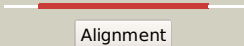

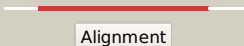

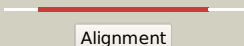







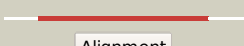











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2334_cysK1_2608806_2609738
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	0a6e992abdcaf116

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4aecB_			100.0	59	PDB header: lyase Chain: B; PDB Molecule: cysteine synthase, mitochondrial; PDBTitle: crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
2	d1z7wa1			100.0	56	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
3	c4lmaA_			100.0	64	PDB header: transferase Chain: A; PDB Molecule: cysteine synthase; PDBTitle: crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
4	c3vbeA_			100.0	53	PDB header: transferase Chain: A; PDB Molecule: beta-cyanoalanine synthase; PDBTitle: crystal structure of beta-cyanoalanine synthase in soybean
5	c3pc3A_			100.0	44	PDB header: lyase Chain: A; PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
6	c4l3vB_			100.0	41	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
7	c5ohxB_			100.0	43	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
8	c5xa2B_			100.0	62	PDB header: transferase Chain: B; PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
9	c2pqmA_			100.0	50	PDB header: lyase Chain: A; PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
10	c3dwgA_			100.0	39	PDB header: transferase Chain: A; PDB Molecule: cysteine synthase b; PDBTitle: crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
11	c2q3bA_			100.0	100	PDB header: transferase Chain: A; PDB Molecule: cysteine synthase a; PDBTitle: 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis

12	d1jbqa_	Alignment		100.0	41	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
13	c1jbqD_	Alignment		100.0	41	PDB header: lyase Chain: D: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
14	c5b1c_	Alignment		100.0	43	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of k42a mutant of cystathionine beta-synthase from2 lactobacillus plantarum in a complex with l-methionine
15	c3x43F_	Alignment		100.0	47	PDB header: transferase Chain: F: PDB Molecule: o-ureido-l-serine synthase; PDBTitle: crystal structure of o-ureido-l-serine synthase
16	c4ilxA_	Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase from helicobacter pylori 26695
17	d1ve1a1	Alignment		100.0	51	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
18	c5xenB_	Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
19	c5d87A_	Alignment		100.0	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable siderophore biosynthesis protein sbna; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbna y152f/s185g2 variant
20	d2bhsa1	Alignment		100.0	44	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
21	c4airB_	Alignment	not modelled	100.0	48	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: leishmania major cysteine synthase
22	d1y7la1	Alignment	not modelled	100.0	57	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
23	c6c2qA_	Alignment	not modelled	100.0	37	PDB header: lyase Chain: A: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structures of cystathionine beta-synthase from saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
24	c5i7wA_	Alignment	not modelled	100.0	37	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: crystal structure of a cysteine synthase from brucella suis
25	c4ql4A_	Alignment	not modelled	100.0	42	PDB header: lyase Chain: A: PDB Molecule: o-acetylserine lyase; PDBTitle: crystal structure of o-acetylserine sulphydrylase from bacillus2 anthracis
26	d1o58a_	Alignment	not modelled	100.0	54	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
27	d1fcja_	Alignment	not modelled	100.0	57	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
28	c2gnvA_	Alignment	not modelled	100.0	50	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase;

28	c2egvA	Alignment	not modelled	100.0	29	PDBTitle: crystal structure of o-acetylserine sulphydrase from geobacillus2 kaustophilus hta426
29	d1wkva1	Alignment	not modelled	100.0	30	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	c1tdjA	Alignment	not modelled	100.0	23	PDB header: allostery Chain: A; PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
31	c3l6cA	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: A; PDB Molecule: serine racemase; PDBTitle: x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
32	c6hulB	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfobolus solfataricus tryptophan synthase ab complex
33	d1pwha	Alignment	not modelled	100.0	21	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
34	c3iauA	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
35	d1v71a1	Alignment	not modelled	100.0	21	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
36	c2gn0A	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
37	c2d1fA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A; PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
38	d1tdja1	Alignment	not modelled	100.0	24	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
39	c1p5jA	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
40	d1p5ja	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
41	c5cvcB	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: B; PDB Molecule: serine racemase; PDBTitle: structure of maize serine racemase
42	d1ve5a1	Alignment	not modelled	100.0	24	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
43	c4qysA	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
44	c6cgqA	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A; PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
45	c5c3uA	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: l-serine ammonia-lyase; PDBTitle: crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
46	c1x1qA	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
47	d1v7ca	Alignment	not modelled	100.0	23	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
48	c5ybwA	Alignment	not modelled	100.0	21	PDB header: isomerase Chain: A; PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
49	d1qopb	Alignment	not modelled	100.0	24	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	c2rkbE	Alignment	not modelled	100.0	23	PDB header: lyase Chain: E; PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
51	c3r0zA	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A; PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium PDB header: lyase

52	c4negA	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
53	c2zsjB	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
54	d1v8za1	Alignment	not modelled	100.0	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
55	c4d9gA	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
56	c5tchH	Alignment	not modelled	100.0	26	PDB header: lyase Chain: H: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
57	c5b54D	Alignment	not modelled	100.0	35	PDB header: transferase Chain: D: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form
58	c5kinD	Alignment	not modelled	100.0	23	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
59	d1e5xa	Alignment	not modelled	100.0	17	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
60	c2o2jA	Alignment	not modelled	100.0	26	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apoforn)
61	c5ygrA	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: diaminopropionate ammonia lyase; PDBTitle: crystal structure of plp bound diaminopropionate ammonia lyase from2 salmonella typhimurium
62	d1j0aa	Alignment	not modelled	100.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
63	c4d8tC	Alignment	not modelled	100.0	19	PDB header: lyase Chain: C: PDB Molecule: d-cysteine desulphydrase; PDBTitle: crystal structure of d-cysteine desulphydrase from salmonella2 typhimurium at 2.2 a resolution
64	d1f2da	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
65	d1tyza	Alignment	not modelled	100.0	22	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	c3v7nA	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from burkholderia2 thailandensis
67	d1vb3a1	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
68	c4f4fB	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
69	d1kl7a	Alignment	not modelled	100.0	15	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	d1vp8a	Alignment	not modelled	91.8	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
71	d1c1da1	Alignment	not modelled	89.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
72	d1o8ca2	Alignment	not modelled	88.3	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
73	c3s8mA	Alignment	not modelled	86.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acp reductase; PDBTitle: the crystal structure of fabv
74	c3iupB	Alignment	not modelled	86.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadph:quinone oxidoreductase; PDBTitle: crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
75	c4ggoA	Alignment	not modelled	85.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola

76	d1o89a2	Alignment	not modelled	83.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
77	c3zu3A	Alignment	not modelled	82.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
78	c3krtC	Alignment	not modelled	81.6	16	PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
79	d1kola2	Alignment	not modelled	79.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
80	d1ml4a2	Alignment	not modelled	74.0	23	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
81	c3o82A	Alignment	not modelled	69.9	13	PDB header: ligase Chain: A: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
82	c3tumA	Alignment	not modelled	69.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
83	c3widC	Alignment	not modelled	68.6	11	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: structure of a glucose dehydrogenase t277f mutant in complex with nadp
84	c3grkE	Alignment	not modelled	68.3	13	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
85	c4qi2B	Alignment	not modelled	66.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: crotonyl-coa carboxylase/reductase; PDBTitle: crotonyl-coa carboxylase/reductase
86	d1tt7a2	Alignment	not modelled	66.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
87	c3pgjB	Alignment	not modelled	65.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
88	c5swvC	Alignment	not modelled	63.6	17	PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquinase dehydratase and shikimate dehydrogenase from s. pombe2 arom
89	c6h1bA	Alignment	not modelled	63.0	14	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospira thermotolerans
90	c5wb4H	Alignment	not modelled	62.7	12	PDB header: transferase Chain: H: PDB Molecule: n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
91	c5xi0B	Alignment	not modelled	62.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabv, a new class of enyl-acyl carrier protein2 reductase from vibrio fischeri
92	c6f3oC	Alignment	not modelled	62.0	14	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
93	d1l7da1	Alignment	not modelled	60.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
94	c3ivrA	Alignment	not modelled	59.2	10	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodospseudomonas palustris cga009
95	c4euhA	Alignment	not modelled	59.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
96	d1t57a	Alignment	not modelled	58.6	21	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
97	c1nytC	Alignment	not modelled	58.5	20	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
98	c6c4nB	Alignment	not modelled	57.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pseudopaline dehydrogenase; PDBTitle: pseudopaline dehydrogenase (paodh) - nadp+ bound
99	c4nimA	Alignment	not modelled	57.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
						Fold: FAD/NAD(P)-binding domain

100	d1hyua1	Alignment	not modelled	57.6	37	Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
101	d1fl2a1	Alignment	not modelled	57.5	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
102	d1llua2	Alignment	not modelled	56.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
103	c4zjuA	Alignment	not modelled	55.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: structure of a nadh-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
104	c3p2yA	Alignment	not modelled	55.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
105	c6fn6A	Alignment	not modelled	55.4	14	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase 1, isoform a; PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
106	d1trba1	Alignment	not modelled	53.7	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
107	d1ekxa2	Alignment	not modelled	53.4	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
108	c4m87B	Alignment	not modelled	52.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
109	d1xa0a2	Alignment	not modelled	51.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
110	c3d4oA	Alignment	not modelled	51.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
111	c3orgA	Alignment	not modelled	51.5	22	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
112	d1pg5a2	Alignment	not modelled	51.4	10	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
113	d1qsga	Alignment	not modelled	50.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
114	c3o8qB	Alignment	not modelled	50.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
115	c2vq3B	Alignment	not modelled	50.1	26	PDB header: oxidoreductase Chain: B: PDB Molecule: metalloreductase steap3; PDBTitle: crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
116	c2rgwD	Alignment	not modelled	50.1	13	PDB header: transferase Chain: D: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
117	c3o82B	Alignment	not modelled	49.8	13	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
118	c2vhyB	Alignment	not modelled	49.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
119	d1vdca1	Alignment	not modelled	49.5	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
120	d1otha2	Alignment	not modelled	49.5	22	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase