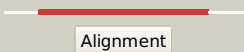

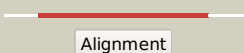
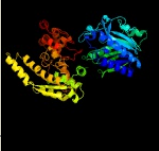
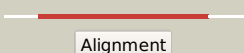

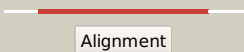

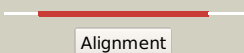
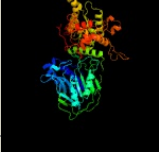
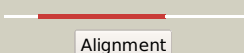







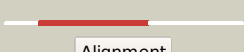

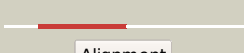



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2438c_(nadE)_2734802_2736841
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	457ccb9298be2540

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dlaD_</a>	 Alignment		100.0	97	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
2	<a href="#">c3ilvA_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
3	<a href="#">c5khaA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad+ synthetase; <b>PDBTitle:</b> structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
4	<a href="#">c4f4hA_</a>	 Alignment		100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine dependent nad+ synthetase; <b>PDBTitle:</b> crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
5	<a href="#">c3n05B_</a>	 Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
6	<a href="#">c5hyyA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nta1p; <b>PDBTitle:</b> crystal structure of n-terminal amidase
7	<a href="#">d1kqpa_</a>	 Alignment		100.0	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
8	<a href="#">c3dpiA_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+ synthetase; <b>PDBTitle:</b> crystal structure of nad+ synthetase from burkholderia pseudomallei
9	<a href="#">c2e18B_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of project ph0182 from pyrococcus horikoshii ot3
10	<a href="#">c1emsB_</a>	 Alignment		100.0	18	<b>PDB header:</b> antitumor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nit-fragile histidine triad fusion protein; <b>PDBTitle:</b> crystal structure of the c. elegans nitfhit protein
11	<a href="#">c2vhiG_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cg3027-pa; <b>PDBTitle:</b> crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster

12	<a href="#">c4q16C_</a>	Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad+ synthetase from deinococcus radiodurans
13	<a href="#">d1uf5a_</a>	Alignment		100.0	22	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
14	<a href="#">c4xfdA_</a>	Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
15	<a href="#">d1wxia1</a>	Alignment		100.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
16	<a href="#">c2e11B_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
17	<a href="#">c2vhhA_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cg3027-pa; <b>PDBTitle:</b> crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
18	<a href="#">c2e2kC_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> formamidase; <b>PDBTitle:</b> helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
19	<a href="#">c2plqA_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> aliphatic amidase; <b>PDBTitle:</b> crystal structure of the amidase from geobacillus pallidus rapc8
20	<a href="#">c5hujB_</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nade from streptococcus pyogenes
21	<a href="#">c5h8IM_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> M; <b>PDB Molecule:</b> n-carbamoylputrescine amidohydrolase; <b>PDBTitle:</b> crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
22	<a href="#">c2w1vA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nitrilase homolog 2; <b>PDBTitle:</b> crystal structure of mouse nitrilase-2 at 1.4a resolution
23	<a href="#">d1emsa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase
24	<a href="#">c6mg6D_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> carbon-nitrogen hydrolase; <b>PDBTitle:</b> crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
25	<a href="#">c3wuyA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nitrilase; <b>PDBTitle:</b> crystal structure of nit6803
26	<a href="#">c3q4gA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad synthetase from vibrio cholerae
27	<a href="#">c4hg3C_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> probable hydrolase nit2; <b>PDBTitle:</b> structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
28	<a href="#">d1j31a_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
						<b>PDB header:</b> hydrolase

29	<a href="#">c6ftqA</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> beta-ureidopropionase; <b>PDBTitle:</b> crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
30	<a href="#">d1f89a</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase
31	<a href="#">c6i00C</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional nitrilase/nitrile hydratase nit4; <b>PDBTitle:</b> cryo-em informed directed evolution of nitrilase 4 leads to a change2 in quaternary structure.
32	<a href="#">c3hkxA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure analysis of an amidase from nesterenkonia sp.
33	<a href="#">c3fiuD</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nmn synthetase from francisella tularensis
34	<a href="#">d1xnga1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
35	<a href="#">c4cyyA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pantetheinase; <b>PDBTitle:</b> the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
36	<a href="#">c3p52B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
37	<a href="#">c5n6mA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa
38	<a href="#">c5vrhA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> apolipoprotein n-acyltransferase c387s active site mutant
39	<a href="#">c2vx0B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
40	<a href="#">c3uowB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
41	<a href="#">c1gpmD</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
42	<a href="#">c5tw7E</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
43	<a href="#">c3tqiB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
44	<a href="#">c2ywcC</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermophilus in2 complex with xmp
45	<a href="#">c2dplA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
46	<a href="#">c2hmaA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna (5-methylaminomethyl-2-thiouridylylate)- <b>PDBTitle:</b> the crystal structure of trna (5-methylaminomethyl-2-thiouridylylate)-2 methyltransferase trmu from streptococcus pneumoniae
47	<a href="#">d1gpma1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
48	<a href="#">c4kr7A</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna sulfurtransferase; <b>PDBTitle:</b> crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
49	<a href="#">c5udwB</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
50	<a href="#">c2derA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylyase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
51	<a href="#">c2c5sA</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine biosynthesis protein thii; <b>PDBTitle:</b> crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
52	<a href="#">d2c5sa1</a>	Alignment	not modelled	99.5	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
53	<a href="#">c3k32D</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mj0690; <b>PDBTitle:</b> the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm <b>PDB header:</b> hydrolase

54	<a href="#">c3bl5E_</a>	Alignment	not modelled	99.3	21	<b>Chain:</b> E: <b>PDB Molecule:</b> queuosine biosynthesis protein quec; <b>PDBTitle:</b> crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
55	<a href="#">d1wy5a1</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
56	<a href="#">d1j20a1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
57	<a href="#">d1vl2a1</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
58	<a href="#">c3vrhA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
59	<a href="#">d2pg3a1</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
60	<a href="#">d1k92a1</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
61	<a href="#">c5udtD_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
62	<a href="#">c5ghaC_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
63	<a href="#">c3a2kB_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
64	<a href="#">d1ni5a1</a>	Alignment	not modelled	98.8	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
65	<a href="#">c2e21A_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
66	<a href="#">d1ct9a1</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
67	<a href="#">c1ct9D_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> asparagine synthetase b; <b>PDBTitle:</b> crystal structure of asparagine synthetase b from2 escherichia coli
68	<a href="#">d1jgta1</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
69	<a href="#">d1q15a1</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
70	<a href="#">c2nz2A_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
71	<a href="#">c1q15A_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
72	<a href="#">c1ni5A_</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
73	<a href="#">c1kh2D_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
74	<a href="#">c4u7jB_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
75	<a href="#">c1m1zB_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
76	<a href="#">d1sura_</a>	Alignment	not modelled	98.4	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
77	<a href="#">c1k97A_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
78	<a href="#">c1vl2C_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
79	<a href="#">c2goyC_</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
80	<a href="#">c4nzpA_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168

81	<a href="#">d1zuna1</a>	Alignment	not modelled	98.2	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
82	<a href="#">c2o8vA</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> paps reductase in a covalent complex with thioredoxin c35a
83	<a href="#">c1zunA</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
84	<a href="#">d1vbkA1</a>	Alignment	not modelled	97.8	7	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
85	<a href="#">d1ru8a</a>	Alignment	not modelled	97.6	24	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
86	<a href="#">d2d13a1</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
87	<a href="#">c4bwwB</a>	Alignment	not modelled	96.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine-phosphosulphate reductase; <b>PDBTitle:</b> structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
88	<a href="#">c2oq2B</a>	Alignment	not modelled	95.6	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
89	<a href="#">c3g59A</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn adenylyltransferase; <b>PDBTitle:</b> crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
90	<a href="#">c2wsiA</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fad synthetase; <b>PDBTitle:</b> crystal structure of yeast fad synthetase (fad1) in complex2 with fad
91	<a href="#">c1vbkA</a>	Alignment	not modelled	90.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1313; <b>PDBTitle:</b> crystal structure of ph1313 from pyrococcus horikoshii ot3
92	<a href="#">c4k3zA</a>	Alignment	not modelled	88.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-erythrose 4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
93	<a href="#">c3vniC</a>	Alignment	not modelled	84.2	4	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
94	<a href="#">d1hnja1</a>	Alignment	not modelled	84.1	14	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
95	<a href="#">d1t5la1</a>	Alignment	not modelled	82.7	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
96	<a href="#">c3qxbB</a>	Alignment	not modelled	80.9	6	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative xylose isomerase; <b>PDBTitle:</b> crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
97	<a href="#">c2hk1D</a>	Alignment	not modelled	77.6	6	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
98	<a href="#">c2qw5B</a>	Alignment	not modelled	77.4	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
99	<a href="#">c3qfnA</a>	Alignment	not modelled	76.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
100	<a href="#">d2eyqa4</a>	Alignment	not modelled	67.6	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
101	<a href="#">d1vlia2</a>	Alignment	not modelled	67.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
102	<a href="#">c3c8uA</a>	Alignment	not modelled	63.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
103	<a href="#">d1su1a</a>	Alignment	not modelled	62.3	12	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
104	<a href="#">c1su1A</a>	Alignment	not modelled	62.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yfce; <b>PDBTitle:</b> structural and biochemical characterization of yfce, a phosphoesterase2 from e. coli

105	<a href="#">c6ncsB_</a>	 Alignment	not modelled	60.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylneuraminic acid (sialic acid) synthetase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
106	<a href="#">c3hjhA_</a>	 Alignment	not modelled	60.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> transcription-repair-coupling factor; <b>PDBTitle:</b> a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
107	<a href="#">c3vylB_</a>	 Alignment	not modelled	59.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> l-ribose 3-epimerase; <b>PDBTitle:</b> structure of l-ribose 3-epimerase
108	<a href="#">d1i60a_</a>	 Alignment	not modelled	58.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> lol1-like
109	<a href="#">c2ou4C_</a>	 Alignment	not modelled	55.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> d-tagatose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
110	<a href="#">d1uf3a_</a>	 Alignment	not modelled	54.9	14	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
111	<a href="#">c4s1aB_</a>	 Alignment	not modelled	54.8	5	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
112	<a href="#">c2c40B_</a>	 Alignment	not modelled	54.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> inosine-uridine preferring nucleoside hydrolase family <b>PDBTitle:</b> crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
113	<a href="#">c1yx0B_</a>	 Alignment	not modelled	53.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxythreonine-4-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
114	<a href="#">c1vliA_</a>	 Alignment	not modelled	53.9	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
115	<a href="#">d1d9ea_</a>	 Alignment	not modelled	52.7	4	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
116	<a href="#">c3dx5A_</a>	 Alignment	not modelled	51.5	8	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
117	<a href="#">d2q02a1</a>	 Alignment	not modelled	50.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> lol1-like
118	<a href="#">c5zfsA_</a>	 Alignment	not modelled	50.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
119	<a href="#">d1ptma_</a>	 Alignment	not modelled	49.9	20	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> PdxA-like
120	<a href="#">d1s3la_</a>	 Alignment	not modelled	49.6	6	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like