
















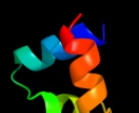





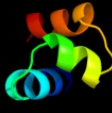
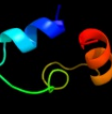


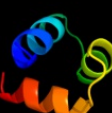






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x48B_	 Alignment		89.8	13	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
2	c2gm4B_	 Alignment		87.0	12	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
3	d1a9xa1	 Alignment		83.9	17	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
4	d1p4wa_	 Alignment		82.4	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)
5	d1s6la1	 Alignment		81.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
6	d1vz0a1	 Alignment		79.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
7	c1x3uA_	 Alignment		79.4	5	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
8	c1h0mD_	 Alignment		78.8	11	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
9	c1r71B_	 Alignment		78.7	28	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
10	d1fsea_	 Alignment		78.5	11	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	c2jpcA_	 Alignment		77.9	8	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein

12	dla04a1	Alignment		77.7	8	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		77.4	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	c1q1hA	Alignment		77.0	30	PDB header: transcription Chain: A: PDB Molecule: transcription factor e; PDBTitle: an extended winged helix domain in general transcription2 factor e/iie alpha
15	dlq1ha	Alignment		77.0	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcription factor E/Ile-alpha, N-terminal domain
16	dlr71a	Alignment		75.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
17	dlyioa1	Alignment		75.6	11	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)
18	c2rnjA	Alignment		75.5	17	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
19	c1zljE	Alignment		75.2	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
20	c2q0oA	Alignment		75.1	11	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
21	c1l0oC	Alignment	not modelled	72.2	5	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
22	dl10oc	Alignment	not modelled	72.2	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
23	c3sztB	Alignment	not modelled	71.3	5	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	c3qp5C	Alignment	not modelled	69.3	8	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
25	dl13la1	Alignment	not modelled	68.1	11	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)
26	c3cloC	Alignment	not modelled	67.8	16	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
27	dlrp3a1	Alignment	not modelled	59.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
28	clu78A	Alignment	not modelled	58.9	6	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 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
29	c3trbA_	Alignment	not modelled	57.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
30	d1ku2a1	Alignment	not modelled	57.6	18	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
31	c3c3wB_	Alignment	not modelled	57.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
32	d1ttya_	Alignment	not modelled	55.5	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
33	c3t76A_	Alignment	not modelled	54.9	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
34	d2a6ca1	Alignment	not modelled	53.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
35	d1ku3a_	Alignment	not modelled	52.7	17	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
36	c3b7hA_	Alignment	not modelled	51.9	15	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
37	c2r0qF_	Alignment	not modelled	51.3	13	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of 2 mycobacterium tuberculosis sigc
38	c2o8xA_	Alignment	not modelled	49.9	19	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome partitioning protein parb; PDBTitle: chromosome segregation protein spoJ from thermus2 thermophilus
39	c1vz0B_	Alignment	not modelled	49.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
40	d1luxca_	Alignment	not modelled	48.9	27	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of 2 carbamoyl phosphate synthetase
41	c1m6vE_	Alignment	not modelled	48.8	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
42	d1trra_	Alignment	not modelled	48.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
43	d1ku7a_	Alignment	not modelled	47.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
44	d1jhga_	Alignment	not modelled	47.9	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
45	d1ic8a2	Alignment	not modelled	46.6	15	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
46	d1q08a_	Alignment	not modelled	46.2	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
47	d1efaa1	Alignment	not modelled	45.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
48	d2p7vb1	Alignment	not modelled	44.4	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
49	d1lcda_	Alignment	not modelled	44.2	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
50	d2hsga1	Alignment	not modelled	43.5	30	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfmf, a putative dna-binding membrane2 protein from staphylococcus aureus
51	c3fymA_	Alignment	not modelled	42.2	12	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
52	d1r8ea1	Alignment	not modelled	41.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
53	d1s7oa_	Alignment	not modelled	40.7	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains
54	d1r69a_	Alignment	not modelled	40.0	12	

					Family: Phage repressors
55	dlz6ra1	Alignment	not modelled	39.8	26 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
56	c2k9lA_	Alignment	not modelled	39.5	28 PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
57	dlv9qa1	Alignment	not modelled	39.0	15 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
58	dlsmvf2	Alignment	not modelled	38.8	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
59	dlb0na2	Alignment	not modelled	38.8	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
60	c3klnC_	Alignment	not modelled	38.4	14 PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
61	dluxda_	Alignment	not modelled	38.0	27 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
62	c2wusR_	Alignment	not modelled	37.4	9 PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape2 protein rodz
63	dlijwc_	Alignment	not modelled	37.2	27 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
64	c3mzyA_	Alignment	not modelled	36.8	15 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
65	d2bjca1	Alignment	not modelled	36.5	38 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
66	c3d6zA_	Alignment	not modelled	36.2	15 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
67	clrnIA_	Alignment	not modelled	36.2	8 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
68	c3t72o_	Alignment	not modelled	35.9	13 PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
69	dladra_	Alignment	not modelled	35.6	9 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
70	c3frwF_	Alignment	not modelled	35.4	19 PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
71	dlhcra_	Alignment	not modelled	35.1	27 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
72	c3omtA_	Alignment	not modelled	34.8	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
73	dlor7a1	Alignment	not modelled	34.4	19 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
74	dlxsva_	Alignment	not modelled	34.4	11 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
75	c3clcC_	Alignment	not modelled	33.4	30 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
76	c2ebyA_	Alignment	not modelled	33.3	19 PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
77	c2q1zA_	Alignment	not modelled	33.1	22 PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
78	dl5ya1	Alignment	not modelled	32.9	18 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
79	c2jvlA_	Alignment	not modelled	32.9	9 PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
80	dl1dpuA_	Alignment	not modelled	32.7	10 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: C-terminal domain of RPA32
81	c1dpuA	Alignment	not modelled	32.7	10	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)
82	d1vola2	Alignment	not modelled	32.5	13	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
83	d2iv2x2	Alignment	not modelled	32.2	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
84	d1bl0a2	Alignment	not modelled	31.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
85	c3hugA	Alignment	not modelled	31.5	14	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
86	d2icta1	Alignment	not modelled	31.4	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
87	c3hh0C	Alignment	not modelled	30.8	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal strcure of a transcriptional regulator, merr family2 from bacillus cereus
88	d1h0ha2	Alignment	not modelled	30.6	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
89	d1hq1a	Alignment	not modelled	30.3	6	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
90	c1h0hA	Alignment	not modelled	29.9	15	PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
91	d1dula	Alignment	not modelled	29.6	6	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
92	d1pdnc	Alignment	not modelled	29.4	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
93	c1or7A	Alignment	not modelled	29.3	19	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
94	d2cyya1	Alignment	not modelled	29.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
95	d1z05a1	Alignment	not modelled	29.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
96	d2o38a1	Alignment	not modelled	29.0	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
97	c2o38A	Alignment	not modelled	29.0	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
98	c2l8nA	Alignment	not modelled	28.4	24	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
99	c2iv2X	Alignment	not modelled	28.4	19	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
100	c3op9A	Alignment	not modelled	28.1	12	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
101	d1y7ya1	Alignment	not modelled	28.1	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
102	d2croa	Alignment	not modelled	28.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
103	d1qpza1	Alignment	not modelled	27.7	38	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
104	d1j5ya1	Alignment	not modelled	27.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
105	d1kqfa2	Alignment	not modelled	27.4	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
106	c3f52A	Alignment	not modelled	27.3	12	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum

107	d1utxa_	Alignment	not modelled	27.2	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
108	c2e7zA_	Alignment	not modelled	27.1	23	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
109	c3dfgA_	Alignment	not modelled	27.0	14	PDB header: recombination Chain: A: PDB Molecule: regulatory protein recx; PDBTitle: crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
110	d2et1a1	Alignment	not modelled	26.9	0	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
111	c2v45A_	Alignment	not modelled	26.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
112	d1sq8a_	Alignment	not modelled	26.6	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
113	c2npuA_	Alignment	not modelled	26.6	22	PDB header: transferase Chain: A: PDB Molecule: fkbp12-rapamycin complex-associated protein; PDBTitle: the solution structure of the rapamycin-binding domain of2 mtor (frb)
114	c2kpiA_	Alignment	not modelled	26.5	5	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
115	d2cg4a1	Alignment	not modelled	26.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
116	c2vpyE_	Alignment	not modelled	25.9	19	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
117	c2lcvA_	Alignment	not modelled	25.7	24	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
118	c3cecA_	Alignment	not modelled	25.6	26	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
119	d2r1jl1	Alignment	not modelled	25.5	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
120	d1k78a1	Alignment	not modelled	25.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain