Phyre2

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Description	P76214
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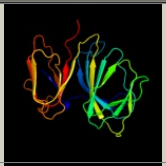
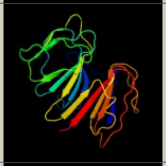
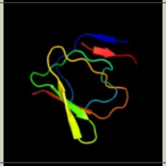
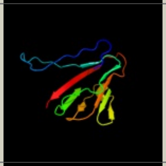
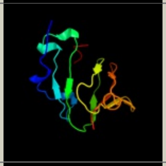
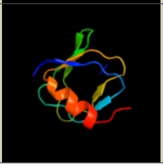
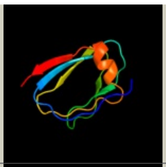
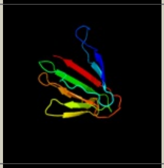
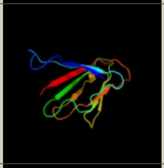
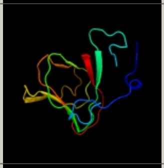
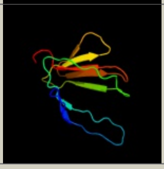
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3esgA_	Alignment		100.0	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hutd from pseudomonas fluorescens sbw25
2	d1ylla1	Alignment		100.0	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**PA5104-like
3	d1vj2a_	Alignment		95.2	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
4	d1y9qa2	Alignment		94.4	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
5	c3bcwB_	Alignment		93.7	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
6	d1sq4a_	Alignment		93.1	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
7	d2pyta1	Alignment		92.2	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
8	c3rnsA_	Alignment		91.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** cupin 2 conserved barrel domain protein from leptotrichia buccalis
9	d1tq5a1	Alignment		91.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
10	c1y9qA_	Alignment		91.2	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
11	d1o5ua_	Alignment		90.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112

12	c3es4B_	Alignment		89.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
13	d1sefa_	Alignment		87.1	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
14	c1sefA_	Alignment		87.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
15	c3lwcA_	Alignment		87.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
16	c3es1A_	Alignment		85.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
17	c3ht2A_	Alignment		80.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
18	d1yhfa1	Alignment		76.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
19	c3myxA_	Alignment		76.5	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
20	c2bnoA_	Alignment		74.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
21	d1y3ta1	Alignment	not modelled	74.4	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
22	d1rc6a_	Alignment	not modelled	71.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
23	c2i45C_	Alignment	not modelled	64.8	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
24	d2f4pa1	Alignment	not modelled	63.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
25	c3kgzA_	Alignment	not modelled	56.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
26	d2phla2	Alignment	not modelled	55.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
27	c2pfwB_	Alignment	not modelled	54.4	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
28	c3ibmB_	Alignment	not modelled	53.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila

29	c3h7yA_	Alignment	not modelled	49.6	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
30	c2gu9B_	Alignment	not modelled	48.2	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
31	c3d82A_	Alignment	not modelled	42.9	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
32	d2bnma2	Alignment	not modelled	42.4	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
33	c2o8qA_	Alignment	not modelled	39.5	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
34	d1v70a_	Alignment	not modelled	36.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
35	d1j1la_	Alignment	not modelled	34.9	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
36	c3fjsC_	Alignment	not modelled	31.5	15	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
37	d1dgwa_	Alignment	not modelled	29.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
38	d1sfna_	Alignment	not modelled	28.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
39	d2phla1	Alignment	not modelled	27.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
40	d1o4ta_	Alignment	not modelled	23.8	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
41	c3fljA_	Alignment	not modelled	23.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
42	c3o14B_	Alignment	not modelled	23.2	14	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**anti-ecfsigma factor, chrr; **PDBTitle:** crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
43	c2fqpD_	Alignment	not modelled	20.0	6	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hypothetical protein bp2299; **PDBTitle:** crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
44	c3prdA_	Alignment	not modelled	19.1	14	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
45	c3h1yA_	Alignment	not modelled	17.1	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
46	d1uija1	Alignment	not modelled	16.5	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
47	d1uika1	Alignment	not modelled	16.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	c3cewA_	Alignment	not modelled	16.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
49	c2vqaC_	Alignment	not modelled	16.1	9	**PDB header:**metal-binding protein **Chain:** C: **PDB Molecule:**sll1358 protein; **PDBTitle:** protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
50	c1cauB_	Alignment	not modelled	15.6	18	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
51	d1b7yb4	Alignment	not modelled	15.5	20	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
52			not modelled	15.1	14	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak;

52	c2vecA_	Alignment	not modelled	15.1	14	**PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
53	d1jjcb4	Alignment	not modelled	13.3	20	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
54	c3h8uA_	Alignment	not modelled	12.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
55	c3sf5D_	Alignment	not modelled	10.8	18	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**urease accessory protein ureh; **PDBTitle:** crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
56	d1uija2	Alignment	not modelled	9.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
57	d1juha_	Alignment	not modelled	9.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
58	c3i7dB_	Alignment	not modelled	9.4	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase; **PDBTitle:** crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution
59	c2ozjB_	Alignment	not modelled	9.2	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
60	c3f8xD_	Alignment	not modelled	9.0	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative delta-5-3-ketosteroid isomerase; **PDBTitle:** crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
61	c2kdoA_	Alignment	not modelled	8.9	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ribosome maturation protein sbds; **PDBTitle:** structure of the human shwachman-bodian-diamond syndrome protein, sbds
62	c3ghnA_	Alignment	not modelled	8.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a disintegrin and metalloproteinase with thrombospondin **PDBTitle:** crystal structure of the exosite-containing fragment of human adamts132 (form-2)
63	d1lr5a_	Alignment	not modelled	7.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	c2h6oA_	Alignment	not modelled	7.6	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer envelope glycoprotein gp350; **PDBTitle:** epstein barr virus major envelope glycoprotein
65	c2q30C_	Alignment	not modelled	7.2	8	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
66	d1pmia_	Alignment	not modelled	7.1	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
67	c3pr9A_	Alignment	not modelled	6.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
68	c3l2hD_	Alignment	not modelled	6.8	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative sugar phosphate isomerase; **PDBTitle:** crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
69	c3h0mE_	Alignment	not modelled	6.2	32	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
70	d1uika2	Alignment	not modelled	5.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein