













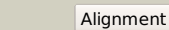

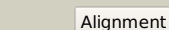


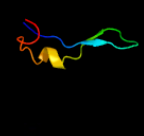



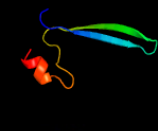
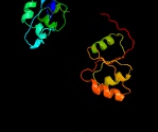



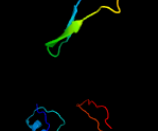




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2567_(-)_2889805_2892459
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	b25837f5df45c609

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n6xA_	 Alignment		100.0	30	PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
2	c2ioaA_	 Alignment		99.2	16	PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine PDBTitle: e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
3	c2vpmB_	 Alignment		99.1	15	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
4	c1gshA_	 Alignment		96.5	15	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
5	d2io8a3	 Alignment		95.3	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Glutathionylspermidine synthase ATP-binding domain-like
6	c4iwyA_	 Alignment		90.1	13	PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
7	c1m0tB_	 Alignment		86.2	14	PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase; PDBTitle: yeast glutathione synthase
8	c1i7nA_	 Alignment		86.1	13	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
9	c5i47A_	 Alignment		84.7	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: rimk domain protein atp-grasp; PDBTitle: crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745
10	c3vpbC_	 Alignment		80.1	21	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
11	c1kjaA_	 Alignment		79.4	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s

12	c3kalB	Alignment		77.4	11	PDB header: ligase Chain: B: PDB Molecule: homogluthatione synthetase; PDBTitle: structure of homogluthatione synthetase from glycine max in2 closed conformation with homogluthatione, adp, a sulfate3 ion, and three magnesium ions bound
13	c1pk8D	Alignment		76.4	13	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
14	c3wvqA	Alignment		75.8	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
15	c3tinA	Alignment		75.1	22	PDB header: ligase Chain: A: PDB Molecule: ttl protein; PDBTitle: tubulin tyrosine ligase
16	c5ig9H	Alignment		73.9	17	PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
17	d1pk8a2	Alignment		71.9	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
18	c5ig8A	Alignment		71.5	14	PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnb from microcystis aeruginosa mrc
19	c1ehiB	Alignment		71.3	11	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides
20	c2p0aA	Alignment		70.4	14	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
21	d1gsaa2	Alignment	not modelled	69.3	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
22	d1i7na2	Alignment	not modelled	68.7	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
23	c2qb5B	Alignment	not modelled	67.7	18	PDB header: transferase Chain: B: PDB Molecule: inositol-tetrakisphosphate 1-kinase; PDBTitle: crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
24	d1kjqA3	Alignment	not modelled	67.0	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
25	c3i12A	Alignment	not modelled	66.5	21	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
26	c3lp8A	Alignment	not modelled	65.5	9	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
27	c5oetB	Alignment	not modelled	64.9	14	PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase-like effector 30 (gpa-gss30-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss30) from2 globodera pallida in apoform.
28	c5oevB	Alignment	not modelled	60.7	14	PDB header: transferase Chain: B: PDB Molecule: glutathione synthetase-like effector 22 (gpa-gss22-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.

29	c1e4eB_	Alignment	not modelled	59.7	23	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
30	d1iowa2	Alignment	not modelled	57.5	20	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
31	c4fu0B_	Alignment	not modelled	56.8	15	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis
32	c3e5nA_	Alignment	not modelled	53.6	21	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
33	c4ijjF_	Alignment	not modelled	53.4	16	PDB header: cell cycle Chain: F: PDB Molecule: tubulin tyrosine ligase, ttl; PDBTitle: crystal structure of tubulin-stathmin-ttl-apo complex
34	c3tqtB_	Alignment	not modelled	52.7	13	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
35	c4wd3B_	Alignment	not modelled	52.7	9	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
36	c6dgiA_	Alignment	not modelled	51.6	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: the crystal structure of d-alanyl-alanine synthetase a from vibrio2 cholerae o1 biovar eltor str. n16961
37	c5cviB_	Alignment	not modelled	50.3	12	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
38	c1w96B_	Alignment	not modelled	48.8	16	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
39	c2yyaB_	Alignment	not modelled	47.0	10	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
40	c2dlnA_	Alignment	not modelled	46.3	23	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
41	d1e4ea2	Alignment	not modelled	45.7	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
42	d2qxfa1	Alignment	not modelled	45.1	12	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
43	d1a9xa5	Alignment	not modelled	44.6	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
44	d1omha_	Alignment	not modelled	42.9	20	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain
45	c3soyA_	Alignment	not modelled	41.1	10	PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
46	c2ip4A_	Alignment	not modelled	40.1	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
47	c5kciA_	Alignment	not modelled	39.9	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ypl067c; PDBTitle: crystal structure of htc1
48	c2xd4A_	Alignment	not modelled	39.5	12	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
49	c4mamB_	Alignment	not modelled	38.5	10	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp
50	c2i80B_	Alignment	not modelled	38.0	14	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
51	c3se7A_	Alignment	not modelled	37.2	35	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
52	d1uc8a2	Alignment	not modelled	37.0	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
53	c1z2pX_	Alignment	not modelled	36.8	21	PDB header: transferase Chain: X: PDB Molecule: inositol 1,3,4-trisphosphate 5/6-kinase; PDBTitle: inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3
54	c5k2mG_	Alignment	not modelled	35.6	21	PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis

						with lysw-gamma-2 aaa
55	c6o5cB	Alignment	not modelled	35.2	15	PDB header: dna binding protein Chain: B: PDB Molecule: putative metal-dependent transcriptional regulator; PDBTitle: x-ray crystal structure of metal-dependent transcriptional regulator2 mtsr
56	c1vkzA	Alignment	not modelled	33.9	12	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
57	c3oetF	Alignment	not modelled	33.8	19	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
58	d1gsoa3	Alignment	not modelled	33.5	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
59	d1ewqa4	Alignment	not modelled	31.9	22	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
60	c3gidB	Alignment	not modelled	31.1	16	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with soraphen a
61	c5oevD	Alignment	not modelled	31.0	13	PDB header: transferase Chain: D: PDB Molecule: glutathione synthetase-like effector 22 (gpa-gss22-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.
62	c3ln6A	Alignment	not modelled	29.9	9	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
63	c4egqD	Alignment	not modelled	28.3	14	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
64	d2r85a2	Alignment	not modelled	28.1	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
65	c6jdxC	Alignment	not modelled	27.3	16	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of acric2 dimer in complex with partial nme1cas92 preprocessed with protease alpha-chymotrypsin
66	d3c0na2	Alignment	not modelled	27.2	16	Fold: Aerolisin/ETX pore-forming domain Superfamily: Aerolisin/ETX pore-forming domain Family: (Pro)aerolysin, pore-forming lobe
67	c2hjaA	Alignment	not modelled	26.4	17	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
68	c4qdfA	Alignment	not modelled	24.6	16	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
69	c3c8iA	Alignment	not modelled	23.8	27	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of a putative membrane protein from corynebacterium2 diphtheriae
70	c3h75A	Alignment	not modelled	23.1	37	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
71	c3orgA	Alignment	not modelled	22.7	10	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
72	c2zdqA	Alignment	not modelled	22.0	23	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
73	c5dt9A	Alignment	not modelled	21.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
74	c1wtaA	Alignment	not modelled	21.5	20	PDB header: transferase Chain: A: PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
75	c4njmA	Alignment	not modelled	21.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
76	c6fanC	Alignment	not modelled	21.0	23	PDB header: metal binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of putative coot from carboxydotherrmus2 hydrogenoformans
77	d2r7ka2	Alignment	not modelled	20.3	8	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
78	c2o4cB	Alignment	not modelled	20.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
79	c2llpB	Alignment	not modelled	19.7	7	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c;

79	c3i4B_	Alignment	not modelled	19.7	7	PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate PDB header: hydrolase
80	c3diyB_	Alignment	not modelled	19.4	15	Chain: B; PDB Molecule: hyaluronidase; PDBTitle: thermobaculum terrenum o-glcnac hydrolase mutant - d120n
81	c3dktD_	Alignment	not modelled	19.3	13	PDB header: structural protein/virus like particle Chain: D; PDB Molecule: maritimacin; PDBTitle: crystal structure of thermotoga maritima encapsulin
82	c1ik6A_	Alignment	not modelled	18.6	22	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate dehydrogenase; PDBTitle: 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
83	c2e5qA_	Alignment	not modelled	18.5	17	PDB header: transcription Chain: A; PDB Molecule: phd finger protein 19; PDBTitle: solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
84	c3hruA_	Alignment	not modelled	18.1	15	PDB header: transcription Chain: A; PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
85	c4prkB_	Alignment	not modelled	17.7	20	PDB header: oxidoreductase Chain: B; PDB Molecule: 4-phosphoerythronate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
86	d2dlad2	Alignment	not modelled	17.7	10	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
87	c3ecjC_	Alignment	not modelled	17.3	11	PDB header: oxidoreductase Chain: C; PDB Molecule: protein (homoprotocatechuate 2,3-dioxygenase); PDBTitle: structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
88	c4p16A_	Alignment	not modelled	17.2	20	PDB header: hydrolase Chain: A; PDB Molecule: orf1a; PDBTitle: crystal structure of the papain-like protease of middle-east2 respiratory syndrome coronavirus
89	c4yakD_	Alignment	not modelled	17.1	7	PDB header: ligase Chain: D; PDB Molecule: beta subunit of acyl-coa synthetase (ndp forming); PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 in complex with coenzyme a, acetyl-coenzyme a and with3 phosphorylated phosphohistidine segment (site i orientation)
90	c2lc0A_	Alignment	not modelled	17.0	24	PDB header: protein binding Chain: A; PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: rv0020c_nter structure
91	c3wwyA_	Alignment	not modelled	17.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
92	c3bb9D_	Alignment	not modelled	16.9	19	PDB header: unknown function Chain: D; PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
93	c3bg5C_	Alignment	not modelled	16.6	20	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
94	c2e5pA_	Alignment	not modelled	16.2	21	PDB header: transcription Chain: A; PDB Molecule: phd finger protein 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
95	c3wvzB_	Alignment	not modelled	16.1	18	PDB header: oxidoreductase Chain: B; PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
96	c2hwgA_	Alignment	not modelled	16.1	20	PDB header: transferase Chain: A; PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
97	c4qdfB_	Alignment	not modelled	16.0	6	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B; PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
98	c3r23B_	Alignment	not modelled	15.9	19	PDB header: ligase Chain: B; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
99	c2pvpB_	Alignment	not modelled	15.7	13	PDB header: ligase Chain: B; PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori