
97	c3qksC_	Alignment	not modelled	8.4	57	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** mre11 rad50 binding domain bound to rad50
98	c3hn5B_	Alignment	not modelled	8.4	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative exported protein bf0290; **PDBTitle:** crystal structure of bf0290 (yp_210027.1) from bacteroides fragilis2 nctc 9343 at 1.70 a resolution
99	c3hrzA_	Alignment	not modelled	8.4	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b