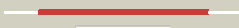
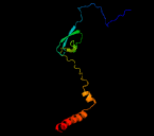

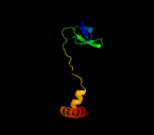
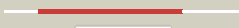
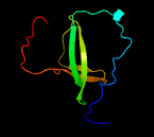



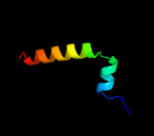

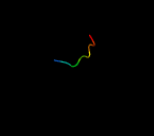

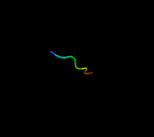

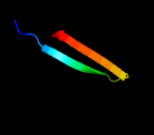

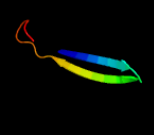

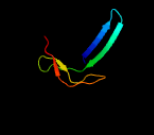
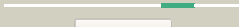



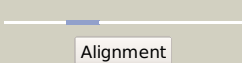
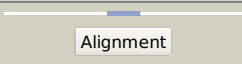
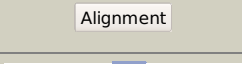
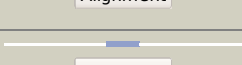
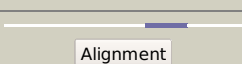
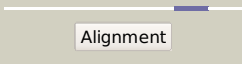
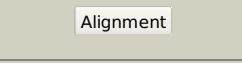
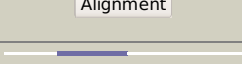
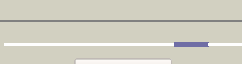
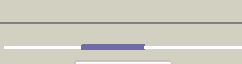

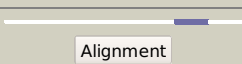
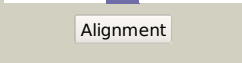
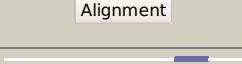
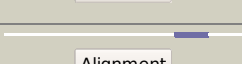
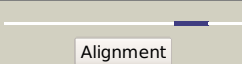
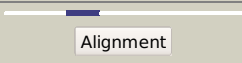
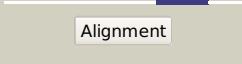
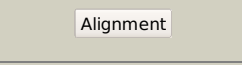


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2050_(-)_2307829_2308164
Date	Mon Aug 5 13:25:16 BST 2019
Unique Job ID	464e354003c02fe7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c04J_	 Alignment		100.0	100	PDB header: transcription/dna Chain: J: PDB Molecule: rna polymerase-binding protein rbpa; PDBTitle: mtb rnap holo/rbpa/double fork dna -closed clamp
2	c5tw1J_	 Alignment		100.0	89	PDB header: transcription activator/transferase/dna Chain: J: PDB Molecule: rna polymerase-binding protein rbpa; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
3	c2m4vA_	 Alignment		100.0	100	PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: mycobacterium tuberculosis rna polymerase binding protein a (rbpa) and2 its interactions with sigma factors
4	c2m6oA_	 Alignment		99.8	45	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
5	c4x8kB_	 Alignment		99.4	100	PDB header: transcription activator Chain: B: PDB Molecule: rna polymerase-binding protein rbpa; PDBTitle: mycobacterium tuberculosis rbpa-sid in complex with sigmaa domain 2
6	c5xknE_	 Alignment		66.0	44	PDB header: transferase/signaling protein Chain: E: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epf4
7	c5xknF_	 Alignment		66.0	44	PDB header: transferase/signaling protein Chain: F: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epf4
8	c3f6zB_	 Alignment		63.1	25	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
9	c5my7A_	 Alignment		58.2	13	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
10	c2m4IA_	 Alignment		47.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein bt_0846; PDBTitle: nmr structure of the protein bt_0846 from bacteroides thetaiotaomicron2 vpi-5482 (np_809759.1)
11	c5y81E_	 Alignment		47.0	63	PDB header: transcription Chain: E: PDB Molecule: chromatin modification-related protein eaf1; PDBTitle: nua4 teeaa sub-complex

12	c2ms3A_	Alignment		38.3	27	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
13	c3oe3B_	Alignment		31.6	16	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of plic-st, periplasmic lysozyme inhibitor of c-type2 lysozyme from salmonella typhimurium
14	d2jne1	Alignment		28.4	17	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
15	c2jneA_	Alignment		28.4	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.
16	d1h7va_	Alignment		27.5	6	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
17	c2kn9A_	Alignment		27.3	29	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
18	c1dvbA_	Alignment		27.0	21	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
19	d6rxna_	Alignment		26.9	25	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
20	d2dsxa1	Alignment		26.6	25	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
21	d1rb9a_	Alignment	not modelled	26.6	24	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
22	d2rdva_	Alignment	not modelled	26.4	25	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
23	d1qcva_	Alignment	not modelled	25.8	25	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
24	d1dx8a_	Alignment	not modelled	25.7	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
25	d1iroa_	Alignment	not modelled	25.7	29	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
26	d4rxna_	Alignment	not modelled	25.6	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
27	c1s24A_	Alignment	not modelled	25.5	31	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
28	d1s24a_	Alignment	not modelled	25.5	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
29	c2v3bB_	Alignment	not modelled	25.4	31	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.

30	c2jrpA		Alignment	not modelled	24.5	33	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
31	d1iu5a		Alignment	not modelled	24.2	40	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
32	d1brfa		Alignment	not modelled	23.8	31	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
33	d1x6ha1		Alignment	not modelled	21.7	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	c5xpda		Alignment	not modelled	20.6	36	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
35	c4uciA		Alignment	not modelled	18.1	24	PDB header: transferase Chain: A: PDB Molecule: rna-directed rna polymerase I; PDBTitle: x-ray structure and activities of an essential mononegavirales l-2 protein domain
36	c5h7pB		Alignment	not modelled	15.3	38	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: nmr structure of the vta1ntd-did2(176-204) complex
37	c3ggzH		Alignment	not modelled	15.2	38	PDB header: protein transport, endocytosis Chain: H: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
38	c2pg1J		Alignment	not modelled	14.3	45	PDB header: structural protein Chain: J: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
39	c2pg1L		Alignment	not modelled	14.3	45	PDB header: structural protein Chain: L: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2; PDBTitle: structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
40	c3fqia		Alignment	not modelled	14.1	18	PDB header: protein binding Chain: A: PDB Molecule: protein dom3z; PDBTitle: crystal structure of the mouse dom3z
41	c3ggzF		Alignment	not modelled	13.9	38	PDB header: protein transport, endocytosis Chain: F: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
42	c3ggzE		Alignment	not modelled	13.9	38	PDB header: protein transport, endocytosis Chain: E: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
43	c2ofqa		Alignment	not modelled	13.5	23	PDB header: protein transport/protein transport Chain: A: PDB Molecule: trao; PDBTitle: nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
44	c3ir9A		Alignment	not modelled	13.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from methanosarcina2 mazei.
45	c3mk4B		Alignment	not modelled	12.7	47	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray structure of human pex3 in complex with a pex19 derived peptide
46	c2m4ya		Alignment	not modelled	11.9	33	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: rubredoxin type protein from mycobacterium ulcerans
47	c2ktvA		Alignment	not modelled	11.5	13	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
48	c3tweA		Alignment	not modelled	10.3	43	PDB header: unknown function Chain: A: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
49	c3tweB		Alignment	not modelled	10.1	43	PDB header: unknown function Chain: B: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
50	c3ggzG		Alignment	not modelled	9.9	40	PDB header: protein transport, endocytosis Chain: G: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
51	d2ok5a4		Alignment	not modelled	9.8	22	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
52	c5jnpB		Alignment	not modelled	9.6	22	PDB header: transferase Chain: B: PDB Molecule: probable cellulose synthase a catalytic subunit 8 [udp- PDBTitle: crystal structure of a rice (oryza sativa) cellulose synthase plant2 conserved region (p-cr)
53	c6oegY		Alignment	not modelled	9.0	13	PDB header: translocase Chain: Y: PDB Molecule: type iv secretion system apparatus protein cag; PDBTitle: structure of cagx from a cryo-em reconstruction of a t4ss
54	c3aihB		Alignment	not modelled	8.9	27	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 19;

54	c9ajub_	Alignment	not modelled	8.9	37	PDBTitle: crystal structure of human pex3p in complex with n-terminal pex19p2 peptide PDB header: viral protein
55	c4xalA_	Alignment	not modelled	8.9	46	Chain: A: PDB Molecule: tegument protein vp22; PDBTitle: crystal structure of the conserved core domain of vp22 from hsv-1
56	d2f09a1	Alignment	not modelled	8.5	10	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
57	d1xx6a2	Alignment	not modelled	8.3	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
58	c5m2uA_	Alignment	not modelled	8.0	35	PDB header: photosynthesis Chain: A: PDB Molecule: ycf54; PDBTitle: the structure of the ycf54 protein from synechocystis sp. pcc6803
59	d3ci0j1	Alignment	not modelled	7.9	17	Fold: Pili subunits Superfamily: Pili subunits Family: Epsj-like
60	c6a68A_	Alignment	not modelled	7.9	33	PDB header: exocytosis Chain: A: PDB Molecule: calcium-dependent secretion activator 1; PDBTitle: the crystal structure of rat calcium-dependent activator protein for2 secretion (caps) damh domain
61	c1odpA_	Alignment	not modelled	7.8	38	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
62	c1odrA_	Alignment	not modelled	7.8	38	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
63	c1odqA_	Alignment	not modelled	7.8	38	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
64	c2iwiA_	Alignment	not modelled	7.7	33	PDB header: transferase Chain: A: PDB Molecule: gag-pol polyprotein; PDBTitle: solution structure of the zn complex of hiv-2 ncp(23-49)2 peptide, encompassing protein cchc-linker, distal cchc zn-3 binding motif and c-terminal tail.
65	c5btoA_	Alignment	not modelled	7.7	24	PDB header: hydrolase Chain: A: PDB Molecule: ssrai1; PDBTitle: crystal structure of scheffersomyces stipitis rail
66	c3izr_	Alignment	not modelled	7.6	33	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
67	c3cc4Z_	Alignment	not modelled	7.6	22	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
68	d1vqoz1	Alignment	not modelled	7.6	22	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
69	c2qa4Z_	Alignment	not modelled	7.6	22	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
70	c2e1xA_	Alignment	not modelled	7.6	33	PDB header: viral protein Chain: A: PDB Molecule: gag-pol polyprotein (pr160gag-pol); PDBTitle: nmr structure of the hiv-2 nucleocapsid protein
71	c2zkrz_	Alignment	not modelled	7.5	22	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
72	c3zf7o_	Alignment	not modelled	7.5	23	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
73	c1yshD_	Alignment	not modelled	7.3	33	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
74	c4pogC_	Alignment	not modelled	7.3	21	PDB header: replication, dna binding protein/dna Chain: C: PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure
75	d1zswa1	Alignment	not modelled	7.2	11	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: BC1024-like
76	d1jj2y_	Alignment	not modelled	7.2	33	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
77	c3j39p_	Alignment	not modelled	7.1	33	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
78	c3jyw9_	Alignment	not modelled	7.1	22	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution

79	d1ffkw_	Alignment	not modelled	7.1	33	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
80	c3j21i_	Alignment	not modelled	7.1	33	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
81	c3jsrA_	Alignment	not modelled	7.1	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: all0216 protein; PDBTitle: x-ray structure of all0216 protein from nostoc sp. pcc 7120 at the2 resolution 1.8a. northeast structural genomics consortium target3 nsr236
82	d1p91a_	Alignment	not modelled	7.1	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RlmA
83	d1lqta2	Alignment	not modelled	6.9	22	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradial dioxygenases
84	c5h3vA_	Alignment	not modelled	6.6	13	PDB header: protein binding Chain: A: PDB Molecule: cag8; PDBTitle: crystal structure of a type iv secretion system component cagx in2 helicobacter pylori
85	c4ed9A_	Alignment	not modelled	6.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: caib/baif family protein; PDBTitle: crystal structure of a caib/baif family protein from brucella suis
86	d1i42a_	Alignment	not modelled	6.4	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
87	c5da5R_	Alignment	not modelled	6.4	38	PDB header: oxidoreductase Chain: R: PDB Molecule: rrru_a0973; PDBTitle: crystal structure of rhodospirillum rubrum rru_a0973
88	c2ysaA_	Alignment	not modelled	6.4	33	PDB header: metal binding protein Chain: A: PDB Molecule: retinoblastoma-binding protein 6; PDBTitle: solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
89	c4a17Y_	Alignment	not modelled	6.4	22	PDB header: ribosome Chain: Y: PDB Molecule: rp137a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
90	d1mbya_	Alignment	not modelled	6.4	15	Fold: Polo-box domain Superfamily: Polo-box domain Family: Swapped Polo-box domain
91	d1ed7a_	Alignment	not modelled	6.2	13	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
92	c5xyiG_	Alignment	not modelled	6.2	27	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6; PDBTitle: small subunit of trichomonas vaginalis ribosome
93	c5vb0E_	Alignment	not modelled	6.1	8	PDB header: transferase Chain: E: PDB Molecule: fosfomycin resistance protein fosa3; PDBTitle: crystal structure of fosfomycin resistance protein fosa3
94	c2n37A_	Alignment	not modelled	6.1	48	PDB header: unknown function Chain: A: PDB Molecule: avr-pia protein; PDBTitle: solution structure of avr-pia
95	c2lvhA_	Alignment	not modelled	5.6	33	PDB header: metal binding protein Chain: A: PDB Molecule: putative zinc finger protein orf59a; PDBTitle: solution structure of the zinc finger afv1p06 protein from the2 hyperthermophilic archaeal virus afv1
96	d1s3sg_	Alignment	not modelled	5.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
97	c5g5oC_	Alignment	not modelled	5.4	14	PDB header: viral protein Chain: C: PDB Molecule: lh3 hexon-interlacing capsid protein; PDBTitle: structure of the snake adenovirus 1 hexon-interlacing lh3 protein,2 native
98	d1wj4a_	Alignment	not modelled	5.4	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
99	d1qpqa_	Alignment	not modelled	5.3	18	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase