Phyre^2

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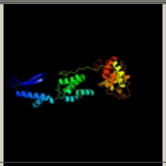
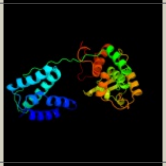
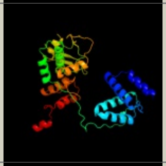
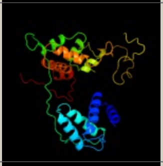
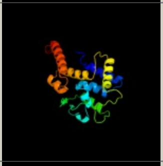
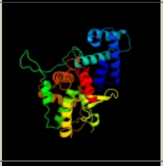
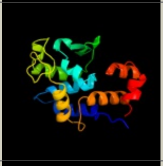
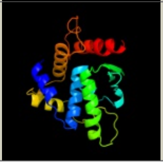
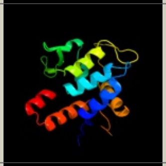
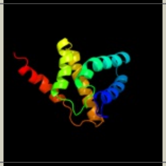
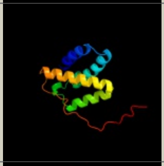
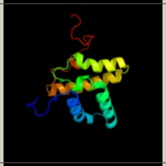
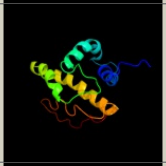
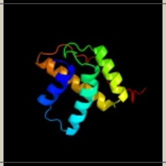
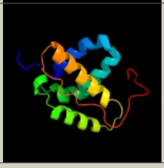
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z1bA_	Alignment		100.0	16	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a lambda integrase dimer bound to a2 coc' core site
2	d1p7da_	Alignment		100.0	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
3	c1ma7A_	Alignment		100.0	15	**PDB header:**hydrolase, ligase/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
4	c1crxA_	Alignment		100.0	15	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cre recombinase; **PDBTitle:** cre recombinase/dna complex reaction intermediate i
5	c2a3vA_	Alignment		99.9	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase inti4; **PDBTitle:** structural basis for broad dna-specificity in integron2 recombination
6	c3nkhB_	Alignment		99.9	18	**PDB header:**recombination **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus
7	c1a0pA_	Alignment		99.9	14	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**site-specific recombinase xerd; **PDBTitle:** site-specific recombinase, xerd
8	d1aiha_	Alignment		99.9	15	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
9	d1f44a2	Alignment		99.8	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
10	c3ju0A_	Alignment		99.8	44	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
11	d1a0pa2	Alignment		99.8	13	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core

12	d1ae9a_	Alignment		99.8	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
13	c3jtzA_	Alignment		99.8	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
14	d5crxb2	Alignment		99.6	16	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
15	c2kj8A_	Alignment		99.5	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
16	c2kiwA_	Alignment		99.4	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**int protein; **PDBTitle:** solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
17	c2kj9A_	Alignment		99.4	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e
18	c2kkvA_	Alignment		99.4	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
19	c2khqA_	Alignment		99.4	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
20	c2kd1A_	Alignment		99.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
21	c2kkpA_	Alignment	not modelled	99.3	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
22	c3lysC_	Alignment	not modelled	99.3	13	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
23	c2oxoA_	Alignment	not modelled	99.3	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
24	c2kj5A_	Alignment	not modelled	99.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
25	c2khvA_	Alignment	not modelled	99.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
26	c2kobA_	Alignment	not modelled	99.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase;

27	c2keyA_	Alignment	not modelled	99.0	10	**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
28	c3nrwA_	Alignment	not modelled	98.7	10	**PDB header:**recombination **Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase; **PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
29	c2v6eB_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protelemorase; **PDBTitle:** protelomerase telk complexed with substrate dna
30	d1a0pa1	Alignment	not modelled	97.5	13	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
31	c2f4qA_	Alignment	not modelled	97.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type i topoisomerase, putative; **PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib
32	c2h7fX_	Alignment	not modelled	96.9	14	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
33	d1f44a1	Alignment	not modelled	95.9	10	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
34	d1a41a_	Alignment	not modelled	94.5	18	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
35	d1k4ta2	Alignment	not modelled	92.6	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
36	c2b9sA_	Alignment	not modelled	92.5	15	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
37	d1rr8c1	Alignment	not modelled	91.0	12	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
38	d1z1ba1	Alignment	not modelled	89.9	20	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
39	c1kjkA_	Alignment	not modelled	89.1	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
40	c1a31A_	Alignment	not modelled	80.9	12	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
41	c1nh3A_	Alignment	not modelled	79.0	12	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
42	d1gcca_	Alignment	not modelled	75.6	15	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
43	c3igmA_	Alignment	not modelled	44.2	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
44	d1uxca_	Alignment	not modelled	25.9	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
45	c2l8nA_	Alignment	not modelled	16.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
46	d2iw5b1	Alignment	not modelled	16.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
47	d2csba1	Alignment	not modelled	16.0	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
48	d2gf5a1	Alignment	not modelled	15.7	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
49	d1uxda_	Alignment	not modelled	15.3	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
50	c1v9nA_	Alignment	not modelled	11.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of malate dehydrogenase from pyrococcus horikoshii ot3
51	c2nogA_	Alignment	not modelled	10.9	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
52	d1xc5a1	Alignment	not modelled	10.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
						Fold:L-sulfolactate dehydrogenase-like

53	d1xrha_	Alignment	not modelled	10.7	8	**Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
54	d1p4ea2	Alignment	not modelled	9.8	14	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
55	d1lcda_	Alignment	not modelled	9.6	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
56	d1e6vc_	Alignment	not modelled	9.5	19	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
57	c2g8yB_	Alignment	not modelled	9.1	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
58	d1qpza1	Alignment	not modelled	9.0	0	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
59	c2lcvA_	Alignment	not modelled	9.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
60	d1r8da_	Alignment	not modelled	8.9	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
61	d2bjca1	Alignment	not modelled	8.8	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
62	c2x0lB_	Alignment	not modelled	8.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of a neuro-specific splicing variant of2 human histone lysine demethylase lsd1.
63	c2iw5B_	Alignment	not modelled	8.6	14	**PDB header:**oxidoreductase/transcription regulator **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis for corest-dependent demethylation of2 nucleosomes by the human lsd1 histone demethylase
64	c2v1dB_	Alignment	not modelled	8.6	14	**PDB header:**oxidoreductase/repressor **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
65	c2xajB_	Alignment	not modelled	8.6	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rest corepressor 1; **PDBTitle:** crystal structure of lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine
66	c2eqrA_	Alignment	not modelled	8.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1
67	c1u24A_	Alignment	not modelled	8.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**myo-inositol hexaphosphate phosphohydrolase; **PDBTitle:** crystal structure of selenomonas ruminantium phytase
68	c1p4eB_	Alignment	not modelled	7.9	14	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
69	d2auwa1	Alignment	not modelled	7.9	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
70	c3kmpA_	Alignment	not modelled	7.8	13	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**smad1-mh1; **PDBTitle:** crystal structure of smad1-mh1/dna complex
71	c3lgbB_	Alignment	not modelled	7.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of the fe-s domain of the yeast dna primase
72	c3d6zA_	Alignment	not modelled	7.5	7	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
73	c2daeA_	Alignment	not modelled	7.5	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0733 protein; **PDBTitle:** solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)
74	c3cuqA_	Alignment	not modelled	7.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
75	d1hbnc_	Alignment	not modelled	7.4	13	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
76	d2hsga1	Alignment	not modelled	7.3	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	c1wtjB_	Alignment	not modelled	7.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
78	d1nxua_	Alignment	not modelled	7.1	11	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
79	c2v4xA_	Alignment	not modelled	7.0	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p27; **PDBTitle:** crystal structure of jaagsiekte sheep retrovirus capsid n-

						2 terminal domain
80	d1jhfa1	Alignment	not modelled	7.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
81	c3sqgF_	Alignment	not modelled	6.8	31	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methyl-coenzyme m reductase, gamma subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
82	c3i0pA_	Alignment	not modelled	6.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
83	c2kscA_	Alignment	not modelled	6.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
84	c4a69C_	Alignment	not modelled	6.5	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**nuclear receptor corepressor 2; **PDBTitle:** structure of hdac3 bound to corepressor and inositol tetraphosphate
85	d1u5ta1	Alignment	not modelled	6.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
86	d1j98a_	Alignment	not modelled	6.5	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
87	d1e6yc_	Alignment	not modelled	6.4	19	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase gamma chain
88	d1efaa1	Alignment	not modelled	6.4	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
89	c3ol0C_	Alignment	not modelled	6.4	31	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
90	c3n3fB_	Alignment	not modelled	6.3	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
91	c1vbiA_	Alignment	not modelled	6.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
92	c3aq8A_	Alignment	not modelled	6.3	19	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
93	d1r8ea1	Alignment	not modelled	6.2	6	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
94	d1j6xa_	Alignment	not modelled	5.9	20	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
95	d2crga1	Alignment	not modelled	5.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
96	d1vmha_	Alignment	not modelled	5.7	15	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
97	c1or7A_	Alignment	not modelled	5.6	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
98	c3qaoA_	Alignment	not modelled	5.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
99	d1qu6a2	Alignment	not modelled	5.6	13	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)