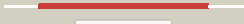



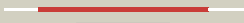




















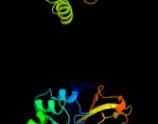




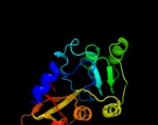


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2504c_(scoA)_2819134_2819880
 Date Wed Aug 7 12:50:13 BST 2019
 Unique Job ID d2e4029a3b2091b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ooya2	 Alignment		100.0	56	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
2	d2ahua2	 Alignment		100.0	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
3	d1poia_	 Alignment		100.0	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
4	c3rrlC_	 Alignment		100.0	53	PDB header: transferase Chain: C: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
5	c6co9A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: probable coa-transferase alpha subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab cochea-coa complex
6	c3cdkA_	 Alignment		100.0	61	PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
7	c5mzyA_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: glutaconate coa-transferase family, subunit a; PDBTitle: crystal structure of the decarboxylase aiba/aibb in complex with a2 possible transition state analog
8	c4kqbB_	 Alignment		100.0	47	PDB header: transferase Chain: B: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase; PDBTitle: structure of succinyl-coa: 3-ketoacid coa transferase from drosophila2 melanogaster
9	c1ooyA_	 Alignment		100.0	56	PDB header: transferase Chain: A: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase, PDBTitle: succinyl-coa:3-ketoacid coa transferase from pig heart
10	c2ahvC_	 Alignment		100.0	25	PDB header: transferase Chain: C: PDB Molecule: putative enzyme ydif; PDBTitle: crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
11	d1k6da_	 Alignment		100.0	43	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like

12	c2hj0A_	Alignment		100.0	18	PDB header: lyase Chain: A; PDB Molecule: putative citrate lyase, alfa subunit; PDBTitle: crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 .
13	c3q1kB_	Alignment		100.0	23	PDB header: transferase Chain: B; PDB Molecule: coenzyme a transferase; PDBTitle: crystal structure of ripa from yersinia pestis
14	c1xr4B_	Alignment		100.0	21	PDB header: hydrolase/transferase Chain: B; PDB Molecule: putative citrate lyase alpha chain/citrate-acp transferase; PDBTitle: x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
15	c4eu4A_	Alignment		100.0	23	PDB header: transferase Chain: A; PDB Molecule: succinyl-coa:acetate coenzyme a transferase; PDBTitle: succinyl-coa: acetate coa-transferase (aarch6) in complex with coa2 (hexagonal lattice)
16	c3gk7A_	Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
17	c2oasA_	Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: 4-hydroxybutyrate coenzyme a transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
18	c2g39A_	Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: acetyl-coa hydrolase; PDBTitle: crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
19	c5vitP_	Alignment		99.9	23	PDB header: transferase Chain: P; PDB Molecule: mdca; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
20	c2nvvF_	Alignment		99.9	20	PDB header: hydrolase Chain: F; PDB Molecule: acetyl-coa hydrolase/transferase family protein; PDBTitle: crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
21	d1xr4a1	Alignment	not modelled	99.9	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
22	c3eh7A_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A; PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
23	c3d3uA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A; PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
24	d2g39a1	Alignment	not modelled	99.9	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
25	c6eepA_	Alignment	not modelled	98.1	26	PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
26	c5uf2A_	Alignment	not modelled	97.9	26	PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
27	c5dbnD_	Alignment	not modelled	97.8	18	PDB header: transferase Chain: D; PDB Molecule: acetate coa-transferase subunit beta; PDBTitle: crystal structure of atoda complex
28	c1m0sA_	Alignment	not modelled	97.8	25	PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
29	c3l7oB_	Alignment	not modelled	97.8	23	PDB header: isomerase Chain: B; PDB Molecule: ribose-5-phosphate isomerase a;

29	c3r0b_	Alignment	not modelled	97.8	29	PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
30	d2g39a2	Alignment	not modelled	97.8	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
31	c2f8mB_	Alignment	not modelled	97.7	22	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
32	d1m0sa1	Alignment	not modelled	97.6	27	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
33	c4gmkB_	Alignment	not modelled	97.6	23	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
34	c6j1kA_	Alignment	not modelled	97.5	25	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from ochrobactrum2 sp. csl1
35	c1k5C_	Alignment	not modelled	97.5	29	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
36	c1lkzB_	Alignment	not modelled	97.5	27	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
37	c3hheA_	Alignment	not modelled	97.5	18	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
38	c3kwmC_	Alignment	not modelled	97.4	27	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
39	d1xr4a2	Alignment	not modelled	97.4	23	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
40	c5n02B_	Alignment	not modelled	97.2	22	PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant
41	c1uj6A_	Alignment	not modelled	97.1	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
42	d1uj4a1	Alignment	not modelled	97.0	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
43	c2pjmA_	Alignment	not modelled	96.7	15	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
44	c3cdkD_	Alignment	not modelled	96.7	19	PDB header: transferase Chain: D: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase PDBTitle: crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
45	c4nmIA_	Alignment	not modelled	96.5	23	PDB header: isomerase Chain: A: PDB Molecule: ribulose 5-phosphate isomerase; PDBTitle: 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
46	c3u7JA_	Alignment	not modelled	96.3	22	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
47	d1k5a1	Alignment	not modelled	96.2	28	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
48	c4x84C_	Alignment	not modelled	96.1	32	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
49	c6conF_	Alignment	not modelled	96.0	25	PDB header: hydrolase Chain: F: PDB Molecule: coa-transferase subunit beta; PDBTitle: crystal structure of mycobacterium tuberculosis ipdab
50	d1poib_	Alignment	not modelled	95.4	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
51	d1ooya1	Alignment	not modelled	95.2	27	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
52	c1xtzA_	Alignment	not modelled	95.1	24	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
53	c6co6B_	Alignment	not modelled	95.1	23	PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab
54	d2ahua1	Alignment	not modelled	93.3	28	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
						PDB header: transferase

55	c3rrlD_	Alignment	not modelled	93.2	22	Chain: D: PDB Molecule: succinyl-coa:3-ketoacid-coenzyme a transferase subunit b; PDBTitle: complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
56	c3ecsd_	Alignment	not modelled	91.2	20	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
57	d1t9ka_	Alignment	not modelled	90.3	23	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
58	c5b04B_	Alignment	not modelled	89.3	25	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
59	c6qg0G_	Alignment	not modelled	88.1	18	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
60	d1t5oa_	Alignment	not modelled	85.9	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
61	c5b04G_	Alignment	not modelled	85.3	17	PDB header: translation Chain: G: PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
62	c4zemB_	Alignment	not modelled	81.3	16	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
63	d1o8bb1_	Alignment	not modelled	79.1	26	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
64	c6i7tB_	Alignment	not modelled	78.5	20	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
65	c6i3mD_	Alignment	not modelled	77.4	17	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
66	c5b04C_	Alignment	not modelled	74.0	10	PDB header: translation Chain: C: PDB Molecule: probable translation initiation factor eif-2b subunit beta; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
67	c3a11D_	Alignment	not modelled	72.9	17	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
68	d1vb5a_	Alignment	not modelled	68.6	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
69	d2a0ua1_	Alignment	not modelled	65.3	12	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
70	c4zeoH_	Alignment	not modelled	64.7	22	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
71	c6a34B_	Alignment	not modelled	64.5	15	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i
72	c4oqgA_	Alignment	not modelled	62.1	17	PDB header: transcription Chain: A: PDB Molecule: deoxyribonucleoside regulator; PDBTitle: structure of the effector-binding domain of deoxyribonucleoside2 regulator deor from bacillus subtilis
73	c6ezoD_	Alignment	not modelled	56.0	18	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
74	c2yvka_	Alignment	not modelled	55.4	15	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
75	c3rwrE_	Alignment	not modelled	53.1	17	PDB header: transferase Chain: E: PDB Molecule: tm-1 protein; PDBTitle: crystal structure of the n-terminal domain of resistance protein
76	c3smaD_	Alignment	not modelled	52.7	25	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
77	c6mb6A_	Alignment	not modelled	48.8	31	PDB header: transferase Chain: A: PDB Molecule: aac(3)-iiib protein; PDBTitle: aac-iiib binary with coash
78	c5ht0B_	Alignment	not modelled	47.1	22	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside acetyltransferase hmb0005; PDBTitle: crystal structure of an antibiotic_nat family

						aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
79	c3nzeB_	Alignment	not modelled	45.2	15	PDB header: transcription regulator Chain: B; PDB Molecule: putative transcriptional regulator, sugar-binding family; PDBTitle: the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aureusens tc1.
80	d2nyga1	Alignment	not modelled	43.7	23	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
81	d2r5fa1	Alignment	not modelled	43.6	10	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
82	c6i3mF_	Alignment	not modelled	42.7	11	PDB header: translation Chain: F; PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
83	c5dboA_	Alignment	not modelled	42.0	26	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
84	c4r9nA_	Alignment	not modelled	42.0	16	PDB header: transcription Chain: A; PDB Molecule: lmo0547 protein; PDBTitle: deor family transcriptional regulator from listeria monocytogenes.
85	d2gnpa1	Alignment	not modelled	41.9	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
86	d3efba1	Alignment	not modelled	31.3	21	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
87	c3e4fB_	Alignment	not modelled	30.3	17	PDB header: transferase Chain: B; PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
88	c1dbgA_	Alignment	not modelled	28.3	16	PDB header: lyase Chain: A; PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
89	d1o8ba1	Alignment	not modelled	25.0	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
90	c2w48D_	Alignment	not modelled	24.6	15	PDB header: transcription Chain: D; PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
91	d2grea1	Alignment	not modelled	23.6	26	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Aminoamidase/glucanase lid domain Family: Aminoamidase/glucanase lid domain
92	c5mvrA_	Alignment	not modelled	23.6	18	PDB header: transferase Chain: A; PDB Molecule: trna threonylcarbamoyladenosine biosynthesis protein tsa;e; PDBTitle: crystal structure of bacillus subtilus ydib
93	c6bc3A_	Alignment	not modelled	22.2	15	PDB header: transferase/antibiotic Chain: A; PDB Molecule: aac 3-vi protein; PDBTitle: cryo x-ray structure of sisomicin bound aac-via
94	c3izbP_	Alignment	not modelled	21.2	13	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein rps11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
95	c6mn5A_	Alignment	not modelled	20.4	25	PDB header: transferase/antibiotic Chain: A; PDB Molecule: aminoglycoside n(3)-acetyltransferase, aac(3)-iva; PDBTitle: crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
96	c3iz6P_	Alignment	not modelled	20.2	19	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
97	d1ofla_	Alignment	not modelled	19.9	16	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
98	d1jb7a3	Alignment	not modelled	18.6	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
99	d1soua_	Alignment	not modelled	18.5	10	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase