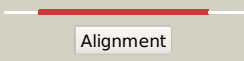

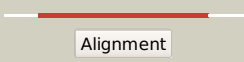

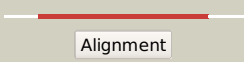

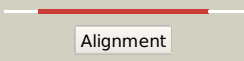

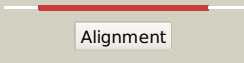

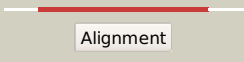

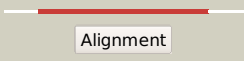

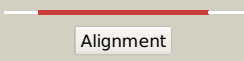

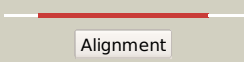

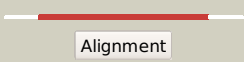

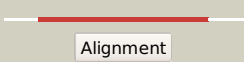
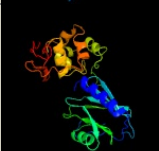








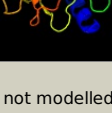


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2464c (-)_2766869_2767675
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	033dc5b2a79f0f06

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f5qA_			100.0	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
2	c1k82D_			100.0	26	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
3	c1nnjA_			100.0	24	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
4	c1ee8A_			100.0	28	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
5	c2opfA_			100.0	25	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
6	c3twkB_			100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
7	c3a46B_			100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
8	c3w0fA_			100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3)
9	c4mb7A_			100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like l720; PDBTitle: crystal structure of a viral dna glycosylase
10	c1tdhA_			100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: nei endonuclease viii-like 1; PDBTitle: crystal structure of human endonuclease viii-like 1 (nei1)
11	c5ituB_			100.0	22	PDB header: dna binding protein/dna Chain: B: PDB Molecule: endonuclease 8-like 1; PDBTitle: crystal structure of human nei1(242k) bound to duplex dna containing2 thf

12	d1r2za1	Alignment		100.0	34	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
13	d1k82a1	Alignment		100.0	27	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
14	d1ee8a1	Alignment		100.0	35	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
15	d1tdza1	Alignment		100.0	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
16	d1k3xa1	Alignment		100.0	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
17	d1k82a2	Alignment		99.9	19	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
18	d1ee8a2	Alignment		99.9	21	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
19	d1r2za2	Alignment		99.9	17	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
20	d1tdza2	Alignment		99.9	19	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
21	d1k3xa2	Alignment	not modelled	99.9	20	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
22	d1tdha1	Alignment	not modelled	99.8	27	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
23	d1tdha2	Alignment	not modelled	99.8	18	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
24	d2hkja1	Alignment	not modelled	99.7	12	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
25	d1ee8a3	Alignment	not modelled	99.6	34	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
26	d1r2za3	Alignment	not modelled	99.5	38	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
27	d1tdza3	Alignment	not modelled	99.5	36	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
28	d1k82a3	Alignment	not modelled	99.5	44	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
						Fold: Glucocorticoid receptor-like (DNA-binding domain)

29	d1l1ta3	Alignment	not modelled	99.5	41	Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
30	d1k3xa3	Alignment	not modelled	99.5	46	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
31	c3doA	Alignment	not modelled	97.4	12	PDB header: protein binding Chain: A: PDB Molecule: fibrinogen binding protein; PDBTitle: the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
32	d2uubm1	Alignment	not modelled	97.0	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
33	c3iz6M	Alignment	not modelled	96.8	22	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
34	c2zkqm	Alignment	not modelled	96.7	27	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
35	d2gy9m1	Alignment	not modelled	96.7	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
36	c5o5jM	Alignment	not modelled	96.7	17	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
37	c2xznM	Alignment	not modelled	96.7	18	PDB header: ribosome Chain: M: PDB Molecule: rps18e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
38	d1i94m	Alignment	not modelled	96.6	20	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
39	c3j20O	Alignment	not modelled	96.5	14	PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
40	c5xyiS	Alignment	not modelled	96.4	24	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
41	c3zeyM	Alignment	not modelled	96.0	14	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
42	c5mmjm	Alignment	not modelled	95.6	14	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
43	c1mx0D	Alignment	not modelled	94.9	14	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
44	c5h3xA	Alignment	not modelled	94.6	13	PDB header: cell adhesion Chain: A: PDB Molecule: fibrinectin/fibrinogen binding protein; PDBTitle: the structure of the n-terminal of the fibrinectin/fibrinogen-binding2 protein from streptococcus suis (fbps)
45	c6ifsB	Alignment	not modelled	93.8	21	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
46	c4gc5A	Alignment	not modelled	93.3	12	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m
47	d2i0za2	Alignment	not modelled	93.3	18	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
48	c4itqA	Alignment	not modelled	93.1	25	PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
49	c6erpJ	Alignment	not modelled	91.8	5	PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter
50	c3fuxB	Alignment	not modelled	90.1	17	PDB header: transferase Chain: B: PDB Molecule: dimethyladenosine transferase; PDBTitle: t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
51	c2gb5B	Alignment	not modelled	89.4	21	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
52	c3fteA	Alignment	not modelled	88.9	16	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
53	d1qyra	Alignment	not modelled	88.7	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like

54	d2gqfa2	Alignment	not modelled	85.9	8	Fold: HI0933 insert domain-like Superfamily: HI0933 insert domain-like Family: HI0933 insert domain-like
55	c2m6nA_	Alignment	not modelled	85.1	21	PDB header: cell cycle Chain: A: PDB Molecule: ef-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
56	c4rulA_	Alignment	not modelled	84.4	26	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
57	c3uzuA_	Alignment	not modelled	84.4	15	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
58	c3bbnM_	Alignment	not modelled	84.3	17	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein s13; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
59	c4jxA_	Alignment	not modelled	83.3	15	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
60	d2fiya1	Alignment	not modelled	83.1	23	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
61	d2f4ma1	Alignment	not modelled	82.3	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
62	c4ui9S_	Alignment	not modelled	80.6	14	PDB header: cell cycle Chain: S: PDB Molecule: ef-box only protein 5; PDBTitle: atomic structure of the human anaphase-promoting complex
63	c1yuzB_	Alignment	not modelled	79.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
64	c6o3pA_	Alignment	not modelled	74.5	13	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
65	c3u50C_	Alignment	not modelled	74.0	24	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
66	c3tqsB_	Alignment	not modelled	73.7	16	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
67	c2h1rA_	Alignment	not modelled	73.6	11	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase, putative; PDBTitle: crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
68	d2jneal	Alignment	not modelled	72.2	17	Fold: Rubredoxin-like Superfamily: YfgJ-like Family: YfgJ-like
69	c2jneA_	Alignment	not modelled	72.2	17	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein yfgj; PDBTitle: nmr structure of e.coli yfgj modelled with two zn+2 bound. northeast2 structural genomics consortium target er317.
70	c5fywW_	Alignment	not modelled	72.0	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
71	c1dvbA_	Alignment	not modelled	71.1	20	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
72	c2jrpA_	Alignment	not modelled	70.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
73	c6i52C_	Alignment	not modelled	70.5	21	PDB header: dna binding protein Chain: C: PDB Molecule: replication factor a protein 1; PDBTitle: yeast rpa bound to ssdna
74	c2lcqA_	Alignment	not modelled	69.0	20	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
75	c4gopC_	Alignment	not modelled	66.4	32	PDB header: dna binding protein/dna Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
76	c4kblA_	Alignment	not modelled	66.2	18	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase arih1; PDBTitle: structure of hhari, a ring-ibr-ring ubiquitin ligase: autoinhibition2 of an ariadne-family e3 and insights into ligation mechanism
77	c5fmrR_	Alignment	not modelled	64.9	23	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
78	c2ztkB_	Alignment	not modelled	64.3	15	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b;

78	c2z0k6	Alignment	not modelled	64.3	13	PDBTitle: crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms PDB header: transcription
79	c5oqmW	Alignment	not modelled	62.9	23	Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiie and2 core mediator
80	c5ijlA	Alignment	not modelled	61.9	41	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
81	c1dgsB	Alignment	not modelled	61.3	39	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
82	c5oqiW	Alignment	not modelled	61.2	31	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiie
83	d1l1oc	Alignment	not modelled	59.2	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
84	d1qf8a	Alignment	not modelled	59.1	28	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
85	c5d5hA	Alignment	not modelled	58.4	13	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
86	d1pfta	Alignment	not modelled	57.6	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
87	c6hmsB	Alignment	not modelled	57.4	41	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
88	c2owoA	Alignment	not modelled	57.3	38	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
89	d1odha	Alignment	not modelled	56.7	17	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
90	d1x3za1	Alignment	not modelled	56.4	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
91	c6gymW	Alignment	not modelled	56.0	23	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
92	d2k4xa1	Alignment	not modelled	55.7	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
93	c2kpiA	Alignment	not modelled	55.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sco3027; PDBTitle: solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
94	c5ah5B	Alignment	not modelled	54.8	38	PDB header: ligase/rna Chain: B: PDB Molecule: leucine--trna ligase; PDBTitle: crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agn2 leu-trna-leuams
95	d2akla2	Alignment	not modelled	54.6	30	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
96	c5edvB	Alignment	not modelled	54.3	26	PDB header: ligase/transferase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rnf31; PDBTitle: structure of the hoip-rbr/ubch5b~ubiquitin transfer complex
97	c2mvwA	Alignment	not modelled	53.8	35	PDB header: metal binding protein Chain: A: PDB Molecule: protein pml; PDBTitle: solution structure of the trim19 b-box1 (b1) of human promyelocytic leukemia (pml)
98	c3eg9B	Alignment	not modelled	53.3	23	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
99	c4k95G	Alignment	not modelled	53.1	31	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
100	c5f4tA	Alignment	not modelled	52.6	33	PDB header: cell adhesion Chain: A: PDB Molecule: izumo sperm-egg fusion protein 1; PDBTitle: crystal structure of the human sperm izumo1 residues 22-254
101	c2hr5B	Alignment	not modelled	52.4	25	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
102	c4u3eA	Alignment	not modelled	51.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
103	c5iy9Q	Alignment	not modelled	51.8	31	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)

104	c2m9yA_	Alignment	not modelled	51.7	27	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase arih1; PDBTitle: solution structure of the catalytic domain of hhari
105	c2js4A_	Alignment	not modelled	51.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein bb2007; PDBTitle: solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
106	c1pd0A_	Alignment	not modelled	51.6	23	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
107	c3wwnB_	Alignment	not modelled	51.3	27	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
108	c1wz2B_	Alignment	not modelled	49.8	31	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
109	c2m48A_	Alignment	not modelled	49.5	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: solution structure of ibr-ring2 tandem domain from parkin
110	d1twfi2	Alignment	not modelled	49.4	24	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
111	d2avue1	Alignment	not modelled	49.4	32	Fold: FlhC-like Superfamily: FlhC-like Family: FlhC-like
112	c2xzn9_	Alignment	not modelled	49.2	29	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
113	c2jr6A_	Alignment	not modelled	48.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein nma0874; PDBTitle: solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
114	c1m2vB_	Alignment	not modelled	48.6	23	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
115	c5b5kA_	Alignment	not modelled	48.0	33	PDB header: cell adhesion Chain: A: PDB Molecule: izumo sperm-egg fusion protein 1; PDBTitle: crystal structure of izumo1, the mammalian sperm ligand for egg juno
116	d1jwhc_	Alignment	not modelled	47.7	28	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
117	c6f5zC_	Alignment	not modelled	47.2	8	PDB header: transferase Chain: C: PDB Molecule: upf0434 family protein; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
118	c2riqA_	Alignment	not modelled	46.9	24	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
119	d1ctla1	Alignment	not modelled	46.8	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
120	d1libia1	Alignment	not modelled	46.7	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain