Phyre^2

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Description	P69791
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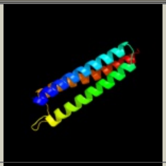
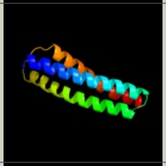
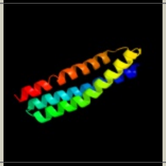
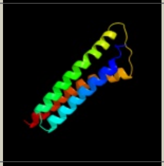
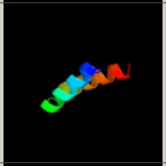
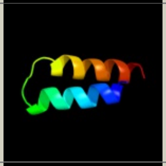
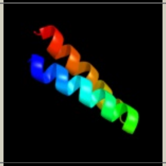
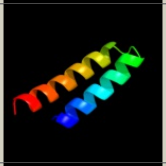
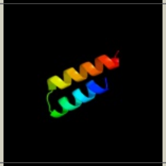
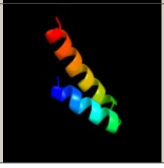
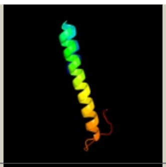
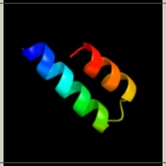
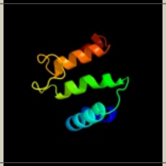
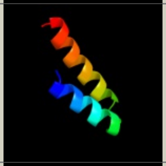
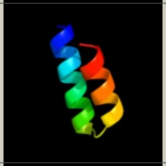
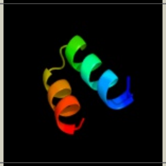
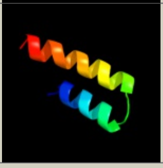
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1wcrA_	Alignment		100.0	99	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, n, n'-diacetylchitobiose-specific **PDBTitle:** trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
2	d2e2aa_	Alignment		100.0	33	**Fold:**Spectrin repeat-like **Superfamily:**Enzyme IIa from lactose specific PTS, IIa-lac **Family:**Enzyme IIa from lactose specific PTS, IIa-lac
3	c3l8rA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative pts system, cellobiose-specific iia **PDBTitle:** the crystal structure of ptca from s. mutans
4	c3k1sE_	Alignment		100.0	45	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
5	c2w2uA_	Alignment		60.5	26	**PDB header:**hydrolase/transport **Chain:** A: **PDB Molecule:**hypothetical p60 katanin; **PDBTitle:** structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
6	d2jq9a1	Alignment		50.2	17	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
7	d1wr0a1	Alignment		49.1	20	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
8	d2cpta1	Alignment		46.2	21	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
9	c2v6xA_	Alignment		43.1	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** stractural insight into the interaction between escrt-iii2 and vps4
10	c2v6yA_	Alignment		43.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aaa family atpase, p60 katanin; **PDBTitle:** structure of the mit domain from a s. solfataricus vps4-2 like atpase
11	d1wfda_	Alignment		39.4	11	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain

12	c3zxpC_	Alignment		34.1	13	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**bro1 domain-containing protein brox; **PDBTitle:** structural and functional analyses of the bro1 domain protein brox
13	d2hr2a1	Alignment		32.2	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**CT2138-like
14	c3bu8B_	Alignment		26.9	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**telomeric repeat-binding factor 2; **PDBTitle:** crystal structure of trf2 trfh domain and tin2 peptide2 complex
15	d2crba1	Alignment		26.6	21	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain-like **Family:**MIT domain
16	d1hh8a_	Alignment		26.3	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
17	c2xevB_	Alignment		24.6	22	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
18	d1hxia_	Alignment		21.8	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
19	c1xofA_	Alignment		21.2	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**bbahett1; **PDBTitle:** heterooligomeric beta beta alpha miniprotein
20	d2gy9t1	Alignment		20.3	18	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
21	d2c2la1	Alignment	not modelled	17.7	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
22	c3r9mA_	Alignment	not modelled	17.5	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bro1 domain-containing protein brox; **PDBTitle:** crystal structure of the brox bro1 domain
23	c2avpA_	Alignment	not modelled	17.2	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
24	d2uubt1	Alignment	not modelled	17.1	21	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
25	d1elwa_	Alignment	not modelled	16.1	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
26	c2xcbA_	Alignment	not modelled	14.1	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**regulatory protein pcrh; **PDBTitle:** crystal structure of pcrh in complex with the chaperone2 binding region of popd
27	c2hyzA_	Alignment	not modelled	14.0	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form)
28	c1na3A_	Alignment	not modelled	13.7	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
						Fold:alpha-alpha superhelix

29	d2buga1	Alignment	not modelled	13.4	26	**Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
30	c2j7aE_	Alignment	not modelled	13.2	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c nitrite reductase nrfa; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
31	c1sfcJ_	Alignment	not modelled	12.6	12	**PDB header:**transport protein **Chain:** J: **PDB Molecule:**protein (syntaxin 1a); **PDBTitle:** neuronal synaptic fusion complex
32	d1qhla_	Alignment	not modelled	12.4	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
33	c2ae3A_	Alignment	not modelled	12.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
34	c2c2lD_	Alignment	not modelled	12.1	17	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
35	c2q00B_	Alignment	not modelled	12.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**orf c02003 protein; **PDBTitle:** crystal structure of the p95883_sulso protein from2 sulfolobus solfataricus. nesg target ssr10.
36	d1tjca_	Alignment	not modelled	11.9	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
37	c3dzaB_	Alignment	not modelled	11.8	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized putative membrane protein; **PDBTitle:** crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
38	d1wiva_	Alignment	not modelled	11.5	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
39	c2vyiA_	Alignment	not modelled	11.4	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sgta protein; **PDBTitle:** crystal structure of the tpr domain of human sgt
40	c3sz7A_	Alignment	not modelled	11.1	11	**PDB header:**chaperone regulator **Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt); **PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus
41	d1ndba2	Alignment	not modelled	10.9	17	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
42	c3ipdB_	Alignment	not modelled	10.6	15	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
43	c1gk9A_	Alignment	not modelled	10.6	37	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin g acylase alpha subunit; **PDBTitle:** crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
44	d2pqrb1	Alignment	not modelled	10.4	29	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
45	c3ct5A_	Alignment	not modelled	10.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
46	c3oxgA_	Alignment	not modelled	9.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3; **PDBTitle:** human lysine methyltransferase smyd3 in complex with adohcy (form iii)
47	c3q49B_	Alignment	not modelled	9.6	14	**PDB header:**ligase/chaperone **Chain:** B: **PDB Molecule:**stip1 homology and u box-containing protein 1; **PDBTitle:** crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
48	c1ajnA_	Alignment	not modelled	9.3	37	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** penicillin acylase complexed with p-nitrophenylacetic acid
49	c2npsB_	Alignment	not modelled	9.3	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 13; **PDBTitle:** crystal structure of the early endosomal snare complex
50	d1xl7a2	Alignment	not modelled	9.2	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
51	c1cp9A_	Alignment	not modelled	8.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** crystal structure of penicillin g acylase from the bro12 mutant strain of providencia rettgeri
52	c3k3wA_	Alignment	not modelled	8.6	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin g acylase; **PDBTitle:** thermostable penicillin g acylase from alcaligence faecalis2 in orthorhombic form
53	d1a17a_	Alignment	not modelled	8.5	26	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
						PDB header:structural genomics, unknown function

54	c2kckA_	Alignment	not modelled	8.3	7	**Chain:** A: **PDB Molecule:**tpr repeat; **PDBTitle:** nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
55	d2joka1	Alignment	not modelled	8.2	23	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
56	c2if4A_	Alignment	not modelled	8.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
57	d1xb2b1	Alignment	not modelled	7.9	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
58	c2vr0A_	Alignment	not modelled	7.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase, catalytic subunit nfra; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex bound to the hqno inhibitor
59	c3qkyA_	Alignment	not modelled	7.4	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
60	c3ceqB_	Alignment	not modelled	7.4	19	**PDB header:**motor protein, transport protein **Chain:** B: **PDB Molecule:**kinesin light chain 2; **PDBTitle:** the tpr domain of human kinesin light chain 2 (hklc2)
61	d2choa1	Alignment	not modelled	7.3	7	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
62	c1n7sB_	Alignment	not modelled	7.2	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 1a; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
63	d2bcgg2	Alignment	not modelled	7.1	0	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
64	c2r5sB_	Alignment	not modelled	7.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp0806; **PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
65	c3b5nF_	Alignment	not modelled	7.0	13	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**protein sso1; **PDBTitle:** structure of the yeast plasma membrane snare complex
66	d1aipc1	Alignment	not modelled	6.9	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
67	c2wybA_	Alignment	not modelled	6.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
68	d2cbia1	Alignment	not modelled	6.6	14	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
69	d1p5qa1	Alignment	not modelled	6.4	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
70	c1kt0A_	Alignment	not modelled	6.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**51 kda fk506-binding protein; **PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
71	c2r0bA_	Alignment	not modelled	6.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
72	c3rauB_	Alignment	not modelled	6.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 23; **PDBTitle:** crystal structure of the hd-ptp bro1 domain
73	d1vh6a_	Alignment	not modelled	5.9	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
74	c1vh6A_	Alignment	not modelled	5.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of a flagellar protein
75	d1iqpa1	Alignment	not modelled	5.7	17	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
76	d2ivxa2	Alignment	not modelled	5.7	37	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
77	c1ii8A_	Alignment	not modelled	5.6	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
78	c1efuB_	Alignment	not modelled	5.6	30	**PDB header:**complex (two elongation factors) **Chain:** B: **PDB Molecule:**elongation factor ts; **PDBTitle:** elongation factor complex ef-tu/ef-ts from escherichia coli
79	d3blhb1	Alignment	not modelled	5.6	42	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
						Fold: Four-helical up-and-down bundle

80	d256ba_	Alignment	not modelled	5.5	29	**Superfamily:**Cytochromes **Family:**Cytochrome b562
81	c3kvhA_	Alignment	not modelled	5.4	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
82	d2cp9a1	Alignment	not modelled	5.4	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
83	c1xexA_	Alignment	not modelled	5.4	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
84	c1ycsB_	Alignment	not modelled	5.3	16	**PDB header:**complex (anti-oncogene/ankyrin repeats) **Chain:** B: **PDB Molecule:**53bp2; **PDBTitle:** p53-53bp2 complex
85	d2idga1	Alignment	not modelled	5.2	10	**Fold:**TorD-like **Superfamily:**TorD-like **Family:**TorD-like
86	c2oudA_	Alignment	not modelled	5.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
87	c2kc7A_	Alignment	not modelled	5.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bfr218_protein; **PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
88	c3gyzB_	Alignment	not modelled	5.1	14	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri