

Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3251c_(rubA)_3630568_3630735
 Date Thu Aug 8 16:20:45 BST 2019
 Unique Job ID 9596fd9acff967e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2m4yA_	Alignment		100.0	84	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: rubredoxin type protein from mycobacterium ulcerans
2	d4rxna_	Alignment		99.9	47	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
3	d1iroa_	Alignment		99.9	46	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
4	c2v3bB_	Alignment		99.9	58	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
5	d2rdva_	Alignment		99.9	45	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
6	d2dsxa1	Alignment		99.9	49	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
7	c1s24A_	Alignment		99.9	48	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
8	d1s24a_	Alignment		99.9	48	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
9	d1iu5a_	Alignment		99.9	49	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
10	d1brfa_	Alignment		99.9	44	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
11	d1qcva_	Alignment		99.9	37	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin

12	d1h7va_	Alignment		99.9	35	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
13	c2kn9A_	Alignment		99.9	52	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
14	d1dx8a_	Alignment		99.9	34	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
15	c2ms3A_	Alignment		99.9	35	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the nmr structure of the rubredoxin domain of the no reductase2 flavorubredoxin from escherichia coli
16	d1rb9a_	Alignment		99.9	46	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
17	d6rxna_	Alignment		99.8	52	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
18	c5xpdA_	Alignment		99.7	46	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
19	d1lkoa2	Alignment		98.4	53	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
20	c2hr5B_	Alignment		98.2	35	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
21	c1dvvA_	Alignment	not modelled	98.1	44	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
22	c1yuzB_	Alignment	not modelled	98.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
23	d1nnqa2	Alignment	not modelled	98.0	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
24	d1yuza2	Alignment	not modelled	98.0	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
25	c4tpuA_	Alignment	not modelled	97.6	42	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: crystal structure of ferredoxin-dependent disulfide reductase from2 methanosarcina acetivorans
26	c3a44D_	Alignment	not modelled	92.6	36	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
27	c5fywW_	Alignment	not modelled	90.7	30	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
28	d2gmg1	Alignment	not modelled	89.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like PDB header: metal-binding protein

29	c2kdxA	Alignment	not modelled	89.4	26	Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
30	c5zb8B	Alignment	not modelled	89.4	33	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
31	c5iy9Q	Alignment	not modelled	88.9	29	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)
32	c6gymW	Alignment	not modelled	88.9	26	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccdlist)
33	c5fmrR	Alignment	not modelled	87.0	26	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
34	c6o9lQ	Alignment	not modelled	86.2	29	PDB header: transcription/dna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
35	c5oqmW	Alignment	not modelled	85.8	26	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
36	c5oqjW	Alignment	not modelled	85.6	26	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
37	c4zlhB	Alignment	not modelled	82.5	31	PDB header: metal binding protein Chain: B: PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
38	c6ok1B	Alignment	not modelled	77.7	35	PDB header: transport protein Chain: B: PDB Molecule: chsh2(duf35); PDBTitle: ltp2-chsh2(duf35) aldolase
39	c5l9wC	Alignment	not modelled	77.3	22	PDB header: ligase Chain: C: PDB Molecule: acetophenone carboxylase beta subunit; PDBTitle: crystal structure of the apc core complex
40	c2m6oA	Alignment	not modelled	76.7	38	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
41	c3h0gl	Alignment	not modelled	76.5	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
42	c5mg5W	Alignment	not modelled	76.4	23	PDB header: transferase Chain: W: PDB Molecule: 2,4-diacetylphloroglucinol biosynthesis protein; PDBTitle: a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
43	d1vd4a	Alignment	not modelled	75.7	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
44	c3glsC	Alignment	not modelled	74.5	27	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
45	c4u3eA	Alignment	not modelled	73.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase
46	d2gnra1	Alignment	not modelled	68.2	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
47	d1m2ka	Alignment	not modelled	67.4	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
48	c2lcqA	Alignment	not modelled	67.0	38	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
49	d1yc5a1	Alignment	not modelled	66.4	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
50	d1hk8a	Alignment	not modelled	65.9	17	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
51	c1hk8A	Alignment	not modelled	65.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
52	c5ol0B	Alignment	not modelled	65.5	19	PDB header: hydrolase Chain: B: PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
53	c6et9H	Alignment	not modelled	64.7	34	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus

						thermolithotrophicus at 2.75 a
54	c4o64C	Alignment	not modelled	64.6	26	PDB header: metal binding protein Chain: C: PDB Molecule: lysine-specific demethylase 2b; PDBTitle: zinc fingers of kdm2b
55	c1i3ql	Alignment	not modelled	63.7	24	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
56	d1fp0a1	Alignment	not modelled	61.3	20	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
57	d1q1aa	Alignment	not modelled	60.7	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
58	d2ak3a2	Alignment	not modelled	60.1	17	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
59	c5flml	Alignment	not modelled	57.9	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
60	c1fp0A	Alignment	not modelled	57.8	20	PDB header: transcription Chain: A: PDB Molecule: kap-1 corepressor; PDBTitle: solution structure of the phd domain from the kap-12 corepressor
61	c4c2mX	Alignment	not modelled	57.5	20	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
62	c3g9yA	Alignment	not modelled	56.4	40	PDB header: transcription/rna Chain: A: PDB Molecule: zinc finger ran-binding domain-containing protein 2; PDBTitle: crystal structure of the second zinc finger from zranb2/znf265 bound to 6 nt ssrna sequence agguaa
63	c6nmiF	Alignment	not modelled	53.3	32	PDB header: transcription Chain: F: PDB Molecule: general transcription factor iih subunit 3, p34; PDBTitle: cryo-em structure of the human tfiih core complex
64	d2akla2	Alignment	not modelled	51.0	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
65	c1bboA	Alignment	not modelled	50.7	14	PDB header: dna-binding protein Chain: A: PDB Molecule: human enhancer-binding protein mbp-1; PDBTitle: high-resolution solution structure of the double cys2*his22 zinc finger from the human enhancer binding protein mbp-1
66	c5m45l	Alignment	not modelled	50.3	14	PDB header: ligase Chain: I: PDB Molecule: acetone carboxylase gamma subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
67	d1wila	Alignment	not modelled	48.6	20	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: variant PHD-like domain
68	c2k1A	Alignment	not modelled	48.1	40	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
69	d1wgma	Alignment	not modelled	47.6	12	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
70	c2k0A	Alignment	not modelled	46.6	40	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
71	c3zg6A	Alignment	not modelled	46.1	16	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
72	c1q14A	Alignment	not modelled	46.0	27	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of sir2
73	c5jneA	Alignment	not modelled	45.7	31	PDB header: ligase/signaling protein Chain: A: PDB Molecule: e3 sumo-protein ligase siz1,ubiquitin-like protein smt3; PDBTitle: e2-sumo-siz1 e3-sumo-pcna complex
74	d1t1ha	Alignment	not modelled	45.0	27	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
75	c2k5cA	Alignment	not modelled	44.7	22	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
76	c2e61A	Alignment	not modelled	44.5	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: zinc finger cw-type pwwp domain protein 1; PDBTitle: solution structure of the zf-cw domain in zinc finger cw-type pwwp2 domain protein 1
77	c2mxvA	Alignment	not modelled	43.8	44	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 10; PDBTitle: nmr structure of the first zinc finger domain of rbm10
78	c5fjal	Alignment	not modelled	43.7	11	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
79	c4bbqA	Alignment	not modelled	43.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 2a; PDBTitle: crystal structure of the cxxc and phd domain of human

						lysine-specific2 demethylase 2a (kdm2a)(fbx11)
80	d1e4va2	Alignment	not modelled	43.0	7	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
81	c5iy9M	Alignment	not modelled	43.0	50	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)
82	d1mm2a	Alignment	not modelled	42.9	26	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
83	c1n0zA	Alignment	not modelled	42.0	55	PDB header: transcription Chain: A: PDB Molecule: znf265; PDBTitle: solution structure of the first zinc-finger domain from2 znf265
84	d1mm3a	Alignment	not modelled	40.6	26	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
85	d1akya2	Alignment	not modelled	40.4	10	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
86	c3i2dA	Alignment	not modelled	40.0	33	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase siz1; PDBTitle: crystal structure of s. cerevisiae sumo e3 ligase siz1
87	c3ja82	Alignment	not modelled	39.8	20	PDB header: hydrolase Chain: 2: PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
88	c5vbnB	Alignment	not modelled	39.4	19	PDB header: transferase Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
89	c3pkfF	Alignment	not modelled	39.1	17	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
90	d1p3ja2	Alignment	not modelled	39.0	17	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
91	d1zina2	Alignment	not modelled	39.0	17	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
92	c3k7aM	Alignment	not modelled	39.0	46	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
93	c4i5iA	Alignment	not modelled	38.7	32	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
94	c6g5iy	Alignment	not modelled	37.9	26	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
95	c2kreA	Alignment	not modelled	37.8	21	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin conjugation factor e4 b; PDBTitle: solution structure of e4b/ufd2a u-box domain
96	c3k35D	Alignment	not modelled	37.4	17	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
97	d1s3ga2	Alignment	not modelled	37.0	17	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
98	c5hh7A	Alignment	not modelled	36.8	23	PDB header: transcription Chain: A: PDB Molecule: origin of replication complex subunit 1b; PDBTitle: crystal structure of arabidopsis orc1b bah-phd cassette in complex2 with unmodified h3 peptide
99	c3k1fM	Alignment	not modelled	35.8	46	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
100	c5btrB	Alignment	not modelled	35.8	32	PDB header: hydrolase/substrate Chain: B: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of sirt1 in complex with resveratrol and an amc-2 containing peptide
101	c4fo9A	Alignment	not modelled	34.9	40	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase pias2; PDBTitle: crystal structure of the e3 sumo ligase pias2
102	c4mvtC	Alignment	not modelled	34.8	44	PDB header: ligase Chain: C: PDB Molecule: e3 sumo-protein ligase pias3; PDBTitle: crystal structure of sumo e3 ligase pias3
103	c3u5pF	Alignment	not modelled	34.4	27	PDB header: transcription Chain: F: PDB Molecule: e3 ubiquitin-protein ligase trim33; PDBTitle: crystal structure of the complex of trim33 phd-bromo and h3(1-28)2 k9me3k14ack18ack23ac histone peptide
104	c2f9iD	Alignment	not modelled	34.4	24	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
						PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a,

105	c3a1bA_	Alignment	not modelled	34.1	29	histone h3.1; PDBTitle: crystal structure of the dnmt3a add domain in complex with histone h3
106	c6g99B_	Alignment	not modelled	33.8	32	PDB header: rna binding protein Chain: B; PDB Molecule: rna-binding protein fus; PDBTitle: solution structure of fus-znf bound to uggug
107	d2c2la2	Alignment	not modelled	33.4	33	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
108	c2aklA_	Alignment	not modelled	32.7	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
109	c2kvgA_	Alignment	not modelled	31.9	33	PDB header: transcription Chain: A; PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
110	c1xwhA_	Alignment	not modelled	31.6	27	PDB header: transcription Chain: A; PDB Molecule: autoimmune regulator; PDBTitle: nmr structure of the first phd finger of autoimmune2 regulator protein (aire1): insights into apeced
111	d1pd0a5	Alignment	not modelled	31.1	25	Fold: Rubredoxin-like Superfamily: Zn-finger domain of Sec23/24 Family: Zn-finger domain of Sec23/24
112	c4pogC_	Alignment	not modelled	31.1	16	PDB header: replication, dna binding protein/dna Chain: C; PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure
113	c2lv9A_	Alignment	not modelled	30.9	27	PDB header: transferase Chain: A; PDB Molecule: histone-lysine n-methyltransferase ml15; PDBTitle: solution nmr structure of the phd domain of human ml15, northeast2 structural genomics consortium target hr6512a
114	c4wz1B_	Alignment	not modelled	30.9	42	PDB header: ligase Chain: B; PDB Molecule: e3 ubiquitin-protein ligase lubx; PDBTitle: crystal structure of u-box 2 of lubx / legu2 / lpp2887 from legionella2 pneumophila str. paris, wild-type
115	c5fz5M_	Alignment	not modelled	30.7	46	PDB header: transcription Chain: M; PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
116	c2j9uB_	Alignment	not modelled	30.2	50	PDB header: protein transport Chain: B; PDB Molecule: vacuolar protein sorting-associated protein 36; PDBTitle: 2 angstrom x-ray structure of the yeast escrt-i vps28 c-terminus in2 complex with the nzf-n domain from escrt-ii
117	d2j9ub1	Alignment	not modelled	30.2	50	Fold: Rubredoxin-like Superfamily: Ran binding protein zinc finger-like Family: Ran binding protein zinc finger-like
118	c2d9gA_	Alignment	not modelled	29.6	38	PDB header: transcription Chain: A; PDB Molecule: yy1-associated factor 2; PDBTitle: solution structure of the zf-ranbp domain of yy1-associated2 factor 2
119	c3s32A_	Alignment	not modelled	29.5	13	PDB header: transcription Chain: A; PDB Molecule: set1/ash2 histone methyltransferase complex subunit ash2; PDBTitle: crystal structure of ash2l n-terminal domain
120	c4me3A_	Alignment	not modelled	28.9	17	PDB header: replication Chain: A; PDB Molecule: dna replication licensing factor mcm related protein; PDBTitle: 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm