
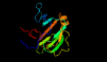































Phyre2

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Description	RVBD2891 (-) _3200276_3201025
Date	Thu Aug 8 16:20:04 BST 2019
Unique Job ID	88ef8df217a35415

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sluB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
2	c2hsiB_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
3	c2gu1A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
4	c4rnzA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal
5	d1qwya_	 Alignment		100.0	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
6	c3nyyA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
7	c4bh5B_	 Alignment		100.0	26	PDB header: cell cycle Chain: B: PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
8	c4lxcA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from staphylococcus simulans
9	c5kqbA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu
10	c2b44A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
11	c5kvpA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: zoocin a endopeptidase; PDBTitle: solution structure of the catalytic domain of zoocin a

12	c3tufB	Alignment		100.0	24	PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
13	c4qpbB	Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from <i>Staphylococcus simulans</i> crystallized in the absence of phosphate
14	c5j1mD	Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
15	c3uz0D	Alignment		100.0	23	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiiah and spoiiq complex
16	c5gt1A	Alignment		100.0	28	PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from <i>L. salivarius</i> ren
17	c5j1lA	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i
18	c3it5B	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from <i>Pseudomonas aeruginosa</i>
19	c5b0hB	Alignment		99.9	19	PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
20	c3csqC	Alignment		99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall-degrading enzyme in the bacteriophage phi29 tail
21	c4iqzD	Alignment	not modelled	95.9	23	PDB header: unknown function Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: the crystal structure of a large insert in rna polymerase (rpoC)2 subunit from <i>E. coli</i>
22	c2lmcB	Alignment	not modelled	94.3	23	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
23	d2f3ga	Alignment	not modelled	93.5	14	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
24	d1glaf	Alignment	not modelled	93.1	16	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
25	d1gpaa	Alignment	not modelled	93.1	14	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
26	d2gpaa	Alignment	not modelled	92.7	17	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
27	d1e2wa2	Alignment	not modelled	92.7	24	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
28	c4cgaA	Alignment	not modelled	92.5	13	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from <i>Streptococcus pneumoniae</i>

29	c2aukA	Alignment	not modelled	92.1	30	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
30	d1ci3m2	Alignment	not modelled	89.7	18	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
31	c1q90A	Alignment	not modelled	87.6	26	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
32	c1e2vB	Alignment	not modelled	87.5	26	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
33	d1brwa3	Alignment	not modelled	85.4	13	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
34	c2jxmB	Alignment	not modelled	81.6	18	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
35	d2tpa3	Alignment	not modelled	76.6	19	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
36	c3n6rK	Alignment	not modelled	74.5	29	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
37	c4xcmB	Alignment	not modelled	70.3	23	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus
38	c2aujD	Alignment	not modelled	70.1	16	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
39	c2dsjA	Alignment	not modelled	69.8	16	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
40	c2j0fC	Alignment	not modelled	68.9	30	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
41	c4p6vA	Alignment	not modelled	68.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
42	c5xu0B	Alignment	not modelled	68.2	18	PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6
43	d1vf7a	Alignment	not modelled	66.4	9	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
44	c5c22A	Alignment	not modelled	64.8	31	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
45	c1otpA	Alignment	not modelled	64.4	19	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
46	c2x5cB	Alignment	not modelled	63.7	18	PDB header: viral protein Chain: B: PDB Molecule: hypothetical protein orf131; PDBTitle: crystal structure of hypothetical protein orf131 from pyrobaculum2 spherical virus
47	c1ctmA	Alignment	not modelled	63.3	10	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
48	d1o78a	Alignment	not modelled	63.1	29	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
49	c3h5qA	Alignment	not modelled	62.2	14	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
50	c1tu2B	Alignment	not modelled	61.7	24	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
51	c2qj8B	Alignment	not modelled	61.1	25	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
52	d1tu2b2	Alignment	not modelled	60.8	26	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
53	c3bg3A	Alignment	not modelled	59.4	22	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)

54	c2f1mA	Alignment	not modelled	56.5	12	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
55	c1brwB	Alignment	not modelled	56.5	17	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
56	d1bdoa	Alignment	not modelled	55.7	19	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
57	c3fmcC	Alignment	not modelled	55.4	29	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
58	c2ejmA	Alignment	not modelled	54.3	26	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
59	c4hnbB	Alignment	not modelled	53.5	36	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
60	d1laba	Alignment	not modelled	53.3	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
61	c3lnnB	Alignment	not modelled	52.5	25	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
62	c2kccA	Alignment	not modelled	52.3	13	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
63	d1uoua3	Alignment	not modelled	52.2	31	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
64	c3na6A	Alignment	not modelled	50.8	18	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
65	c4tkoB	Alignment	not modelled	50.8	18	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
66	c3cdxB	Alignment	not modelled	48.4	24	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
67	c3hblA	Alignment	not modelled	48.2	36	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
68	c2jkuA	Alignment	not modelled	47.9	26	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, mitochondrial; PDBTitle: crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase
69	c3bg5B	Alignment	not modelled	46.7	36	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
70	d1pmra	Alignment	not modelled	46.3	25	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
71	c2l5tA	Alignment	not modelled	45.9	16	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
72	c5vz0D	Alignment	not modelled	45.3	18	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
73	c2q8iB	Alignment	not modelled	44.8	17	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
74	c2k33A	Alignment	not modelled	44.4	12	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
75	d2pnrc1	Alignment	not modelled	44.1	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
76	c3fppB	Alignment	not modelled	44.1	25	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
77	d1y8ob1	Alignment	not modelled	44.0	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

78	c1k8ma	Alignment	not modelled	43.8	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
79	c5ks8F	Alignment	not modelled	43.6	37	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from <i>2 methylobacillus flagellatus</i>
80	c4dk1B	Alignment	not modelled	42.6	18	PDB header: membrane protein Chain: B: PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the 2 pseudomonas aeruginosa mexa alpha-hairpin domain.
81	c4qskB	Alignment	not modelled	41.7	21	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of <i>I. monocytogenes</i> pyruvate carboxylase in complex 2 with cyclic-di-amp
82	d1qjoa	Alignment	not modelled	41.5	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
83	c3InnA	Alignment	not modelled	40.4	25	PDB header: metal transport Chain: A: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from <i>Cupriavidus metallidurans</i>
84	c3tw6B	Alignment	not modelled	39.7	11	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the 2 allosteric activator, acetyl coenzyme-a
85	c2v4dM	Alignment	not modelled	39.0	19	PDB header: membrane protein Chain: M: PDB Molecule: multidrug resistance protein mexa; PDBTitle: re-refinement of mexa adaptor protein
86	c2b8gA	Alignment	not modelled	38.7	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of <i>Bacillus subtilis</i> blp biotinylated-2 form (energy minimized mean structure)
87	c1t5eB	Alignment	not modelled	37.3	10	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
88	c3camB	Alignment	not modelled	37.1	20	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from <i>Neisseria meningitidis</i>
89	c4dk0A	Alignment	not modelled	34.6	18	PDB header: membrane protein Chain: A: PDB Molecule: putative maca; PDBTitle: crystal structure of maca from <i>Actinobacillus actinomycetemcomitans</i>
90	c2e75C	Alignment	not modelled	33.0	22	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from <i>M. lamosus</i>
91	c5v5sH	Alignment	not modelled	32.8	9	PDB header: membrane protein Chain: H: PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
92	d1dcza	Alignment	not modelled	31.4	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
93	c5nenA	Alignment	not modelled	31.3	32	PDB header: hydrolase Chain: A: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion 2 protein of a type i secretion system
94	c2dncA	Alignment	not modelled	31.2	21	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from 2 human 2-oxoacid dehydrogenase
95	c2ejgD	Alignment	not modelled	31.1	20	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and 2 biotin carboxyl carrier protein complex from <i>Pyrococcus horikoshii</i> 3 ot3
96	c5bn4A	Alignment	not modelled	28.1	11	PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: structure of a unique atp synthase neqa-neqb in complex with anp from 2 nanoarchaeum equitans
97	c2dneA	Alignment	not modelled	27.7	11	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of 2 human 2-oxoacid dehydrogenase
98	c5niIG	Alignment	not modelled	26.8	21	PDB header: transport protein Chain: G: PDB Molecule: macrolide export protein maca; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section
99	c3u9sA	Alignment	not modelled	25.9	37	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of <i>P. aeruginosa</i> 3-methylcrotonyl-coa carboxylase 2 (mcc) 750 kd holoenzyme, coa complex
100	c2qf7A	Alignment	not modelled	24.4	16	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase 2 from <i>Rhizobium etli</i>
101	c3j9vC	Alignment	not modelled	24.1	15	PDB header: hydrolase Chain: C: PDB Molecule: v-type proton atpase catalytic subunit a; PDBTitle: yeast v-atpase state 3
102	c3b9iB	Alignment	not modelled	24.0	31	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb;

102	c3h9b_	Alignment	not modelled	24.0	31	PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
103	d2e1ba1	Alignment	not modelled	23.6	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: AlaX-M N-terminal domain-like
104	c1vdzA_	Alignment	not modelled	22.3	19	PDB header: hydrolase Chain: A; PDB Molecule: a-type atpase subunit a; PDBTitle: crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
105	c3va7A_	Alignment	not modelled	21.0	26	PDB header: ligase Chain: A; PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase