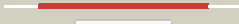



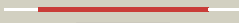






















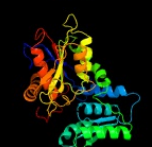





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1295_(thrC)_1450703_1451785
Date	Wed Jul 31 22:05:39 BST 2019
Unique Job ID	40d4fb42e2d0580b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2d1fA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
2	<a href="#">c2zsjB_</a>	 Alignment		100.0	61	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase from aquifex aeolicus vf5
3	<a href="#">d1v7ca_</a>	 Alignment		100.0	58	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
4	<a href="#">d1e5xa_</a>	 Alignment		100.0	36	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
5	<a href="#">c6cggA_</a>	 Alignment		100.0	57	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
6	<a href="#">c4l3vB_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structure of delta516-525 human cystathionine beta-synthase
7	<a href="#">c3pc3A_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> cg1753, isoform a; <b>PDBTitle:</b> full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
8	<a href="#">c6hulB_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> tryptophan synthase beta chain 1; <b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase ab complex
9	<a href="#">c3l6cA_</a>	 Alignment		100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
10	<a href="#">d1jbqa_</a>	 Alignment		100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
11	<a href="#">c1jbqD_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein

12	<a href="#">c5ohxB_</a>	Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of active cystathionine b-synthase from apis mellifera
13	<a href="#">c1tdjA_</a>	Alignment		100.0	22	<b>PDB header:</b> allostery <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic threonine deaminase; <b>PDBTitle:</b> threonine deaminase (biosynthetic) from e. coli
14	<a href="#">d1pwha_</a>	Alignment		100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
15	<a href="#">c3r0zA_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> d-serine dehydratase; <b>PDBTitle:</b> crystal structure of apo d-serine deaminase from salmonella2 typhimurium
16	<a href="#">c2gn0A_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine dehydratase catabolic; <b>PDBTitle:</b> 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)
17	<a href="#">d1ve1a1</a>	Alignment		100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
18	<a href="#">c3iauA_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine deaminase; <b>PDBTitle:</b> the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
19	<a href="#">d1v71a1</a>	Alignment		100.0	20	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	<a href="#">c4qysA_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain 2; <b>PDBTitle:</b> trpb2 enzymes
21	<a href="#">c1p5jA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure analysis of human serine dehydratase
22	<a href="#">d1p5ja_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
23	<a href="#">c2pqmA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
24	<a href="#">c4d9gA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diaminopropionate ammonia-lyase; <b>PDBTitle:</b> crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
25	<a href="#">d2bhsa1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	<a href="#">c3x43F_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> o-ureido-l-serine synthase; <b>PDBTitle:</b> crystal structure of o-ureido-l-serine synthase
27	<a href="#">c3vbeA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-cyanoalanine synthase; <b>PDBTitle:</b> crystal structure of beta-cyanoalanine synthase in soybean
						<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent

28	<a href="#">dlz7wa1</a>	Alignment	not modelled	100.0	24	enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
29	<a href="#">c6c2qA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structures of cystathionine beta-synthase from saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
30	<a href="#">dlwkva1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
31	<a href="#">d1tdja1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
32	<a href="#">c2rkbE_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
33	<a href="#">c4aecB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of the arabidopsis thaliana o-acetyl-serine-(thiol)-2 lyase c
34	<a href="#">c5i7wA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine synthase a; <b>PDBTitle:</b> crystal structure of a cysteine synthase from brucella suis
35	<a href="#">c5d87A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable siderophore biosynthesis protein sbna; <b>PDBTitle:</b> staphyloferrin b precursor biosynthetic enzyme sbna y152f/s185g2 variant
36	<a href="#">c5cvcB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> structure of maize serine racemase
37	<a href="#">c4lmaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
38	<a href="#">c3dwgA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine synthase b; <b>PDBTitle:</b> crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
39	<a href="#">c5xa2B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
40	<a href="#">c5ybwA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate racemase; <b>PDBTitle:</b> crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
41	<a href="#">d1ve5a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
42	<a href="#">c5b1iC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structure of k42a mutant of cystathionine beta-synthase from2 lactobacillus plantarum in a complex with l-methionine
43	<a href="#">c5xenB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
44	<a href="#">c5c3uA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> l-serine ammonia-lyase; <b>PDBTitle:</b> crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
45	<a href="#">c4airB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> leishmania major cysteine synthase
46	<a href="#">d1y7la1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
47	<a href="#">d1o58a_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
48	<a href="#">c5ygrA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> diaminopropionate ammonia lyase; <b>PDBTitle:</b> crystal structure of plp bound diaminopropionate ammonia lyase from2 salmonella typhimurium
49	<a href="#">d1v8za1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	<a href="#">c2q3ba_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine synthase a; <b>PDBTitle:</b> 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
51	<a href="#">c1x1qA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase beta chain from

						thermus2 thermophilus hb8
52	<a href="#">c4ql4A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetylserine lyase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrylase from bacillus2 anthracis
53	<a href="#">d1qopb_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
54	<a href="#">c4i1xA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase from helicobacter pylori 26695
55	<a href="#">c5tchH_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
56	<a href="#">d1fcja_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
57	<a href="#">c2eguA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrylase from geobacillus2 kaustophilus hta426
58	<a href="#">c5kinD_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
59	<a href="#">c4negA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
60	<a href="#">c4d8tC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> d-cysteine desulfhydrase; <b>PDBTitle:</b> crystal structure of d-cysteine desulfhydrase from salmonella2 typhimurium at 2.2 a resolution
61	<a href="#">d1j0aa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
62	<a href="#">c2o2jA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apoform)
63	<a href="#">d1f2da_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
64	<a href="#">d1tyza_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
65	<a href="#">c5b54D_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form
66	<a href="#">d1vb3a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	<a href="#">c4f4fB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
68	<a href="#">c3v7nA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase (thrc) from burkholderia2 thailandensis
69	<a href="#">d1ki7a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	<a href="#">d1vp8a_</a>	Alignment	not modelled	97.2	20	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
71	<a href="#">d1t57a_</a>	Alignment	not modelled	94.5	15	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
72	<a href="#">c3d3jA_</a>	Alignment	not modelled	87.0	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
73	<a href="#">d2ay1a_</a>	Alignment	not modelled	86.8	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
74	<a href="#">d2q7wa1</a>	Alignment	not modelled	86.4	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
75	<a href="#">d1xgka_</a>	Alignment	not modelled	84.7	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
						<b>PDB header:</b> oxidoreductase

76	<a href="#">c3zu3A_</a>	Alignment	not modelled	84.4	15	<b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ypo4104/y4119/yp_4011; <b>PDBTitle:</b> structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
77	<a href="#">d7aata_</a>	Alignment	not modelled	83.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
78	<a href="#">c3iupB_</a>	Alignment	not modelled	83.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph:quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
79	<a href="#">d1o8ca2</a>	Alignment	not modelled	82.2	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
80	<a href="#">d3tata_</a>	Alignment	not modelled	81.7	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
81	<a href="#">d1yaaa_</a>	Alignment	not modelled	81.1	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
82	<a href="#">d2ioja1</a>	Alignment	not modelled	81.0	9	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
83	<a href="#">c5epoD_</a>	Alignment	not modelled	80.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> the three-dimensional structure of clostridium absonum 7alpha-2 hydroxysteroid dehydrogenase
84	<a href="#">c4j2hA_</a>	Alignment	not modelled	78.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain alcohol dehydrogenase-related dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative short-chain alcohol dehydrogenase from2 sinorhizobium meliloti 1021 (target nysgrc-011708)
85	<a href="#">d1c1da1</a>	Alignment	not modelled	77.9	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
86	<a href="#">c5ig2B_</a>	Alignment	not modelled	77.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
87	<a href="#">c5dj3B_</a>	Alignment	not modelled	77.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> plp-dependent l-arginine hydroxylase mppp; <b>PDBTitle:</b> structure of the plp-dependent l-arginine hydroxylase mppp with d-2 arginine bound
88	<a href="#">c4urfB_</a>	Alignment	not modelled	76.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclohexanol dehydrogenase; <b>PDBTitle:</b> molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
89	<a href="#">c4wuvB_</a>	Alignment	not modelled	76.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-hydroxycyclohexanecarboxyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative d-mannonate oxidoreductase from2 haemophilus influenza (avi_5165, target efi-513796) with bound nad
90	<a href="#">c4iboA_</a>	Alignment	not modelled	76.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
91	<a href="#">c3krtC_</a>	Alignment	not modelled	75.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> crotonyl coa reductase; <b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
92	<a href="#">d1l7da1</a>	Alignment	not modelled	74.8	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
93	<a href="#">d1ml4a2</a>	Alignment	not modelled	74.1	14	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
94	<a href="#">c5yhvA_</a>	Alignment	not modelled	74.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aminotransferase from mycobacterium2 tuberculosis
95	<a href="#">d1f12a1</a>	Alignment	not modelled	73.7	41	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
96	<a href="#">d1ae1a_</a>	Alignment	not modelled	73.7	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
97	<a href="#">c5wb4H_</a>	Alignment	not modelled	73.7	10	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d- <b>PDBTitle:</b> crystal structure of the tara wall teichoic acid glycosyltransferase
98	<a href="#">c1w4zA_</a>	Alignment	not modelled	73.5	14	<b>PDB header:</b> antibiotic biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ketoacyl reductase; <b>PDBTitle:</b> structure of actinorhodin polyketide (actiii) reductase
99	<a href="#">c3omlA_</a>	Alignment	not modelled	73.4	11	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal multifunctional enzyme type 2, cg3415; <b>PDBTitle:</b> structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster

100	<a href="#">c3toxG</a>	Alignment	not modelled	73.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
101	<a href="#">c6ci9D</a>	Alignment	not modelled	72.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
102	<a href="#">d1bg6a2</a>	Alignment	not modelled	72.5	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
103	<a href="#">c4imrA</a>	Alignment	not modelled	72.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from agrobacterium tumefaciens c58 with nadp3 bound
104	<a href="#">c4nbwA</a>	Alignment	not modelled	72.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of fabg from plesiocystis pacifica
105	<a href="#">c3e2yB</a>	Alignment	not modelled	71.9	16	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine-oxoglutarate transaminase 3; <b>PDBTitle:</b> crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
106	<a href="#">c3wtcB</a>	Alignment	not modelled	71.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2036
107	<a href="#">d1u6ea2</a>	Alignment	not modelled	71.2	17	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
108	<a href="#">c5jy1C</a>	Alignment	not modelled	71.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad
109	<a href="#">c3oidA</a>	Alignment	not modelled	70.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadph]; <b>PDBTitle:</b> crystal structure of enoyl-acyl reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
110	<a href="#">d1hyua1</a>	Alignment	not modelled	70.3	29	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
111	<a href="#">c2qx7A</a>	Alignment	not modelled	70.0	13	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
112	<a href="#">d1trba1</a>	Alignment	not modelled	69.8	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
113	<a href="#">d1o89a2</a>	Alignment	not modelled	69.1	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
114	<a href="#">c3r3sD</a>	Alignment	not modelled	68.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from salmonella enterica
115	<a href="#">c3grkE</a>	Alignment	not modelled	68.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
116	<a href="#">d2rhca1</a>	Alignment	not modelled	68.0	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
117	<a href="#">d1mzja2</a>	Alignment	not modelled	68.0	26	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
118	<a href="#">c5eowA</a>	Alignment	not modelled	67.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxynicotinate 3-monoxygenase; <b>PDBTitle:</b> crystal structure of 6-hydroxynicotinic acid 3-monoxygenase from2 pseudomonas putida kt2440
119	<a href="#">c4afnB</a>	Alignment	not modelled	67.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase fabg; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 (fabg) from pseudomonas aeruginosa at 2.3a resolution
120	<a href="#">d1vdca1</a>	Alignment	not modelled	67.0	30	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains