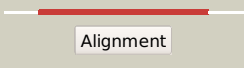

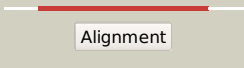

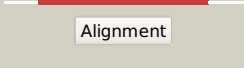

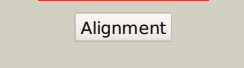

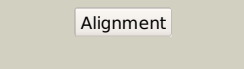

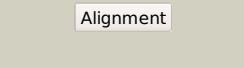

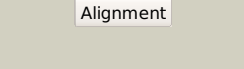

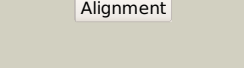

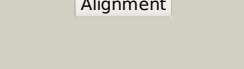

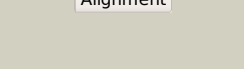

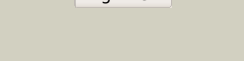



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1086_(-)_1210600_1211388
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	ec070a093dc3ca34

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vg2C_	 Alignment		100.0	35	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
2	c4h8eA_	 Alignment		100.0	30	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
3	c2vfwB_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
4	c5hc7A_	 Alignment		100.0	32	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: prenyltransferase for protein; PDBTitle: crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenylidiphosphate
5	c4q9mA_	 Alignment		100.0	33	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: isoprenyl transferase; PDBTitle: crystal structure of upps in complex with fpp and an allosteric2 inhibitor
6	c5hxpA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: ((2z,6z)-farnesyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
7	c5gukA_	 Alignment		100.0	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: cyclolavandulyl diphosphate synthase; PDBTitle: crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
8	d1ueha_	 Alignment		100.0	33	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
9	c6acsA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: ditrans, polycis-undecaprenyl-diphosphate synthase ((2e,6e)- PDBTitle: poly-cis-prenyltransferase
10	c5xk9F_	 Alignment		100.0	24	PDB header: transferase Chain: F: PDB Molecule: undecaprenyl diphosphate synthase; PDBTitle: crystal structure of isosesquilavandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gssp and dmapp
11	c1jp3A_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase

12	d1f75a_	Alignment		100.0	30	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
13	c3ugsB_	Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
14	c2d2rA_	Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
15	c6jcnB_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: dehydrodolichyl diphosphate synthase complex subunit nus1; PDBTitle: yeast dehydrodolichyl diphosphate synthase complex subunit nus1
16	c4cmxB_	Alignment		99.3	18	PDB header: nuclear protein Chain: B: PDB Molecule: rv3378c; PDBTitle: crystal structure of rv3378c
17	c3cprB_	Alignment		70.0	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
18	c3s5oA_	Alignment		64.1	13	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
19	c5ak1A_	Alignment		62.7	10	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate binding family 6; PDBTitle: the penta-modular cellulosomal arabinoxylanase ctxyl5a2 structure as revealed by x-ray crystallography
20	c3fluD_	Alignment		58.2	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
21	c3n58D_	Alignment	not modelled	58.1	8	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteine; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
22	c2rfqB_	Alignment	not modelled	58.1	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
23	c3si9B_	Alignment	not modelled	57.1	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
24	c5n6yD_	Alignment	not modelled	56.8	12	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
25	c2ou4C_	Alignment	not modelled	56.6	12	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
26	c3daqB_	Alignment	not modelled	55.4	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
27	c5iq5A_	Alignment	not modelled	52.8	17	PDB header: viral protein Chain: A: PDB Molecule: macro domain; PDBTitle: nmr solution structure of mayaro virus macro domain
28	d1hl2a_	Alignment	not modelled	51.7	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

29	c2hk1D	Alignment	not modelled	50.3	14	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
30	c3pueA	Alignment	not modelled	49.9	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from 2 acinetobacter baumannii with lysine at 2.6a resolution
31	c3zddA	Alignment	not modelled	49.7	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
32	d2a6na1	Alignment	not modelled	49.1	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
33	c6c34A	Alignment	not modelled	48.8	15	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
34	c5ud6B	Alignment	not modelled	47.2	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
35	c2v9dB	Alignment	not modelled	47.0	14	PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to 2 the dihydrodipicolinic acid synthase family from e. coli 3 k12
36	c3qfeB	Alignment	not modelled	47.0	13	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family 2 protein from coccidioides immitis
37	d1xxa1	Alignment	not modelled	46.9	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
38	c3bdkB	Alignment	not modelled	46.8	17	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate 2 dehydratase complexed with substrate analogue
39	c3noeA	Alignment	not modelled	46.5	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas 2 aeruginosa
40	c2yxgD	Alignment	not modelled	45.8	14	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
41	c3fkkA	Alignment	not modelled	45.2	12	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
42	c3dx5A	Alignment	not modelled	45.0	9	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in 2 the petrobactin synthesis from bacillus anthracis
43	d1i60a	Alignment	not modelled	44.0	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
44	c3d0cB	Alignment	not modelled	43.6	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus 2 iheyensis at 1.9 a resolution
45	c2vc6A	Alignment	not modelled	43.3	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. melloti with pyruvate bound
46	c3n2xB	Alignment	not modelled	41.9	14	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from e. coli k12 in complex 3 with pyruvate
47	c3b4uB	Alignment	not modelled	39.0	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium 2 tumefaciens str. c58
48	c3lciA	Alignment	not modelled	38.9	16	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
49	c3g0sA	Alignment	not modelled	38.3	9	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
50	c3cnyA	Alignment	not modelled	37.8	9	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole 2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a 3 resolution
51	c3cqbB	Alignment	not modelled	36.5	8	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b) 2 complex with zn2+ and sulfate
52	d1o5ka	Alignment	not modelled	35.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
53	d1xkya1	Alignment	not modelled	35.2	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: biosynthetic protein

54	c4i7vD_	Alignment	not modelled	35.0	15	Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhps with pyruvate
55	c5afdA_	Alignment	not modelled	34.9	12	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: native structure of n-acetylneuraminase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
56	c4ah7C_	Alignment	not modelled	34.6	13	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
57	c3qxbB_	Alignment	not modelled	34.1	15	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
58	c3lerA_	Alignment	not modelled	32.5	18	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
59	c5ktlA_	Alignment	not modelled	31.9	13	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
60	c5ui3C_	Alignment	not modelled	31.7	16	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhps from chlamydomonas reinhardtii
61	c3gqeA_	Alignment	not modelled	30.0	15	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of venezuelan equine encephalitis2 virus
62	c4iqyB_	Alignment	not modelled	28.9	11	PDB header: hydrolase Chain: B: PDB Molecule: o-acetyl-adp-ribose deacetylase macrod2; PDBTitle: crystal structure of the human protein-proximal adp-ribosyl-hydrolase2 macrod2
63	c3oneA_	Alignment	not modelled	28.7	11	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
64	c3eb2A_	Alignment	not modelled	28.5	14	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
65	c3bi8A_	Alignment	not modelled	28.4	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
66	c5c54D_	Alignment	not modelled	27.9	16	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminase lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
67	c4nq1B_	Alignment	not modelled	27.8	9	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
68	c6mqhA_	Alignment	not modelled	27.2	18	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
69	c6d0gA_	Alignment	not modelled	27.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pirin family protein; PDBTitle: 1.78 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii
70	c4umlA_	Alignment	not modelled	25.5	4	PDB header: signaling protein Chain: A: PDB Molecule: ganglioside-induced differentiation-associated protein 2; PDBTitle: crystal structure of ganglioside induced differentiation2 associated protein 2 (gdap2) macro domain
71	c2x47A_	Alignment	not modelled	25.5	7	PDB header: signaling protein Chain: A: PDB Molecule: macro domain-containing protein 1; PDBTitle: crystal structure of human macrod1
72	c6daqA_	Alignment	not modelled	25.1	13	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
73	c2ynmD_	Alignment	not modelled	25.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
74	d1vk1a_	Alignment	not modelled	24.9	38	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Hypothetical protein PF0380
75	d1miob_	Alignment	not modelled	24.1	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
76	c4ur7B_	Alignment	not modelled	23.4	13	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
77	c2f9iC_	Alignment	not modelled	23.2	12	PDB header: transferase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
78	c2ksnA_	Alignment	not modelled	22.8	36	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-

						ubp/ubtd2
79	d1cmwa2	Alignment	not modelled	22.8	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
80	c1cmwA_	Alignment	not modelled	22.1	19	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
81	d2f9ya1	Alignment	not modelled	21.9	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
82	c4uxdC_	Alignment	not modelled	21.9	11	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
83	c4xkyC_	Alignment	not modelled	21.5	12	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
84	c3d64A_	Alignment	not modelled	21.4	9	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
85	c4icnB_	Alignment	not modelled	21.2	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
86	c2d1gB_	Alignment	not modelled	21.1	11	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
87	c2r8wB_	Alignment	not modelled	20.3	11	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
88	c3vylB_	Alignment	not modelled	20.2	11	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
89	c5n6yE_	Alignment	not modelled	19.9	11	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
90	c2pfuA_	Alignment	not modelled	19.8	14	PDB header: transport protein Chain: A: PDB Molecule: biopolymer transport exbd protein; PDBTitle: nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
91	c5by4A_	Alignment	not modelled	19.6	24	PDB header: protein transport Chain: A: PDB Molecule: protein tolr; PDBTitle: structure and function of the escherichia coli tol-pal stator protein2 tolr
92	c2nuxB_	Alignment	not modelled	18.9	12	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
93	c5v96A_	Alignment	not modelled	18.7	13	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
94	c3ktcB_	Alignment	not modelled	18.6	11	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
95	c5j67C_	Alignment	not modelled	18.5	20	PDB header: membrane protein Chain: C: PDB Molecule: astrotactin-2; PDBTitle: structure of astrotactin-2, a conserved vertebrate-specific and2 perforin-like membrane protein involved in neuronal development
96	c5ujeA_	Alignment	not modelled	18.5	23	PDB header: gene regulation Chain: A: PDB Molecule: sbni protein; PDBTitle: sbni with c-terminal truncation from staphylococcus aureus
97	c5kivA_	Alignment	not modelled	18.5	13	PDB header: hydrolase Chain: A: PDB Molecule: protein- <small>adp</small> -ribose hydrolase; PDBTitle: crystal structure of saumacro (sav0325)
98	c3vniC_	Alignment	not modelled	18.0	12	PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
99	c5hm8C_	Alignment	not modelled	17.5	12	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.