
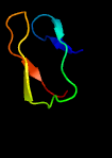
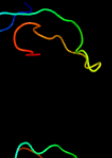

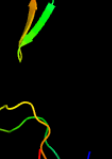

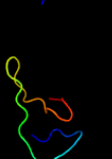
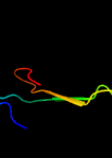
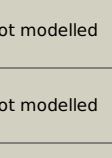


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1684 (-) _1910593_1910817
Date	Fri Aug 2 13:30:28 BST 2019
Unique Job ID	ea0cf2619e246a9b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2js4A_	Alignment		99.9	35	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
2	c2k5rA_	Alignment		99.9	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein xf2673; PDBTitle: solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
3	d2jnya1	Alignment		99.9	54	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
4	d2hf1a1	Alignment		99.9	46	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
5	c2jr6A_	Alignment		99.9	39	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
6	d2pk7a1	Alignment		99.9	46	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
7	c2kpiA_	Alignment		99.9	46	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
8	c6f5zC_	Alignment		99.9	42	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
9	c6g4wr_	Alignment		98.6	35	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
10	c5cm2M_	Alignment		98.6	22	PDB header: transferase Chain: M: PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
11	c2j6aA_	Alignment		98.6	30	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.

12	d1p91a_	Alignment		97.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RImA
13	c3vpbF_	Alignment		95.5	14	PDB header: ligase Chain: F: PDB Molecule: alpha-aminoadipate carrier protein lysw; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
14	c3k1fM_	Alignment		94.1	21	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
15	c3wwnB_	Alignment		93.3	16	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
16	d1dl6a_	Alignment		92.4	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
17	c4v1oM_	Alignment		92.2	22	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
18	c6f42V_	Alignment		92.1	14	PDB header: transcription Chain: V: PDB Molecule: transcription factor iiib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
19	c3k7aM_	Alignment		91.7	17	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
20	c5fz5M_	Alignment		91.6	22	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
21	d2akla2	Alignment	not modelled	91.5	15	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
22	c5jy9M_	Alignment	not modelled	91.2	19	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)
23	d1pfta_	Alignment	not modelled	90.2	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
24	c5k2mF_	Alignment	not modelled	89.9	16	PDB header: biosynthetic protein Chain: F: PDB Molecule: probable lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
25	c2aklA_	Alignment	not modelled	89.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
26	c6cnbR_	Alignment	not modelled	87.2	11	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
27	c2gb5B_	Alignment	not modelled	84.8	12	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
28	c2nb9A_	Alignment	not modelled	82.4	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
						PDB header: transferase activator/transferase

29	c3q87A_	Alignment	not modelled	82.2	21	Chain: A: PDB Molecule: putative uncharacterized protein ecu08_1170; PDBTitle: structure of e. cuculicus mtq2-trm112 complex responsible for the2 methylation of erf1 translation termination factor
30	c2e9hA_	Alignment	not modelled	80.7	15	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
31	c2jrpA_	Alignment	not modelled	78.0	14	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
32	c2dcuB_	Alignment	not modelled	77.5	14	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
33	c6qg3P_	Alignment	not modelled	76.4	10	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)
34	c2jneA_	Alignment	not modelled	74.4	14	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.
35	d2jneA1	Alignment	not modelled	74.4	14	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
36	c3cngC_	Alignment	not modelled	73.0	18	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
37	d1dgsa1	Alignment	not modelled	72.8	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
38	c4c2mX_	Alignment	not modelled	72.8	8	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
39	c2owoA_	Alignment	not modelled	70.5	17	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
40	c2k5cA_	Alignment	not modelled	70.1	28	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
41	c4glxA_	Alignment	not modelled	69.4	16	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
42	c2f5qA_	Alignment	not modelled	68.1	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
43	c5xogM_	Alignment	not modelled	68.1	14	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor 1 homolog; PDBTitle: rna polymerase ii elongation complex bound with spt5 kow5 and elf1
44	d1k81a_	Alignment	not modelled	67.8	16	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
45	c2f9iD_	Alignment	not modelled	65.7	7	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
46	c3h0gl_	Alignment	not modelled	65.2	16	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
47	c1neeA_	Alignment	not modelled	65.2	12	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 beta PDBTitle: structure of archaeal translation factor aif2beta from2 methanobacterium thermoautotrophicum
48	c4ui9S_	Alignment	not modelled	65.2	11	PDB header: cell cycle Chain: S: PDB Molecule: f-box only protein 5; PDBTitle: atomic structure of the human anaphase-promoting complex
49	c1nnjA_	Alignment	not modelled	65.1	8	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
50	c3cw2M_	Alignment	not modelled	64.9	10	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 .
51	d2fiya1	Alignment	not modelled	64.8	16	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
52	d1wiia_	Alignment	not modelled	64.4	11	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
53	c1ee8A_	Alignment	not modelled	64.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
						PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii;

54	c2opfA_	Alignment	not modelled	63.6	8	PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
55	c5iy9Q_	Alignment	not modelled	63.1	15	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)
56	c1k82D_	Alignment	not modelled	61.0	15	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
57	c5oqj3_	Alignment	not modelled	58.6	25	PDB header: transcription Chain: 3: PDB Molecule: rna polymerase ii transcription factor b subunit 3; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
58	c1i3ql_	Alignment	not modelled	58.5	13	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
59	c5fywW_	Alignment	not modelled	58.2	15	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
60	c3w0fA_	Alignment	not modelled	58.0	7	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mneil3)
61	c5fmfR_	Alignment	not modelled	54.4	15	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
62	c6o3pA_	Alignment	not modelled	54.3	22	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
63	c2f9yB_	Alignment	not modelled	53.6	14	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
64	d2f9yb1	Alignment	not modelled	53.6	14	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
65	d1tdza3	Alignment	not modelled	52.5	8	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	d1k82a3	Alignment	not modelled	52.4	15	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
67	d2ct7a1	Alignment	not modelled	52.2	8	Fold: RING/U-box Superfamily: RING/U-box Family: !BR domain
68	c5flml_	Alignment	not modelled	51.8	18	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
69	c2gajA_	Alignment	not modelled	51.4	10	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
70	d1r2za3	Alignment	not modelled	51.1	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
71	d1l1ta3	Alignment	not modelled	49.9	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
72	d1k3xa3	Alignment	not modelled	49.1	8	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
73	c2y43B_	Alignment	not modelled	48.8	11	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rad18; PDBTitle: rad18 ubiquitin ligase ring domain structure
74	c1v9pB_	Alignment	not modelled	47.6	27	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
75	c3twkB_	Alignment	not modelled	47.6	21	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
76	c1dgsB_	Alignment	not modelled	46.2	27	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
77	c2m6nA_	Alignment	not modelled	45.6	10	PDB header: cell cycle Chain: A: PDB Molecule: f-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
78	d1fqta_	Alignment	not modelled	45.4	11	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
79	d1vm9a_	Alignment	not modelled	43.5	15	Fold: ISP domain Superfamily: ISP domain

						Family: Rieske iron-sulfur protein (ISP)
80	c3bvoA	Alignment	not modelled	42.7	16	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
81	d1ee8a3	Alignment	not modelled	42.7	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
82	d1bora	Alignment	not modelled	39.6	12	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
83	d3c0da1	Alignment	not modelled	37.6	8	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
84	d1weva	Alignment	not modelled	36.2	19	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
85	c3ndjA	Alignment	not modelled	36.2	24	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
86	c6qajB	Alignment	not modelled	35.9	20	PDB header: nuclear protein Chain: B: PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
87	c5oqjW	Alignment	not modelled	35.5	16	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
88	c2ecwA	Alignment	not modelled	35.5	23	PDB header: apoptosis Chain: A: PDB Molecule: tripartite motif-containing protein 30; PDBTitle: solution structure of the zinc finger, c3hc4 type (ring2 finger) domain tripartite motif protein 30
89	d2jzaa1	Alignment	not modelled	35.4	24	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
90	c2riqA	Alignment	not modelled	34.8	32	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
91	d1lloc	Alignment	not modelled	34.7	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
92	d1jm7b	Alignment	not modelled	34.2	14	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
93	c5oqmW	Alignment	not modelled	34.1	16	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
94	d1lv3a	Alignment	not modelled	34.0	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
95	c2pptA	Alignment	not modelled	33.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
96	c6o9l3	Alignment	not modelled	33.5	10	PDB header: transcription/dna Chain: 3: PDB Molecule: cdk-activating kinase assembly factor mat1; PDBTitle: human holo-pic in the closed state
97	c6nmiH	Alignment	not modelled	33.5	10	PDB header: transcription Chain: H: PDB Molecule: cdk-activating kinase assembly factor mat1; PDBTitle: cryo-em structure of the human tfiih core complex
98	c2jvnA	Alignment	not modelled	32.3	38	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: domain c of human parp-1
99	c2qkdA	Alignment	not modelled	31.9	18	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
100	c2de7E	Alignment	not modelled	31.1	21	PDB header: oxidoreductase Chain: E: PDB Molecule: ferredoxin component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
101	c4r7eA	Alignment	not modelled	30.8	14	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase bre1; PDBTitle: structure of bre1 ring domain
102	c6gymW	Alignment	not modelled	30.6	16	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
103	c2i7fB	Alignment	not modelled	30.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin component of dioxygenase; PDBTitle: sphingomonas yanoikuyae b1 ferredoxin
104	c3gceA	Alignment	not modelled	29.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin component of carbazole 1,9a- PDBTitle: ferredoxin of carbazole 1,9a-dioxygenase from nocardiooides2 aromaticivorans ic177
105	c6o9lQ	Alignment	not modelled	27.9	15	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state

106	c3d89A_	Alignment	not modelled	27.5	21	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
107	d2baya1	Alignment	not modelled	27.0	23	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
108	c4zdtA_	Alignment	not modelled	26.8	7	PDB header: hydrolase Chain: A: PDB Molecule: structure-specific endonuclease subunit slx1; PDBTitle: crystal structure of the ring finger domain of slx1 in complex with2 the c-terminal domain of slx4
109	c6i52C_	Alignment	not modelled	26.7	11	PDB header: dna binding protein Chain: C: PDB Molecule: replication factor a protein 1; PDBTitle: yeast rpa bound to ssdna
110	c1wcoN_	Alignment	not modelled	26.6	45	PDB header: peptide/antibiotic Chain: N: PDB Molecule: nisin z; PDBTitle: the solution structure of the nisin-lipid ii complex
111	c5fjaI_	Alignment	not modelled	25.9	21	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
112	c2hl7A_	Alignment	not modelled	25.2	29	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
113	c4s3oC_	Alignment	not modelled	24.9	13	PDB header: ligase/transcription Chain: C: PDB Molecule: polycomb group ring finger protein 5; PDBTitle: pcgf5-ring1b-ubch5c complex
114	c2qpzA_	Alignment	not modelled	24.5	8	PDB header: metal binding protein Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase system ferredoxin PDBTitle: naphthalene 1,2-dioxygenase rieske ferredoxin
115	c5aaqA_	Alignment	not modelled	24.3	15	PDB header: calcium-binding protein Chain: A: PDB Molecule: calcium-binding and coiled-coil domain-containing protein PDBTitle: tbk1 recruitment to cytosol-invading salmonella induces2 anti-bacterial autophagy
116	c2yu4A_	Alignment	not modelled	23.9	17	PDB header: apoptosis Chain: A: PDB Molecule: e3 sumo-protein ligase nse2; PDBTitle: solution structure of the sp-ring domain in non-smc element2 2 homolog (mms21, s. cerevisiae)
117	c2kdxA_	Alignment	not modelled	23.8	10	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
118	d1pfva3	Alignment	not modelled	23.6	19	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
119	d1jm7a_	Alignment	not modelled	23.5	16	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
120	c4opxD_	Alignment	not modelled	23.0	32	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