Phyre^2

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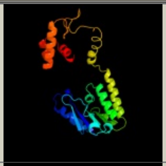
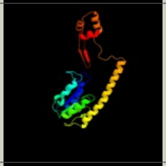
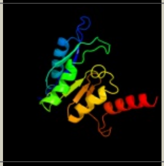
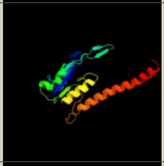
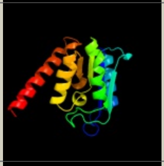
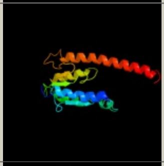
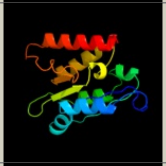
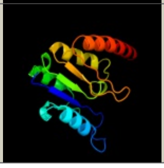
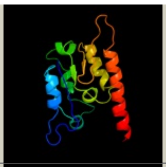
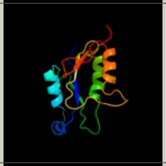
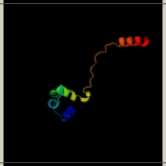
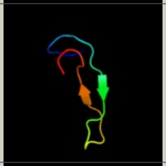
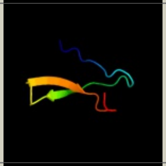
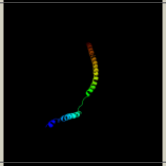
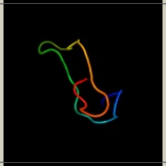
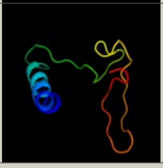
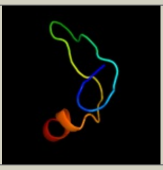
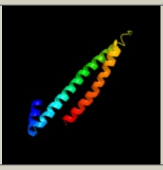
Description	P77698
Date	Thu Jan 5 12:31:47 GMT 2012
Unique Job ID	e615bbdb963a1a78

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r0qF_	Alignment		99.9	20	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
2	c3guvA_	Alignment		99.9	22	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase, resolvase family protein; **PDBTitle:** crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
3	c2gm4B_	Alignment		99.9	21	**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
4	c3g13B_	Alignment		99.9	16	**PDB header:**recombination **Chain:** B: **PDB Molecule:**putative conjugative transposon recombinase; **PDBTitle:** crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
5	d1gdta2	Alignment		99.8	20	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
6	c3bvpB_	Alignment		99.8	27	**PDB header:**recombination **Chain:** B: **PDB Molecule:**tp901-1 integrase; **PDBTitle:** crystal structure of the n-terminal catalytic domain of tp901-12 integrase
7	c3lhkA_	Alignment		99.8	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein mj0014; **PDBTitle:** crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
8	d2gm4a2	Alignment		99.8	20	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
9	c3lhfC_	Alignment		99.8	23	**PDB header:**recombination **Chain:** C: **PDB Molecule:**serine recombinase; **PDBTitle:** the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a
10	c3pkzK_	Alignment		99.7	23	**PDB header:**recombination **Chain:** K: **PDB Molecule:**recombinase sin; **PDBTitle:** structural basis for catalytic activation of a serine recombinase
11	d2rsla_	Alignment		99.7	24	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain

12	c3ploX_	Alignment		99.7	25	**PDB header:**recombination **Chain:** X: **PDB Molecule:**dna-invertase; **PDBTitle:** crystal structure of the fis-independent mutant of gin
13	d1hx7a_	Alignment		99.5	23	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
14	c1u78A_	Alignment		88.4	17	**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
15	c3cngC_	Alignment		86.5	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
16	c1i3ql_	Alignment		83.8	15	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
17	c3ghgK_	Alignment		80.4	8	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
18	c1deqF_	Alignment		76.5	10	**PDB header:** **PDB COMPND:**
19	c2gb5B_	Alignment		73.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
20	c2opfA_	Alignment		72.2	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
21	d1k78a2	Alignment	not modelled	71.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
22	c3h0gI_	Alignment	not modelled	70.4	13	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
23	c2k8dA_	Alignment	not modelled	69.3	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msrb; **PDBTitle:** solution structure of a zinc-binding methionine sulfoxide reductase
24	d2fiya1	Alignment	not modelled	68.7	20	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
25	c1k82D_	Alignment	not modelled	68.7	13	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
26	d6paxa2	Alignment	not modelled	68.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
27	d1k78a1	Alignment	not modelled	68.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
28	c1nnjA_	Alignment	not modelled	65.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna

29	c1deqO_	Alignment	not modelled	63.8	11	**PDB header:** **PDB COMPND:**
30	d2nlya1	Alignment	not modelled	62.9	7	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
31	c2vrwB_	Alignment	not modelled	62.8	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** critical structural role for the ph and c1 domains of the2 vav1 exchange factor
32	d1twfi1	Alignment	not modelled	60.8	15	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
33	d1pvma3	Alignment	not modelled	60.4	21	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
34	d1wo8a1	Alignment	not modelled	59.9	12	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
35	d1dgsa1	Alignment		59.1	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
36	d1p91a_	Alignment	not modelled	58.5	35	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
37	c2dq3A_	Alignment		57.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
38	c2k27A_	Alignment	not modelled	57.0	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
39	d1l1da_	Alignment	not modelled	56.4	8	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
40	d1pdnc_	Alignment	not modelled	55.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
41	c1y1yS_	Alignment	not modelled	55.4	12	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
42	c3gn5B_	Alignment	not modelled	55.4	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
43	d2g9wa1	Alignment	not modelled	54.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
44	c1pqvS_	Alignment	not modelled	54.8	12	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
45	c2f5qA_	Alignment	not modelled	54.1	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
46	d6paxa1	Alignment	not modelled	53.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
47	c2lcqA_	Alignment	not modelled	53.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
48	d1tfia_	Alignment	not modelled	51.6	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
49	d2iw0a1	Alignment	not modelled	49.8	9	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
50	c6paxA_	Alignment	not modelled	48.8	21	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
51	d1dl6a_	Alignment	not modelled	48.6	15	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
52	c2krfB_	Alignment	not modelled	48.3	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
53	d1twfi2	Alignment	not modelled	47.3	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
						PDB header:transferase

54	c2riqA_	Alignment	not modelled	47.0	19	**Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
55	c3lssA_	Alignment	not modelled	46.7	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
56	d1yioa1	Alignment	not modelled	46.3	18	**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)
57	c3pfqA_	Alignment	not modelled	46.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
58	c3izci_	Alignment	not modelled	45.6	16	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein rpl10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
59	c2jpcA_	Alignment	not modelled	45.6	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
60	c1ee8A_	Alignment	not modelled	45.6	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
61	c2j6aA_	Alignment	not modelled	45.1	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
62	c1zljE_	Alignment	not modelled	45.0	15	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
63	d1fsea_	Alignment	not modelled	44.7	21	**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)
64	c3hnwB_	Alignment	not modelled	44.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
65	c3cezA_	Alignment	not modelled	44.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
66	d1p6ra_	Alignment	not modelled	44.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
67	c3hcjB_	Alignment	not modelled	44.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)
68	c2l1uA_	Alignment	not modelled	43.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b2, mitochondrial; **PDBTitle:** structure-functional analysis of mammalian msrb2 protein
69	c2rnjA_	Alignment	not modelled	42.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
70	d1x6ma_	Alignment	not modelled	41.5	33	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
71	c3fxaA_	Alignment	not modelled	41.1	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
72	d1ivsa1	Alignment	not modelled	40.9	16	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
73	d1xm0a1	Alignment	not modelled	40.9	8	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
74	d1p4wa_	Alignment	not modelled	40.9	27	**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)
75	d1ny1a_	Alignment	not modelled	40.1	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
76	c2jeeA_	Alignment	not modelled	39.9	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
77	d1r2za3	Alignment	not modelled	39.2	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
78	d1ee8a3	Alignment	not modelled	38.6	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
79	d1l3la1	Alignment	not modelled	38.4	12	**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)
80	d2cona1	Alignment	not modelled	38.2	36	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
81	c3dtpA_	Alignment	not modelled	37.8	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
82	c2jvmA_	Alignment	not modelled	37.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95
83	d1l1ta3	Alignment	not modelled	37.6	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
84	c2w48D_	Alignment	not modelled	37.6	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
85	d1qypa_	Alignment	not modelled	37.2	30	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
86	c2jvnA_	Alignment	not modelled	37.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
87	d1sd4a_	Alignment	not modelled	37.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
88	d1tdza3	Alignment	not modelled	37.0	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
89	d1k82a3	Alignment	not modelled	36.7	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
90	d1pd0a5	Alignment	not modelled	36.6	18	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
91	c3hugA_	Alignment	not modelled	36.5	17	**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
92	c3eg9B_	Alignment	not modelled	35.8	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
93	d1x68a2	Alignment	not modelled	35.8	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
94	d1k3xa3	Alignment	not modelled	35.3	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
95	c2w3zA_	Alignment	not modelled	35.2	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
96	c1w17A_	Alignment	not modelled	35.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
97	d1tc3c_	Alignment	not modelled	34.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
98	c1ei3C_	Alignment	not modelled	34.3	11	**PDB header:** **PDB COMPND:**
99	c3eh2B_	Alignment	not modelled	34.2	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
100	d1ltla_	Alignment	not modelled	33.9	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
101	c2gajA_	Alignment	not modelled	33.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
102	d1ibia2	Alignment	not modelled	33.6	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
103	c2zq0B_	Alignment	not modelled	33.1	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
104	c3k7aM_	Alignment	not modelled	32.6	24	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
105	c1ei3E_	Alignment	not modelled	32.6	9	**PDB header:**

		Alignment	not modelled			**PDB COMPND:**
106	d1seta1	Alignment	not modelled	32.5	18	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
107	d2eppa1	Alignment	not modelled	32.4	21	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
108	d1x94a_	Alignment	not modelled	32.1	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
109	d2dlda2	Alignment	not modelled	32.0	21	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
110	d1okra_	Alignment	not modelled	31.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
111	d2c71a1	Alignment	not modelled	31.7	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
112	c1x3uA_	Alignment	not modelled	31.3	24	**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
113	c3bjiA_	Alignment	not modelled	30.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
114	c1m2vB_	Alignment	not modelled	30.7	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
115	d1gh9a_	Alignment	not modelled	30.5	23	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein MTH1184 **Family:**Hypothetical protein MTH1184
116	c3e0mB_	Alignment	not modelled	30.5	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
117	d1vd4a_	Alignment	not modelled	30.4	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
118	c3u50C_	Alignment	not modelled	30.1	14	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**telomerase-associated protein 82; **PDBTitle:** crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
119	d1m3sa_	Alignment	not modelled	30.0	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
120	c3egxB_	Alignment	not modelled	30.0	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1