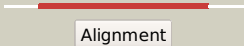








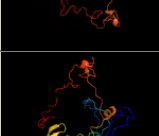

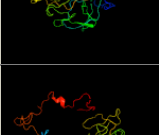
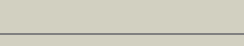
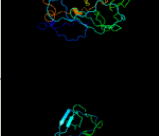

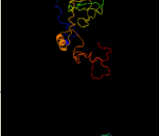


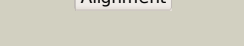
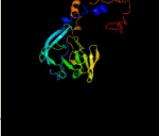


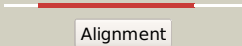

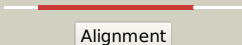

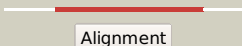
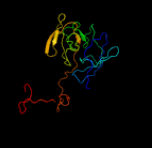

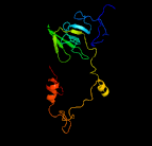
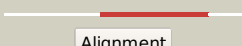
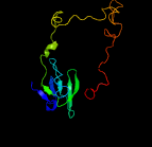

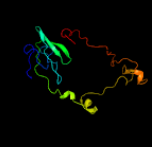
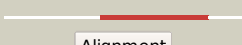
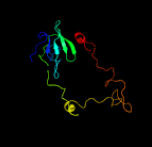

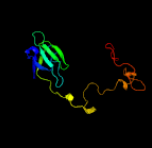



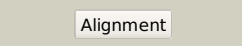




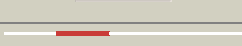
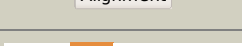
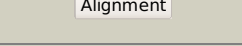


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0704 (rplB) 802531_803373
 Date Fri Jul 26 01:50:27 BST 2019
 Unique Job ID ff851a001e7cb626

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60C	 Alignment		100.0	93	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c3d5bD	 Alignment		100.0	63	PDB header: ribosome Chain: D; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
3	c3j3wC	 Alignment		100.0	62	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l2; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
4	c1vw3B	 Alignment		100.0	44	PDB header: ribosome Chain: B; PDB Molecule: 54s ribosomal protein rml2, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
5	c2z4lC	 Alignment		100.0	56	PDB header: ribosome Chain: C; PDB Molecule: 50s ribosomal protein l2; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with paromomycin and ribosome recycling factor (rrf). this3 file contains the 50s subunit of the first 70s ribosome, with4 paromomycin and rrf bound. the entire crystal structure contains two5 70s ribosomes and is described in remark 400.
6	c3bboE	 Alignment		100.0	54	PDB header: ribosome Chain: E; PDB Molecule: ribosomal protein l2; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
7	c2gyaA	 Alignment		100.0	59	PDB header: ribosome Chain: A; PDB Molecule: 50s ribosomal protein l2; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
8	c4a1cA	 Alignment		100.0	31	PDB header: ribosome Chain: A; PDB Molecule: rpl8; 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 4.
9	c2zkra	 Alignment		100.0	33	PDB header: ribosomal protein/rna Chain: A; PDB Molecule: rna expansion segment es3; 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
10	c1kqsA	 Alignment		100.0	40	PDB header: ribosome Chain: A; PDB Molecule: ribosomal protein l2; PDBTitle: the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
11	c3j2lB	 Alignment		100.0	33	PDB header: ribosome Chain: B; PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)

12	c4v19D	 Alignment		100.0	40	PDB header: ribosome Chain: D: PDB Molecule: mitoribosomal protein ul2m, mrpl2; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
13	c4ce4D	 Alignment		100.0	42	PDB header: ribosome Chain: D: PDB Molecule: mrpl2; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
14	c2b66D	 Alignment		100.0	59	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l2; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
15	c3zf7e	 Alignment		100.0	36	PDB header: ribosome Chain: E: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
16	d2j01d1	 Alignment		100.0	62	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
17	d2qamc1	 Alignment		100.0	58	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
18	d2zjra1	 Alignment		100.0	63	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
19	d1vqoa1	 Alignment		100.0	43	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
20	c1rl2A	 Alignment		100.0	62	PDB header: ribosomal protein Chain: A: PDB Molecule: protein (ribosomal protein l2); PDBTitle: ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
21	c2ftcB	 Alignment	not modelled	100.0	39	PDB header: ribosome Chain: B: PDB Molecule: mitochondrial ribosomal protein l2; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
22	d2j01d2	 Alignment	not modelled	100.0	66	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
23	d2zjra2	 Alignment	not modelled	100.0	66	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	d1rl2a1	 Alignment	not modelled	100.0	60	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
25	d1vqoa2	 Alignment	not modelled	99.9	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
26	d1rl2a2	 Alignment	not modelled	99.9	61	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
27	d2qamc2	 Alignment	not modelled	99.8	59	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
28	c3peiA	 Alignment	not modelled	89.9	25	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
29	d2dy1a1	 Alignment	not modelled	73.0	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins

					Family:Elongation factors
30	c3ij3A	Alignment	not modelled	56.7	28 PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
31	c1lanA	Alignment	not modelled	53.6	21 PDB header: hydrolase (alpha-aminoacylpeptide) Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal
32	c3h8gC	Alignment	not modelled	46.3	17 PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
33	c2jmzA	Alignment	not modelled	45.9	17 PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein mj0781; PDBTitle: solution structure of a kba intein precursor from2 methanococcus jannaschii
34	c1oeiA	Alignment	not modelled	45.7	61 PDB header: prion protein Chain: A: PDB Molecule: major prion protein; PDBTitle: human prion protein 61-84
35	d2cqaa1	Alignment	not modelled	41.3	19 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
36	c4maqB	Alignment	not modelled	40.9	26 PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
37	c5ergA	Alignment	not modelled	40.8	22 PDB header: transferase Chain: A: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
38	c3d4rE	Alignment	not modelled	40.2	18 PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
39	c3kzwD	Alignment	not modelled	38.7	21 PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
40	c5lhkA	Alignment	not modelled	35.0	31 PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 2, chloroplastic; PDBTitle: bottromycin maturation enzyme botp in complex with mn
41	d2bv3a1	Alignment	not modelled	34.7	28 Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
42	c3nx6A	Alignment	not modelled	31.6	33 PDB header: chaperone Chain: A: PDB Molecule: 10kda chaperonin; PDBTitle: crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
43	c1x65A	Alignment	not modelled	30.3	27 PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
44	c3jruB	Alignment	not modelled	29.5	19 PDB header: hydrolase Chain: B: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
45	c6omeA	Alignment	not modelled	27.8	19 PDB header: hydrolase Chain: A: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from chlamydia trachomatis d/uw-3/cx
46	c2kkgA	Alignment	not modelled	27.7	59 PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: nmr structure of the octarepeat region of prion protein2 bound to pentosan polysulfate
47	d1lama1	Alignment	not modelled	27.5	21 Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
48	c5ounA	Alignment	not modelled	26.9	18 PDB header: hydrolase Chain: A: PDB Molecule: rvub-like protein 2; PDBTitle: nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
49	c4gopX	Alignment	not modelled	25.8	13 PDB header: dna binding protein/dna Chain: X: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
50	c6cxdA	Alignment	not modelled	24.7	22 PDB header: hydrolase Chain: A: PDB Molecule: peptidase b; PDBTitle: crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution
51	c3j20J	Alignment	not modelled	24.1	16 PDB header: ribosome Chain: J: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
52	c1gytG	Alignment	not modelled	23.6	23 PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa)
53	c5xxul	Alignment	not modelled	23.1	16 PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein es8; PDBTitle: small subunit of toxoplasma gondii ribosome
54	c3u5cl	Alignment	not modelled	21.8	24 PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome

					a
55	c4zi6D_	Alignment	not modelled	21.5	25 PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of leucine aminopeptidase from helicobacter pylori
56	c3j3al_	Alignment	not modelled	20.5	19 PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: structure of the human 40s ribosomal proteins
57	c4kkuD_	Alignment	not modelled	20.4	8 PDB header: membrane protein Chain: D: PDB Molecule: membrane fusion protein; PDBTitle: structure of besa (selenomethionone derivative - p212121)
58	c1gycA_	Alignment	not modelled	17.2	24 PDB header: oxidoreductase Chain: A: PDB Molecule: laccase 2; PDBTitle: crystal structure determination at room temperature of a laccase from <i>Trametes versicolor</i> in its oxidised form containing a full complement of copper ions
59	c6jymB_	Alignment	not modelled	16.9	33 PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic <i>Exiguobacterium antarcticum</i>
60	d2pi2e1	Alignment	not modelled	16.4	15 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
61	c2pqaB_	Alignment	not modelled	16.4	15 PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
62	c3zey5_	Alignment	not modelled	16.2	19 PDB header: ribosome Chain: 5: PDB Molecule: 40s ribosomal protein s8; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma <i>brucei</i> ribosome
63	c5xyil_	Alignment	not modelled	16.0	16 PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: small subunit of <i>Trichomonas vaginalis</i> ribosome
64	c3r6oA_	Alignment	not modelled	15.6	31 PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioate isomerase from <i>Mycobacterium abscessus</i>
65	c3j38l_	Alignment	not modelled	15.4	19 PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: structure of the <i>D. melanogaster</i> 40s ribosomal proteins
66	c2dfuB_	Alignment	not modelled	15.3	31 PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from <i>Thermus thermophilus</i> hb8
67	d1ulva4	Alignment	not modelled	14.3	16 Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
68	c5lp5F_	Alignment	not modelled	13.9	14 PDB header: hydrolase/antibiotic Chain: F: PDB Molecule: rod shape-determining protein (mrec); PDBTitle: complex between penicillin-binding protein (pbp2) and mrec from <i>Helicobacter pylori</i>
69	c5ntgA_	Alignment	not modelled	13.9	18 PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: structure of leucyl aminopeptidase from <i>Trypanosoma cruzi</i> in complex2 with citrate
70	c2kcoA_	Alignment	not modelled	13.9	19 PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution nmr structure of ribosomal protein sso0164 from <i>Sulfolobus solfataricus</i> . northeast structural genomics3 consortium (nesg) target sst4.
71	c3f1zF_	Alignment	not modelled	13.5	46 PDB header: dna binding protein Chain: F: PDB Molecule: putative nucleic acid-binding lipoprotein; PDBTitle: crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh3 78578 at 2.46 a resolution
72	d1sawa_	Alignment	not modelled	13.0	18 Fold: FAH Superfamily: FAH Family: FAH
73	c2qqsB_	Alignment	not modelled	12.8	13 PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
74	c2j5uB_	Alignment	not modelled	12.6	26 PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec <i>Lysteria monocytogenes</i>
75	c2jz8A_	Alignment	not modelled	11.3	56 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from <i>Bartonella henselae</i> 2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
76	d1q1ca2	Alignment	not modelled	10.9	17 Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
77	c5ohqA_	Alignment	not modelled	10.8	15 PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kow6-kow7 domain of human dsf
78	c5daoA_	Alignment	not modelled	10.7	23 PDB header: oxidoreductase Chain: A: PDB Molecule: laccase; PDBTitle: laccase from <i>Antrodia faginea</i>
					Fold: OB-fold

79	d3d3ra1	Alignment	not modelled	10.5	21	Superfamily: HupF/HypC-like Family: HupF/HypC-like
80	c2xzn2	Alignment	not modelled	10.3	12	PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s8; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
81	c1wzoC	Alignment	not modelled	10.3	26	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
82	c4e2uA	Alignment	not modelled	10.2	19	PDB header: unknown function Chain: A: PDB Molecule: pho rada intein; PDBTitle: crystal structures of radamin intein from pyrococcus horikoshii
83	d2nvna1	Alignment	not modelled	9.8	16	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
84	c6opcZ	Alignment	not modelled	9.7	17	PDB header: motor protein Chain: Z: PDB Molecule: ubx domain-containing protein 1; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
85	c3d3rA	Alignment	not modelled	9.7	21	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
86	c3kf8D	Alignment	not modelled	9.7	17	PDB header: structural protein Chain: D: PDB Molecule: protein ten1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
87	c4tt9A	Alignment	not modelled	9.7	7	PDB header: protein transport Chain: A: PDB Molecule: surface presentation of antigens protein spa0; PDBTitle: structure of the c-terminal spa0 domain of shigella flexneri spa33
88	d1g03a	Alignment	not modelled	9.6	86	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
89	c4uc4A	Alignment	not modelled	9.4	17	PDB header: replication Chain: A: PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
90	d1gta2	Alignment	not modelled	9.4	24	Fold: FAH Superfamily: FAH Family: FAH
91	c2kjpA	Alignment	not modelled	9.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ylbl; PDBTitle: solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
92	c2kcyA	Alignment	not modelled	9.4	16	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nesg) target tr71d
93	d1o6aa	Alignment	not modelled	9.2	7	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
94	c5ifgC	Alignment	not modelled	9.2	24	PDB header: hydrolase/antitoxin Chain: C: PDB Molecule: mrna interferase higb; PDBTitle: crystal structure of higa-higb complex from e. coli
95	c1i7oC	Alignment	not modelled	9.2	26	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
96	d2it9a1	Alignment	not modelled	9.1	21	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
97	c6cztA	Alignment	not modelled	8.9	25	PDB header: cell adhesion Chain: A: PDB Molecule: alginate biosynthesis protein algf; PDBTitle: cs-rosetta determined structures of the n-terminal domain of algf from2 p. aeruginosa
98	d1gta1	Alignment	not modelled	8.8	27	Fold: FAH Superfamily: FAH Family: FAH
99	c4dbhA	Alignment	not modelled	8.3	29	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor