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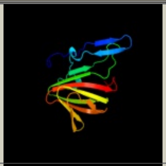
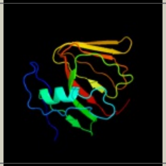
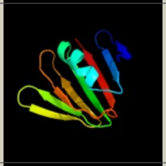
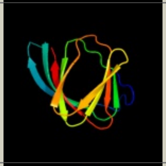
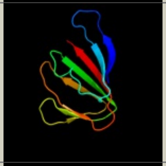
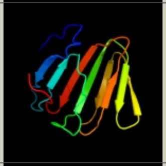
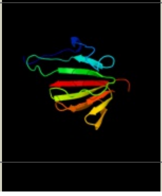
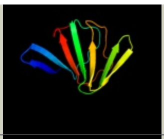
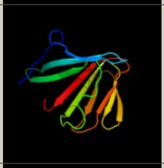
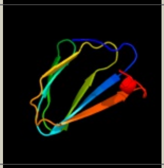
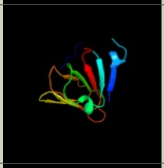
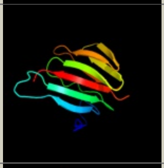
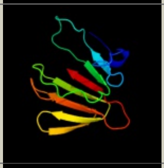
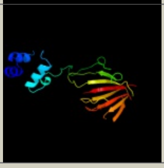
Description	P76555
Date	Thu Jan 5 12:24:33 GMT 2012
Unique Job ID	21e79aa7a1ba43c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pyta1	Alignment		100.0	87	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
2	c3myxA_	Alignment		99.9	15	**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
3	d1o5ua_	Alignment		99.7	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
4	c3lwcA_	Alignment		99.7	24	**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
5	c3bcwB_	Alignment		99.7	22	**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	c3es4B_	Alignment		99.6	18	**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
7	d1vj2a_	Alignment		99.3	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
8	c2vpvA_	Alignment		99.3	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
9	d1y3ta1	Alignment		99.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
10	c2gu9B_	Alignment		99.2	18	**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
11	d2bnma2	Alignment		99.2	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like

12	c2o8qA_	Alignment		99.2	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
13	c2pfwB_	Alignment		99.2	18	**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
14	c3jzvA_	Alignment		99.2	13	**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.
15	d1juha_	Alignment		99.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
16	d1y9qa2	Alignment		99.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
17	c3ht2A_	Alignment		99.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
18	c3ibmB_	Alignment		99.1	14	**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
19	c3kgzA_	Alignment		99.1	15	**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
20	d1sfna_	Alignment		99.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
21	c2bnoA_	Alignment		99.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
22	d1o4ta_	Alignment	not modelled	99.1	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
23	c2ozjB_	Alignment	not modelled	99.1	14	**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
24	c3i7dB_	Alignment	not modelled	99.1	23	**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
25	d2b8ma1	Alignment	not modelled	99.0	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
26	d1sq4a_	Alignment	not modelled	99.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
27	d2f4pa1	Alignment	not modelled	99.0	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like

28	d1sefa_	Alignment	not modelled	99.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
29	c1sefA_	Alignment	not modelled	99.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
30	d1rc6a_	Alignment	not modelled	99.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
31	c3cewA_	Alignment	not modelled	99.0	16	**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
32	c3l2hD_	Alignment	not modelled	99.0	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
33	c2i45C_	Alignment	not modelled	99.0	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
34	c3h8uA_	Alignment	not modelled	99.0	17	**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
35	d1v70a_	Alignment	not modelled	99.0	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
36	c1y9qA_	Alignment	not modelled	99.0	15	**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
37	c2oa2A_	Alignment	not modelled	99.0	16	**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
38	c3fjsC_	Alignment	not modelled	99.0	13	**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
39	d1dgwa_	Alignment	not modelled	98.9	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
40	c2q30C_	Alignment	not modelled	98.9	19	**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
41	c3d82A_	Alignment	not modelled	98.9	22	**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
42	d1uika1	Alignment	not modelled	98.9	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
43	d1yhfa1	Alignment	not modelled	98.9	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
44	c2d40C_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
45	d2phda1	Alignment	not modelled	98.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
46	d1lr5a_	Alignment	not modelled	98.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
47	d1uija1	Alignment	not modelled	98.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	d2d40a1	Alignment	not modelled	98.8	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
49	c3h7yA_	Alignment	not modelled	98.8	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
50	d1x82a_	Alignment	not modelled	98.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
51	d1j3pa_	Alignment	not modelled	98.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
52	c3rnsA_	Alignment	not modelled	98.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein;

52	[illegible]	Alignment	not modelled	98.7	18	**PDBTitle:** cupin 2 conserved barrel domain protein from leptotrichia buccalis
53	c2vqaC_	Alignment	not modelled	98.7	26	**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.
54	d3bu7a1	Alignment	not modelled	98.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
55	c3bu7A_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure and biochemical characterization of gdosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
56	c3es1A_	Alignment	not modelled	98.6	21	**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
57	d1j58a_	Alignment	not modelled	98.5	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
58	d1fxza1	Alignment	not modelled	98.5	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
59	c2xlfA_	Alignment	not modelled	98.5	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
60	d1yfua1	Alignment	not modelled	98.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
61	c1cauB_	Alignment	not modelled	98.5	26	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
62	c2fqpD_	Alignment	not modelled	98.4	14	**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
63	c2cauA_	Alignment	not modelled	98.4	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
64	d2et1a1	Alignment	not modelled	98.4	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
65	d2phla2	Alignment	not modelled	98.4	30	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
66	c2eaaB_	Alignment	not modelled	98.4	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
67	d1uika2	Alignment	not modelled	98.4	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
68	d1zvfa1	Alignment	not modelled	98.4	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
69	c1fxzC_	Alignment	not modelled	98.4	13	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
70	d1uija2	Alignment	not modelled	98.4	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
71	c3s7eB_	Alignment	not modelled	98.4	13	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
72	c1uijA_	Alignment	not modelled	98.3	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
73	c3kglB_	Alignment	not modelled	98.3	16	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
74	c2oziA_	Alignment	not modelled	98.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
75	c3kscD_	Alignment	not modelled	98.3	13	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
76	d1fxza2	Alignment	not modelled	98.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
77	d1zrra1	Alignment	not modelled	98.2	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
78	d2phla1	Alignment	not modelled	98.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

79	c3ehkC_	Alignment	not modelled	98.2	18	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
80	c2opkC_	Alignment	not modelled	98.2	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
81	c2d5fB_	Alignment	not modelled	98.1	20	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
82	d1od5a2	Alignment	not modelled	98.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
83	d2arca_	Alignment	not modelled	98.0	19	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
84	c3c3vA_	Alignment	not modelled	98.0	14	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
85	d1od5a1	Alignment	not modelled	97.9	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
86	c2e9qA_	Alignment	not modelled	97.7	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
87	c3ebrA_	Alignment	not modelled	97.7	15	**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
88	d1vr3a1	Alignment	not modelled	97.5	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
89	c3o14B_	Alignment	not modelled	97.5	17	**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
90	c3balB_	Alignment	not modelled	97.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetylacetone-cleaving enzyme; **PDBTitle:** crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
91	c2y0oA_	Alignment	not modelled	97.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
92	c3cjxE_	Alignment	not modelled	97.3	13	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**protein of unknown function with a cupin-like fold; **PDBTitle:** crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
93	c1ey2A_	Alignment	not modelled	97.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homogentisate 1,2-dioxygenase; **PDBTitle:** human homogentisate dioxygenase with fe(ii)
94	d1eyba_	Alignment	not modelled	97.3	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Homogentisate dioxygenase
95	d1ywka1	Alignment	not modelled	97.2	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Kdul-like
96	c3hqxA_	Alignment	not modelled	97.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
97	c1ywkE_	Alignment	not modelled	97.1	23	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**4-deoxy-l-threo-5-hexosulose-uronate ketol- **PDBTitle:** crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
98	d1xrua1	Alignment	not modelled	97.1	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Kdul-like
99	d1vrba1	Alignment	not modelled	97.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
100	d2o1qa1	Alignment	not modelled	97.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acetylacetone-cleaving enzyme-like
101	c3h1yA_	Alignment	not modelled	96.8	20	**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)
102	d1pmia_	Alignment	not modelled	96.8	27	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
103	c3mpbA_	Alignment	not modelled	96.5	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
						PDB header:structural genomics, unknown function

104	c3eo6B_	Alignment	not modelled	96.5	23	**Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
105	d1qwra_	Alignment	not modelled	96.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
106	c3d0jA_	Alignment	not modelled	96.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
107	d2oyza1	Alignment	not modelled	96.2	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
108	c2qjvB_	Alignment	not modelled	96.0	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**uncharacterized iolb-like protein; **PDBTitle:** crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
109	d1zx5a1	Alignment	not modelled	95.8	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
110	c3gbgA_	Alignment	not modelled	95.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
111	c2qnkA_	Alignment	not modelled	95.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
112	c2vecA_	Alignment	not modelled	95.4	15	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**pirin-like protein yhak; **PDBTitle:** the crystal structure of the protein yhak from escherichia2 coli
113	c2xdvA_	Alignment	not modelled	94.9	21	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
114	c2zklA_	Alignment	not modelled	94.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
115	c3uyjA_	Alignment	not modelled	94.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
116	d1tq5a1	Alignment	not modelled	93.9	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
117	c3k2oB_	Alignment	not modelled	93.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
118	c3al6A_	Alignment	not modelled	93.4	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
119	d2pa7a1	Alignment	not modelled	93.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
120	c3k3nA_	Alignment	not modelled	93.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phd finger protein 8; **PDBTitle:** crystal structure of the catalytic core domain of human phf8