Phyre2

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Description	P41066
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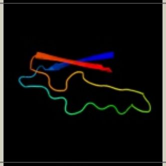
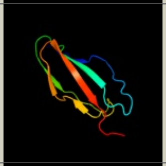
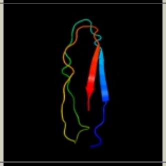
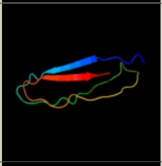
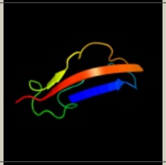
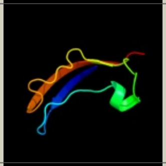
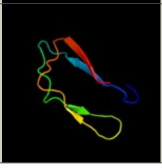
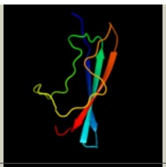
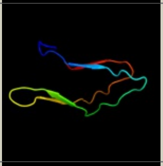
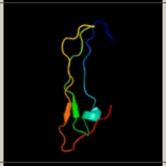
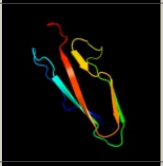
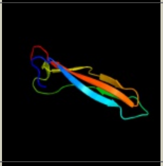
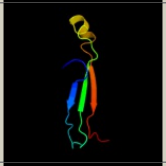
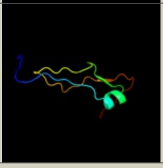
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cfuA_	Alignment		82.1	11	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
2	c2qsvA_	Alignment		61.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
3	d1l4ia1	Alignment		58.3	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
4	d3bwuc1	Alignment		55.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
5	d1p5va1	Alignment		46.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
6	c3jt0B_	Alignment		41.5	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
7	c1so9A_	Alignment		39.6	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cytochrome c oxidase assembly protein ctag; **PDBTitle:** solution structure of apocox11, 30 structures
8	d1so9a_	Alignment		39.6	15	**Fold:**Ctag/Cox11 **Superfamily:**Ctag/Cox11 **Family:**Ctag/Cox11
9	c1yewI_	Alignment		27.5	23	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
10	c3rgbA_	Alignment		27.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
11	c2lllA_	Alignment		25.9	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a

12	d2vzsa2	Alignment		23.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
13	d1ifra_	Alignment		22.9	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
14	c1z9sA_	Alignment		22.5	13	**PDB header:**chaperone/immune system **Chain:** A: **PDB Molecule:**chaperone protein caf1m; **PDBTitle:** crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
15	d2bsya2	Alignment		21.5	10	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
16	c1l4iA_	Alignment		18.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
17	d2j2za1	Alignment		16.7	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
18	c2h6oA_	Alignment		14.5	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer envelope glycoprotein gp350; **PDBTitle:** epstein barr virus major envelope glycoprotein
19	d1ivta_	Alignment		13.6	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
20	d1vyqa1	Alignment		13.4	8	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
21	d2co7b1	Alignment	not modelled	13.2	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
22	c2qlpC_	Alignment	not modelled	13.2	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase:dutpase from mycobacterium tuberculosis,2 apo form
23	c2l0dA_	Alignment	not modelled	12.3	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell surface protein; **PDBTitle:** solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
24	d1rwha2	Alignment	not modelled	11.9	12	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
25	c2k9uA_	Alignment	not modelled	10.8	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**gamma filamin; **PDBTitle:** solution nmr structure of the filamin-migfilin complex
26	c2bt1A_	Alignment	not modelled	10.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** epstein barr virus dutpase in complex with a,b-imino dutp
27	d1bqka_	Alignment	not modelled	9.4	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
28	c3qbtH_	Alignment	not modelled	8.8	10	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with

						rab8a:gppnhp
29	d1ufga_	Alignment	not modelled	8.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
30	c4a19Q_	Alignment	not modelled	8.7	25	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l36; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
31	c3lnnB_	Alignment	not modelled	7.9	17	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
32	d1e42a1	Alignment	not modelled	7.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
33	c2hjjA_	Alignment	not modelled	7.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ykff; **PDBTitle:** solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
34	d2hjja1	Alignment	not modelled	7.7	19	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YkfF-like
35	d1euwa_	Alignment	not modelled	7.7	9	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
36	c2qxxA_	Alignment	not modelled	7.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxycytidine triphosphate deaminase; **PDBTitle:** bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
37	c3mbqC_	Alignment	not modelled	7.5	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of deoxyuridine 5-triphosphate nucleotidohydrolase2 from brucella melitensis, orthorhombic crystal form
38	c3f6iB_	Alignment	not modelled	7.4	7	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein faee; **PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee
39	d1t4wa_	Alignment	not modelled	7.3	9	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
40	c3rfrI_	Alignment	not modelled	7.2	25	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
41	c1pzdA_	Alignment	not modelled	7.1	16	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** structural identification of a conserved appendage domain2 in the carboxyl-terminus of the copi gamma-subunit.
42	c2oxgD_	Alignment	not modelled	7.1	6	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**soxy protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
43	c2p9oB_	Alignment	not modelled	7.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dutp pyrophosphatase-like protein; **PDBTitle:** structure of dutpase from arabidopsis thaliana
44	d1rnja_	Alignment	not modelled	7.0	9	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
45	d1w8oa1	Alignment	not modelled	6.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	c3q48B_	Alignment	not modelled	6.9	5	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
47	d1v05a_	Alignment	not modelled	6.9	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
48	c3ca9A_	Alignment	not modelled	6.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase
49	d1hn0a3	Alignment	not modelled	6.4	14	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
50	c3tqzA_	Alignment	not modelled	6.3	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
51	c2brqA_	Alignment	not modelled	6.3	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
52	c2w0pB_	Alignment	not modelled	6.3	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
53	c3iswB_	Alignment	not modelled	6.3	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
						PDB header:structural genomics, unknown function

54	c2e6jA_	Alignment	not modelled	6.1	11	**Chain:** A: **PDB Molecule:**hydin protein; **PDBTitle:** solution structure of the c-terminal papd-like domain from2 human hydin protein
55	d1xs1a_	Alignment	not modelled	6.0	19	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
56	d1sjna_	Alignment	not modelled	5.9	17	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
57	c2brqB_	Alignment	not modelled	5.9	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
58	d1q5uz_	Alignment	not modelled	5.8	20	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
59	c3ef4A_	Alignment	not modelled	5.6	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**blue copper protein; **PDBTitle:** crystal structure of native pseudoazurin from2 hyphomicrobium denitrificans
60	c1qunA_	Alignment	not modelled	5.5	14	**PDB header:**chaperone/structural protein **Chain:** A: **PDB Molecule:**papd-like chaperone fimc; **PDBTitle:** x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli
61	c1pyuD_	Alignment	not modelled	5.5	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
62	c3sojA_	Alignment	not modelled	5.3	38	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pile; **PDBTitle:** francisella tularensis pilin pile
63	c3fppB_	Alignment	not modelled	5.3	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
64	d1x1ia2	Alignment	not modelled	5.2	15	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
65	c1x1jA_	Alignment	not modelled	5.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xanthan lyase; **PDBTitle:** crystal structure of xanthan lyase (n194a) with a substrate.