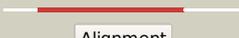
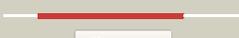
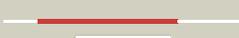
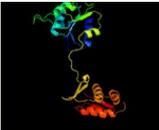
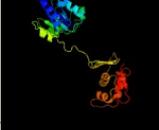


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0260c_(-)_311514_312659
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	a89c86e837666839

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wd7a_	 Alignment		100.0	30	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
2	c3d8tB_	 Alignment		100.0	32	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
3	c4es6A_	 Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
4	c3re1B_	 Alignment		100.0	16	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
5	c1jr2A_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
6	d1jr2a_	 Alignment		100.0	17	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
7	c3mw8A_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
8	c3p9zA_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
9	c1ys7B_	 Alignment		99.9	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
10	c2rv8A_	 Alignment		99.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
11	c2pmuD_	 Alignment		99.9	21	PDB header: transcription regulation Chain: D: PDB Molecule: response regulator phop; PDBTitle: crystal structure of the dna-binding domain of phop

12	c4kfcB	Alignment		99.9	16	PDB header: transcription regulator/dna Chain: B: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
13	c2oqrA	Alignment		99.8	19	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
14	c4s05B	Alignment		99.8	17	PDB header: transcription/dna Chain: B: PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
15	d1ys7a1	Alignment		99.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
16	c4uhtA	Alignment		99.8	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cpxr; PDBTitle: crystal structure of the dna binding domain of cpxr from e. coli
17	c2hqnA	Alignment		99.8	18	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
18	d1gxqa	Alignment		99.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
19	d1p2fa1	Alignment		99.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
20	c2m87A	Alignment		99.8	22	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional regulatory protein basr/pmra; PDBTitle: structural basis of dna recognition by the effector domain of2 klebsiella pneumoniae pmra
21	d1opca	Alignment	not modelled	99.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
22	c3zq7A	Alignment	not modelled	99.8	19	PDB header: transcription Chain: A: PDB Molecule: kdp operon transcriptional regulatory protein kdpe; PDBTitle: the structure of dna-binding domain of response regulator from2 escherichia coli k-12
23	c2jzyA	Alignment	not modelled	99.8	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
24	c5ju7A	Alignment	not modelled	99.8	24	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: dna binding domain of e.coli cadc
25	c4ixaA	Alignment	not modelled	99.8	23	PDB header: transcription Chain: A: PDB Molecule: response regulator saer; PDBTitle: structure of dna-binding domain of the response regulator saer from2 staphylococcus epidermidis
26	c2hqrA	Alignment	not modelled	99.8	15	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
27	c2gwrA	Alignment	not modelled	99.8	22	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
28	c2hvwA	Alignment	not modelled	99.8	24	PDB header: transcription Chain: A: PDB Molecule: dna-binding response regulator vicr; PDBTitle: crystal structure of an essential response regulator dna

					binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
29	c2zxB	Alignment	not modelled	99.8	24 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein walr; PDBTitle: crystal structure of yycf dna-binding domain from staphylococcus2 aureus
30	c3q9vB	Alignment	not modelled	99.8	26 PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
31	c2m1bA	Alignment	not modelled	99.8	22 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein, c terminal family PDBTitle: solution structure of the chxr dna-binding domain
32	c5dcmB	Alignment	not modelled	99.8	28 PDB header: signaling protein Chain: B: PDB Molecule: phob family transcriptional regulator; PDBTitle: structure of a lantibiotic response regulator: c-terminal domain of2 the nisin resistance regulator nsrr
33	c3rjpA	Alignment	not modelled	99.8	22 PDB header: dna binding protein Chain: A: PDB Molecule: covr; PDBTitle: crystal structure of the dna binding domain of covr from streptococcus2 pyogenes
34	d1kgsa1	Alignment	not modelled	99.8	19 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
35	c5u8mA	Alignment	not modelled	99.8	17 PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
36	c2k4jA	Alignment	not modelled	99.8	22 PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: arsr dna binding domain
37	c2nazA	Alignment	not modelled	99.8	24 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein rsta; PDBTitle: the solution nmr structure of the c-terminal effector domain of bfmr2 from acinetobacter baumannii
38	c3r0jA	Alignment	not modelled	99.8	18 PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
39	c1p2fA	Alignment	not modelled	99.7	18 PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
40	c5x5IM	Alignment	not modelled	99.7	26 PDB header: dna binding protein/dna Chain: M: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader dna binding domain in2 complex with an intercistronic region
41	c1kgsA	Alignment	not modelled	99.7	15 PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
42	c3q9sA	Alignment	not modelled	99.6	18 PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
43	c4b09F	Alignment	not modelled	99.6	17 PDB header: transcription Chain: F: PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
44	d2ff4a1	Alignment	not modelled	99.6	26 Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
45	c2ff4B	Alignment	not modelled	99.0	27 PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
46	d7reqa2	Alignment	not modelled	97.0	15 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
47	d1biaa1	Alignment	not modelled	96.8	25 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
48	c3rkxA	Alignment	not modelled	96.8	18 PDB header: ligase Chain: A: PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: structural characterisation of staphylococcus aureus biotin protein2 ligase
49	c2yxB	Alignment	not modelled	96.6	14 PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
50	c1zn2A	Alignment	not modelled	96.5	14 PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
51	c5xt2C	Alignment	not modelled	96.5	19 PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
52	c2ewnA	Alignment	not modelled	96.5	23 PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
53	c4r3uD	Alignment	not modelled	96.4	18 PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
54	d1ccwa	Alignment	not modelled	96.4	16 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain

						Family: Cobalamin (vitamin B12)-binding domain
55	c5yx6D	Alignment	not modelled	95.8	26	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form
56	c3k69A	Alignment	not modelled	95.5	13	PDB header: transcription Chain: A: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
57	d1fmfa	Alignment	not modelled	95.4	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
58	c3klnC	Alignment	not modelled	95.2	14	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
59	c2pjuD	Alignment	not modelled	95.1	15	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
60	c3n58D	Alignment	not modelled	94.8	21	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
61	c3ubmB	Alignment	not modelled	94.8	31	PDB header: transferase Chain: B: PDB Molecule: formyl-coa:oxalate coa-transferase; PDBTitle: formyl-coa:oxalate coa-transferase from acetobacter aceti
62	c3g85A	Alignment	not modelled	94.8	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
63	c4if4A	Alignment	not modelled	94.6	24	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus
64	c4qjiB	Alignment	not modelled	94.5	27	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
65	c6f3oC	Alignment	not modelled	94.4	24	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
66	c6a4tB	Alignment	not modelled	94.3	17	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
67	c3t8tA	Alignment	not modelled	94.3	19	PDB header: unknown function Chain: A: PDB Molecule: staphylococcus aureus cymr (oxidized form); PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form
68	d2vjma1	Alignment	not modelled	94.2	27	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
69	c3d8uA	Alignment	not modelled	94.2	11	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
70	c1xa3B	Alignment	not modelled	94.2	26	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase; PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
71	c5n0sA	Alignment	not modelled	94.1	13	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-delta6 mutant y98a in complex with sam
72	c1rnlA	Alignment	not modelled	94.1	24	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
73	c4hyeB	Alignment	not modelled	94.0	17	PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
74	d1x74a1	Alignment	not modelled	94.0	24	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
75	c6hsdB	Alignment	not modelled	94.0	18	PDB header: transcription Chain: B: PDB Molecule: rrf2 family transcriptional regulator; PDBTitle: crystal structure of the oxidized form of the transcription regulator2 rsrr
76	c3sztB	Alignment	not modelled	94.0	20	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
77	c3gv0A	Alignment	not modelled	94.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family; PDBTitle: crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
						Fold: CoA-transferase family III (CaiB/BaiF)

78	d1xk7a1	Alignment	not modelled	94.0	26	Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
79	c1d4fD	Alignment	not modelled	93.9	19	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
80	c3qk7C	Alignment	not modelled	93.9	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
81	d1j5ya1	Alignment	not modelled	93.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
82	d2pjuA1	Alignment	not modelled	93.9	15	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
83	c4r6iA	Alignment	not modelled	93.8	10	PDB header: transcription Chain: A: PDB Molecule: anthrax toxin expression trans-acting positive regulator; PDBTitle: atxa protein, a virulence regulator from bacillus anthracis.
84	c5f64C	Alignment	not modelled	93.8	25	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
85	c3k4hA	Alignment	not modelled	93.8	10	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator lacI from2 bacillus cereus subsp. cytotoxis nvh 391-98
86	c5o8yG	Alignment	not modelled	93.7	22	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
87	c3dhyC	Alignment	not modelled	93.7	21	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
88	c1e1cA	Alignment	not modelled	93.7	17	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
89	c5hevC	Alignment	not modelled	93.7	24	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the berylliofluoride-activated liar from2 enterococcus faecium
90	c1xrsB	Alignment	not modelled	93.7	11	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
91	c6aphA	Alignment	not modelled	93.6	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
92	c3clkB	Alignment	not modelled	93.6	9	PDB header: transcription regulator Chain: B: PDB Molecule: transcription regulator; PDBTitle: crystal structure of a transcription regulator from lactobacillus2 plantarum
93	c4lfuA	Alignment	not modelled	93.5	12	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
94	c3c3wB	Alignment	not modelled	93.2	20	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
95	d1u7za	Alignment	not modelled	93.1	20	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
96	c5v96A	Alignment	not modelled	93.1	23	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
97	c2eklA	Alignment	not modelled	92.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
98	c4ed9A	Alignment	not modelled	92.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: caib/baif family protein; PDBTitle: crystal structure of a caib/baif family protein from brucella suis
99	c3sqnA	Alignment	not modelled	92.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: conserved domain protein; PDBTitle: putative mga family transcriptional regulator from enterococcus2 faecalis
100	c2y75F	Alignment	not modelled	92.8	20	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
101	d1xrsb1	Alignment	not modelled	92.8	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
102	c4yn8A	Alignment	not modelled	92.7	27	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
103	d1sd4a	Alignment	not modelled	92.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor PDB header: hydrolase/hydrolase substrate

104	c3oneA	Alignment	not modelled	92.3	20	Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
105	c5ojgB	Alignment	not modelled	92.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of the dehydrogenase/reductase sdr family member 42 (dhrs4) from caenorhabditis elegans
106	c3lwfD	Alignment	not modelled	92.1	21	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
107	c3hcvB	Alignment	not modelled	91.8	12	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
108	c2q0aA	Alignment	not modelled	91.6	20	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
109	d1p6ra	Alignment	not modelled	91.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
110	c3h5oB	Alignment	not modelled	91.6	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
111	d2nzug1	Alignment	not modelled	91.5	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
112	c2rgvA	Alignment	not modelled	91.5	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of transcriptional regulator of lacI family from2 burkholderia phytatum
113	c4zgwB	Alignment	not modelled	91.4	27	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: short-chain dehydrogenase/reductase from serratia marcescens bcrc2 10948
114	c3c3kA	Alignment	not modelled	91.4	13	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
115	c1h0mD	Alignment	not modelled	91.4	20	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
116	c1zljE	Alignment	not modelled	91.3	24	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
117	c1ybaC	Alignment	not modelled	91.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
118	c5bt9B	Alignment	not modelled	91.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of folm alternative dihydrofolate reductase 1 from2 brucella canis complexed with nadp
119	c3x2fA	Alignment	not modelled	90.9	21	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
120	d1yifa1	Alignment	not modelled	90.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2