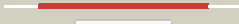



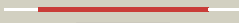







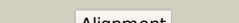











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2503c_(scoB)_2818481_2819137
Date	Wed Aug 7 12:50:13 BST 2019
Unique Job ID	bffb10b934796520

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ooya1	 Alignment		100.0	60	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
2	c3rrlD_	 Alignment		100.0	54	PDB header: transferase 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
3	c3cdkD_	 Alignment		100.0	57	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
4	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
5	c5n02B_	 Alignment		100.0	17	PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant
6	d1poib_	 Alignment		100.0	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
7	c4kgbB_	 Alignment		100.0	57	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
8	c5dbnD_	 Alignment		100.0	53	PDB header: transferase Chain: D: PDB Molecule: acetate coa-transferase subunit beta; PDBTitle: crystal structure of atoda complex
9	d2ahua1	 Alignment		100.0	28	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
10	c2ahvC_	 Alignment		100.0	28	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	c6conF_	 Alignment		100.0	20	PDB header: hydrolase Chain: F: PDB Molecule: coa-transferase subunit beta; PDBTitle: crystal structure of mycobacterium tuberculosis ipdb

12	c6co6B_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab
13	c3gk7A_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
14	c3eh7A_	Alignment		100.0	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
15	c2oasA_	Alignment		100.0	20	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.
16	c2nvvF_	Alignment		100.0	14	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.
17	c2g39A_	Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: acetyl-coa hydrolase; PDBTitle: crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
18	c4eu4A_	Alignment		100.0	19	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)
19	c3qlkB_	Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: coenzyme a transferase; PDBTitle: crystal structure of ripa from yersinia pestis
20	d2g39a2	Alignment		100.0	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
21	c3d3uA_	Alignment	not modelled	100.0	20	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
22	d1xr4a2	Alignment	not modelled	100.0	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
23	c1xr4B_	Alignment	not modelled	100.0	19	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]
24	c2hj0A_	Alignment	not modelled	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 .
25	c5vitP_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: P: PDB Molecule: mdca; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
26	d1m0sa1	Alignment	not modelled	98.6	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
27	c5uf2A_	Alignment	not modelled	98.5	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
						Fold: NagB/RpiA/CoA transferase-like

28	d1uj4a1	Alignment	not modelled	98.5	18	Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
29	c1k5C_	Alignment	not modelled	98.4	25	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
30	c6eepA_	Alignment	not modelled	98.4	21	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
31	c3hheA_	Alignment	not modelled	98.4	20	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
32	c3kwmC_	Alignment	not modelled	98.4	18	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
33	c1m0sA_	Alignment	not modelled	98.3	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
34	c3l7oB_	Alignment	not modelled	98.3	23	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
35	c6j1kA_	Alignment	not modelled	98.3	23	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from ochrobactrum2 sp. cs11
36	d1lk5a1	Alignment	not modelled	98.3	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
37	c4gmkB_	Alignment	not modelled	98.2	21	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
38	c2f8mB_	Alignment	not modelled	98.2	17	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
39	c1lkzB_	Alignment	not modelled	98.2	18	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.
40	c1uj6A_	Alignment	not modelled	98.0	23	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
41	c2pjmA_	Alignment	not modelled	97.7	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
42	c3cdkA_	Alignment	not modelled	97.7	18	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
43	c5mzyA_	Alignment	not modelled	97.4	22	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
44	d1k6da_	Alignment	not modelled	97.4	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
45	c3rrIC_	Alignment	not modelled	97.1	16	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
46	d1ooya2	Alignment	not modelled	97.0	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
47	d2g39a1	Alignment	not modelled	96.9	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
48	d1poia_	Alignment	not modelled	96.7	21	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
49	d1t9ka_	Alignment	not modelled	96.7	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
50	d1t5oa_	Alignment	not modelled	96.4	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
51	c4nmIA_	Alignment	not modelled	96.3	25	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
52	c2yvka_	Alignment	not modelled	96.2	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
53	c6a34B_	Alignment	not modelled	96.1	17	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
54	c6co9A_	Alignment	not modelled	95.8	17	PDB header: hydrolase Chain: A: PDB Molecule: probable coa-transferase alpha subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab coeaa-coa complex
55	c3u7jA_	Alignment	not modelled	95.8	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
56	c4x84C_	Alignment	not modelled	95.4	16	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
57	d2ahua2	Alignment	not modelled	95.3	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
58	d1vb5a_	Alignment	not modelled	95.1	15	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: !F2B-like
59	c3ecsd_	Alignment	not modelled	95.0	16	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
60	c4zemB_	Alignment	not modelled	94.3	16	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
61	c5b04B_	Alignment	not modelled	93.7	20	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
62	c6i3mD_	Alignment	not modelled	93.2	18	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
63	c3a11D_	Alignment	not modelled	93.1	18	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
64	c4zeoH_	Alignment	not modelled	93.0	14	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
65	c1xtzA_	Alignment	not modelled	92.8	20	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
66	d2a0ua1	Alignment	not modelled	92.6	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: !F2B-like
67	c6i7tB_	Alignment	not modelled	92.2	19	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
68	d1xr4a1	Alignment	not modelled	91.5	26	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
69	c5b04G_	Alignment	not modelled	91.4	14	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
70	c4ldrA_	Alignment	not modelled	91.1	16	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
71	c6i3mF_	Alignment	not modelled	91.1	9	PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
72	c5dboA_	Alignment	not modelled	87.1	13	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
73	c5b04C_	Alignment	not modelled	86.7	13	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
74	c6ezoD_	Alignment	not modelled	82.8	14	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
75	d1o8bb1	Alignment	not modelled	82.3	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
76	c3nzeB_	Alignment	not modelled	81.9	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 aureus tc1.

77	d2gnpa1	Alignment	not modelled	79.3	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
78	c6ezoH	Alignment	not modelled	76.2	16	PDB header: membrane protein Chain: H: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
79	c2w48D	Alignment	not modelled	76.0	14	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
80	c4oqqA	Alignment	not modelled	68.0	15	PDB header: transcription Chain: A: PDB Molecule: deoxyribonucleoside regulator; PDBTitle: structure of the effector-binding domain of deoxyribonucleoside2 regulator deor from bacillus subtilis
81	d3efba1	Alignment	not modelled	64.9	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
82	c6gg0G	Alignment	not modelled	48.8	12	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)
83	c1w2wj	Alignment	not modelled	46.8	20	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
84	d1soua	Alignment	not modelled	25.3	18	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
85	d1wkca	Alignment	not modelled	24.0	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
86	c2ri0B	Alignment	not modelled	22.2	24	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
87	c2eo0A	Alignment	not modelled	21.0	24	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein st1444; PDBTitle: crystal structure of holliday junction resolvase st1444
88	d2okga1	Alignment	not modelled	14.2	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
89	c5cl2A	Alignment	not modelled	14.0	15	PDB header: protein binding Chain: A: PDB Molecule: sporulation-control protein spo0m; PDBTitle: crystal structure of spo0m, sporulation control protein, from bacillus2 subtilis.
90	c3kv1A	Alignment	not modelled	11.8	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional repressor; PDBTitle: crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
91	c4go1A	Alignment	not modelled	11.3	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
92	d1gefa	Alignment	not modelled	8.9	27	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
93	c4r9nA	Alignment	not modelled	8.9	11	PDB header: transcription Chain: A: PDB Molecule: lmo0547 protein; PDBTitle: deor family transcriptional regulator from listeria monocytogenes.
94	c2k4mA	Alignment	not modelled	8.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0146 protein mth_1000; PDBTitle: solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
95	d1pvda3	Alignment	not modelled	8.4	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
96	c2o0mA	Alignment	not modelled	7.7	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, sorc family; PDBTitle: the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
97	d2o0ma1	Alignment	not modelled	7.7	10	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
98	c4wt3A	Alignment	not modelled	7.6	13	PDB header: chaperone Chain: A: PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana
99	c2jcbA	Alignment	not modelled	7.5	15	PDB header: ligase Chain: A: PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase family protein; PDBTitle: the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)