Phyre2

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Description	RVBD3833_(-)_4307045_4307836
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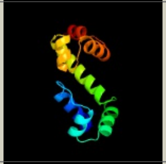
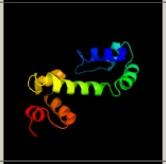
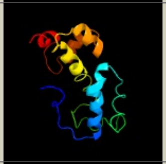
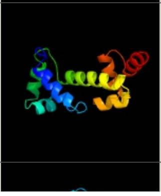
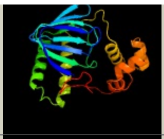
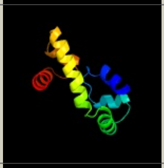
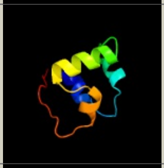
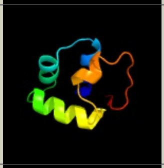
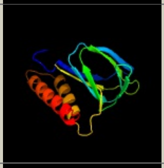
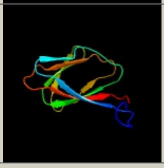
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		100.0	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
2	c1d5yD_	Alignment		99.9	21	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**rob transcription factor; **PDBTitle:** crystal structure of the e. coli rob transcription factor2 in complex with dna
3	c5chhA_	Alignment		99.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arac family transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
4	c3w6vA_	Alignment		99.9	27	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**adpa; **PDBTitle:** crystal structure of the dna-binding domain of adpa, the global2 transcriptional factor, in complex with a target dna
5	c3oioA_	Alignment		99.9	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
6	c3oouA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
7	c2k9sA_	Alignment		99.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
8	c1bl0A_	Alignment		99.9	20	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
9	c3mn2B_	Alignment		99.9	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator; **PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
10	c4fe4C_	Alignment		99.9	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**xylose operon regulatory protein; **PDBTitle:** crystal structure of apo e. coli xylr
11	c3mklB_	Alignment		99.9	26	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12

12	c5nlaA_	Alignment		99.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator transcription regulator **PDBTitle:** crystal structure of the arac-like transcriptional activator cuxr
13	c3lsgD_	Alignment		99.8	23	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
14	d1bl0a2	Alignment		99.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
15	d1d5ya2	Alignment		99.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
16	d1d5ya1	Alignment		99.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
17	c5u9eB_	Alignment		99.1	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional activator rhar; **PDBTitle:** structure of the regulatory domain of the arac family transcriptional2 activator rhar
18	d1bl0a1	Alignment		99.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
19	c6nwoD_	Alignment		99.0	7	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator bgar; **PDBTitle:** structures of the transcriptional regulator bgar, a lactose sensor.
20	c5tg0A_	Alignment		99.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dimethylsulfoniopropionate lyase dddk; **PDBTitle:** crystal structure of the dimethylsulfoniopropionate (dmsp) lyase dddk2 complexed with iron and zinc
21	c3ibmB_	Alignment	not modelled	99.0	19	**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
22	c5j7mB_	Alignment	not modelled	99.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836
23	c5zbfA_	Alignment	not modelled	98.9	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cupin domain protein; **PDBTitle:** crystal structure of 4-hydroxyphenylpyruvic acid bound aere from2 microcystis aeruginosa
24	c1zgwA_	Alignment	not modelled	98.9	31	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
25	c3jzvA_	Alignment	not modelled	98.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
26	c3kgzA_	Alignment	not modelled	98.9	13	**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
27	c3fjsC_	Alignment	not modelled	98.9	17	**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
28	c4rd7A_	Alignment	not modelled	98.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** the crystal structure of a cupin 2 conserved barrel domain protein2 from salinispora arenicola cns-205

29	d2f4pa1	Alignment	not modelled	98.9	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
30	c5j4fB_	Alignment	not modelled	98.9	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
31	d1vj2a_	Alignment	not modelled	98.9	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
32	c4i4aA_	Alignment	not modelled	98.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**similar to unknown protein; **PDBTitle:** crystal structure of plu4264 protein from photorhabdus luminescens
33	c2pfwB_	Alignment	not modelled	98.8	15	**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
34	c5bxxA_	Alignment	not modelled	98.8	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-ectoine synthase; **PDBTitle:** crystal structure of the ectoine synthase from the cold-adapted marine2 bacterium sphingopyxis alaskensis
35	c4e2gE_	Alignment	not modelled	98.8	20	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
36	d1sq4a_	Alignment	not modelled	98.8	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
37	d1y3ta1	Alignment	not modelled	98.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
38	c2ozjB_	Alignment	not modelled	98.8	12	**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
39	d1o4ta_	Alignment	not modelled	98.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
40	c5uqpA_	Alignment	not modelled	98.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cupin; **PDBTitle:** the crystal structure of cupin protein from rhodococcus jostii rha1
41	c3h7yA_	Alignment	not modelled	98.8	15	**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
42	d1sfna_	Alignment	not modelled	98.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
43	c3rnsA_	Alignment	not modelled	98.8	17	**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
44	d1yhfa1	Alignment	not modelled	98.7	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
45	c4la3B_	Alignment	not modelled	98.7	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dimethylsulphoniopropionate (dmsp) lyase dddq; **PDBTitle:** crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
46	c4bifC_	Alignment	not modelled	98.7	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** biochemical and structural characterisation of a novel2 manganese-dependent hydroxynitrile lyase from bacteria
47	d1sefa_	Alignment	not modelled	98.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
48	c1sefA_	Alignment	not modelled	98.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
49	d1y9qa2	Alignment	not modelled	98.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
50	c4e2sE_	Alignment	not modelled	98.7	10	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**ureidoglycine aminohydrolase; **PDBTitle:** crystal structure of (s)-ureidoglycine aminohydrolase from arabidopsis2 thaliana in complex with its substrate, (s)-ureidoglycine
51	c3cewA_	Alignment	not modelled	98.7	15	**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
52	c5onoA_	Alignment	not modelled	98.7	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**l-ectoine synthase; **PDBTitle:** crystal structure of ectoine synthase from p. lautus
53	d1rc6a_	Alignment	not modelled	98.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
54	c5fpzA_	Alignment	not modelled	98.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pectin degradation protein; **PDBTitle:** the structure of kdgf from yersinia enterocolitica with2

						malonate bound in the active site.
55	d2b8ma1	Alignment	not modelled	98.6	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
56	c6b8wB_	Alignment	not modelled	98.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**xre family transcriptional regulator; **PDBTitle:** 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2 07883) of xre family transcriptional regulator from enterobacter3 cloacae.
57	c5fq0A_	Alignment	not modelled	98.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**kdgf; **PDBTitle:** the structure of kdgf from halomonas sp.
58	c2gu9B_	Alignment	not modelled	98.6	22	**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
59	d1lr5a_	Alignment	not modelled	98.6	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
60	c5fljK_	Alignment	not modelled	98.6	18	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**quercetinase qued; **PDBTitle:** enzyme-substrate-dioxygen complex of ni-quercetinase
61	d3bu7a1	Alignment	not modelled	98.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
62	c3bu7A_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure and biochemical characterization of gdosp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi
63	c3ht2A_	Alignment	not modelled	98.6	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
64	c2d40C_	Alignment	not modelled	98.6	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
65	c4b29A_	Alignment	not modelled	98.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dimethylsulfoniopropionate lyase; **PDBTitle:** crystal structures of dmsp lyases rddddp and rndddqii
66	d2d40a1	Alignment	not modelled	98.6	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
67	d1v70a_	Alignment	not modelled	98.6	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
68	d2phda1	Alignment	not modelled	98.6	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
69	c5cu1A_	Alignment	not modelled	98.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dmsp lyase; **PDBTitle:** crystal structure of dmsp lyase dddq from ruegeria pomeroyi dss-3
70	c3i7dB_	Alignment	not modelled	98.5	22	**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
71	c2oa2A_	Alignment	not modelled	98.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
72	c2vpvA_	Alignment	not modelled	98.5	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
73	d2arca_	Alignment	not modelled	98.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
74	c3h8uA_	Alignment	not modelled	98.5	16	**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
75	c3l2hD_	Alignment	not modelled	98.4	16	**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
76	c2o8qA_	Alignment	not modelled	98.4	17	**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
77	c2fqpD_	Alignment	not modelled	98.4	26	**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
78	c2q30C_	Alignment	not modelled	98.4	14	**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
						PDB header:structural genomics, unknown function

79	c2oziA_	Alignment	not modelled	98.3	20	**Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
80	d1juha_	Alignment	not modelled	98.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
81	d1uika1	Alignment	not modelled	98.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
82	c2vqaC_	Alignment	not modelled	98.2	21	**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.
83	d2et1a1	Alignment	not modelled	98.2	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
84	c3d82A_	Alignment	not modelled	98.2	12	**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
85	c5oo9A_	Alignment	not modelled	98.2	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative cupin_2 domain-containing isomerase; **PDBTitle:** streptomyces pac13 (y55f) with uridine
86	c4qglA_	Alignment	not modelled	98.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acireductone dioxygenase; **PDBTitle:** acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
87	d1j58a_	Alignment	not modelled	98.2	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
88	d1dgwa_	Alignment	not modelled	98.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
89	d1yfua1	Alignment	not modelled	98.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
90	d1uika2	Alignment	not modelled	98.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
91	c4axoA_	Alignment	not modelled	98.1	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ethanolamine utilization protein; **PDBTitle:** structure of the clostridium difficile eutq protein
92	c1cauB_	Alignment	not modelled	98.1	15	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
93	d1uija1	Alignment	not modelled	98.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
94	c3lwcA_	Alignment	not modelled	98.1	15	**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
95	c2i45C_	Alignment	not modelled	98.1	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
96	c6b9rD_	Alignment	not modelled	98.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**hydroxyethylphosphonate dioxygenase; **PDBTitle:** streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
97	d2phla2	Alignment	not modelled	98.0	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
98	c4h7lB_	Alignment	not modelled	98.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of plim_4148 protein from planctomyces limnophilus
99	d1fxza1	Alignment	not modelled	98.0	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
100	d1zrra1	Alignment	not modelled	98.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
101	c3es1A_	Alignment	not modelled	97.9	13	**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
102	c4p9gA_	Alignment	not modelled	97.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4'-dihydroxyacetophenone dioxygenase; **PDBTitle:** structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
103	d2bnma2	Alignment	not modelled	97.9	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
104	c5u57B_	Alignment	not modelled	97.9	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**(s)-2-hydroxypropylphosphonic acid epoxidase; **PDBTitle:** psf4 in complex with fe2+ and (s)-2-hpp
						Fold: Double-stranded beta-helix

105	d1uija2	Alignment	not modelled	97.8	13	**Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
106	d1zvfa1	Alignment	not modelled	97.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
107	d1fxza2	Alignment	not modelled	97.8	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
108	c5e1rC_	Alignment	not modelled	97.8	14	**PDB header:**allergen **Chain:** C: **PDB Molecule:**7s vicilin; **PDBTitle:** crystal structure of pecan (carya illinoinensis) vicilin, a new food2 allergen
109	c3ebrA_	Alignment	not modelled	97.8	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
110	d1od5a2	Alignment	not modelled	97.8	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
111	c3bcwB_	Alignment	not modelled	97.8	9	**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
112	d1od5a1	Alignment	not modelled	97.8	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
113	d1j3pa_	Alignment	not modelled	97.7	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
114	d1x82a_	Alignment	not modelled	97.7	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
115	c1fxzC_	Alignment	not modelled	97.6	19	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
116	c3kglB_	Alignment	not modelled	97.6	11	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from brassica napus
117	c1y9qA_	Alignment	not modelled	97.5	11	**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
118	c2cauA_	Alignment	not modelled	97.5	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
119	c5yjsB_	Alignment	not modelled	97.5	15	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**vicilin-like antimicrobial peptides 2-2; **PDBTitle:** structure of vicilin from capsicum annuum
120	c3kscD_	Alignment	not modelled	97.5	19	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.