


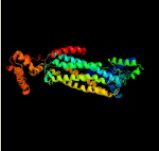
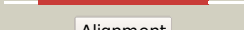

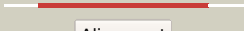






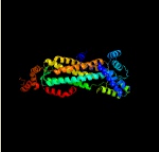


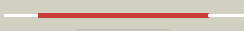
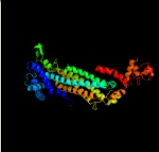






Phyre2

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 Description RVBD0777_(purB)_870011_871429
 Date Fri Jul 26 01:50:36 BST 2019
 Unique Job ID 9c55f3234b203d05

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nleB_	 Alignment		100.0	82	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of apo adenylosuccinate lyase from mycobacterium2 smegmatis
2	c5vkwB_	 Alignment		100.0	31	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase ade13 from candida2 albicans
3	c2vd6B_	 Alignment		100.0	30	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
4	c2pfmA_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
5	d1c3ca_	 Alignment		100.0	26	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
6	d1re5a_	 Alignment		100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
7	c1yisA_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: structural genomics of caenorhabditis elegans: adenylosuccinate lyase
8	c5xnzA_	 Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: cred; PDBTitle: crystal structure of cred complex with fumarate
9	c4eeiA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from francisella2 tularensis complexed with amp and succinate
10	c5eyvB_	 Alignment		100.0	30	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from schistosoma mansoni2 in apo form.
11	d1q5na_	 Alignment		100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase

12	d1i0aa_	Alignment		100.0	16	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
13	d1tj7a_	Alignment		100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
14	d1dofa_	Alignment		100.0	27	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
15	d1hy0a_	Alignment		100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
16	c6igaB_	Alignment		100.0	17	PDB header: lyase Chain: B: PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of argininosuccinate lyase from mycobacterium2 tuberculosis
17	d1tjva_	Alignment		100.0	17	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
18	c2qgaC_	Alignment		100.0	17	PDB header: lyase Chain: C: PDB Molecule: adenylosuccinate lyase; PDBTitle: plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
19	d1k62a_	Alignment		100.0	17	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
20	c3c8tA_	Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: fumarate lyase; PDBTitle: crystal structure of fumarate lyase from mesorhizobium sp. bnc1
21	c2e9fC_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
22	c4efcA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from trypanosoma brucei,2 tb427tmp.160.5560
23	c3bhgA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from legionella2 pneumophila
24	c4mx2C_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: C: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from leishmania donovani
25	c6g3eA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of edds lyase in complex with formate
26	c2ptsA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of wild type escherichia coli adenylosuccinate lyase
27	d1fuoa_	Alignment	not modelled	100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
28	c6n1mA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of fumarate hydratase class ii from legionella2 pneumophila philadelphia 1
						Fold: L-aspartase-like

29	dlj3ua_	Alignment	not modelled	100.0	18	Superfamily: L-aspartase-like Family: L-aspartase/fumarase
30	c1yfmA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: fumarase; PDBTitle: recombinant yeast fumarase
31	d1yfmA_	Alignment	not modelled	100.0	17	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
32	c4hgvD_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: D: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of a fumarate hydratase
33	d1vdka_	Alignment	not modelled	100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
34	d1jswa_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
35	c3gtdA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
36	d1jswc_	Alignment	not modelled	100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
37	c3no9C_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
38	c2fenA_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: A: PDB Molecule: 3-carboxy-cis,cis-muconate lactonizing enzyme; PDBTitle: 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
39	c3ocfB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: fumarate lyase:delta crystallin; PDBTitle: crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
40	d1f1oa_	Alignment	not modelled	100.0	25	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
41	c4hgvC_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of a fumarate hydratase
42	c3e04A_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
43	c3e04C_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
44	c3gtdB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
45	c3r6yG_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: G: PDB Molecule: aspartase; PDBTitle: crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
46	c2xgvA_	Alignment	not modelled	46.1	24	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from 2 rabbit endogenous lentivirus (relik)
47	d2ahra1	Alignment	not modelled	36.1	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
48	c2rcyB_	Alignment	not modelled	31.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
49	c2ctoA_	Alignment	not modelled	27.7	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein flj14904
50	d1yqqa1	Alignment	not modelled	24.2	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
51	c5nvkF_	Alignment	not modelled	24.1	36	PDB header: translation Chain: F: PDB Molecule: grb10-interacting gyf protein 1; PDBTitle: crystal structure of the human 4ehp-gigyf1 complex
52	c1nvtA_	Alignment	not modelled	23.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
53	c2ag8A_	Alignment	not modelled	20.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
54	d1g3pa2	Alignment	not modelled	17.6	20	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
55	d1u5ta1	Alignment	not modelled	17.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain

56	c3bbnC_	Alignment	not modelled	17.0	30	PDB header: ribosome Chain: C; PDB Molecule: ribosomal protein s3; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
57	c1dipA_	Alignment	not modelled	16.4	17	PDB header: acetylation Chain: A; PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
58	c2digA_	Alignment	not modelled	14.8	67	PDB header: dna binding protein Chain: A; PDB Molecule: lamin-b receptor; PDBTitle: solusion structure of the todor domain of human lamin-b2 receptor
59	c4ug3C_	Alignment	not modelled	14.3	14	PDB header: cell cycle Chain: C; PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb n-terminal domain
60	c2hk8B_	Alignment	not modelled	13.9	8	PDB header: oxidoreductase Chain: B; PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
61	d1nvtA2	Alignment	not modelled	13.3	25	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
62	c3fbtB_	Alignment	not modelled	13.0	13	PDB header: oxidoreductase, lyase Chain: B; PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
63	d2gj4a1	Alignment	not modelled	13.0	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
64	c2wukD_	Alignment	not modelled	12.2	16	PDB header: cell cycle Chain: D; PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
65	c2l81A_	Alignment	not modelled	11.6	17	PDB header: cell adhesion Chain: A; PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
66	d1p77a2	Alignment	not modelled	11.3	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
67	d1vi2a2	Alignment	not modelled	11.2	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
68	c1wjvA_	Alignment	not modelled	11.2	56	PDB header: dna binding protein Chain: A; PDB Molecule: cell growth regulating nucleolar protein lyar; PDBTitle: solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar
69	c2ev9B_	Alignment	not modelled	11.1	17	PDB header: oxidoreductase Chain: B; PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
70	c5w16D_	Alignment	not modelled	10.9	14	PDB header: isomerase Chain: D; PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate
71	d2qalc1	Alignment	not modelled	10.7	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
72	c3no7A_	Alignment	not modelled	10.7	23	PDB header: dna binding protein Chain: A; PDB Molecule: putative plasmid related protein; PDBTitle: crystal structure of the centromere-binding protein parb from plasmid2 pcxc100
73	c2jfqA_	Alignment	not modelled	10.7	20	PDB header: isomerase Chain: A; PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate racemase in2 complex with d- glutamate
74	c2gzmB_	Alignment	not modelled	10.6	14	PDB header: isomerase Chain: B; PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus anthracis
75	d1d1da2	Alignment	not modelled	10.6	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
76	c2zmeA_	Alignment	not modelled	10.6	17	PDB header: protein transport Chain: A; PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
77	c5ns5A_	Alignment	not modelled	10.5	8	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+
78	c4ardA_	Alignment	not modelled	10.3	12	PDB header: viral protein Chain: A; PDB Molecule: capsid protein p27; PDBTitle: structure of the immature retroviral capsid at 8a resolution by cryo-2 electron microscopy
79	c5dzaA_	Alignment	not modelled	10.1	25	PDB header: oxidoreductase Chain: A; PDB Molecule: shikimate dehydrogenase (nadp(+)); PDBTitle: 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile.
80	c1vi2B_	Alignment	not modelled	10.1	14	PDB header: oxidoreductase Chain: B; PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad

81	d1npya2	Alignment	not modelled	10.0	25	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
82	c3pgjB	Alignment	not modelled	10.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
83	c3hfrA	Alignment	not modelled	9.8	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
84	c4ug1A	Alignment	not modelled	9.7	16	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
85	d1p7na	Alignment	not modelled	9.6	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
86	c3cuqA	Alignment	not modelled	9.5	17	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
87	c3pwzA	Alignment	not modelled	9.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
88	c2dwuA	Alignment	not modelled	9.3	14	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
89	c5ybxA	Alignment	not modelled	9.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: bouquet formation protein 4; PDBTitle: crystal structure of the n-terminal domain of bqt4 in s.pombe
90	c5ijwA	Alignment	not modelled	9.2	17	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
91	d1gg2g	Alignment	not modelled	9.1	13	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
92	c6fxyA	Alignment	not modelled	9.0	37	PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
93	c5z4yB	Alignment	not modelled	9.0	13	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
94	d1em9a	Alignment	not modelled	9.0	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
95	c2v4xA	Alignment	not modelled	8.9	8	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
96	c1l6nA	Alignment	not modelled	8.7	29	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
97	c4g9qA	Alignment	not modelled	8.6	15	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
98	c3gt0A	Alignment	not modelled	8.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
99	c1p74B	Alignment	not modelled	8.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae