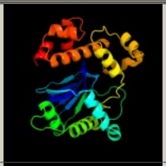
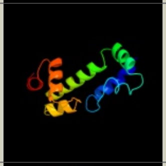
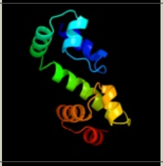
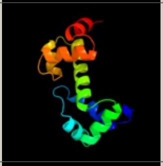
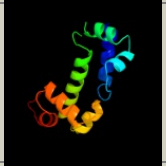
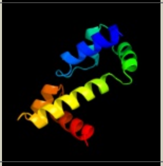
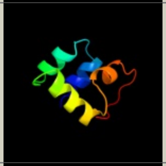
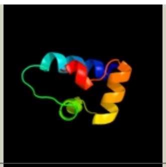
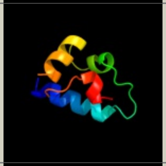
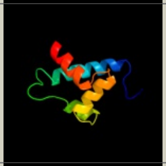
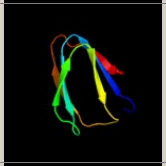
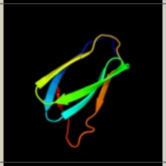
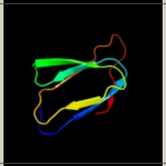
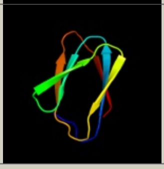
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P33234
Date	Thu Jan 5 11:51:34 GMT 2012
Unique Job ID	9c1e40ebccdad6aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		100.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
2	c3mklB_	Alignment		99.9	44	**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
3	c1d5yD_	Alignment		99.9	17	**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
4	c3oouA_	Alignment		99.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
5	c3oioA_	Alignment		99.9	20	**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	c1bl0A_	Alignment		99.9	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
7	c3mn2B_	Alignment		99.9	18	**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
8	c2k9sA_	Alignment		99.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
9	c3lsgD_	Alignment		99.8	22	**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
10	d1d5ya2	Alignment		99.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1bl0a2	Alignment		99.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	d1d5ya1	Alignment		98.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
13	d1bl0a1	Alignment		98.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	c1zgwA_	Alignment		98.7	15	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
15	d2arca_	Alignment		97.0	7	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
16	c2o8qA_	Alignment		96.8	11	**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
17	d2b8ma1	Alignment		96.6	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
18	c3kgzA_	Alignment		96.4	7	**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
19	c3ibmB_	Alignment		96.4	5	**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
20	c3fjsC_	Alignment		96.4	16	**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
21	d1vj2a_	Alignment	not modelled	96.3	0	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
22	c3cewA_	Alignment	not modelled	96.2	11	**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
23	c2vpvA_	Alignment	not modelled	96.2	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
24	d2f4pa1	Alignment	not modelled	96.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
25	c2i45C_	Alignment	not modelled	96.2	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
26	c2pfwB_	Alignment	not modelled	96.2	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
27	c3jzvA_	Alignment	not modelled	96.1	7	**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.
28	c3rnsA_	Alignment	not modelled	96.1	15	**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
29	d1y9qa2	Alignment	not modelled	96.1	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
30	c2q30C_	Alignment	not modelled	96.1	7	**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
31	d1yfua1	Alignment	not modelled	96.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
32	c3h7yA_	Alignment	not modelled	96.0	6	**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
33	c2d40C_	Alignment	not modelled	95.9	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
34	d1o4ta_	Alignment	not modelled	95.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
35	d2phda1	Alignment	not modelled	95.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
36	c2ozjB_	Alignment	not modelled	95.8	7	**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
37	c3h8uA_	Alignment	not modelled	95.8	10	**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
38	c2gu9B_	Alignment	not modelled	95.8	8	**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
39	c2opkC_	Alignment	not modelled	95.8	13	**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
40	d1y3ta1	Alignment	not modelled	95.8	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
41	d1yhfa1	Alignment	not modelled	95.7	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
42	d1juha_	Alignment	not modelled	95.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
43	d1x82a_	Alignment	not modelled	95.7	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
44	d2bnma2	Alignment	not modelled	95.6	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
45	c3lwcA_	Alignment	not modelled	95.6	10	**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
46	d1o5ua_	Alignment	not modelled	95.6	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
47	d1j3pa_	Alignment	not modelled	95.5	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
48	d2d40a1	Alignment	not modelled	95.5	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
49	d1v70a_	Alignment	not modelled	95.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
50	d1sfna_	Alignment	not modelled	95.4	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
51	d1uika1	Alignment	not modelled	95.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
52	c3iwfA_	Alignment	not modelled	95.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
53	d2hsga1	Alignment	not modelled	95.3	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family: GalR/LacI-like bacterial regulator
54	c3d82A_	Alignment	not modelled	95.3	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
55	c1sefA_	Alignment	not modelled	95.3	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
56	d1sefa_	Alignment	not modelled	95.3	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
57	d1rc6a_	Alignment	not modelled	95.3	4	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
58	d1dgwa_	Alignment	not modelled	95.3	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
59	d1sq4a_	Alignment	not modelled	95.3	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
60	c3bcwB_	Alignment	not modelled	95.2	6	**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
61	c3bu7A_	Alignment	not modelled	95.2	5	**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
62	d3bu7a1	Alignment	not modelled	95.2	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
63	d1lr5a_	Alignment	not modelled	95.1	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	d1uija1	Alignment	not modelled	95.1	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
65	d2bjca1	Alignment	not modelled	95.1	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
66	d2pyta1	Alignment	not modelled	95.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
67	c2eaaB_	Alignment	not modelled	95.1	11	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
68	d1efaa1	Alignment	not modelled	95.1	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	c3l2hD_	Alignment	not modelled	95.0	10	**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
70	d1zvfa1	Alignment	not modelled	95.0	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
71	c3i7dB_	Alignment	not modelled	95.0	13	**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
72	c3ht2A_	Alignment	not modelled	94.8	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
73	c2cauA_	Alignment	not modelled	94.8	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
74	c2oa2A_	Alignment	not modelled	94.7	8	**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
75	d1qpza1	Alignment	not modelled	94.6	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
76	d1fxza1	Alignment	not modelled	94.6	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
77	c1uijA_	Alignment	not modelled	94.5	11	**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)
78	c3myxA_	Alignment	not modelled	94.3	7	**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
79	c3es1A_	Alignment	not modelled	94.2	4	**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
80	c2gfnA_	Alignment	not modelled	94.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator pksa related protein; **PDBTitle:** crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
81	c3on4D_	Alignment	not modelled	93.9	6	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
82	c3es4B_	Alignment	not modelled	93.7	8	**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
83	c3kjxD_	Alignment	not modelled	93.5	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
84	c3kscD_	Alignment	not modelled	93.5	6	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
85	d1jt6a1	Alignment	not modelled	93.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
86	d1zrra1	Alignment	not modelled	93.3	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
87	d1pmia_	Alignment	not modelled	93.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
88	c2bnoA_	Alignment	not modelled	93.3	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
89	c1vi0B_	Alignment	not modelled	93.2	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
90	c2qtqB_	Alignment	not modelled	93.2	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
91	c1fxzC_	Alignment	not modelled	93.1	6	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
92	c1y9qA_	Alignment	not modelled	93.0	5	**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
93	c1jumB_	Alignment	not modelled	93.0	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical transcriptional regulator in qaca **PDBTitle:** crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
94	c2f07A_	Alignment	not modelled	93.0	4	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
95	c1u78A_	Alignment	not modelled	92.9	11	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
96	c3s7eB_	Alignment	not modelled	92.9	13	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
97	c3geuC_	Alignment	not modelled	92.8	8	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**intercellular adhesion protein r; **PDBTitle:** crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family
98	c3bruA_	Alignment	not modelled	92.8	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
99	c3gziA_	Alignment	not modelled	92.8	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
100	d2fq4a1	Alignment	not modelled	92.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
101	c1cauB_	Alignment	not modelled	92.6	14	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
102	d1t56a1	Alignment	not modelled	92.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

103	d2i10a1	Alignment	not modelled	92.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
104	d1sgma1	Alignment	not modelled	92.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
105	d2gfna1	Alignment	not modelled	92.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
106	c2ibdB_	Alignment	not modelled	92.4	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
107	c2dg7A_	Alignment	not modelled	92.4	4	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
108	c3h5tA_	Alignment	not modelled	92.4	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
109	d1od5a1	Alignment	not modelled	92.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
110	c3iuvA_	Alignment	not modelled	92.4	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized tetr family protein; **PDBTitle:** the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
111	c2eh3A_	Alignment	not modelled	92.3	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
112	c3ppbB_	Alignment	not modelled	92.3	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr family transcription regulator; **PDBTitle:** crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
113	d1ui5a1	Alignment	not modelled	92.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
114	d1lcda_	Alignment	not modelled	92.3	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
115	d2phla2	Alignment	not modelled	92.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
116	c2g3bB_	Alignment	not modelled	92.2	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
117	c2nx4A_	Alignment	not modelled	92.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family protein; **PDBTitle:** the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
118	d2fbqa1	Alignment	not modelled	92.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
119	c3e7lD_	Alignment	not modelled	92.1	28	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
120	d2fx0a1	Alignment	not modelled	92.1	2	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain