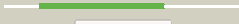
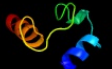
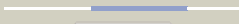
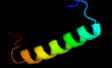






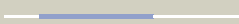
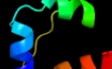

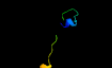










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2808 (-)_3115056_3115313
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	f8dd0637cae70e31

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lq1a_	 Alignment		58.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
2	d3e9va1	 Alignment		28.1	20	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
3	c5nm7A_	 Alignment		27.7	31	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan-binding domain 1; PDBTitle: crystal structure of burkholderia ap3 phage endolysin
4	c5ecfj_	 Alignment		26.7	14	PDB header: lipid binding protein Chain: J: PDB Molecule: cell wall antigen; PDBTitle: ligand binding domain 1 of penicillium marneffeii mp1 protein complexed2 with arachidonic acids
5	c2q01A_	 Alignment		25.8	28	PDB header: isomerase Chain: A: PDB Molecule: uronate isomerase; PDBTitle: crystal structure of glucuronate isomerase from caulobacter crescentus
6	d1fc3a_	 Alignment		25.3	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: Spo0A
7	c3w3sA_	 Alignment		19.8	19	PDB header: ligase/rna Chain: A: PDB Molecule: type-2 serine--trna ligase; PDBTitle: crystal structure of a. aeolicus trnasec in complex with m. kandleri2 serrs
8	d1dvka_	 Alignment		18.8	26	Fold: Functional domain of the splicing factor Prp18 Superfamily: Functional domain of the splicing factor Prp18 Family: Functional domain of the splicing factor Prp18
9	c4i6vA_	 Alignment		17.9	21	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase 2; PDBTitle: the crystal structure of an amidohydrolase 2 from planctomyces2 limnophilus dsm 3776
10	c2ky4A_	 Alignment		17.0	43	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
11	c5ietA_	 Alignment		17.0	38	PDB header: gene regulation Chain: A: PDB Molecule: bacterial proteasome activator; PDBTitle: crystal structure of mycobacterium tuberculosis atp-independent2 proteasome activator

12	c3ohwB_	Alignment		16.8	38	PDB header: protein binding Chain: B: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: x-ray structure of phycobilisome lcm core-membrane linker polypeptide2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e
13	c3b0bA_	Alignment		16.6	21	PDB header: dna binding protein Chain: A: PDB Molecule: centromere protein s; PDBTitle: crystal structure of the chicken cenp-s/cenp-x complex
14	c3pruD_	Alignment		16.1	43	PDB header: photosynthesis Chain: D: PDB Molecule: phycobilisome 32.1 kda linker polypeptide, phycocyanin- PDBTitle: crystal structure of phycobilisome 32.1 kda linker polypeptide,2 phycocyanin-associated, rod 1 (fragment 14-158) from synechocystis3 sp. pcc 6803, northeast structural genomics consortium target sgr182a
15	c6neqj_	Alignment		15.4	29	PDB header: ribosomal protein Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: structure of human mitochondrial translation initiation factor 3 bound2 to the small ribosomal subunit-class-ii
16	c3vh5A_	Alignment		15.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: cenp-s; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
17	d1jqna_	Alignment		14.6	31	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
18	d1uerc2	Alignment		14.3	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
19	c2i06A_	Alignment		13.8	37	PDB header: protein binding Chain: A: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
20	d3deoa1	Alignment		13.4	63	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
21	d1kkca2	Alignment	not modelled	13.0	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
22	d1rqba2	Alignment	not modelled	12.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
23	d2p4ka2	Alignment	not modelled	12.3	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
24	d1gyxa_	Alignment	not modelled	12.2	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
25	c1ma1E_	Alignment	not modelled	11.9	20	PDB header: oxidoreductase Chain: E: PDB Molecule: superoxide dismutase; PDBTitle: structure and properties of the atypical iron superoxide2 dismutase from methanobacterium thermoautotrophicum
26	c5tirB_	Alignment	not modelled	11.5	25	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of mn superoxide dismutase mutant m27v from2 trichoderma reesei
27	d2ouwa1	Alignment	not modelled	11.2	18	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
28	d1j5sa_	Alignment	not modelled	11.0	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
29	c1ddzA_	Alignment	not modelled	10.7	30	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase;

29	c1002A	Alignment	not modelled	10.7	30	PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
30	c2lxeA	Alignment	not modelled	10.7	21	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suvr4; PDBTitle: s4wyild
31	c4br6B	Alignment	not modelled	10.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of chaetomium thermophilum mnsod
32	d1ma1a2	Alignment	not modelled	10.5	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
33	c3dc5C	Alignment	not modelled	10.5	30	PDB header: oxidoreductase Chain: C: PDB Molecule: superoxide dismutase [mn] 2; PDBTitle: crystal structure of a manganese superoxide dismutases from2 caenorhabditis elegans
34	c3hj1A	Alignment	not modelled	10.5	24	PDB header: proton transport Chain: A: PDB Molecule: flagellar motor switch protein flig; PDBTitle: the structure of full-length flig from aquifex aeolicus
35	c1n0nB	Alignment	not modelled	10.4	25	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase [mn]; PDBTitle: catalytic and structural effects of amino-acid substitution at his302 in human manganese superoxide dismutase
36	d1jr9a2	Alignment	not modelled	10.1	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
37	c4lrcC	Alignment	not modelled	9.8	18	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
38	c3ak1C	Alignment	not modelled	9.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: superoxide dismutase [mn/fe]; PDBTitle: superoxide dismutase from aeropyrum pernix k1, apo-form
39	c2l3waA	Alignment	not modelled	9.6	37	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome rod linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
40	c4dh4A	Alignment	not modelled	9.5	21	PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
41	d1nvma2	Alignment	not modelled	9.4	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
42	c1p7gL	Alignment	not modelled	9.3	20	PDB header: oxidoreductase Chain: L: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of superoxide dismutase from pyrobaculum2 aerophilum
43	d1unfx2	Alignment	not modelled	9.0	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
44	d1ddza2	Alignment	not modelled	8.9	29	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
45	d1y67a2	Alignment	not modelled	8.8	35	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
46	c6bejA	Alignment	not modelled	8.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of manganese superoxide dismutase from xanthomonas2 citri
47	d1bsma2	Alignment	not modelled	8.4	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
48	c2kwpA	Alignment	not modelled	8.3	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa
49	c1kkcB	Alignment	not modelled	8.3	25	PDB header: oxidoreductase Chain: B: PDB Molecule: manganese superoxide dismutase; PDBTitle: crystal structure of aspergillus fumigatus mnsod
50	c2mqkA	Alignment	not modelled	8.2	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
51	c4ffkA	Alignment	not modelled	8.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase; PDBTitle: x-ray structure of iron superoxide dismutase from acidilobus2 saccharovorans
52	c1qnnD	Alignment	not modelled	7.9	25	PDB header: oxidoreductase Chain: D: PDB Molecule: superoxide dismutase; PDBTitle: cambialistic superoxide dismutase from porphyromonas gingivalis
53	c3lw9B	Alignment	not modelled	7.7	32	PDB header: protein transport Chain: B: PDB Molecule: invasion protein inva; PDBTitle: structure of a cytoplasmic domain of salmonella inva
54	d2aala1	Alignment	not modelled	7.7	25	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like

55	c4h3eB	Alignment	not modelled	7.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of a putative iron superoxide dismutase from <i>Trypanosoma cruzi</i> bound to iron
56	c2mt4A	Alignment	not modelled	7.6	24	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: solution structure of the n-terminal domain of nusa from <i>B. subtilis</i>
57	d1dt0a2	Alignment	not modelled	7.6	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
58	c1nvmG	Alignment	not modelled	7.6	18	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
59	c3pl4A	Alignment	not modelled	7.6	6	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flag (residue 116-343) from <i>H. pylori</i>
60	c1xreB	Alignment	not modelled	7.5	35	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of soda-2 (ba5696) from <i>Bacillus anthracis</i> at 1.8 Å resolution.
61	c6j9eF	Alignment	not modelled	7.5	12	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryo-em structure of <i>Xanthomonas oryzae</i> transcription elongation complex with nusa and the bacteriophage protein p7
62	d1gv3a2	Alignment	not modelled	7.4	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
63	d1idsa2	Alignment	not modelled	7.4	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
64	c3h1sB	Alignment	not modelled	7.4	30	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of superoxide dismutase from <i>Francisella tularensis</i> subsp. <i>tularensis</i> schu s4
65	d1uera2	Alignment	not modelled	7.3	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
66	c1gv3B	Alignment	not modelled	7.3	25	PDB header: manganese superoxide dismutase Chain: B: PDB Molecule: manganese superoxide dismutase; PDBTitle: the 2.0 Å resolution structure of the catalytic portion of a cyanobacterial membrane-bound manganese superoxide dismutase
67	c5aj3i	Alignment	not modelled	7.3	25	PDB header: ribosome Chain: I: PDB Molecule: mitoribosomal protein us9m, mrps9; PDBTitle: structure of the small subunit of the mammalian mitoribosome
68	c3cvfA	Alignment	not modelled	7.2	45	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
69	c4jn6C	Alignment	not modelled	7.2	22	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from <i>Mycobacterium tuberculosis</i> hrv37
70	c4ds1C	Alignment	not modelled	7.2	24	PDB header: structural protein/transport protein Chain: C: PDB Molecule: dynein light chain 1, cytoplasmic; PDBTitle: the structure of a yeast dyn2-nup159 complex and the molecular basis for the dynein light chain - nuclear pore interaction
71	c4c7uB	Alignment	not modelled	7.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: superoxide dismutase [mn] 1, mitochondrial; PDBTitle: crystal structure of manganese superoxide dismutase from <i>Arabidopsis thaliana</i>
72	d1hjra	Alignment	not modelled	7.1	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
73	d1b06a2	Alignment	not modelled	7.1	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
74	c3cveC	Alignment	not modelled	7.0	39	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
75	d1mnga2	Alignment	not modelled	6.9	35	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
76	d1qxoa	Alignment	not modelled	6.9	19	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
77	c6btcA	Alignment	not modelled	6.8	35	PDB header: dna binding protein Chain: A: PDB Molecule: lp1413 - sccmec type iv-encoded dna binding protein; PDBTitle: sccmec type iv lp1413 - nucleic acids binding protein
78	c1unfX	Alignment	not modelled	6.8	25	PDB header: oxidoreductase Chain: X: PDB Molecule: iron superoxide dismutase; PDBTitle: the crystal structure of the eukaryotic feso from <i>Vigna unguiculata</i> suggests a new enzymatic mechanism
79	c3l1nA	Alignment	not modelled	6.8	20	PDB header: lipid binding protein Chain: A: PDB Molecule: cell wall antigen; PDBTitle: crystal structure of mp1p ligand binding domain 2 complexed with 2 palmitic acid
80	c3hvvB	Alignment	not modelled	6.7	22	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase;

80	c3np2B_	Alignment	not modelled	6.7	42	PDBTitle: crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644) PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif;
81	c2k5jB_	Alignment	not modelled	6.7	36	PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1 PDB header: oxidoreductase Chain: A: PDB Molecule: manganese-containing superoxide dismutase;
82	c3qvnA_	Alignment	not modelled	6.6	25	PDBTitle: crystal structure of cytosolic mnsod3 from candida albicans PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [mn];
83	d1lkvx_	Alignment	not modelled	6.5	27	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
84	c3abfB_	Alignment	not modelled	6.5	14	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
85	c1y67D_	Alignment	not modelled	6.4	35	PDB header: oxidoreductase Chain: D: PDB Molecule: manganese superoxide dismutase; PDBTitle: crystal structure of manganese superoxide dismutase from deinococcus2 radiodurans
86	c2rcvA_	Alignment	not modelled	6.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase [mn]; PDBTitle: crystal structure of the bacillus subtilis superoxide dismutase
87	d1wb8a2	Alignment	not modelled	6.4	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
88	c4ecdB_	Alignment	not modelled	6.2	29	PDB header: lyase Chain: B: PDB Molecule: chorismate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of bifidobacterium longum2 chorismate synthase
89	d2z15a1	Alignment	not modelled	6.2	20	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
90	d1jmx1	Alignment	not modelled	6.1	28	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
91	d1p7ga2	Alignment	not modelled	6.1	20	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
92	d1my6a2	Alignment	not modelled	6.1	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
93	d3sdpa2	Alignment	not modelled	6.0	25	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
94	c1avmA_	Alignment	not modelled	5.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase; PDBTitle: the cambialistic superoxide dismutase (fe-sod) of p. shermanii2 coordinated by azide
95	c6h9mA_	Alignment	not modelled	5.9	11	PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
96	c6ms4B_	Alignment	not modelled	5.8	40	PDB header: translation Chain: B: PDB Molecule: density-regulated protein; PDBTitle: crystal structure of the denr-mct-1 complex
97	c4f2nL_	Alignment	not modelled	5.8	25	PDB header: oxidoreductase Chain: L: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of iron superoxide dismutase from leishmania major
98	c2kqeA_	Alignment	not modelled	5.8	27	PDB header: lyase Chain: A: PDB Molecule: aprataxin and pnk-like factor; PDBTitle: second pbz domain of human aplf protein in complex with2 ribofuranosyladenosine
99	c3b64A_	Alignment	not modelled	5.7	7	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major