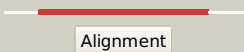

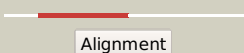

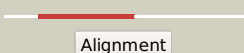

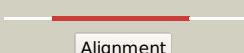






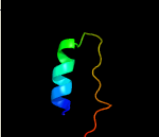
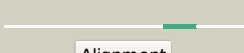


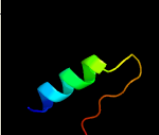




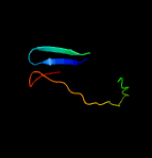
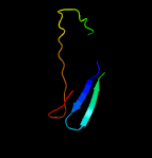
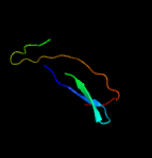
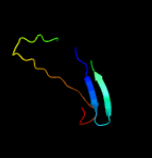

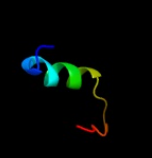
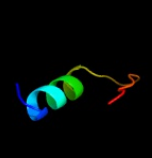

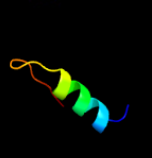


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1635c_(-)_1840579_1842249
Date	Fri Aug 2 13:30:23 BST 2019
Unique Job ID	e9a9ab08deb076cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5f15A_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
2	c6p2rB_	 Alignment		99.8	13	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
3	c6p25A_	 Alignment		99.8	15	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
4	c3wajA_	 Alignment		99.7	14	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
5	c3rceA_	 Alignment		99.7	12	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
6	c6eznF_	 Alignment		99.5	16	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	d2jfga2	 Alignment		79.5	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
8	c3uagA_	 Alignment		42.3	21	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
9	c3lk7A_	 Alignment		37.3	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
10	c3mvnA_	 Alignment		29.3	32	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
11	d1xq4a_	 Alignment		27.7	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like

12	c2fleA	Alignment		27.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
13	c5hdwA	Alignment		26.0	24	PDB header: protein binding Chain: A: PDB Molecule: f-box only protein 3; PDBTitle: apag domain of fbxo3
14	d1tzaa	Alignment		25.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
15	d1xvsa	Alignment		25.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
16	c5n6mA	Alignment		19.9	13	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa
17	d1p3da2	Alignment		18.7	36	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
18	c3hn7A	Alignment		18.6	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
19	c4bucA	Alignment		18.1	13	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of murd ligase from thermotoga maritima in apo form
20	d1e8ca2	Alignment		14.5	23	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
21	c3tr7A	Alignment	not modelled	14.3	14	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: structure of a uracil-dna glycosylase (ung) from coxiella burnetii
22	c6nbxG	Alignment	not modelled	12.9	14	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
23	d1vk3a3	Alignment	not modelled	11.8	18	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
24	c3gt2A	Alignment	not modelled	11.3	18	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
25	c4c13A	Alignment	not modelled	11.2	23	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; PDBTitle: x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys
26	d1h9aa1	Alignment	not modelled	11.1	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	c2fynH	Alignment	not modelled	10.9	14	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
28	c1e8cB	Alignment	not modelled	10.7	23	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylanyl-d-glutamate--2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide

						synthetase from2 e. coli
29	d1s04a_	Alignment	not modelled	10.7	27	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
30	c1zrtD_	Alignment	not modelled	10.6	11	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
31	c2f00A_	Alignment	not modelled	10.6	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
32	d2evra2	Alignment	not modelled	10.5	21	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
33	c4afpA_	Alignment	not modelled	10.1	23	PDB header: hydrolase Chain: A: PDB Molecule: metacaspase mca2; PDBTitle: the structure of metacaspase 2 from t. brucei determined in the2 presence of samarium
34	c5ifiA_	Alignment	not modelled	10.0	18	PDB header: ligase Chain: A: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99
35	c6b8cA_	Alignment	not modelled	10.0	36	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlpC/p60 domain of peptidoglycan hydrolase saga
36	c4bubA_	Alignment	not modelled	9.9	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine PDBTitle: crystal structure of mure ligase from thermotoga maritima2 in complex with adp
37	c1gqgA_	Alignment	not modelled	9.8	36	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
38	d1vkya_	Alignment	not modelled	9.8	31	Fold: QueA-like Superfamily: QueA-like Family: QueA-like
39	c4uy5A_	Alignment	not modelled	9.7	11	PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egtD; PDBTitle: crystal structure of histidine-specific methyltransferase egtD from2 mycobacterium smegmatis
40	c2yiuE_	Alignment	not modelled	9.7	11	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
41	d1ofla_	Alignment	not modelled	9.6	17	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
42	c2lkjA_	Alignment	not modelled	9.5	50	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-m; PDBTitle: structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
43	c5eqnA_	Alignment	not modelled	9.3	50	PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase
44	d3c9ua2	Alignment	not modelled	9.3	33	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
45	d1jr7a_	Alignment	not modelled	9.2	33	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Gab protein (hypothetical protein YgaT)
46	c3n2aA_	Alignment	not modelled	9.2	18	PDB header: ligase Chain: A: PDB Molecule: bifunctional folylpolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
47	c5ey8D_	Alignment	not modelled	9.2	18	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
48	d1wdia_	Alignment	not modelled	9.2	25	Fold: QueA-like Superfamily: QueA-like Family: QueA-like
49	c3cwbQ_	Alignment	not modelled	9.1	8	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
50	c1yy3A_	Alignment	not modelled	9.1	44	PDB header: isomerase Chain: A: PDB Molecule: s-adenosylmethionine:trna ribosyltransferase- PDBTitle: structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
51	c4e9iB_	Alignment	not modelled	9.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
52	c3on0D_	Alignment	not modelled	9.0	18	PDB header: dna binding protein/dna Chain: D: PDB Molecule: protein tram; PDBTitle: crystal structure of the ped208 tram-sbma complex
53	c3etcB_	Alignment	not modelled	8.9	10	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and

						cys298
54	c1qkiE_	Alignment	not modelled	8.9	33	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459l) complexed with structural nadp+
55	c3rg2H_	Alignment	not modelled	8.8	15	PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
56	c1qcrD_	Alignment	not modelled	8.7	5	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
57	d2zoda2	Alignment	not modelled	8.7	25	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
58	c1w78A_	Alignment	not modelled	8.7	36	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
59	d1xnea_	Alignment	not modelled	8.6	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
60	c1dbgA_	Alignment	not modelled	8.5	18	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
61	c2bhlB_	Alignment	not modelled	8.5	33	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
62	c2xivA_	Alignment	not modelled	8.5	12	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
63	d2pyta1	Alignment	not modelled	8.3	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
64	d1t33a2	Alignment	not modelled	8.1	12	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
65	c2xjaD_	Alignment	not modelled	8.1	32	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate-2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
66	c1h9aA_	Alignment	not modelled	8.1	29	PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
67	c4r0mA_	Alignment	not modelled	8.0	10	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
68	d1pg4a_	Alignment	not modelled	7.9	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
69	c6ijbA_	Alignment	not modelled	7.9	9	PDB header: ligase Chain: A: PDB Molecule: amp-binding domain protein; PDBTitle: structure of 3-methylmercaptopyruvate coa ligase mutant k523a in2 complex with amp and mmpa
70	c1p84D_	Alignment	not modelled	7.7	8	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
71	c3rkoF_	Alignment	not modelled	7.7	11	PDB header: oxidoreductase Chain: F: PDB Molecule: nahd-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
72	c4cmrB_	Alignment	not modelled	7.7	41	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase/deacetylase family protein; PDBTitle: the crystal structure of novel exo-type maltose-forming2 amylase(py04_0872) from pyrococcus sp. st04
73	d3euga_	Alignment	not modelled	7.5	12	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Uracil-DNA glycosylase
74	d1iz0a1	Alignment	not modelled	7.5	5	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
75	c5mvrA_	Alignment	not modelled	7.4	24	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
76	c4gr5B_	Alignment	not modelled	7.4	11	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
77	c6biqA_	Alignment	not modelled	7.4	19	PDB header: hydrolase Chain: A: PDB Molecule: clan ca, family c40, nlpc/p60 superfamily cysteine PDBTitle: structure of nlpc2 from trichomonas vaginalis
78	d1clia2	Alignment	not modelled	7.4	27	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like

						Family: PurM C-terminal domain-like
79	c3ibmB_	Alignment	not modelled	7.3	15	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
80	d2z1ea2	Alignment	not modelled	7.3	53	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
81	c2wtzC_	Alignment	not modelled	7.2	32	PDB header: ligase Chain: C; PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis
82	c5vrhA_	Alignment	not modelled	7.1	11	PDB header: transferase Chain: A; PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
83	c2fg0B_	Alignment	not modelled	7.1	21	PDB header: hydrolase Chain: B; PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
84	c5oynB_	Alignment	not modelled	7.0	12	PDB header: lyase Chain: B; PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
85	c4lqvA_	Alignment	not modelled	7.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
86	c3fp9E_	Alignment	not modelled	7.0	60	PDB header: hydrolase Chain: E; PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
87	c2k1gA_	Alignment	not modelled	7.0	27	PDB header: lipoprotein Chain: A; PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
88	c2yvaB_	Alignment	not modelled	6.8	29	PDB header: dna binding protein Chain: B; PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
89	c4wd1A_	Alignment	not modelled	6.8	15	PDB header: ligase Chain: A; PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
90	d2f4la1	Alignment	not modelled	6.8	50	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
91	c5odnG_	Alignment	not modelled	6.8	5	PDB header: dna binding protein Chain: G; PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
92	c3mjjD_	Alignment	not modelled	6.7	50	PDB header: hydrolase Chain: D; PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
93	c4pa5A_	Alignment	not modelled	6.7	32	PDB header: transferase Chain: A; PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: tgl - a bacterial spore coat transglutaminase - cystamine complex
94	c4eatB_	Alignment	not modelled	6.7	14	PDB header: ligase Chain: B; PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
95	c2ii1A_	Alignment	not modelled	6.7	33	PDB header: hydrolase Chain: A; PDB Molecule: acetamidase; PDBTitle: crystal structure of acetamidase (10172637) from bacillus halodurans2 at 1.95 a resolution
96	c2zw3B_	Alignment	not modelled	6.7	17	PDB header: cell adhesion Chain: B; PDB Molecule: gap junction beta-2 protein; PDBTitle: structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
97	c4f6oA_	Alignment	not modelled	6.7	18	PDB header: hydrolase Chain: A; PDB Molecule: metacaspase-1; PDBTitle: crystal structure of the yeast metacaspase yca1
98	c5ym0A_	Alignment	not modelled	6.7	17	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
99	c3kj0B_	Alignment	not modelled	6.7	38	PDB header: apoptosis Chain: B; PDB Molecule: bc1-2-like protein 11; PDBTitle: mcl-1 in complex with bim bh3 mutant i2dy