
















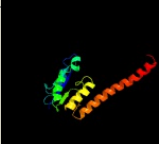




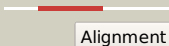

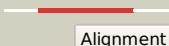
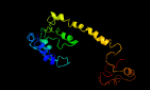





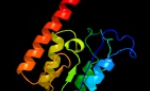

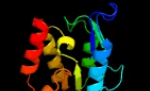











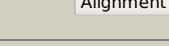
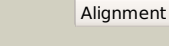



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1586c_(-)_1787103_1788512
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	aea76f02f57c2120

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bqqB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.
2	c4kisA_	 Alignment		100.0	19	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a Isr-dna complex
3	c3g13B_	 Alignment		100.0	21	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
4	c3guvA_	 Alignment		99.9	20	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
5	c2r0qF_	 Alignment		99.9	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
6	c2gm4B_	 Alignment		99.9	17	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
7	c6dgcA_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: isc1926 tnpa c-terminal catalytic domain; PDBTitle: crystal structure of the c-terminal catalytic domain of isc1926 tnpa,2 an is607-like serine recombinase
8	c3bvpB_	 Alignment		99.9	20	PDB header: recombination Chain: B: PDB Molecule: tp901-1 integrase; PDBTitle: crystal structure of the n-terminal catalytic domain of tp901-12 integrase
9	d1gdta2	 Alignment		99.9	16	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
10	c2mhcA_	 Alignment		99.9	18	PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpx
11	d2gm4a2	 Alignment		99.9	16	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain

12	c3lhkA	 Alignment		99.9	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.
13	c4m6fA	 Alignment		99.9	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-invertase; PDBTitle: dimer of the g-segment invertase bound to a dna substrate
14	c3lhfC	 Alignment		99.8	15	PDB header: recombination Chain: C: PDB Molecule: serine recombinase; PDBTitle: the crystal structure of a serine recombinase from sulfolobus2 solfataricus to 2.3a
15	d2rsla	 Alignment		99.8	17	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
16	c3ploX	 Alignment		99.8	24	PDB header: recombination Chain: X: PDB Molecule: dna-invertase; PDBTitle: crystal structure of the fis-independent mutant of gin
17	c3pkzK	 Alignment		99.8	21	PDB header: recombination Chain: K: PDB Molecule: recombinase sin; PDBTitle: structural basis for catalytic activation of a serine recombinase
18	c6dgbA	 Alignment		99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: is607 family transposase is1535; PDBTitle: crystal structure of the c-terminal catalytic domain of is1535 tnpa,2 an is607-like serine recombinase
19	d1hx7a	 Alignment		99.6	15	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
20	c2pmzB	 Alignment		93.0	13	PDB header: translation, transferase Chain: B: PDB Molecule: dna-directed rna polymerase subunit b; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
21	d1twfb	 Alignment	not modelled	92.8	16	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta
22	c4rulA	 Alignment	not modelled	92.3	14	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
23	c5flmB	 Alignment	not modelled	92.1	17	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase ii subunit rpb2; PDBTitle: structure of transcribing mammalian rna polymerase ii
24	c4c2mQ	 Alignment	not modelled	91.2	17	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase i subunit rpa135; PDBTitle: structure of rna polymerase i at 2.8 a resolution
25	c2gajA	 Alignment	not modelled	89.1	16	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
26	d2fiya1	 Alignment	not modelled	88.5	19	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
27	c3twkB	 Alignment	not modelled	88.3	9	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
28	c1k82D	 Alignment	not modelled	88.0	22	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

29	c3cngC	Alignment	not modelled	87.9	25	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
30	c4qiwB	Alignment	not modelled	87.4	12	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
31	c5flmI	Alignment	not modelled	87.1	27	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
32	c1i3qI	Alignment	not modelled	86.3	22	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
33	c6j6qF	Alignment	not modelled	85.9	12	PDB header: splicing Chain: F: PDB Molecule: splicing factor yju2; PDBTitle: cryo-em structure of the yeast b*-b2 complex at an average resolution2 of 3.7 angstrom
34	c5xonU	Alignment	not modelled	84.7	12	PDB header: transcription/rna Chain: U: PDB Molecule: general transcription elongation factor tfiis; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
35	c3h0gN	Alignment	not modelled	84.7	13	PDB header: transcription Chain: N: PDB Molecule: dna-directed rna polymerase ii subunit rpb2; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
36	c4c2mX	Alignment	not modelled	84.6	29	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
37	c1u78A	Alignment	not modelled	84.1	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposease; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposease bound to transposon dna
38	c2gb5B	Alignment	not modelled	82.9	24	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
39	c1ee8A	Alignment	not modelled	81.7	19	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
40	c3w0fA	Alignment	not modelled	81.1	18	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3)
41	c3gn5B	Alignment	not modelled	81.1	10	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)
42	c5fjaI	Alignment	not modelled	80.8	26	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
43	c5d5hA	Alignment	not modelled	80.6	16	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
44	c4mb7A	Alignment	not modelled	80.3	16	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like I720; PDBTitle: crystal structure of a viral dna glycosylase
45	c2kdxA	Alignment	not modelled	79.3	15	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
46	c1pqvS	Alignment	not modelled	77.8	16	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
47	c2k8dA	Alignment	not modelled	76.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
48	c1nnjA	Alignment	not modelled	76.5	16	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
49	c2f5qA	Alignment	not modelled	75.2	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
50	c2opfA	Alignment	not modelled	74.8	15	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
51	c3h0gI	Alignment	not modelled	73.3	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
52	d1dgsa1	Alignment	not modelled	69.2	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
53	d1twfi1	Alignment	not modelled	68.7	22	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain PDB header: transferase

54	c3pfqA	Alignment	not modelled	68.4	23	Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii
55	c1y1yS	Alignment	not modelled	68.2	27	PDB header: transferase/transcription/dna-rna hybrid Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
56	c6qg3P	Alignment	not modelled	68.1	23	PDB header: translation Chain: P: PDB Molecule: eukaryotic translation initiation factor 2 subunit beta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model b)
57	c5lycU	Alignment	not modelled	66.1	16	PDB header: transcription, transferase/dna Chain: U: PDB Molecule: transcription elongation factor a protein 1; PDBTitle: human core-pic in the initial transcribing state
58	c4l9mA	Alignment	not modelled	65.1	18	PDB header: signaling protein Chain: A: PDB Molecule: ras guanyl-releasing protein 1; PDBTitle: autoinhibited state of the ras-specific exchange factor rasgrp1
59	d1x6mA	Alignment	not modelled	64.7	29	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
60	d1p91a	Alignment	not modelled	64.3	26	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RlmA
61	c6o3pA	Alignment	not modelled	64.2	23	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
62	c2lvsA	Alignment	not modelled	63.2	22	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
63	c5z6vA	Alignment	not modelled	62.3	6	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
64	c3egxB	Alignment	not modelled	61.5	16	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1
65	d1ee8a3	Alignment	not modelled	61.5	25	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
66	d1l1da	Alignment	not modelled	61.3	12	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
67	d1tdza3	Alignment	not modelled	61.0	22	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
68	c2rowA	Alignment	not modelled	60.8	22	PDB header: transferase Chain: A: PDB Molecule: rho-associated protein kinase 2; PDBTitle: the c1 domain of rock ii
69	d1dl6a	Alignment	not modelled	60.4	16	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
70	c3cw2M	Alignment	not modelled	60.3	19	PDB header: translation Chain: M: PDB Molecule: translation initiation factor 2 subunit beta; PDBTitle: crystal structure of the intact archaeal translation initiation factor2 2 from sulfobolus solfataricus .
71	c2dcuB	Alignment	not modelled	59.9	23	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
72	c5ijlA	Alignment	not modelled	59.5	27	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
73	d1r2za3	Alignment	not modelled	59.4	23	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
74	c6paxA	Alignment	not modelled	59.2	15	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
75	d1l1ta3	Alignment	not modelled	59.1	23	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
76	c1neeA	Alignment	not modelled	58.9	23	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 beta PDBTitle: structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
77	d1wiia	Alignment	not modelled	58.9	23	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
78	c3a44D	Alignment	not modelled	58.4	15	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
79	c3nklA	Alignment	not modelled	58.2	10	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase;

79	c3lka	Alignment	not modelled	58.2	10	PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
80	d2g9wa1	Alignment	not modelled	58.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
81	d1sd4a	Alignment	not modelled	57.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
82	d1k81a	Alignment	not modelled	56.6	19	Fold: Zinc-binding domain of translation initiation factor 2 beta Superfamily: Zinc-binding domain of translation initiation factor 2 beta Family: Zinc-binding domain of translation initiation factor 2 beta
83	d1k82a3	Alignment	not modelled	56.2	19	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	c3k1fM	Alignment	not modelled	56.1	24	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
85	c4m1bA	Alignment	not modelled	55.5	11	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
86	c6hmsB	Alignment	not modelled	55.5	27	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
87	d1tfia	Alignment	not modelled	55.4	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
88	d1ivsa1	Alignment	not modelled	55.2	11	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
89	c4y66D	Alignment	not modelled	55.1	13	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
90	c3eswA	Alignment	not modelled	55.1	27	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
91	d1k3xa3	Alignment	not modelled	55.1	24	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
92	d1x3za1	Alignment	not modelled	54.6	23	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
93	d1libia2	Alignment	not modelled	54.2	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
94	c2riqA	Alignment	not modelled	53.4	15	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: crystal structure of the third zinc-binding domain of human parp-1
95	c2e9hA	Alignment	not modelled	52.8	23	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
96	d1okra	Alignment	not modelled	52.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
97	c5iy9M	Alignment	not modelled	52.1	16	PDB header: transcription, transferase/dna/rna Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: human holo-pic in the initial transcribing state (no iis)
98	c2vrwB	Alignment	not modelled	51.6	16	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
99	d2f4ma1	Alignment	not modelled	51.3	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
100	c4v1oM	Alignment	not modelled	51.1	19	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
101	c3eg9B	Alignment	not modelled	50.2	22	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
102	d1pd0a5	Alignment	not modelled	50.0	13	Fold: Rubredoxin-like Superfamily: Zn-finger domain of Sec23/24 Family: Zn-finger domain of Sec23/24
103	c4opxD	Alignment	not modelled	49.2	15	PDB header: transferase/dna/transferase inhibitor Chain: D: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: structure of human parp-1 bound to a dna double strand break in2 complex with (2r)-5-fluoro-2-methyl-2,3-dihydro-1-benzofuran-7-3 carboxamide
104	c1m2vB	Alignment	not modelled	49.2	13	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
105	c2e2zA	Alignment	not modelled	48.8	21	PDB header: protein transport, chaperone regulator Chain: A: PDB Molecule: tim15; PDBTitle: solution nmr structure of yeast tim15, co-chaperone of2

						mitochondrial hsp70
106	d1tc3c_	Alignment	not modelled	48.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
107	d1pfta_	Alignment	not modelled	47.9	20	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
108	c3eh2B_	Alignment	not modelled	47.8	19	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
109	c3hcb_	Alignment	not modelled	47.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
110	c3u50C_	Alignment	not modelled	47.2	23	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
111	d1pdnc_	Alignment	not modelled	47.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
112	c5fa9B_	Alignment	not modelled	46.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
113	d1tbna_	Alignment	not modelled	46.4	30	Fold: Cysteine-rich domain Superfamily: Cysteine-rich domain Family: Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
114	c3cezA_	Alignment	not modelled	46.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
115	d1p6ra_	Alignment	not modelled	46.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
116	d1xm0a1	Alignment	not modelled	45.8	17	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
117	c2eliA_	Alignment	not modelled	45.5	25	PDB header: transferase Chain: A: PDB Molecule: protein kinase c alpha type; PDBTitle: solution structure of the second phorbol2 esters/diacylglycerol binding domain of human protein3 kinase c alpha type
118	c4cgkA_	Alignment	not modelled	45.4	8	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
119	c2l1uA_	Alignment	not modelled	45.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
120	c3ky9B_	Alignment	not modelled	44.6	16	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1