Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q9JMT4
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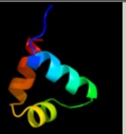
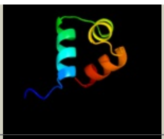
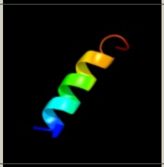
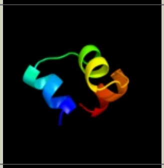
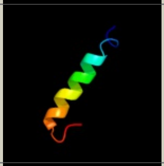
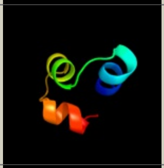
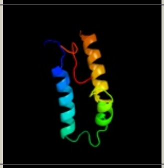
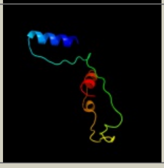
Unique Job ID	1d2b5dea1f46d245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fsea_	Alignment		48.8	17	**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)
2	d1p4wa_	Alignment		45.9	15	**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)
3	c2rnjA_	Alignment		44.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
4	d1sqwa2	Alignment		38.4	32	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Nip7p homolog, N-terminal domain
5	c1zljE_	Alignment		30.9	19	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
6	c2krfB_	Alignment		30.8	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
7	d1yioa1	Alignment		30.3	22	**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)
8	d1rp3a2	Alignment		28.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
9	c2jpcA_	Alignment		26.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
10	d1a04a1	Alignment		22.8	15	**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)
11	d1l3la1	Alignment		21.5	17	**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)

12	c3cloC_	Alignment		20.3	28	**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
13	c1x3uA_	Alignment		19.3	17	**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
14	d1nh2b_	Alignment		15.9	17	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
15	d1or7a1	Alignment		15.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
16	c2latA_	Alignment		13.3	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
17	c3hugA_	Alignment		13.1	31	**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
18	d2ixoa1	Alignment		13.1	23	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
19	c2pcoA_	Alignment		12.6	78	**PDB header:**toxin **Chain:** A: **PDB Molecule:**latarcin-1; **PDBTitle:** spatial structure and membrane permeabilization for2 latarcin-1, a spider antimicrobial peptide
20	d1gxla_	Alignment		12.3	21	**Fold:**Smc hinge domain **Superfamily:**Smc hinge domain **Family:**Smc hinge domain
21	d1nvpb_	Alignment	not modelled	11.6	22	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
22	c1nvpB_	Alignment	not modelled	11.6	22	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
23	c3sztB_	Alignment	not modelled	11.5	22	**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
24	c3c3wB_	Alignment	not modelled	7.9	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
25	c2x3gA_	Alignment	not modelled	7.8	80	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sirv1 hypothetical protein orf119; **PDBTitle:** crystal structure of the hypothetical protein orf119 from2 sulfolobus islandicus rod-shaped virus 1
26	d1u1ha1	Alignment	not modelled	7.7	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
27	d1xsva_	Alignment	not modelled	6.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
28	c2uvpB_	Alignment	not modelled	6.5	58	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hoba; **PDBTitle:** crystal structure of hoba (hp1230)from helicobacter pylori
						Fold:lambda repressor-like DNA-binding domains

29	d1b0na2	Alignment	not modelled	6.5	15	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
30	d1vp7a_	Alignment	not modelled	6.4	25	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
31	c3e3vA_	Alignment	not modelled	6.1	26	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
32	d1kxpd3	Alignment	not modelled	5.9	40	**Fold:**Serum albumin-like **Superfamily:**Serum albumin-like **Family:**Serum albumin-like
33	c3d5lA_	Alignment	not modelled	5.9	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of regulatory protein recx
34	c3mzyA_	Alignment	not modelled	5.9	22	**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
35	c2cxaA_	Alignment	not modelled	5.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
36	d2cxaa1	Alignment	not modelled	5.7	27	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
37	d2go8a1	Alignment	not modelled	5.7	31	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
38	c2jmlA_	Alignment	not modelled	5.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
39	c2o8xA_	Alignment	not modelled	5.4	13	**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
40	c3ltiA_	Alignment	not modelled	5.3	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
41	c1u22A_	Alignment	not modelled	5.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
42	c3zr8X_	Alignment	not modelled	5.2	31	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**avr3a11; **PDBTitle:** crystal structure of rxlr effector avr3a11 from phytophthora capsici
43	c2lc2A_	Alignment	not modelled	5.1	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**avr3a4; **PDBTitle:** solution structure of the rxlr effector p. capsici avr3a4
44	c2a7uB_	Alignment	not modelled	5.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase delta chain; **PDBTitle:** nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
45	d1abva_	Alignment	not modelled	5.1	13	**Fold:**ATPD N-terminal domain-like **Superfamily:**N-terminal domain of the delta subunit of the F1F0-ATP synthase **Family:**N-terminal domain of the delta subunit of the F1F0-ATP synthase