Phyre2

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Description	P32690
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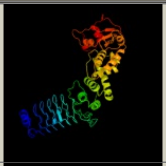
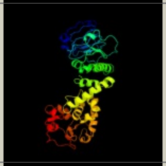
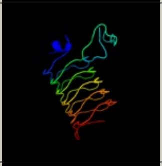
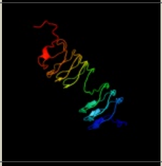
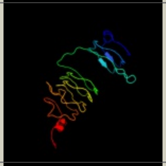
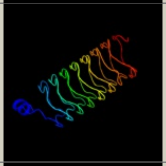
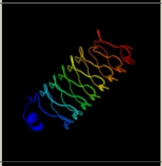
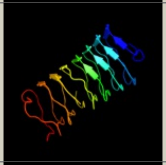
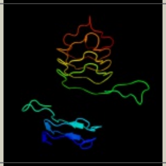
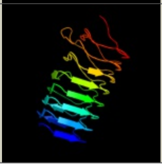
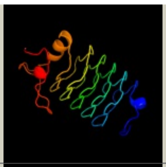
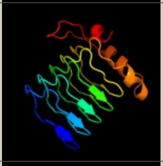
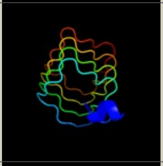
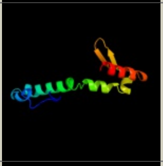
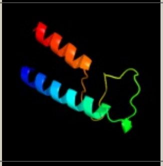
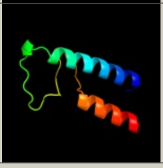
Unique Job ID	1553516dc34a8b86

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nb2B_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nlel
2	c2qzaA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of salmonella effector protein sopa
3	c3du1X_	Alignment		99.9	13	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**all3740 protein; **PDBTitle:** the 2.0 angstrom resolution crystal structure of hetl, a pentapeptide2 repeat protein involved in heterocyst differentiation regulation from3 the cyanobacterium nostoc sp. strain pcc 7120
4	c2o6wA_	Alignment		99.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**repeat five residue (rfr) protein or **PDBTitle:** crystal structure of a pentapeptide repeat protein (rfr23)2 from the cyanobacterium cyanothece 51142
5	c2xt4B_	Alignment		99.9	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
6	c3pssB_	Alignment		99.9	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnr; **PDBTitle:** crystal structure of ahqnr, the qnr protein from aeromonas hydrophila2 (p21 crystal form)
7	d2j8ka1	Alignment		99.9	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
8	c2j8kA_	Alignment		99.9	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**np275-np276; **PDBTitle:** structure of the fusion of np275 and np276, pentapeptide2 repeat proteins from nostoc punctiforme
9	c2w7zB_	Alignment		99.8	16	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**pentapeptide repeat family protein; **PDBTitle:** structure of the pentapeptide repeat protein efsqnr, a dna2 gyrase inhibitor. free amines modified by cyclic3 pentylation with glutaraldehyde.
10	c2xtwB_	Alignment		99.8	15	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnrb1; **PDBTitle:** structure of qnrb1 (full length), a plasmid-mediated2 fluoroquinolone resistance protein
11	c2xt4A_	Alignment		99.8	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.

12	c3n90A_	Alignment		99.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thylakoid lumenal 15 kda protein 1, chloroplastic; **PDBTitle:** the 1.7 angstrom resolution crystal structure of at2g44920, a2 pentapeptide repeat protein from arabidopsis thaliana thylakoid3 lumen.
13	c2g0yA_	Alignment		99.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pentapeptide repeat protein; **PDBTitle:** crystal structure of a lumenal pentapeptide repeat protein from2 cyanothece sp 51142 at 2.3 angstrom resolution. tetragonal crystal3 form
14	d2bm5a1	Alignment		99.8	9	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
15	d2f3la1	Alignment		99.8	11	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
16	c2j8iB_	Alignment		99.8	15	**PDB header:**toxin **Chain:** B: **PDB Molecule:**np275; **PDBTitle:** structure of np275, a pentapeptide repeat protein from2 nostoc punctiforme
17	d2j8ia1	Alignment		99.5	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
18	c3etvA_	Alignment		78.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein tip20,linker,protein **PDBTitle:** crystal structure of a tip20p-dsl1p fusion protein
19	d3buxb2	Alignment		52.8	13	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
20	c3bunB_	Alignment		47.1	13	**PDB header:**ligase/signaling protein **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase cbl; **PDBTitle:** crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
21	c2cblA_	Alignment	not modelled	42.8	13	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
22	d1td6a_	Alignment	not modelled	39.9	16	**Fold:**Hypothetical protein MPN330 **Superfamily:**Hypothetical protein MPN330 **Family:**Hypothetical protein MPN330
23	d1h8ba_	Alignment	not modelled	37.4	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
24	c3ddrC_	Alignment	not modelled	36.0	11	**PDB header:**membrane protein/heme binding protein **Chain:** C: **PDB Molecule:**hemophore hasa; **PDBTitle:** structure of the serratia marcescens hemophore receptor hasr-ile671gly2 mutant in complex with its hemophore hasa and heme
25	c1fbvA_	Alignment	not modelled	35.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
26	d1dlya_	Alignment	not modelled	33.4	22	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
27	c1dlyA_	Alignment	not modelled	33.4	22	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
28	d1idra_	Alignment	not modelled	30.7	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin

29	c2kscA_	Alignment	not modelled	28.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
30	d1dk0a_	Alignment	not modelled	26.9	12	**Fold:**Heme-binding protein A (HasA) **Superfamily:**Heme-binding protein A (HasA) **Family:**Heme-binding protein A (HasA)
31	c3aq8A_	Alignment	not modelled	25.6	26	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
32	d1s69a_	Alignment	not modelled	23.4	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
33	d1m8na_	Alignment	not modelled	23.3	11	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**An insect antifreeze protein **Family:**An insect antifreeze protein
34	d1dlwa_	Alignment	not modelled	21.5	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
35	d1ngka_	Alignment	not modelled	20.6	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
36	c3op0B_	Alignment	not modelled	17.2	8	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
37	c1z9eA_	Alignment	not modelled	16.0	11	**PDB header:**protein binding/transcription **Chain:** A: **PDB Molecule:**pc4 and sfrs1 interacting protein 2; **PDBTitle:** solution structure of the hiv-1 integrase-binding domain in2 ledgf/p75
38	d1ogmx2	Alignment	not modelled	15.1	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Dextranase, catalytic domain
39	d2b4jc1	Alignment	not modelled	15.0	11	**Fold:**N-cbl like **Superfamily:**HIV integrase-binding domain **Family:**HIV integrase-binding domain
40	d1fqia_	Alignment	not modelled	14.1	14	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
41	c2crpA_	Alignment	not modelled	12.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 5; **PDBTitle:** solution structure of the rgs domain of regulator of g-2 protein signalling 5 (rgs 5)
42	c2p90B_	Alignment	not modelled	11.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
43	d1ko7a1	Alignment	not modelled	11.5	20	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
44	c2bmmA_	Alignment	not modelled	11.3	9	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
45	c2gtpD_	Alignment	not modelled	10.4	19	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**regulator of g-protein signaling 1; **PDBTitle:** crystal structure of the heterodimeric complex of human rgs1 and2 activated gi alpha 1
46	c2pbiA_	Alignment	not modelled	10.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 9; **PDBTitle:** the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
47	c2d9jA_	Alignment	not modelled	8.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signalling 7; **PDBTitle:** solution structure of the rgs domain of regulator of g-2 protein signaling 7
48	c1d0rA_	Alignment	not modelled	8.7	0	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
49	d3buxb3	Alignment	not modelled	8.2	17	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
50	d1jg5a_	Alignment	not modelled	7.6	31	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
51	c2xykB_	Alignment	not modelled	7.1	11	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**2-on-2 hemoglobin; **PDBTitle:** group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens
52	d2etda1	Alignment	not modelled	6.3	24	**Fold:**Bromodomain-like **Superfamily:**LemA-like **Family:**LemA-like
53	c2af0A_	Alignment	not modelled	6.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 2; **PDBTitle:** structure of the regulator of g-protein signaling domain of2 rgs2
54	d7pcka_	Alignment	not modelled	6.1	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
						PDB header:hormone/growth factor

55	c1jrjA_	Alignment	not modelled	5.8	6	**Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
56	c2ebzA_	Alignment	not modelled	5.6	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 12; **PDBTitle:** solution structure of the rgs domain from human regulator2 of g-protein signaling 12 (rgs12)