Phyre2

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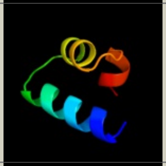
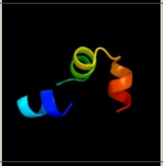
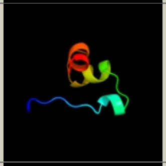
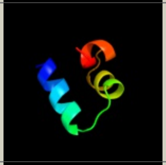
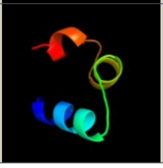
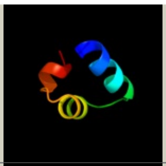
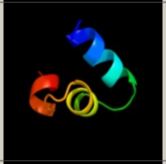
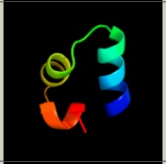
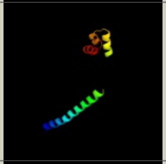
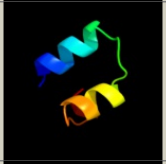
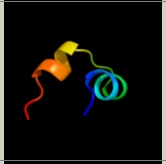
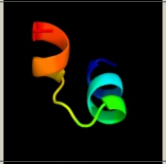
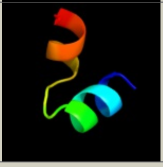
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a9xa1	Alignment		90.0	11	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
2	c2x48B_	Alignment		86.0	18	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
3	d1p4wa_	Alignment		64.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
4	d1s6la1	Alignment		64.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
5	d2etla1	Alignment		61.1	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
6	d1fsea_	Alignment		60.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
7	d1vz0a1	Alignment		57.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
8	c1x3uA_	Alignment		54.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
9	d1yioa1	Alignment		54.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
10	c3fymA_	Alignment		53.8	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
11	c2jpcA_	Alignment		52.9	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein

12	d1a04a1	Alignment		52.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
13	c2krfB_	Alignment		52.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
14	c1zljE_	Alignment		49.8	16	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
15	c1h0mD_	Alignment		49.7	9	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
16	c2gm4B_	Alignment		48.6	11	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
17	d1trra_	Alignment		48.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
18	d1j58a_	Alignment		48.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
19	d1l0oc_	Alignment		48.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
20	c1l0oC_	Alignment		48.3	26	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
21	c2phcB_	Alignment	not modelled	47.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
22	d1fxza2	Alignment	not modelled	47.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
23	c2q0oA_	Alignment	not modelled	47.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
24	d1jhga_	Alignment	not modelled	45.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
25	c2rnjA_	Alignment	not modelled	45.6	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
26	c1r71B_	Alignment	not modelled	44.9	18	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
27	d1ttya_	Alignment	not modelled	43.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
28	c3cloC_	Alignment	not modelled	42.6	9	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from

						bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
29	c2wusR_	Alignment	not modelled	42.1	25	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
30	c3sztB_	Alignment	not modelled	42.0	6	**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
31	d1r71a_	Alignment	not modelled	41.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
32	d1ku3a_	Alignment	not modelled	41.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
33	c3mmlD_	Alignment	not modelled	41.6	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
34	d1od5a2	Alignment	not modelled	41.3	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
35	d1ic8a2	Alignment	not modelled	39.8	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
36	d1fxza1	Alignment	not modelled	38.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
37	d1od5a1	Alignment	not modelled	38.2	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
38	c2vqaC_	Alignment	not modelled	37.1	13	**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.
39	d1ku2a1	Alignment	not modelled	36.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
40	d1bl0a2	Alignment	not modelled	35.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
41	d1ku7a_	Alignment	not modelled	35.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
42	c3trbA_	Alignment	not modelled	35.4	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
43	d1q1ha_	Alignment	not modelled	35.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
44	c1q1hA_	Alignment	not modelled	35.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
45	c2r0qF_	Alignment	not modelled	34.2	16	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
46	c3qp5C_	Alignment	not modelled	33.2	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
47	c3kglB_	Alignment	not modelled	32.8	30	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
48	d1l3la1	Alignment	not modelled	32.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
49	d2p7vb1	Alignment	not modelled	31.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
50	c2o8xA_	Alignment	not modelled	31.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
51	c1m6vE_	Alignment	not modelled	30.5	12	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
52	c1u78A_	Alignment	not modelled	29.6	15	**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
53	c3b7hA_	Alignment	not modelled	29.2	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
54	c3t72o	Alignment	not modelled	29.1	9	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1);

54	c3t72o_	Alignment	not modelled	29.1	9	**PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
55	c3d6zA_	Alignment	not modelled	28.9	31	**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
56	c2d5fB_	Alignment	not modelled	28.8	9	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
57	c3oepA_	Alignment	not modelled	28.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
58	d5crxb2	Alignment	not modelled	28.6	37	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Lambda integrase-like, catalytic core
59	c3mzyA_	Alignment	not modelled	28.5	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
60	d1dpua_	Alignment	not modelled	27.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
61	c1dpuA_	Alignment	not modelled	27.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
62	c3t76A_	Alignment	not modelled	26.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
63	c3c3vA_	Alignment	not modelled	26.7	17	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
64	d2ga1a1	Alignment	not modelled	26.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
65	c3c3wB_	Alignment	not modelled	26.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
66	d1or7a1	Alignment	not modelled	26.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
67	d1smyf2	Alignment	not modelled	26.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
68	d1d5ya1	Alignment	not modelled	26.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
69	c3kscD_	Alignment	not modelled	25.2	17	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
70	c3ehkC_	Alignment	not modelled	25.1	13	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
71	d1g8ma1	Alignment	not modelled	25.0	30	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
72	d1rp3a1	Alignment	not modelled	24.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
73	d2iv2x2	Alignment	not modelled	24.2	27	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
74	c1fxzC_	Alignment	not modelled	23.5	13	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
75	d1r8ea1	Alignment	not modelled	23.4	31	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
76	d1q08a_	Alignment	not modelled	23.4	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
77	d2a6ca1	Alignment	not modelled	23.3	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
78	c1cauB_	Alignment	not modelled	23.3	17	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
79	d1k1va_	Alignment	not modelled	23.1	27	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
						PDB header:nuclear protein

80	c1vz0B_	Alignment	not modelled	22.8	21	**Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; **PDBTitle:** chromosome segregation protein spo0j from thermus2 thermophilus
81	c2e9qA_	Alignment	not modelled	22.7	23	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
82	d1s7oa_	Alignment	not modelled	22.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
83	d1pkxa1	Alignment	not modelled	21.6	30	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
84	c3hugA_	Alignment	not modelled	21.5	15	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
85	d1ijwc_	Alignment	not modelled	21.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
86	c2cauA_	Alignment	not modelled	21.0	17	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
87	d1h0ha2	Alignment	not modelled	20.7	18	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
88	c3frwF_	Alignment	not modelled	20.4	23	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
89	c1dgrW_	Alignment	not modelled	20.2	17	**PDB header:**plant protein **Chain:** W: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
90	d1hcra_	Alignment	not modelled	20.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
91	c3klnC_	Alignment	not modelled	20.1	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
92	c2k9lA_	Alignment	not modelled	19.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
93	d1y9qa1	Alignment	not modelled	19.1	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
94	c2q1zA_	Alignment	not modelled	18.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
95	d1kqfa2	Alignment	not modelled	18.9	5	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
96	c3clcC_	Alignment	not modelled	18.8	26	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
97	d1uija2	Alignment	not modelled	18.8	4	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
98	d1bl0a1	Alignment	not modelled	18.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
99	d1xsva_	Alignment	not modelled	18.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like