Phyre²

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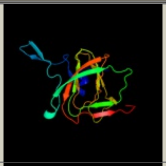
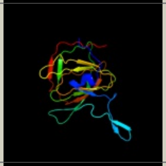
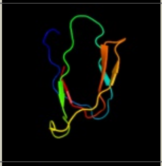
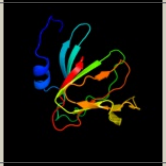
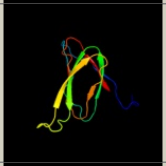
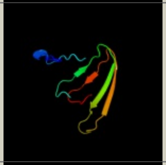
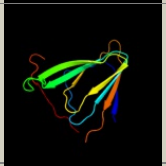
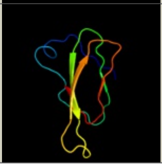
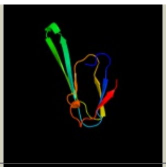
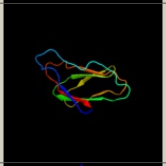
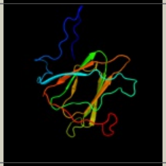
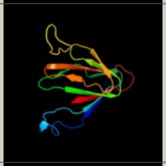
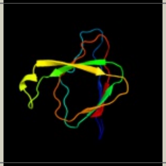
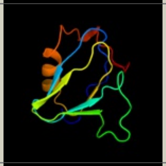
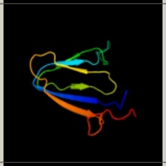
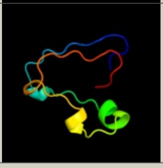
Description	P77731
Date	Thu Jan 5 12:32:12 GMT 2012
Unique Job ID	dd9193e546759fff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bdra1	Alignment		100.0	51	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
2	d1xsqa_	Alignment		100.0	95	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
3	c3d0jA_	Alignment		98.2	18	**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
4	c3mpbA_	Alignment		90.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
5	c2oa2A_	Alignment		89.7	14	**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
6	c3kgzA_	Alignment		88.6	17	**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
7	c3jzvA_	Alignment		88.6	15	**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.
8	d1nxma_	Alignment		88.5	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
9	d2phla2	Alignment		86.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
10	d1zvfa1	Alignment		85.9	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
11	d2pa7a1	Alignment		85.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase

12	c2i45C_	Alignment		85.2	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
13	d1v70a_	Alignment		84.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
14	c3ejkA_	Alignment		81.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dtdp sugar isomerase; **PDBTitle:** crystal structure of dtdp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
15	d1o4ta_	Alignment		78.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
16	c2oziA_	Alignment		76.6	17	**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
17	c2y0oA_	Alignment		73.1	15	**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
18	c3cewA_	Alignment		65.7	13	**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
19	c2gu9B_	Alignment		64.6	14	**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
20	c3d82A_	Alignment		63.8	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
21	c2fqpD_	Alignment	not modelled	61.7	11	**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
22	c2vqaC_	Alignment	not modelled	61.0	12	**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.
23	d2et1a1	Alignment	not modelled	60.4	22	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
24	c3h8uA_	Alignment	not modelled	59.7	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
25	d1juha_	Alignment	not modelled	59.6	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
26	d1ep0a_	Alignment	not modelled	53.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
27	d1wlta1	Alignment	not modelled	49.6	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
						PDB header:metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein;

28	c2o8qA_	Alignment	not modelled	45.7	18	**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
29	c1cauB_	Alignment	not modelled	43.2	12	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
30	d2ixha1	Alignment	not modelled	39.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
31	d2f4pa1	Alignment	not modelled	36.3	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
32	d1vj2a_	Alignment	not modelled	35.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
33	d1j3pa_	Alignment	not modelled	35.5	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
34	c3ibmB_	Alignment	not modelled	35.3	21	**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
35	d2cupa1	Alignment	not modelled	34.8	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
36	d1x82a_	Alignment	not modelled	34.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
37	d1x63a1	Alignment	not modelled	33.6	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	c2c0zA_	Alignment	not modelled	30.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**novw; **PDBTitle:** the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
39	d1rc6a_	Alignment	not modelled	29.0	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
40	c2cauA_	Alignment	not modelled	28.0	11	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
41	d2fcta1	Alignment	not modelled	26.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
42	d1y3ta1	Alignment	not modelled	25.4	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
43	c3l2hD_	Alignment	not modelled	25.2	17	**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
44	d2ixca1	Alignment	not modelled	23.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
45	d1ukwa2	Alignment	not modelled	21.5	21	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
46	c3chxE_	Alignment	not modelled	20.7	16	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
47	d1j58a_	Alignment	not modelled	20.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	d1uija1	Alignment	not modelled	20.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
49	c3rgbA_	Alignment	not modelled	18.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
50	c3rfrI_	Alignment	not modelled	17.9	16	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
51	d1oi6a_	Alignment	not modelled	17.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
52	c3ht2A_	Alignment	not modelled	16.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
53	d1fxza2	Alignment	not modelled	16.3	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
						Fold: Double-stranded beta-helix

54	d1lr5a_	Alignment	not modelled	15.9	12	**Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
55	d2c0za1	Alignment	not modelled	15.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
56	c3rykB_	Alignment	not modelled	14.5	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
57	d1vyqa1	Alignment	not modelled	14.2	38	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
58	c1yewI_	Alignment	not modelled	13.7	29	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
59	c3i7dB_	Alignment	not modelled	12.8	8	**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
60	c1sefA_	Alignment	not modelled	12.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
61	d1sefa_	Alignment	not modelled	12.6	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
62	c3nnlB_	Alignment	not modelled	12.6	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
63	c2xdvA_	Alignment	not modelled	11.8	16	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
64	d2b8ma1	Alignment	not modelled	11.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
65	d1to3a_	Alignment	not modelled	11.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
66	c2xxzA_	Alignment	not modelled	11.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
67	d2jzaa1	Alignment	not modelled	11.3	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
68	d1dgwa_	Alignment	not modelled	10.9	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
69	d1o7na1	Alignment	not modelled	10.9	3	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
70	d1oiha_	Alignment	not modelled	10.9	29	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
71	d2jo6a1	Alignment	not modelled	10.7	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
72	c1upiA_	Alignment	not modelled	10.6	13	**PDB header:**epimerase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** mycobacterium tuberculosis rmlc epimerase (rv3465)
73	d2cupa2	Alignment	not modelled	10.5	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
74	d1vrba1	Alignment	not modelled	10.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
75	d1dzra_	Alignment	not modelled	9.6	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
76	c3fjsC_	Alignment	not modelled	9.6	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
77	d1x4da1	Alignment	not modelled	9.2	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
78	c3h7yA_	Alignment	not modelled	8.7	11	**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
79	c2vpvA_	Alignment	not modelled	8.5	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
						PDB header:cell adhesion

80	c1za4A_	Alignment	not modelled	8.0	19	**Chain:** A: **PDB Molecule:**thrombospondin 1; **PDBTitle:** crystal structure of the thrombospondin-1 n-terminal domain2 in complex with arixtra
81	c3ic3C_	Alignment	not modelled	8.0	35	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative pyruvate dehydrogenase; **PDBTitle:** structure of a putative pyruvate dehydrogenase from the photosynthetic2 bacterium rhodopseudomonas palustrus cga009
82	c2d40C_	Alignment	not modelled	7.8	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
83	c2d9oA_	Alignment	not modelled	7.7	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**dnaj (hsp40) homolog, subfamily c, member 17; **PDBTitle:** solution structure of rna binding domain in hypothetical2 protein flj10634
84	c3es1A_	Alignment	not modelled	7.7	16	**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
85	d1uika2	Alignment	not modelled	7.7	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
86	d2erfa1	Alignment	not modelled	7.1	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Laminin G-like module
87	d1yfua1	Alignment	not modelled	7.0	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
88	c3ctrA_	Alignment	not modelled	7.0	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of the rrm-domain of the poly(a)-specific2 ribonuclease parn bound to m7gtp
89	d2d8za1	Alignment	not modelled	6.9	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
90	d1sq4a_	Alignment	not modelled	6.9	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
91	c3rnsA_	Alignment	not modelled	6.5	10	**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
92	d1txka1	Alignment	not modelled	6.4	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
93	c3bu7A_	Alignment	not modelled	6.4	19	**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
94	d3bu7a1	Alignment	not modelled	6.4	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
95	d2cura2	Alignment	not modelled	6.0	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
96	d3ehwa1	Alignment	not modelled	6.0	31	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
97	c2pfwB_	Alignment	not modelled	6.0	14	**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
98	d1ei5a2	Alignment	not modelled	5.9	13	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
99	d1zrra1	Alignment	not modelled	5.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase