Phyre^2

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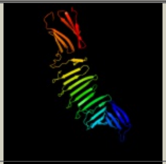
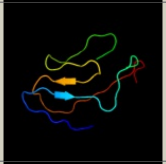
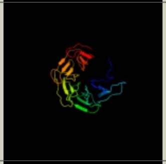
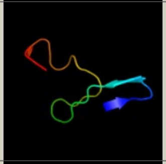
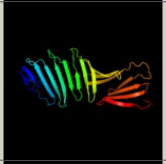
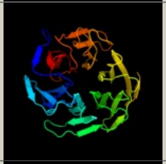
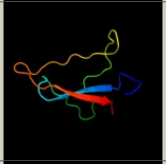
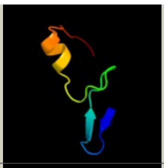
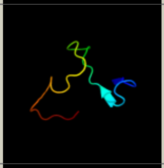
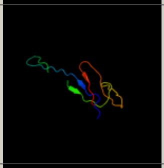
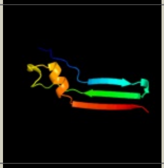
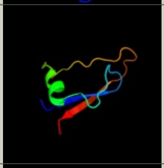
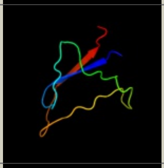
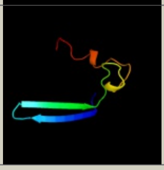
Detailed template information

#	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	d1hnga1	Alignment		92.7	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
3	d1hnfa1	Alignment		68.3	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
4	c1n7dA_	Alignment		67.7	12	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
5	d1x3za1	Alignment		39.1	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
6	d1ospo_	Alignment		33.3	16	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
7	c2w8bB_	Alignment		31.4	12	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
8	c3e5zA_	Alignment		31.0	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.
9	c3rwxA_	Alignment		25.0	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
10	d2j44a2	Alignment		23.8	18	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
11	c2ivzD_	Alignment		22.0	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		21.0	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
13	c3eswA_	Alignment		20.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
14	d1sska_	Alignment		20.3	21	**Fold:**Coronavirus RNA-binding domain **Superfamily:**Coronavirus RNA-binding domain **Family:**Coronavirus RNA-binding domain
15	c3mswA_	Alignment		20.3	20	**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
16	c1j5qB_	Alignment		20.0	28	**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.
17	d2j43a1	Alignment		17.2	16	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
18	d2j44a1	Alignment		17.2	15	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
19	d1ei5a1	Alignment		15.5	32	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
20	c3k8hA_	Alignment		15.5	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**30klp; **PDBTitle:** structure of crystal form i of tp0453
21	c1t3dB_	Alignment	not modelled	14.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
22	c3hd4A_	Alignment	not modelled	13.8	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** mhv nucleocapsid protein ntd
23	c3ilwA_	Alignment	not modelled	13.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
24	d1o5ua_	Alignment	not modelled	13.6	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
25	c2ksnA_	Alignment	not modelled	13.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
26	c2x12A_	Alignment	not modelled	12.6	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
27	c3s88I_	Alignment	not modelled	12.6	19	**PDB header:**immune system/viral protein **Chain:** I: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
28	c2kijA_	Alignment	not modelled	12.1	25	**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
						PDB header:hydrolase

29	c3bmxB_	Alignment	not modelled	12.1	42	**Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis
30	d1xata_	Alignment	not modelled	11.8	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
31	d1t3da_	Alignment	not modelled	11.6	32	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
32	d1pk6c_	Alignment	not modelled	11.4	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
33	c2wlgA_	Alignment	not modelled	11.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
34	d1td6a_	Alignment	not modelled	11.1	31	**Fold:**Hypothetical protein MPN330 **Superfamily:**Hypothetical protein MPN330 **Family:**Hypothetical protein MPN330
35	c2j44A_	Alignment	not modelled	11.1	15	**PDB header:**carbohydrate-binding module **Chain:** A: **PDB Molecule:**alkaline amylopullulanase; **PDBTitle:** alpha-glucan binding by a streptococcal virulence factor
36	c2gopB_	Alignment	not modelled	11.0	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trilobed protease; **PDBTitle:** the beta-propeller domain of the trilobed protease from pyrococcus2 furiosus reveals an open velcro topology
37	d1bcoa1	Alignment	not modelled	11.0	17	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
38	c3ifzA_	Alignment	not modelled	10.8	21	**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
39	d2bxxa1	Alignment	not modelled	10.8	24	**Fold:**Coronavirus RNA-binding domain **Superfamily:**Coronavirus RNA-binding domain **Family:**Coronavirus RNA-binding domain
40	c2ka3C_	Alignment	not modelled	10.7	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
41	d1brwa3	Alignment	not modelled	10.5	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
42	d2i52a1	Alignment	not modelled	10.2	17	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
43	d1bcga_	Alignment	not modelled	10.2	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
44	d1pk6b_	Alignment	not modelled	10.1	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
45	d1pk6a_	Alignment	not modelled	10.1	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
46	c3jroA_	Alignment	not modelled	10.0	12	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
47	d1mr7a_	Alignment	not modelled	9.7	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
48	d2tpta3	Alignment	not modelled	9.7	23	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
49	d2jdqd1	Alignment	not modelled	9.5	20	**Fold:**PB2 C-terminal domain-like **Superfamily:**PB2 C-terminal domain-like **Family:**PB2 C-terminal domain-like
50	d1f00i2	Alignment	not modelled	9.5	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
51	d1m3ya2	Alignment	not modelled	9.4	39	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
52	c3bgyA_	Alignment	not modelled	9.4	20	**PDB header:**hydrolase, viral protein **Chain:** A: **PDB Molecule:**polynucleotide 5'-triphosphatase; **PDBTitle:** triclinic structure of mimivirus capping enzyme2 triphosphatase at 1.65 a
53	c3fsbB_	Alignment	not modelled	9.1	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtc; **PDBTitle:** crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
54	d1c3ha_	Alignment	not modelled	9.0	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
55	c3vh0C_	Alignment	not modelled	9.0	9	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce;

						PDBTitle: crystal structure of e. coli ynce complexed with dna
56	c2hc8A_	Alignment	not modelled	9.0	28	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
57	d1krra_	Alignment	not modelled	8.9	29	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
58	c1gr3A_	Alignment	not modelled	8.9	45	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
59	d1gr3a_	Alignment	not modelled	8.9	45	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
60	d1j2za_	Alignment	not modelled	8.7	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
61	c2xzmG_	Alignment	not modelled	8.7	17	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein s7 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
62	c2iu9C_	Alignment	not modelled	8.6	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
63	d1jnpa_	Alignment	not modelled	8.6	26	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
64	c1m4xC_	Alignment	not modelled	8.5	39	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
65	c2vtwF_	Alignment	not modelled	8.4	32	**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
66	d2geca1	Alignment	not modelled	8.3	24	**Fold:**Coronavirus RNA-binding domain **Superfamily:**Coronavirus RNA-binding domain **Family:**Coronavirus RNA-binding domain
67	c3di4A_	Alignment	not modelled	8.3	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf1989; **PDBTitle:** crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
68	d1azpa_	Alignment	not modelled	7.9	17	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
69	d1a1xa_	Alignment	not modelled	7.9	21	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
70	c3qx3B_	Alignment	not modelled	7.9	34	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
71	d1ufya_	Alignment	not modelled	7.8	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
72	d1f1sa3	Alignment	not modelled	7.8	18	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
73	c3eevC_	Alignment	not modelled	7.8	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
74	d2oqea2	Alignment	not modelled	7.6	25	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
75	d2pyta1	Alignment	not modelled	7.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
76	c3myxA_	Alignment	not modelled	7.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
77	c3r0sA_	Alignment	not modelled	7.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
78	c2kssA_	Alignment	not modelled	7.3	31	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**carotenogenesis protein cars; **PDBTitle:** nmr structure of myxococcus xanthus antirepressor cars1
79	c2gacA_	Alignment	not modelled	7.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
80	d1jsga_	Alignment	not modelled	7.1	26	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
81	d1k8wa3	Alignment	not modelled	7.0	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like

						Family:PUA domain
82	d1w9pa2	Alignment	not modelled	7.0	18	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
83	c2j43A_	Alignment	not modelled	7.0	16	**PDB header:**carbohydrate-binding module **Chain:** A: **PDB Molecule:**spydx; **PDBTitle:** alpha-glucan recognition by family 41 carbohydrate-binding2 modules from streptococcal virulence factors
84	d1jofa_	Alignment	not modelled	7.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
85	c2l92A_	Alignment	not modelled	6.9	44	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone family protein nucleoid-structuring protein h-ns; **PDBTitle:** solution structure of the c-terminal domain of h-ns like protein bv3f
86	d1oi0a_	Alignment	not modelled	6.9	15	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain
87	c7apiB_	Alignment	not modelled	6.9	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
88	c3i3aC_	Alignment	not modelled	6.8	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
89	d2ax3a2	Alignment	not modelled	6.8	14	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
90	c1jjoE_	Alignment	not modelled	6.8	22	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**neuroserpin; **PDBTitle:** crystal structure of mouse neuroserpin (cleaved form)
91	d1jiwi_	Alignment	not modelled	6.8	15	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
92	c1n0nB_	Alignment	not modelled	6.7	57	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase [mn]; **PDBTitle:** catalytic and structural effects of amino-acid substitution at his302 in human manganese superoxide dismutase
93	c3jqyB_	Alignment	not modelled	6.7	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo
94	c3izbF_	Alignment	not modelled	6.7	14	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**40s ribosomal protein rps5 (s7p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
95	c1y10C_	Alignment	not modelled	6.7	32	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
96	c1p7gL_	Alignment	not modelled	6.6	43	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from pyrobaculum2 aerophilum
97	d1ulva3	Alignment	not modelled	6.6	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CBD9-like **Family:**Glucodextranase, domain C
98	c1gn4B_	Alignment	not modelled	6.6	43	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** h145e mutant of mycobacterium tuberculosis iron-superoxide2 dismutase.
99	c3dr2A_	Alignment	not modelled	6.6	15	**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