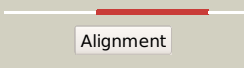

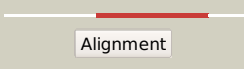

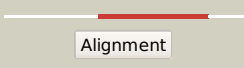

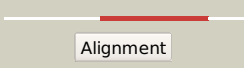

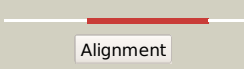

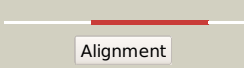

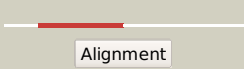

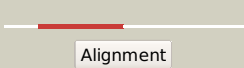

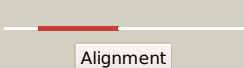

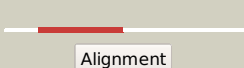

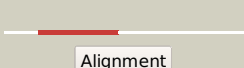

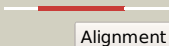

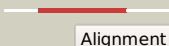







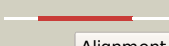













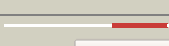



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1391_(dfp)_1565447_1566703
Date	Wed Jul 31 22:05:49 BST 2019
Unique Job ID	b4e48bbdfe1f57af

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1u7za_</a>	 Alignment		100.0	42	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
2	<a href="#">c4qjiB_</a>	 Alignment		100.0	83	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase; <b>PDBTitle:</b> crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
3	<a href="#">c5intB_</a>	 Alignment		100.0	42	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of coenzyme a biosynthesis2 bifunctional protein coabc
4	<a href="#">c2gk4A_</a>	 Alignment		100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
5	<a href="#">c6aikB_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase cab2; <b>PDBTitle:</b> cab2 mutant h337a complex with phosphopantothenoyl-cmp
6	<a href="#">d1p9oa_</a>	 Alignment		100.0	28	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
7	<a href="#">c5h75B_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mersacidin decarboxylase,immunoglobulin g-binding protein <b>PDBTitle:</b> crystal structure of the mrsd-protein a fusion protein
8	<a href="#">d1g5qa_</a>	 Alignment		100.0	18	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
9	<a href="#">d1p3y1_</a>	 Alignment		100.0	25	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
10	<a href="#">c3qjgD_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> epidermin biosynthesis protein epid; <b>PDBTitle:</b> epidermin biosynthesis protein epid from staphylococcus aureus
11	<a href="#">c6jlsA_</a>	 Alignment		100.0	31	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavoprotein decarboxylase; <b>PDBTitle:</b> crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis

12	<a href="#">c6jddA_</a>	 Alignment		100.0	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> cypemycin cysteine dehydrogenase (decarboxylating); <b>PDBTitle:</b> crystal structure of the cypemycin decarboxylase cypd.
13	<a href="#">c1mvIA_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> ppc decarboxylase athal3a; <b>PDBTitle:</b> ppc decarboxylase mutant c175s
14	<a href="#">d1mvIA_</a>	 Alignment		100.0	30	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
15	<a href="#">c6eoaA_</a>	 Alignment		100.0	31	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphopantothenoylecysteine decarboxylase; <b>PDBTitle:</b> crystal structure of hal3 from cryptococcus neoformans
16	<a href="#">c3mCuF_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
17	<a href="#">c3lqkA_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
18	<a href="#">c2ejbA_</a>	 Alignment		100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
19	<a href="#">c6qlgD_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> flavin prenyltransferase pad1, mitochondrial; <b>PDBTitle:</b> crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
20	<a href="#">d1qzuA_</a>	 Alignment		100.0	34	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
21	<a href="#">d1sbza_</a>	 Alignment	not modelled	100.0	18	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
22	<a href="#">c1qzuB_</a>	 Alignment	not modelled	100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein mds018; <b>PDBTitle:</b> crystal structure of human phosphopantothenoylecysteine decarboxylase
23	<a href="#">c4rheB_</a>	 Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-octaprenyl-4-hydroxybenzoate carboxylase; <b>PDBTitle:</b> crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
24	<a href="#">c3zquA_</a>	 Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
25	<a href="#">c3wisA_</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative dihydromethanopterin reductase (afpa); <b>PDBTitle:</b> crystal structure of burkholderia xenovorans dmrB in complex with fmn:2 a cubic protein cage for redox transfer
26	<a href="#">c1z7eC_</a>	 Alignment	not modelled	97.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
27	<a href="#">d1rkxA_</a>	 Alignment	not modelled	97.7	16	<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> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative nucleotide sugar epimerase/

28	<a href="#">c2q1uA</a>	Alignment	not modelled	97.7	19	dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
29	<a href="#">d1wvga1</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
30	<a href="#">c3qvoA</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nmra family protein; <b>PDBTitle:</b> structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
31	<a href="#">c4idgB</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain dehydrogenase/reductase superfamily2 protein from agrobacterium tumefaciens (target efi-506441) with bound3 nad, monoclinic form 2
32	<a href="#">d1hdoa</a>	Alignment	not modelled	97.4	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
33	<a href="#">c2z1mC</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-d-mannose dehydratase; <b>PDBTitle:</b> crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
34	<a href="#">c4wuvB</a>	Alignment	not modelled	97.4	15	<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
35	<a href="#">d1db3a</a>	Alignment	not modelled	97.3	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c3nzoB</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
37	<a href="#">c3zu3A</a>	Alignment	not modelled	97.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ypo4104/yp4119/yp_4011; <b>PDBTitle:</b> structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
38	<a href="#">c4b8wB</a>	Alignment	not modelled	97.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-l-fucose synthase; <b>PDBTitle:</b> crystal structure of human gdp-l-fucose synthase with bound nadp and2 gdp, tetragonal crystal form
39	<a href="#">c4j2oD</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase/5-epimerase; <b>PDBTitle:</b> crystal structure of nadp-bound wbjb from a. baumannii community2 strain d1279779
40	<a href="#">c5l3zA</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide ketoreductase simc7; <b>PDBTitle:</b> polyketide ketoreductase simc7 - binary complex with nadp+
41	<a href="#">c6a41A</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehalogenase; <b>PDBTitle:</b> dehalogenation enzyme
42	<a href="#">c3tpcG</a>	Alignment	not modelled	97.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain alcohol dehydrogenase-related dehydrogenase; <b>PDBTitle:</b> crystal structure of a hypothetical protein sma1452 from sinorhizobium2 meliloti 1021
43	<a href="#">c4nbtA</a>	Alignment	not modelled	97.2	25	<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 fabg from acholeplasma laidlawii
44	<a href="#">d1luaa1</a>	Alignment	not modelled	97.2	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
45	<a href="#">c3vtzD</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose 1-dehydrogenase; <b>PDBTitle:</b> structure of thermoplasma volcanium aldohexose dehydrogenase
46	<a href="#">c3ctmH</a>	Alignment	not modelled	97.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
47	<a href="#">c1zbqB</a>	Alignment	not modelled	97.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 17-beta-hydroxysteroid dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 42 in complex with nad
48	<a href="#">d1zbqa1</a>	Alignment	not modelled	97.1	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
49	<a href="#">c3lu1C</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> wbgu; <b>PDBTitle:</b> crystal structure analysis of wbgu: a udp-galnac 4-epimerase
50	<a href="#">c5f1pB</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ptmo8; <b>PDBTitle:</b> crystal structure of dehydrogenase from streptomyces platensis
51	<a href="#">c2x4gA</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
52	<a href="#">c6bwcA</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide biosynthesis protein capd; <b>PDBTitle:</b> x-ray structure of open pen from bacillus thuringiensis

53	<a href="#">c1n7gB_</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-d-mannose-4,6-dehydratase; <b>PDBTitle:</b> crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
54	<a href="#">c4zrmB_</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
55	<a href="#">c2et6A_</a>	Alignment	not modelled	97.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
56	<a href="#">d1gz6a_</a>	Alignment	not modelled	97.1	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
57	<a href="#">c4twrA_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad binding site:nad-dependent epimerase/dehydratase:udp- <b>PDBTitle:</b> structure of udp-glucose 4-epimerase from brucella abortus
58	<a href="#">d1n7ha_</a>	Alignment	not modelled	97.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
59	<a href="#">c3pvzD_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
60	<a href="#">d1bxka_</a>	Alignment	not modelled	97.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
61	<a href="#">c4euhA_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ca_c0462; <b>PDBTitle:</b> crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
62	<a href="#">d1i24a_</a>	Alignment	not modelled	97.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
63	<a href="#">d1ulua_</a>	Alignment	not modelled	97.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
64	<a href="#">c2pk3B_</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
65	<a href="#">c2dteB_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase related protein; <b>PDBTitle:</b> structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh
66	<a href="#">c4q9nD_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of chlamydia trachomatis enoyl-acyl reductase (fabI)2 in complex with nadh and afn-1252
67	<a href="#">c4ni5A_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from brucella suis
68	<a href="#">c3grkE_</a>	Alignment	not modelled	97.0	19	<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
69	<a href="#">c4zjuA_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> structure of a nadh-dependent enoyl-acyl reductase from acinetobacter2 baumannii in complex with nad
70	<a href="#">c3i1jB_</a>	Alignment	not modelled	97.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> structure of a putative short chain dehydrogenase from pseudomonas2 syringae
71	<a href="#">c2fwmX_</a>	Alignment	not modelled	96.9	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; <b>PDBTitle:</b> crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
72	<a href="#">c5f5nA_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monoxygenase; <b>PDBTitle:</b> the structure of monoxygenase ksta11 in complex with nad and its2 substrate
73	<a href="#">c5koiH_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of a possible enoyl-(acyl-carrier-protein) reductase2 from brucella melitensis
74	<a href="#">c2rirA_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
75	<a href="#">c4yqyA_</a>	Alignment	not modelled	96.9	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative dehydrogenase from sulfotobacter sp.2 (cog1028) (target efi-513936) in its apo form
76	<a href="#">c2q1wC_</a>	Alignment	not modelled	96.9	26	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme

						wbmh in2 complex with nad+
77	<a href="#">c4ggoA_</a>	Alignment	not modelled	96.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
78	<a href="#">c3t7cC_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
79	<a href="#">d2c5aa1</a>	Alignment	not modelled	96.9	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
80	<a href="#">c4m8sB_</a>	Alignment	not modelled	96.9	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl -(acyl carrier protein) reductase2 (fabg) from neisseria meningitidis
81	<a href="#">d1qsga_</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
82	<a href="#">d2o23a1</a>	Alignment	not modelled	96.9	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">d1e6ua_</a>	Alignment	not modelled	96.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
84	<a href="#">c5epoD_</a>	Alignment	not modelled	96.9	23	<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
85	<a href="#">c3un1D_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
86	<a href="#">c1luaA_</a>	Alignment	not modelled	96.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylene tetrahydromethanopterin dehydrogenase; <b>PDBTitle:</b> structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
87	<a href="#">c2gn9B_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glcnac c6 dehydratase; <b>PDBTitle:</b> crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
88	<a href="#">c2ydyA_</a>	Alignment	not modelled	96.8	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine adenosyltransferase 2 subunit beta; <b>PDBTitle:</b> crystal structure of human s-adenosylmethionine synthetase 2, beta2 subunit in orthorhombic crystal form
89	<a href="#">d1cyda_</a>	Alignment	not modelled	96.8	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
90	<a href="#">c4h15B_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain alcohol dehydrogenase-related dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain alcohol dehydrogenase-related2 dehydrogenase (target id nysgrc-011812) from sinorhizobium meliloti3 1021 in space group p21
91	<a href="#">c3sx2F_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative 3-ketoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
92	<a href="#">c6aayD_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> gdp-l-fucose synthetase; <b>PDBTitle:</b> crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
93	<a href="#">c6dntA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4-epimerase from methanobrevibacter2 ruminantium m1 in complex with udp-n-acetylmuramic acid
94	<a href="#">c2jahB_</a>	Alignment	not modelled	96.8	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> clavulanic acid dehydrogenase; <b>PDBTitle:</b> biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
95	<a href="#">c1z45A_</a>	Alignment	not modelled	96.8	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gal10 bifunctional protein; <b>PDBTitle:</b> crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
96	<a href="#">c4yqzD_</a>	Alignment	not modelled	96.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from thermus2 thermophilus hb27 (tt_p0034, target efi-513932) in its apo form
97	<a href="#">d1y5ma1</a>	Alignment	not modelled	96.8	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
98	<a href="#">c3w1vA_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> capsular polysaccharide synthesis enzyme cap8e; <b>PDBTitle:</b> crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor
99	<a href="#">c4w4tA_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mxaa; <b>PDBTitle:</b> the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway

100	<a href="#">c4m87B_</a>	Alignment	not modelled	96.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
101	<a href="#">c2hunB_</a>	Alignment	not modelled	96.8	31	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 336aa long hypothetical dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
102	<a href="#">d1q7ba_</a>	Alignment	not modelled	96.8	38	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
103	<a href="#">c5h5xH_</a>	Alignment	not modelled	96.7	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of nadh bound carbonyl reductase from streptomyces2 coelicolor
104	<a href="#">c3dqpA_</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase ylbe; <b>PDBTitle:</b> crystal structure of the oxidoreductase ylbe from lactococcus lactis,2 northeast structural genomics consortium target kr121.
105	<a href="#">c3c1oA_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase; <b>PDBTitle:</b> the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
106	<a href="#">d1yxma1</a>	Alignment	not modelled	96.7	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
107	<a href="#">d1kewa_</a>	Alignment	not modelled	96.7	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
108	<a href="#">c4rgbB_</a>	Alignment	not modelled	96.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative carveol dehydrogenase from2 mycobacterium avium bound to nad
109	<a href="#">d1h5qa_</a>	Alignment	not modelled	96.7	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
110	<a href="#">d1ek6a_</a>	Alignment	not modelled	96.7	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
111	<a href="#">c3slgB_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pbgp3 protein; <b>PDBTitle:</b> crystal structure of pbgp3 protein from burkholderia pseudomallei
112	<a href="#">c3ijrF_</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
113	<a href="#">c3tscB_</a>	Alignment	not modelled	96.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of short chain dehydrogenase map_2410 from2 mycobacterium paratuberculosis bound to nad
114	<a href="#">c5uzhA_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nafoa.00085.b; <b>PDBTitle:</b> crystal structure of a gdp-mannose dehydratase from naegleria fowleri
115	<a href="#">c3rfxB_</a>	Alignment	not modelled	96.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uronate dehydrogenase; <b>PDBTitle:</b> crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
116	<a href="#">c4tqgA_</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dtdp-d-glucose 4 6-dehydratase; <b>PDBTitle:</b> crystal structure of megavirus udp-glcnac 4,6-dehydratase, 5-epimerase2 mg534
117	<a href="#">c3pxxE_</a>	Alignment	not modelled	96.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
118	<a href="#">c5xi0B_</a>	Alignment	not modelled	96.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of fabv, a new class of enyl-acyl carrier protein2 reductase from vibrio fischeri
119	<a href="#">c5k9zB_</a>	Alignment	not modelled	96.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400
120	<a href="#">d1ae1a_</a>	Alignment	not modelled	96.7	46	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases