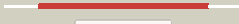



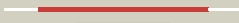




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3709c_ask_4152396_4153661
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	26d21f5c4af05005

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3l76B_	 Alignment		100.0	47	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
2	c5yeiG_	 Alignment		100.0	48	PDB header: transferase Chain: G: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
3	c2cdqB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
4	c3c1nA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
5	c3ab4K_	 Alignment		100.0	70	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
6	c2j0wA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
7	c3tviD_	 Alignment		100.0	23	PDB header: transferase Chain: D: PDB Molecule: aspartokinase; PDBTitle: crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production
8	d2cdqa1	 Alignment		100.0	36	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
9	d2hmf1	 Alignment		100.0	40	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
10	d2j0wa1	 Alignment		100.0	39	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
11	d1ybd1	 Alignment		100.0	25	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like

12	c3ek5A	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: uridylylate kinase; PDBTitle: unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
13	c2e9yA	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: carbamate kinase; PDBTitle: crystal structure of project ape1968 from aeropyrum pernix k1
14	d1e19a	Alignment		100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
15	d2bnea1	Alignment		100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
16	c2rd5A	Alignment		100.0	19	PDB header: protein binding Chain: A: PDB Molecule: acetylglutamate kinase-like protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
17	d1z9da1	Alignment		100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
18	d2a1fa1	Alignment		100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
19	c2jjxC	Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: uridylylate kinase; PDBTitle: the crystal structure of ump kinase from bacillus anthracis (ba1797)
20	d2bufa1	Alignment		100.0	21	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
21	c3nwyB	Alignment	not modelled	100.0	27	PDB header: transferase Chain: B: PDB Molecule: uridylylate kinase; PDBTitle: structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
22	c2dtjA	Alignment	not modelled	100.0	67	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
23	c4a7xF	Alignment	not modelled	100.0	22	PDB header: transferase Chain: F: PDB Molecule: uridylylate kinase; PDBTitle: crystal structure of uridylylate kinase from helicobacter pylori
24	c3k4yB	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
25	d1gs5a	Alignment	not modelled	100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
26	d1b7ba	Alignment	not modelled	100.0	18	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
27	c3l86A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: the crystal structure of smu.665 from streptococcus mutans ua159
28	c3s1tB	Alignment	not modelled	100.0	99	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis

29	d2ij9a1	Alignment	not modelled	100.0	28	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
30	c4axsA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: carbamate kinase; PDBTitle: structure of carbamate kinase from mycoplasma penetrans
31	d2btya1	Alignment	not modelled	100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
32	c2v5hB	Alignment	not modelled	100.0	18	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
33	c2w21A	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
34	c2j5tF	Alignment	not modelled	100.0	19	PDB header: transferase Chain: F: PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
35	d2brxa1	Alignment	not modelled	100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
36	c3ll9A	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: x-ray structures of isopentenyl phosphate kinase
37	c2eqxA	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetylglutamate kinase; PDBTitle: crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
38	c5yeiF	Alignment	not modelled	100.0	45	PDB header: transferase Chain: F: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
39	c3ll5C	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyl kinase related protein; PDBTitle: crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
40	d2ap9a1	Alignment	not modelled	100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
41	c2va1A	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: uridylate kinase; PDBTitle: crystal structure of ump kinase from ureaplasma parvum
42	d2akoa1	Alignment	not modelled	100.0	16	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
43	c2zhoB	Alignment	not modelled	100.0	41	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
44	c3kzfC	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: carbamate kinase; PDBTitle: structure of giardia carbamate kinase
45	c2j4kC	Alignment	not modelled	100.0	21	PDB header: transferase Chain: C: PDB Molecule: uridylate kinase; PDBTitle: crystal structure of uridylate kinase from sulfobolus solfataricus in2 complex with ump to 2.2 angstrom resolution
46	c2re1A	Alignment	not modelled	100.0	42	PDB header: transferase Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
47	c6mx1A	Alignment	not modelled	100.0	26	PDB header: transferase, hydrolase Chain: A: PDB Molecule: bifunctional aspartokinase/homoserine dehydrogenase 1; PDBTitle: the crystal structure of the regulatory domain of aspartokinase in the2 bifunctional aspartokinase/homoserine dehydrogenase 1 from3 escherichia coli str. k-12 substr. mg1655
48	c2ogxB	Alignment	not modelled	100.0	18	PDB header: metal binding protein Chain: B: PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
49	c3d40A	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: foma protein; PDBTitle: crystal structure of fosfomicin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
50	c2r98A	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: putative acetylglutamate synthase; PDBTitle: crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
51	c4f6tA	Alignment	not modelled	100.0	21	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein (mosto) from2 azotobacter vinelandii loaded with various polyoxometalates
52	c2ogxA	Alignment	not modelled	99.9	23	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
53	c3zzgC	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of the amino acid kinase domain from saccharomyces2 cerevisiae acetylglutamate kinase without ligands

54	c3mahA	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
55	c4q1tD	Alignment	not modelled	99.9	22	PDB header: transferase Chain: D: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of a glutamate 5-kinase from burkholderia2 thailandensis
56	c2f06B	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
57	c4ab7C	Alignment	not modelled	99.8	15	PDB header: transferase Chain: C: PDB Molecule: protein arg5,6, mitochondrial; PDBTitle: crystal structure of a tetrameric acetylglutamate kinase from2 saccharomyces cerevisiae complexed with its substrate n-3 acetylglutamate
58	c3s7yX	Alignment	not modelled	99.8	17	PDB header: transferase Chain: X: PDB Molecule: n-acetylglutamate kinase / n-acetylglutamate synthase; PDBTitle: crystal structure of mmnags in space group p3121 at 4.3 a resolution
59	c3s6kA	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of xcngns
60	d2cdqa3	Alignment	not modelled	99.6	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
61	d2hmfA2	Alignment	not modelled	99.6	34	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
62	d2j0wa3	Alignment	not modelled	99.6	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
63	d2hmfA3	Alignment	not modelled	99.5	31	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
64	d2cdqa2	Alignment	not modelled	98.9	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
65	d2j0wa2	Alignment	not modelled	98.7	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
66	c2nyiB	Alignment	not modelled	97.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
67	c1u8sB	Alignment	not modelled	96.7	22	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
68	c5i2cA	Alignment	not modelled	96.2	16	PDB header: signaling protein Chain: A: PDB Molecule: gats-like protein 3; PDBTitle: arginine-bound castor1 from homo sapiens
69	c1zhvA	Alignment	not modelled	95.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
70	d2f06a1	Alignment	not modelled	94.3	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
71	c2pc6C	Alignment	not modelled	94.2	13	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
72	c2fgcA	Alignment	not modelled	94.0	12	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
73	d2f06a2	Alignment	not modelled	93.9	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
74	c2f1fA	Alignment	not modelled	93.5	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetoxyhydroxyacid2 synthase isozyme iii from e. coli
75	c3mwbA	Alignment	not modelled	92.9	11	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureescens to 2.0a
76	d1zpvA1	Alignment	not modelled	92.5	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
77	d1zpvA2	Alignment	not modelled	92.0	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like
78	c1zvpB	Alignment	not modelled	91.7	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein vc0802; PDBTitle: crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein

79	d1sc6a3	Alignment	not modelled	91.6	20	Supersfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
80	d1zhva2	Alignment	not modelled	91.3	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
81	d1u8sa1	Alignment	not modelled	91.1	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
82	c1ygyA	Alignment	not modelled	91.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
83	d1ygya3	Alignment	not modelled	90.5	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
84	c2qmwA	Alignment	not modelled	89.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
85	c3ibwA	Alignment	not modelled	89.7	18	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
86	d2qmwA2	Alignment	not modelled	89.3	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
87	c2qmxB	Alignment	not modelled	88.3	9	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
88	d1u8sa2	Alignment	not modelled	87.4	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
89	d2f1fa1	Alignment	not modelled	86.5	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
90	c5uscB	Alignment	not modelled	86.4	16	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
91	d2pc6a2	Alignment	not modelled	85.4	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
92	d2ftsA3	Alignment	not modelled	85.0	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
93	c3kbqA	Alignment	not modelled	84.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
94	c3n0vD	Alignment	not modelled	84.6	12	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
95	d2fgca2	Alignment	not modelled	82.3	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
96	c2phmA	Alignment	not modelled	81.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
97	c6dzsD	Alignment	not modelled	80.7	25	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
98	c5jk5A	Alignment	not modelled	80.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
99	d1phza1	Alignment	not modelled	79.8	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
100	c3rfqC	Alignment	not modelled	78.2	24	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
101	c4uuwA	Alignment	not modelled	77.9	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: cina-like protein; PDBTitle: competence or damage-inducible protein cina from thermus thermophilus
102	c2mdaB	Alignment	not modelled	77.2	6	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
103	d2ngra3	Alignment	not modelled	76.5	22	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
104	c2lvwA	Alignment	not modelled	76.2	13	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetoxyacid synthase i (ahas i)

105	c2fu3A_	Alignment	not modelled	74.4	18	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
106	c3mtjA_	Alignment	not modelled	72.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
107	c2pjkA_	Alignment	not modelled	70.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfobolus tokodaii
108	c3luyA_	Alignment	not modelled	69.8	14	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
109	c2nqgA_	Alignment	not modelled	68.0	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
110	c4lubA_	Alignment	not modelled	66.8	10	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
111	d1y5ea1	Alignment	not modelled	65.5	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
112	c5denA_	Alignment	not modelled	65.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
113	c3o1lB_	Alignment	not modelled	64.0	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
114	c2pvpB_	Alignment	not modelled	60.6	14	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
115	c2is8A_	Alignment	not modelled	59.8	15	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
116	d2g2ca1	Alignment	not modelled	55.5	27	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
117	c3ewiB_	Alignment	not modelled	55.1	15	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
118	c4lhbC_	Alignment	not modelled	55.0	23	PDB header: transferase Chain: C: PDB Molecule: molybdopterin adenyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
119	c2g4rB_	Alignment	not modelled	54.1	30	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
120	c3nrbd_	Alignment	not modelled	52.1	10	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution