Phyre^2

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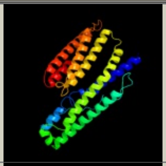
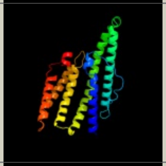
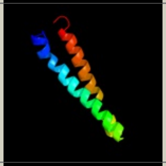
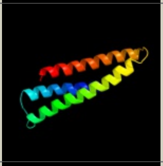
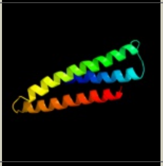
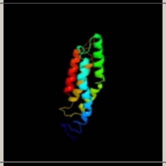
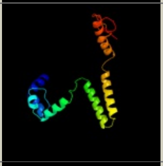
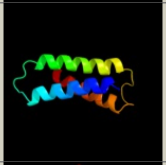
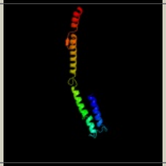
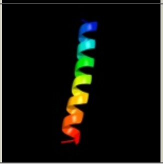
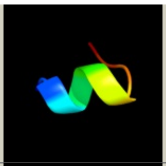
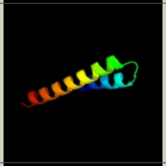
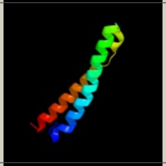
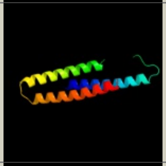
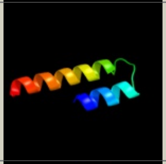
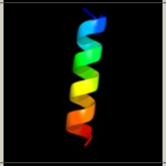
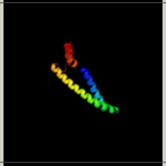
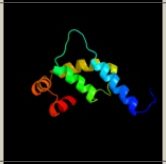
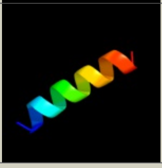
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ieeA_	Alignment		99.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of hypothetical protein bf3319 from bacteroides2 fragilis (yp_212931.1) from bacteroides fragilis nctc 9343 at 1.70 a3 resolution
2	c3rh3A_	Alignment		99.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized duf3829-like protein; **PDBTitle:** crystal structure of an uncharacterized duf3829-like protein (bt_1908)2 from bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
3	d1vlta_	Alignment		31.5	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Aspartate receptor, ligand-binding domain **Family:**Aspartate receptor, ligand-binding domain
4	d1s94a_	Alignment		21.1	16	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
5	c1s94A_	Alignment		21.1	16	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**s-syntaxin; **PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
6	c2kdtA_	Alignment		15.8	33	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
7	c3ls1A_	Alignment		15.2	13	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
8	c3c4mA_	Alignment		13.7	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fusion protein of maltose-binding periplasmic protein and **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
9	c2kmfA_	Alignment		12.8	17	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
10	d1ykhb1	Alignment		12.2	18	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**CSE2-like
11	c1pq1B_	Alignment		12.2	27	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl2-like protein 11; **PDBTitle:** crystal structure of bcl-xl/bim

12	d1pgya_	Alignment		12.0	60	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
13	c3fyqA_	Alignment		11.7	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cg6831-pa (talin); **PDBTitle:** structure of drosophila melanogaster talin ibs2 domain2 (residues 1981-2168)
14	d2liga_	Alignment		11.3	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Aspartate receptor, ligand-binding domain **Family:**Aspartate receptor, ligand-binding domain
15	d1ez3a_	Alignment		11.3	10	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
16	d1sj8a2	Alignment		10.0	17	**Fold:**I/LWEQ domain **Superfamily:**I/LWEQ domain **Family:**I/LWEQ domain
17	c3d7vB_	Alignment		9.1	22	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of mcl-1 in complex with an mcl-12 selective bh3 ligand
18	c2j1dG_	Alignment		8.7	9	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**disheveled-associated activator of morphogenesis 1; **PDBTitle:** crystallization of hdaam1 c-terminal fragment
19	d2jdia1	Alignment		8.6	13	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
20	c2nl9B_	Alignment		8.5	28	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of the mcl-1:bim bh3 complex
21	c3gvmA_	Alignment	not modelled	8.0	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
22	d1wa8b1	Alignment	not modelled	7.9	10	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
23	c3kj1B_	Alignment	not modelled	7.9	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** mcl-1 in complex with bim bh3 mutant i2da
24	c2e76D_	Alignment	not modelled	7.8	14	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
25	d1tuba2	Alignment	not modelled	7.7	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
26	c2d4uA_	Alignment	not modelled	7.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** crystal structure of the ligand binding domain of the bacterial serine2 chemoreceptor tsr
27	c2z6eC_	Alignment	not modelled	6.9	8	**PDB header:**protein fibril regulator **Chain:** C: **PDB Molecule:**disheveled-associated activator of morphogenesis **PDBTitle:** crystal structure of human daam1 fh2
28	d1nm8a1	Alignment	not modelled	6.9	20	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase

29	d1hx1b_	Alignment	not modelled	6.8	16	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
30	c3tekA_	Alignment	not modelled	6.8	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
31	d1ndba1	Alignment	not modelled	6.6	20	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
32	c2b8kD_	Alignment	not modelled	6.6	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase ii 32 kda **PDBTitle:** 12-subunit rna polymerase ii
33	c2dkdA_	Alignment	not modelled	6.5	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoacetylglucosamine mutase; **PDBTitle:** crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
34	d1v54e_	Alignment	not modelled	6.5	20	**Fold:**alpha-alpha superhelix **Superfamily:**Cytochrome c oxidase subunit E **Family:**Cytochrome c oxidase subunit E
35	c3kz0C_	Alignment	not modelled	6.4	28	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
36	c3kz0D_	Alignment	not modelled	6.4	28	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
37	c2vs0B_	Alignment	not modelled	6.4	16	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
38	c2y69R_	Alignment	not modelled	6.3	20	**PDB header:**electron transport **Chain:** R: **PDB Molecule:**cytochrome c oxidase subunit 5a; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
39	d2f43a1	Alignment	not modelled	6.1	12	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
40	c2k7wB_	Alignment	not modelled	6.1	29	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bax activation is initiated at a novel interaction site
41	c3s90B_	Alignment	not modelled	6.1	9	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
42	c3s90A_	Alignment	not modelled	6.1	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
43	c2qr4B_	Alignment	not modelled	6.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
44	d1skyb1	Alignment	not modelled	6.0	12	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
45	c2jofA_	Alignment	not modelled	5.9	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**trp-cage; **PDBTitle:** the trp-cage: optimizing the stability of a globular2 miniprotein
46	c1jrjA_	Alignment	not modelled	5.8	7	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
47	c2npuA_	Alignment	not modelled	5.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fkbp12-rapamycin complex-associated protein; **PDBTitle:** the solution structure of the rapamycin-binding domain of2 mtor (frb)
48	d1tubb2	Alignment	not modelled	5.8	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
49	d1u84a_	Alignment	not modelled	5.7	29	**Fold:**YugE-like **Superfamily:**YugE-like **Family:**YugE-like
50	d1fioa_	Alignment	not modelled	5.6	10	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
51	d1p42a1	Alignment	not modelled	5.6	16	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
52	d1fx0a1	Alignment	not modelled	5.5	10	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
53	c2l81A_	Alignment	not modelled	5.5	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**enhancer of filamentation 1; **PDBTitle:** solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast

						structural genomics3 consortium target hr5554a
54	c3mtuE_	Alignment	not modelled	5.5	23	**PDB header:**contractile protein **Chain:** E: **PDB Molecule:**head morphogenesis protein, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
55	c3tj5A_	Alignment	not modelled	5.5	10	**PDB header:**protein binding/toxin **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head domain (vh1, residues 1-258) in complex with the2 vinculin binding site of the surface cell antigen 4 (sca4-vbs-n;3 residues 412-434) from rickettsia rickettsii
56	c1y9jA_	Alignment	not modelled	5.3	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec1 family domain containing protein 1; **PDBTitle:** solution structure of the rat sly1 n-terminal domain