





















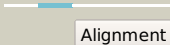
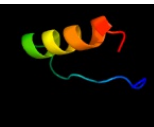
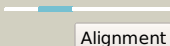

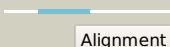



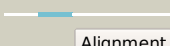
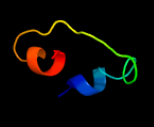
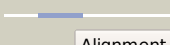
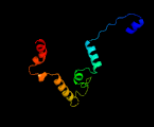
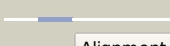

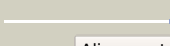
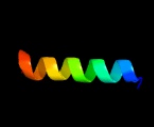
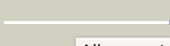
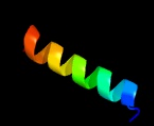
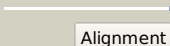

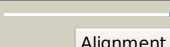

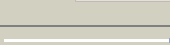

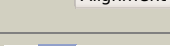
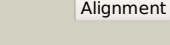


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1376 (-)_1549154_1550647
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	ae72d8ba7c74e18b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2n03A_	 Alignment		76.2	19	PDB header: structural protein Chain: A; PDB Molecule: plectin; PDBTitle: solution nmr structure plectin repeat domain 6 (4403-4606) of plectin2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr6354e
2	d1lm5a_	 Alignment		74.9	19	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Plakin repeat Family: Plakin repeat
3	c3ff4A_	 Alignment		64.5	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
4	c4qmdB_	 Alignment		60.0	18	PDB header: cell adhesion Chain: B; PDB Molecule: envoplakin; PDBTitle: crystal structure of human envoplakin plakin repeat domain
5	c3mogA_	 Alignment		58.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
6	c5dzzA_	 Alignment		55.4	19	PDB header: structural protein Chain: A; PDB Molecule: desmoplakin; PDBTitle: structural characterization of intermediate filaments binding domain2 of desmoplakin
7	c4kueA_	 Alignment		53.7	23	PDB header: oxidoreductase Chain: A; PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
8	d1lm7a_	 Alignment		50.1	24	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Plakin repeat Family: Plakin repeat
9	c3btuD_	 Alignment		48.3	10	PDB header: transcription Chain: D; PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
10	c4ex8A_	 Alignment		42.1	21	PDB header: ligase Chain: A; PDB Molecule: alna; PDBTitle: crystal structure of the prealnumycin c-glycosynthase alna
11	c2duwA_	 Alignment		34.0	14	PDB header: ligand binding protein Chain: A; PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae

12	c3k96B_	 Alignment		33.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
13	c2obnA_	 Alignment		32.5	19	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anaebaena2 variabilis atcc 29413 at 2.30 a resolution
14	c3lyeA_	 Alignment		32.3	16	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
15	c3v5nA_	 Alignment		31.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
16	c4qmkB_	 Alignment		30.4	32	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
17	c5w8sA_	 Alignment		29.1	11	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
18	c4akfA_	 Alignment		27.9	26	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
19	c4gdlC_	 Alignment		27.0	43	PDB header: protein binding Chain: C: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
20	c4nawC_	 Alignment		27.0	43	PDB header: protein transport/ligase Chain: C: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
21	c4nawO_	 Alignment	not modelled	27.0	43	PDB header: protein transport/ligase Chain: O: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
22	c4gdkC_	 Alignment	not modelled	27.0	43	PDB header: protein binding Chain: C: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
23	c4nawK_	 Alignment	not modelled	27.0	43	PDB header: protein transport/ligase Chain: K: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
24	c4nawG_	 Alignment	not modelled	27.0	43	PDB header: protein transport/ligase Chain: G: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
25	c4gdkF_	 Alignment	not modelled	26.6	43	PDB header: protein binding Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
26	c4gijC_	 Alignment	not modelled	25.5	19	PDB header: hydrolase Chain: C: PDB Molecule: pseudouridine-5'-phosphate glycosidase; PDBTitle: crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
27	c5uncB_	 Alignment	not modelled	25.2	23	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
28	c2d3tB_	 Alignment	not modelled	24.6	19	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
						Fold: NAD(P)-binding Rossmann-fold domains

29	d1ks9a2	Alignment	not modelled	24.0	29	Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
30	c3e18A	Alignment	not modelled	23.7	37	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
31	c6aunB	Alignment	not modelled	23.0	23	PDB header: hydrolase Chain: B: PDB Molecule: pla2g6, ipla2beta; PDBTitle: calcium-independent phospholipase a2 beta
32	c6iunB	Alignment	not modelled	22.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa PDBTitle: crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
33	d1vyua2	Alignment	not modelled	22.1	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
34	d1vyva2	Alignment	not modelled	21.7	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
35	c4b3hA	Alignment	not modelled	21.6	27	PDB header: oxidoreductase/transferase Chain: A: PDB Molecule: fatty acid beta-oxidation complex alpha-chain fadb; PDBTitle: crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
36	c3oa2B	Alignment	not modelled	20.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: wbpb; PDBTitle: crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
37	c4hadD	Alignment	not modelled	20.3	26	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
38	d1t3la2	Alignment	not modelled	20.1	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
39	c3I09B	Alignment	not modelled	19.9	9	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
40	d1iuKa	Alignment	not modelled	19.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
41	c2r60A	Alignment	not modelled	19.1	21	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
42	d1xbta1	Alignment	not modelled	19.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
43	d1t0hb	Alignment	not modelled	19.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
44	c2csuB	Alignment	not modelled	18.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
45	c2qytA	Alignment	not modelled	17.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
46	c2xmpB	Alignment	not modelled	17.6	19	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
47	c6hrdD	Alignment	not modelled	17.6	32	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadb2 (rv0468)
48	d1y81a1	Alignment	not modelled	17.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
49	d1sgva1	Alignment	not modelled	17.0	11	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
50	c3j4rA	Alignment	not modelled	16.9	22	PDB header: transferase Chain: A: PDB Molecule: ta-kinase anchor protein 18; PDBTitle: pseudo-atomic model of the akap18-pka complex in a linear conformation2 derived from electron microscopy
51	d2nu7a1	Alignment	not modelled	16.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
52	d1s96a	Alignment	not modelled	16.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
53	c4ix1B	Alignment	not modelled	16.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
54	d1guza1	Alignment	not modelled	16.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
						PDB header: oxyqen storageq/transport

55	c1dlyA	Alignment	not modelled	15.6	17	Chain: A; PDB Molecule: hemoglobin; PDBTitle: x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
56	d1dlyA	Alignment	not modelled	15.6	17	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
57	c5zqzC	Alignment	not modelled	15.4	17	PDB header: lyase,hydrolase/transferase Chain: C; PDB Molecule: trifunctional enzyme subunit alpha, mitochondrial; PDBTitle: structure of human mitochondrial trifunctional protein, tetramer
58	c6jczL	Alignment	not modelled	15.1	20	PDB header: isomerase Chain: L; PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfobolus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
59	c3dfzB	Alignment	not modelled	15.1	29	PDB header: oxidoreductase Chain: B; PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
60	d1llda1	Alignment	not modelled	15.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
61	c4akxB	Alignment	not modelled	15.0	18	PDB header: transport protein Chain: B; PDB Molecule: exou; PDBTitle: structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
62	c3mebB	Alignment	not modelled	14.9	19	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
63	c3gmiA	Alignment	not modelled	14.7	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: supf0348 protein mj0951; PDBTitle: crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
64	d9ldta1	Alignment	not modelled	14.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
65	c5vbaA	Alignment	not modelled	14.2	19	PDB header: chaperone, hydrolase Chain: A; PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
66	d1luxja1	Alignment	not modelled	14.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
67	d1xea1	Alignment	not modelled	14.1	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	c4qicB	Alignment	not modelled	13.9	33	PDB header: signaling protein/dna binding protein Chain: B; PDB Molecule: anti-sigma factor nepr; PDBTitle: co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
69	d1bg6a2	Alignment	not modelled	13.8	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
70	c3e82A	Alignment	not modelled	13.3	30	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
71	c3moiA	Alignment	not modelled	13.3	19	PDB header: oxidoreductase Chain: A; PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
72	d1np3a2	Alignment	not modelled	13.2	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
73	c1xeaD	Alignment	not modelled	13.2	19	PDB header: oxidoreductase Chain: D; PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
74	d1mv8a2	Alignment	not modelled	13.1	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
75	c1m67A	Alignment	not modelled	13.1	27	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
76	d1qhxa	Alignment	not modelled	13.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Chloramphenicol phosphotransferase
77	d1gv0a1	Alignment	not modelled	12.8	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
78	c4tq0D	Alignment	not modelled	12.7	43	PDB header: protein binding Chain: D; PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
79	c4o19A	Alignment	not modelled	12.4	40	PDB header: oxidoreductase Chain: A; PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
80	c3vbaA	Alignment	not modelled	12.4	19	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, gfo/idh/moca family;

80	c3evnA	Alignment	not modelled	12.4	13	PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r PDB header: transferase
81	c4hlnA	Alignment	not modelled	12.4	18	Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide
82	c4tq0B	Alignment	not modelled	12.4	43	PDB header: protein binding Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
83	c5t2xC	Alignment	not modelled	12.3	29	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein lpg1670; PDBTitle: crystal structure of uncharacterised protein lpg1670
84	d1ojua1	Alignment	not modelled	12.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
85	c5yi4A	Alignment	not modelled	12.2	36	PDB header: protein binding Chain: A: PDB Molecule: disrupted in schizophrenia 1 homolog,nuclear distribution PDBTitle: solution structure of the disc1/ndel1 complex
86	c1z82A	Alignment	not modelled	12.1	36	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
87	d2f1ka2	Alignment	not modelled	12.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
88	c3ec7C	Alignment	not modelled	12.0	11	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
89	d1kgda	Alignment	not modelled	11.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
90	d1ldna1	Alignment	not modelled	11.9	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
91	c2qq0B	Alignment	not modelled	11.9	24	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
92	c6jnkA	Alignment	not modelled	11.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p)(+)); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
93	c3k6jA	Alignment	not modelled	11.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
94	d2ou3a1	Alignment	not modelled	11.6	14	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
95	c6aqjB	Alignment	not modelled	11.6	36	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
96	d1pzga1	Alignment	not modelled	11.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
97	d1dlja2	Alignment	not modelled	11.6	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
98	c2hdnE	Alignment	not modelled	11.6	71	PDB header: translation Chain: E: PDB Molecule: elongation factor ef-tu; PDBTitle: trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
99	d1i1qb	Alignment	not modelled	11.5	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)