Phyre^2

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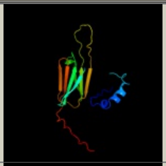
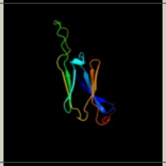
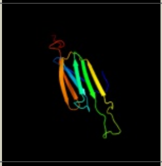
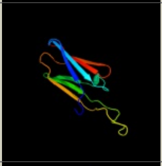
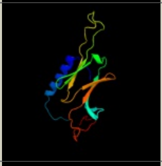
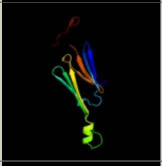
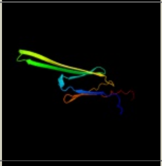
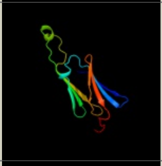
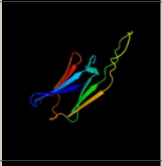
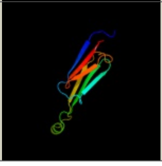
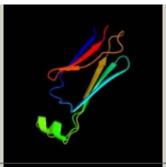
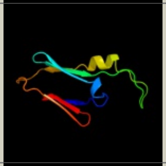
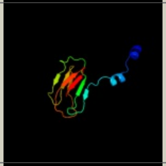
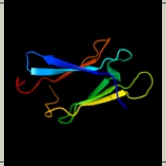
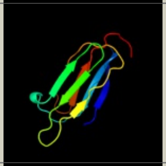
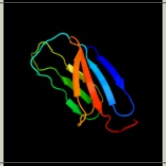
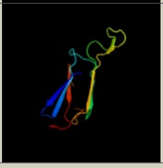
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gmea_	Alignment		99.9	22	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
2	d1gmeb_	Alignment		99.9	23	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
3	d1shsa_	Alignment		99.9	23	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
4	c1shsD_	Alignment		99.9	23	**PDB header:**heat shock protein **Chain:** D: **PDB Molecule:**small heat shock protein; **PDBTitle:** small heat shock protein from methanococcus jannaschii
5	c3glaA_	Alignment		99.8	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**low molecular weight heat shock protein; **PDBTitle:** crystal structure of the hspa from xanthomonas axonopodis
6	c2bolA_	Alignment		99.8	22	**PDB header:**heat shock protein **Chain:** A: **PDB Molecule:**small heat shock protein; **PDBTitle:** crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
7	c3l1eA_	Alignment		99.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin a chain; **PDBTitle:** bovine alphaa crystallin zinc bound
8	c2wj5A_	Alignment		99.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein beta-6; **PDBTitle:** rat alpha crystallin domain
9	c3aabA_	Alignment		99.8	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative uncharacterized protein st1653; **PDBTitle:** small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
10	d2h50a1	Alignment		99.7	24	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**HSP20
11	c2klrA_	Alignment		99.7	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers

12	c3q9qB_	Alignment		99.7	15	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
13	c2wj7D_	Alignment		99.5	18	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin
14	c3igfB_	Alignment		98.0	25	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**all4481 protein; **PDBTitle:** crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
15	d1rl1a_	Alignment		97.8	16	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**GS domain
16	c2jkiS_	Alignment		97.8	13	**PDB header:**chaperone **Chain:** S: **PDB Molecule:**sgt1-like protein; **PDBTitle:** complex of hsp90 n-terminal and sgt1 cs domain
17	c3eudE_	Alignment		96.8	16	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the cs domain of the essential h/aca rnp2 assembly protein shq1p
18	d1wh0a_	Alignment		96.7	8	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**GS domain
19	c1x5mA_	Alignment		96.4	16	**PDB header:**apoptosis, signaling protein **Chain:** A: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of the core domain of calcyclin binding2 protein; siah-interacting protein (sip)
20	d1ejfa_	Alignment		96.3	10	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Co-chaperone p23-like
21	d1wfia_	Alignment	not modelled	96.0	13	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Nuclear movement domain
22	d1wgva_	Alignment	not modelled	95.8	7	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Nuclear movement domain
23	c2k8qA_	Alignment	not modelled	95.5	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** nmr structure of shq1p n-terminal domain
24	d1xo9a_	Alignment	not modelled	95.1	19	**Fold:**HSP20-like chaperones **Superfamily:**HSP20-like chaperones **Family:**Co-chaperone p23-like
25	c2o30A_	Alignment	not modelled	93.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nuclear movement protein; **PDBTitle:** nuclear movement protein from e. cuniculi gb-m1
26	c2rh0B_	Alignment	not modelled	92.2	9	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**nudc domain-containing protein 2; **PDBTitle:** crystal structure of nudc domain-containing protein 22 (13542905) from mus musculus at 1.95 a resolution
27	c2cg9Y_	Alignment	not modelled	70.5	14	**PDB header:**chaperone **Chain:** Y: **PDB Molecule:**co-chaperone protein sba1; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
28	d2fqla1	Alignment	not modelled	65.2	11	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
29	d2ga5a1	Alignment	not modelled	65.0	11	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like

						Family: Frataxin-like
30	d1ew4a_	Alignment	not modelled	50.8	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
31	d2cqla1	Alignment	not modelled	47.4	30	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
32	d1ekga_	Alignment	not modelled	46.2	19	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
33	d1vqoe1	Alignment	not modelled	38.2	24	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
34	d1rl6a1	Alignment	not modelled	37.1	24	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
35	d2j01h1	Alignment	not modelled	31.9	24	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
36	c4a1eE_	Alignment	not modelled	29.3	24	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein l9; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
37	c3iz5F_	Alignment	not modelled	28.7	24	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l9 (l6p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	c2zkre_	Alignment	not modelled	28.7	41	**PDB header:**ribosomal protein/rna **Chain:** E: **PDB Molecule:**rna expansion segment es7 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
39	c3ccmE_	Alignment	not modelled	24.3	24	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**50s ribosomal protein l6p; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
40	d1h8la1	Alignment	not modelled	21.9	12	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
41	c3ho6B_	Alignment	not modelled	19.1	16	**PDB header:**toxin **Chain:** B: **PDB Molecule:**toxin a; **PDBTitle:** structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
42	c3muwU_	Alignment	not modelled	18.9	10	**PDB header:**virus **Chain:** U: **PDB Molecule:**structural polyprotein; **PDBTitle:** pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
43	c2hguH_	Alignment	not modelled	18.5	24	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
44	c2xfbl_	Alignment	not modelled	16.7	20	**PDB header:**virus **Chain:** I: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
45	c3n43B_	Alignment	not modelled	16.6	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.
46	c3petA_	Alignment	not modelled	16.0	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative adhesin; **PDBTitle:** crystal structure of a putative adhesin (bf0245) from bacteroides2 fragilis nctc 9343 at 2.07 a resolution
47	c3n40P_	Alignment	not modelled	15.5	20	**PDB header:**viral protein **Chain:** P: **PDB Molecule:**p62 envelope glycoprotein; **PDBTitle:** crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.
48	c3ipfA_	Alignment	not modelled	15.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
49	c2gjhA_	Alignment	not modelled	13.7	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
50	d2zjre2	Alignment	not modelled	13.4	18	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
51	c487dJ_	Alignment	not modelled	13.2	17	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**protein (50s l6 ribosomal protein); **PDBTitle:** seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
52	c3j0cH_	Alignment	not modelled	13.0	10	**PDB header:**virus **Chain:** H: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
53	c3bbol_	Alignment	not modelled	12.2	47	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l6; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
54	c3livA	Alignment	not modelled	10.8	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative adhesin;

54	c3ljyA_	Alignment	not modelled	10.8	8	**PDBTitle:** crystal structure of putative adhesin (yp_001304413.1) from2 parabacteroides distasonis atcc 8503 at 2.41 a resolution
55	c2wvsD_	Alignment	not modelled	10.5	3	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
56	d1v7wa1	Alignment	not modelled	10.4	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
57	d1uwya1	Alignment	not modelled	10.2	13	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
58	c2lezA_	Alignment	not modelled	9.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**secreted effector protein pipb2; **PDBTitle:** solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a
59	d2qamg1	Alignment	not modelled	9.8	18	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
60	c2i2vG_	Alignment	not modelled	9.3	18	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** crystal structure of ribosome with messenger rna and the2 anticodon stem-loop of p-site trna. this file contains the3 50s subunit of one 70s ribosome. the entire crystal4 structure contains two 70s ribosomes and is described in5 remark 400.
61	c1sm1E_	Alignment	not modelled	8.7	18	**PDB header:**ribosome/antibiotic **Chain:** E: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
62	c2nsmA_	Alignment	not modelled	8.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
63	c1qysA_	Alignment	not modelled	7.8	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
64	c3pa8A_	Alignment	not modelled	7.5	11	**PDB header:**toxin/peptide inhibitor **Chain:** A: **PDB Molecule:**toxin b; **PDBTitle:** structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
65	c3muuA_	Alignment	not modelled	6.9	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**structural polyprotein; **PDBTitle:** crystal structure of the sindbis virus e2-e1 heterodimer at low ph
66	c2x89G_	Alignment	not modelled	6.6	10	**PDB header:**immune system **Chain:** G: **PDB Molecule:**beta-2-microglobulin; **PDBTitle:** structure of the beta2_microglobulin involved in2 amyloidogenesis
67	c1uwyA_	Alignment	not modelled	6.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
68	d1c12b2	Alignment	not modelled	6.2	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
69	d1mvfd_	Alignment	not modelled	6.0	20	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
70	d1ji1a2	Alignment	not modelled	6.0	17	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
71	c2y9jt_	Alignment	not modelled	5.9	13	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
72	d1r3ha1	Alignment	not modelled	5.9	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
73	d1pz5b2	Alignment	not modelled	5.7	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
74	d1je6a1	Alignment	not modelled	5.5	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)