Phyre^2

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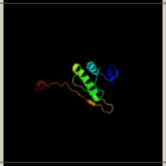
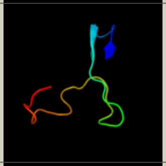
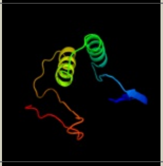
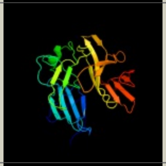
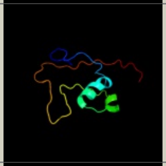
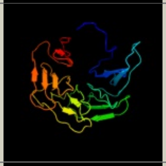
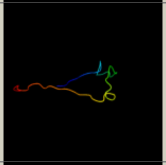
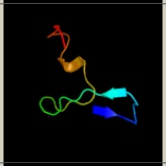
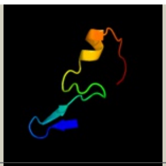
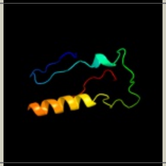
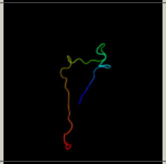
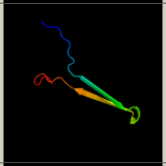
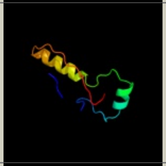
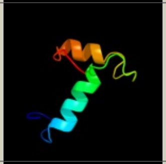
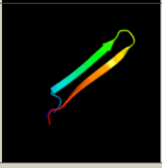
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oy7A_	Alignment		96.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer surface protein a; **PDBTitle:** the crystal structure of ospa mutant
2	d1rypi_	Alignment		46.2	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
3	d1x3za1	Alignment		46.0	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
4	d1irua_	Alignment		43.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
5	c3nqhA_	Alignment		42.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
6	c1j5qB_	Alignment		37.5	25	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**major capsid protein; **PDBTitle:** the structure and evolution of the major capsid protein of a large,2 lipid-containing, dna virus.
7	c1n7dA_	Alignment		36.6	10	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
8	d1j2pa_	Alignment		33.2	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
9	c1m4xC_	Alignment		30.7	29	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
10	c3eswA_	Alignment		30.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
11	c2ivzD_	Alignment		30.3	11	**PDB header:**protein transport/hydrolase **Chain:** D: **PDB Molecule:**protein tolb; **PDBTitle:** structure of tolb in complex with a peptide of the colicin2 e9 t-domain

12	d2f4ma1	Alignment		28.5	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
13	d1wc9a_	Alignment		27.0	22	**Fold:**Ligand-binding domain in the NO signalling and Golgi transport **Superfamily:**Ligand-binding domain in the NO signalling and Golgi transport **Family:**TRAPP components
14	c3e5zA_	Alignment		26.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
15	d1m3ya2	Alignment		26.1	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
16	c3mswA_	Alignment		24.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (bf3112) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
17	c2cfhA_	Alignment		23.9	25	**PDB header:**transport **Chain:** A: **PDB Molecule:**trafficking protein particle complex subunit 3; **PDBTitle:** structure of the bet3-tpc6b core of trapp
18	c1rz2A_	Alignment		22.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein ba4783; **PDBTitle:** 1.6a crystal structure of the protein ba4783/q81l49 (similar to2 sortase b) from bacillus anthracis.
19	c3ifzA_	Alignment		22.7	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
20	c2x12A_	Alignment		22.4	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
21	c3rwxA_	Alignment	not modelled	22.2	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical bacterial outer membrane protein; **PDBTitle:** crystal structure of a hypothetical bacterial outer membrane protein2 (bf2706) from bacteroides fragilis nctc 9343 at 2.40 a resolution
22	c2zcyM_	Alignment	not modelled	20.2	16	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**proteasome component pre4; **PDBTitle:** yeast 20s proteasome:syringolin a-complex
23	d1ryp2_	Alignment	not modelled	20.2	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
24	c1bqfA_	Alignment	not modelled	20.1	70	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**protein (growth-blocking peptide); **PDBTitle:** growth-blocking peptide (gbp) from pseudaletia separata
25	d1rype_	Alignment	not modelled	19.9	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
26	c2kijA_	Alignment	not modelled	19.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
27	c2oryA_	Alignment	not modelled	18.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of m37 lipase
28	c3bmxB_	Alignment	not modelled	17.8	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis

29	d1ri9a_	Alignment	not modelled	17.3	24	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
30	c1ri9A_	Alignment	not modelled	17.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fyn-binding protein; **PDBTitle:** structure of a helically extended sh3 domain of the t cell2 adapter protein adap
31	d1pk6c_	Alignment	not modelled	17.0	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
32	d1qwza_	Alignment	not modelled	16.4	18	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
33	c2ka3C_	Alignment	not modelled	15.7	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
34	d1rh1a1	Alignment	not modelled	15.4	20	**Fold:**Cloacin translocation domain **Superfamily:**Cloacin translocation domain **Family:**Cloacin translocation domain
35	c3nzwH_	Alignment	not modelled	15.3	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**proteasome component pup1; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with 2b
36	d2oqza1	Alignment	not modelled	15.1	15	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
37	d1bcga_	Alignment	not modelled	15.1	35	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
38	c2gacA_	Alignment	not modelled	15.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
39	c3h4pB_	Alignment	not modelled	15.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus2 jannaschii
40	d1bcoa1	Alignment	not modelled	14.8	17	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
41	c3lk6A_	Alignment	not modelled	14.7	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
42	d1pk6b_	Alignment	not modelled	14.7	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
43	d1iruc_	Alignment	not modelled	14.6	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
44	c3ilwA_	Alignment	not modelled	14.4	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
45	d1xata_	Alignment	not modelled	14.2	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
46	c2kkyA_	Alignment	not modelled	14.1	53	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ecs2156; **PDBTitle:** solution structure of c-terminal domain of oxidized nleg2-3 (residue2 90-191) from pathogenic e. coli o157:h7. northeast structural3 genomics consortium and midwest center for structural genomics target4 et109a
47	d1rypc_	Alignment	not modelled	13.8	22	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
48	c3ghpA_	Alignment	not modelled	13.7	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)
49	c1t3dB_	Alignment	not modelled	13.7	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
50	d1c3ha_	Alignment	not modelled	13.5	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
51	c2novD_	Alignment	not modelled	13.4	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
52	c2b59A_	Alignment	not modelled	13.2	24	**PDB header:**hydrolase/structural protein **Chain:** A: **PDB Molecule:**cog1196: chromosome segregation atpases; **PDBTitle:** the type ii cohesin dockerin complex
53	d1rypj_	Alignment	not modelled	13.0	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
54	c3vh0C_	Alignment	not modelled	12.9	9	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce;

						PDBTitle: crystal structure of e. coli ynce complexed with dna
55	c1zvuA_	Alignment	not modelled	12.9	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
56	c2gtjA_	Alignment	not modelled	12.7	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fyn-binding protein; **PDBTitle:** reduced form of adap hsh3-n-domain
57	d1tyja1	Alignment	not modelled	12.6	27	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
58	d1zv9a1	Alignment	not modelled	12.6	36	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
59	d1irug_	Alignment	not modelled	12.5	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
60	c2xetB_	Alignment	not modelled	12.4	5	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
61	d1xaka_	Alignment	not modelled	12.4	44	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Accessory protein X4 (ORF8, ORF7a) **Family:**Accessory protein X4 (ORF8, ORF7a)
62	c2w8bB_	Alignment	not modelled	12.4	11	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
63	c2e5pA_	Alignment	not modelled	12.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
64	c3qx3B_	Alignment	not modelled	12.2	50	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
65	d1ng5a_	Alignment	not modelled	12.1	18	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
66	d1m7xa2	Alignment	not modelled	12.0	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
67	c2wl2B_	Alignment	not modelled	11.8	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
68	c2iu9C_	Alignment	not modelled	11.7	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
69	d1ab4a_	Alignment	not modelled	11.5	22	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
70	c1p4vA_	Alignment	not modelled	11.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(4)-(beta-n-acetylglucosaminyl)-l-asparaginase **PDBTitle:** crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
71	c2wlgA_	Alignment	not modelled	11.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
72	d2jdqd1	Alignment	not modelled	11.4	15	**Fold:**PB2 C-terminal domain-like **Superfamily:**PB2 C-terminal domain-like **Family:**PB2 C-terminal domain-like
73	c2hc8A_	Alignment	not modelled	11.4	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
74	c2xkjE_	Alignment	not modelled	11.3	36	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**topoisomerase iv; **PDBTitle:** crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate)
75	c3fnkA_	Alignment	not modelled	11.3	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
76	d1bjta_	Alignment	not modelled	11.2	60	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
77	c1bjtA_	Alignment	not modelled	11.2	60	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
78	d1t3da_	Alignment	not modelled	11.2	32	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
79	c2vtwF_	Alignment	not modelled	11.2	27	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fiber protein 2; **PDBTitle:** structure of the c-terminal head domain of the fowl2 adenovirus type 1 short fibre

80	c1yo4A_	Alignment	not modelled	11.1	47	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hypothetical protein x4; **PDBTitle:** solution structure of the sars coronavirus orf 7a coded x42 protein
81	c1hrlA_	Alignment	not modelled	11.0	60	**PDB header:**toxin **Chain:** A: **PDB Molecule:**paralytic peptide i; **PDBTitle:** structure of a paralytic peptide from an insect, manduca2 sexta
82	d1iruh_	Alignment	not modelled	10.9	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
83	d1j2qh_	Alignment	not modelled	10.8	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
84	d1iruk_	Alignment	not modelled	10.8	22	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
85	d1pk6a_	Alignment	not modelled	10.7	22	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
86	d1w7pd2	Alignment	not modelled	10.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
87	c3dr2A_	Alignment	not modelled	10.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exported gluconolactonase; **PDBTitle:** structural and functional analyses of xc5397 from2 xanthomonas campestris: a gluconolactonase important in3 glucose secondary metabolic pathways
88	d1x38a2	Alignment	not modelled	10.5	25	**Fold:**Flavodoxin-like **Superfamily:**Beta-D-glucan exohydrolase, C-terminal domain **Family:**Beta-D-glucan exohydrolase, C-terminal domain
89	c2wh7A_	Alignment	not modelled	10.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-phage associated; **PDBTitle:** the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
90	d1rypd_	Alignment	not modelled	10.0	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
91	d1eaic_	Alignment	not modelled	9.9	25	**Fold:**Serine protease inhibitors **Superfamily:**Serine protease inhibitors **Family:**ATI-like
92	c2xk0A_	Alignment	not modelled	9.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
93	c2hh9A_	Alignment	not modelled	9.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** thiamin pyrophosphokinase from candida albicans
94	d1krra_	Alignment	not modelled	9.8	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
95	d1o5ua_	Alignment	not modelled	9.8	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
96	d1o91a_	Alignment	not modelled	9.7	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
97	c1o91B_	Alignment	not modelled	9.7	31	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
98	d1jnpa_	Alignment	not modelled	9.7	26	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
99	c7apiB_	Alignment	not modelled	9.6	6	**PDB header:**proteinase inhibitor **Chain:** B: **PDB Molecule:**alpha 1-antitrypsin; **PDBTitle:** the s variant of human alpha1-antitrypsin, structure and implications2 for function and metabolism