Phyre2

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Description	P32677
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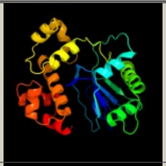
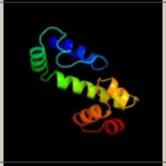
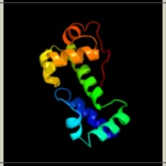
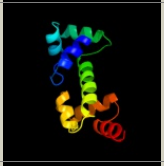
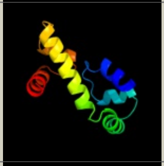
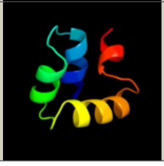
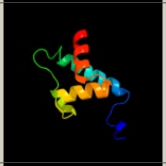
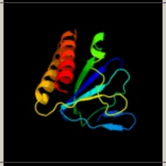
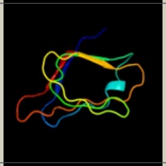
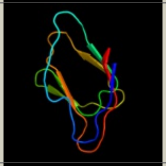
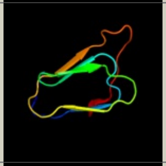
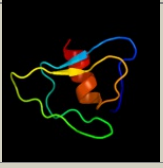
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		100.0	12	**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	19	**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	c3oouA_	Alignment		99.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
4	c3oioA_	Alignment		99.9	21	**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
5	c1bl0A_	Alignment		99.9	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
6	c3mn2B_	Alignment		99.9	24	**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
7	c2k9sA_	Alignment		99.9	34	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
8	c3mklB_	Alignment		99.9	22	**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
9	c3lsgD_	Alignment		99.8	38	**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	d1bl0a2	Alignment		99.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1d5ya2	Alignment		99.5	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	d1bl0a1	Alignment		99.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
13	d1d5ya1	Alignment		99.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	c1zgwA_	Alignment		98.9	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		98.3	17	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
16	c3ibmB_	Alignment		97.6	20	**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
17	c3cewA_	Alignment		97.6	17	**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
18	d1y3ta1	Alignment		97.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
19	c3kgzA_	Alignment		97.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
20	c3d82A_	Alignment		97.2	20	**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	c2i45C_	Alignment	not modelled	97.2	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
22	c3fjsC_	Alignment	not modelled	97.2	26	**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
23	d1v70a_	Alignment	not modelled	97.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
24	c2gu9B_	Alignment	not modelled	97.2	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
25	d2pyta1	Alignment	not modelled	97.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
26	d1juha_	Alignment	not modelled	97.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
27	d1sfna_	Alignment	not modelled	97.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
						PDB header:biosynthetic protein

28	c3h7yA_	Alignment	not modelled	97.1	8	**Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
29	c3jzvA_	Alignment	not modelled	97.1	17	**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.
30	c2pfwB_	Alignment	not modelled	97.1	16	**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
31	d1yhfa1	Alignment	not modelled	97.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
32	c2ozjB_	Alignment	not modelled	97.1	24	**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
33	c3lwcA_	Alignment	not modelled	97.0	22	**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
34	d1vj2a_	Alignment	not modelled	97.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
35	c3i7dB_	Alignment	not modelled	97.0	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
36	c1sefA_	Alignment	not modelled	97.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
37	d1sefa_	Alignment	not modelled	97.0	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
38	c2o8qA_	Alignment	not modelled	97.0	18	**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
39	d1o4ta_	Alignment	not modelled	96.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
40	c2q30C_	Alignment	not modelled	96.9	15	**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	c2vpvA_	Alignment	not modelled	96.9	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
42	c3l2hD_	Alignment	not modelled	96.9	14	**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
43	d2phda1	Alignment	not modelled	96.9	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
44	c2d40C_	Alignment	not modelled	96.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
45	d1sq4a_	Alignment	not modelled	96.8	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
46	d1lr5a_	Alignment	not modelled	96.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
47	d1o5ua_	Alignment	not modelled	96.8	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
48	d1j58a_	Alignment	not modelled	96.8	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
49	d1y9qa2	Alignment	not modelled	96.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
50	d2d40a1	Alignment	not modelled	96.7	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
51	c2oa2A_	Alignment	not modelled	96.6	15	**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
52	c3rnsA_	Alignment	not modelled	96.6	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
						PDB header:unknown function

53	c3bcwB_	Alignment	not modelled	96.6	17	**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
54	d1rc6a_	Alignment	not modelled	96.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
55	d2f4pa1	Alignment	not modelled	96.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
56	d1zvfa1	Alignment	not modelled	96.5	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
57	d1j3pa_	Alignment	not modelled	96.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
58	c2vqaC_	Alignment	not modelled	96.4	23	**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.
59	c1cauB_	Alignment	not modelled	96.4	14	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
60	c3h8uA_	Alignment	not modelled	96.3	15	**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
61	c3bu7A_	Alignment	not modelled	96.3	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
62	d3bu7a1	Alignment	not modelled	96.3	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
63	d1dgwa_	Alignment	not modelled	96.3	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	d2et1a1	Alignment	not modelled	96.1	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
65	d2phla2	Alignment	not modelled	96.1	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
66	d1uija1	Alignment	not modelled	96.1	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
67	d2bnma2	Alignment	not modelled	96.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
68	c2opkC_	Alignment	not modelled	96.0	23	**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
69	d1yfua1	Alignment	not modelled	96.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
70	d1x82a_	Alignment	not modelled	96.0	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
71	c3myxA_	Alignment	not modelled	95.9	11	**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
72	c3ht2A_	Alignment	not modelled	95.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
73	c1uijA_	Alignment	not modelled	95.9	27	**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)
74	c2eaaB_	Alignment	not modelled	95.9	26	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**7s globulin-3; **PDBTitle:** crystal structure of adzuki bean 7s globulin-3
75	d1uika1	Alignment	not modelled	95.8	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
76	d2b8ma1	Alignment	not modelled	95.7	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
77	c2fqpD_	Alignment	not modelled	95.7	10	**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	d1uika2	Alignment	not modelled	95.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins

						Family: Germin/Seed storage 7S protein
79	d1fxza2	Alignment	not modelled	95.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
80	d1uija2	Alignment	not modelled	95.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
81	d2hsga1	Alignment	not modelled	95.4	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
82	d1zrra1	Alignment	not modelled	95.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
83	c3es4B_	Alignment	not modelled	95.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
84	c3ebrA_	Alignment	not modelled	95.2	11	**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
85	d1fxza1	Alignment	not modelled	95.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
86	d1sgma1	Alignment	not modelled	95.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
87	c2cauA_	Alignment	not modelled	95.1	23	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
88	c3gziA_	Alignment	not modelled	95.1	14	**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
89	c1sgmA_	Alignment	not modelled	94.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf
90	c1y9qA_	Alignment	not modelled	94.8	13	**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
91	c3iwfA_	Alignment	not modelled	94.7	22	**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
92	d2bjca1	Alignment	not modelled	94.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
93	c1vi0B_	Alignment	not modelled	94.5	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
94	d1efaa1	Alignment	not modelled	94.5	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
95	d1vrba1	Alignment		94.5	19	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
96	c3o14B_	Alignment	not modelled	94.5	25	**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
97	c3h5tA_	Alignment	not modelled	94.3	19	**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
98	c3kglB_	Alignment	not modelled	94.3	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
99	d1od5a2	Alignment	not modelled	94.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
100	d1qpza1	Alignment	not modelled	94.2	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
101	c2f07A_	Alignment	not modelled	94.1	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
102	c3kjxD_	Alignment	not modelled	94.1	23	**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
103	c1fxzC_	Alignment	not modelled	94.0	14	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b

						homotrimer
104	d1vi0a1	Alignment	not modelled	94.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
105	c3kscD_	Alignment	not modelled	94.0	18	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
106	d1ui5a1	Alignment	not modelled	94.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
107	d2gfna1	Alignment	not modelled	93.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
108	c3on4D_	Alignment	not modelled	93.9	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
109	c2qnkA_	Alignment	not modelled	93.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyanthranilate 3,4-dioxygenase; **PDBTitle:** crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase
110	d1jt6a1	Alignment	not modelled	93.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
111	d2i10a1	Alignment	not modelled	93.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
112	d1j5ya1	Alignment	not modelled	93.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
113	c2oziA_	Alignment	not modelled	93.5	15	**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
114	c3s7eB_	Alignment	not modelled	93.5	14	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
115	c2eh3A_	Alignment	not modelled	93.5	12	**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
116	c2ibdB_	Alignment	not modelled	93.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
117	c2gfnA_	Alignment	not modelled	93.4	20	**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
118	c1jumB_	Alignment	not modelled	93.4	12	**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
119	c3iuvA_	Alignment	not modelled	93.4	16	**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
120	c2bnoA_	Alignment	not modelled	93.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.