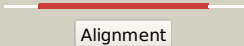

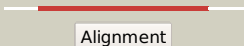

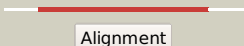







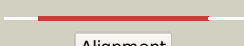











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1714_(- )_1941860_1942672
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	fc0d180b33645697

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pr9a_</a>	 Alignment		100.0	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
2	<a href="#">c5u9pB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gluconate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate
3	<a href="#">c3awdD_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase; <b>PDBTitle:</b> crystal structure of gox2181
4	<a href="#">c5itvC_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroantocapsin 7-dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus subtilis bacc dihydroantocapsin 7-2 dehydrogenase in complex with nadh
5	<a href="#">d2ae2a_</a>	 Alignment		100.0	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
6	<a href="#">c4z9yA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-deoxy-d-gluconate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum
7	<a href="#">c3wtcB_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2036
8	<a href="#">c5ojgB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4; <b>PDBTitle:</b> crystal structure of the dehydrogenase/reductase sdr family member 42 (dhrs4) from caenorhabditis elegans
9	<a href="#">c6d9yB_</a>	 Alignment		100.0	20	<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 with partially occupied nad
10	<a href="#">c5unlA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-acyl-p carrier protein reductase; <b>PDBTitle:</b> crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
11	<a href="#">c3cxtA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase with different specificities; <b>PDBTitle:</b> quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2

12	<a href="#">c3lf2B_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain oxidoreductase q9hya2; <b>PDBTitle:</b> nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
13	<a href="#">c4g81A_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexonate dehydrogenase; <b>PDBTitle:</b> crystal structure of a hexonate dehydrogenase ortholog (target efi-2 506402 from salmonella enterica, unliganded structure
14	<a href="#">c4npcA_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> crystal structure of an oxidoreductase, short-chain2 dehydrogenase/reductase family protein from brucella suis
15	<a href="#">c6ds1C_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of cj0485 dehydrogenase in complex with nadp+
16	<a href="#">c5idxB_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of an oxidoreductase from burkholderia vietnamiensis
17	<a href="#">c4egfA_</a>	Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-xylulose reductase; <b>PDBTitle:</b> crystal structure of a l-xylulose reductase from mycobacterium2 smegmatis
18	<a href="#">c6ci9D_</a>	Alignment		100.0	27	<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
19	<a href="#">c4imrA_</a>	Alignment		100.0	22	<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
20	<a href="#">d1fmca_</a>	Alignment		100.0	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
21	<a href="#">c3gr6A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabI) in complex with nadp and triclosan
22	<a href="#">c4wecA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
23	<a href="#">d1xhla_</a>	Alignment	not modelled	100.0	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
24	<a href="#">c4i5eC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase/short-chain dehydrogenase; <b>PDBTitle:</b> crystal structure of ralstonia sp. alcohol dehydrogenase in complex2 with nadp+
25	<a href="#">d2rhca1</a>	Alignment	not modelled	100.0	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
26	<a href="#">d1ae1a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
27	<a href="#">c3rihB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
28	<a href="#">c5g4kB_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase <b>PDBTitle:</b> phloroglucinol reductase from clostridium sp. apo-form <b>PDB header:</b> oxidoreductase

29	<a href="#">c4urfB</a>	Alignment	not modelled	100.0	26	<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
30	<a href="#">d1yxma1</a>	Alignment	not modelled	100.0	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
31	<a href="#">d1g0oa</a>	Alignment	not modelled	100.0	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
32	<a href="#">c3tzqD</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
33	<a href="#">d1iy8a</a>	Alignment	not modelled	100.0	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
34	<a href="#">c3gvcB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of probable short-chain dehydrogenase-reductase from2 mycobacterium tuberculosis
35	<a href="#">c5h5xH</a>	Alignment	not modelled	100.0	25	<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
36	<a href="#">c1w4zA</a>	Alignment	not modelled	100.0	23	<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
37	<a href="#">d1w6ua</a>	Alignment	not modelled	100.0	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
38	<a href="#">d1k2wa</a>	Alignment	not modelled	100.0	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
39	<a href="#">c3toxG</a>	Alignment	not modelled	100.0	29	<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
40	<a href="#">c4nbvA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase putative short- <b>PDBTitle:</b> crystal structure of fabg from cupriavidus taiwanensis
41	<a href="#">c4trrH</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> putative d-beta-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative putative d-beta-hydroxybutyrate2 dehydrogenase from burkholderia cenocepacia j2315
42	<a href="#">c3ak4C</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-dependent quinuclidinone reductase; <b>PDBTitle:</b> crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
43	<a href="#">c4j2hA</a>	Alignment	not modelled	100.0	30	<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)
44	<a href="#">c4iboA</a>	Alignment	not modelled	100.0	21	<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)
45	<a href="#">c4iuyB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase (apo-form)2 from a. baumannii clinical strain wm99c
46	<a href="#">c4wuvB</a>	Alignment	not modelled	100.0	25	<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
47	<a href="#">c4fc6B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> studies on dcr shed new light on peroxisomal beta-oxidation: crystal2 structure of the ternary complex of pdcr
48	<a href="#">c4cr8D</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> n-acylmannosamine 1-dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-acetyl-d-mannosamine dehydrogenase2 with nad
49	<a href="#">c3k31B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
50	<a href="#">c4afnB</a>	Alignment	not modelled	100.0	23	<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
51	<a href="#">c5epoD</a>	Alignment	not modelled	100.0	25	<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
52	<a href="#">c4o0A</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-dependent 3-quinuclidinone reductase;

						<b>PDBTitle:</b> crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
53	<a href="#">c3itdA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 17beta-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
54	<a href="#">c3ai3A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-sorbose reductase; <b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
55	<a href="#">c3uf0A_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
56	<a href="#">d2bgka1</a>	Alignment	not modelled	100.0	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
57	<a href="#">c2zatC_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4; <b>PDBTitle:</b> crystal structure of a mammalian reductase
58	<a href="#">c5jy1C_</a>	Alignment	not modelled	100.0	22	<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
59	<a href="#">c4nbrA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase from2 brucella melitensis atcc 23457
60	<a href="#">c3sjuA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> keto reductase; <b>PDBTitle:</b> hedamycin polyketide ketoreductase bound to nadph
61	<a href="#">c3v2gA_</a>	Alignment	not modelled	100.0	24	<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 a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
62	<a href="#">c2cfcB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-(r)-hydroxypropyl-com dehydrogenase; <b>PDBTitle:</b> structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
63	<a href="#">c3svtA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
64	<a href="#">d1ydea1</a>	Alignment	not modelled	100.0	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
65	<a href="#">c3pk0B_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
66	<a href="#">d1hdca_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
67	<a href="#">c5t2uC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family <b>PDBTitle:</b> short chain dehydrogenase/reductase family protein
68	<a href="#">c5x8hA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase reductase; <b>PDBTitle:</b> crystal structure of the ketone reductase chkred20 from the genome of2 chryseobacterium sp. ca49
69	<a href="#">c2q2gG_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
70	<a href="#">c3gdfA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
71	<a href="#">c3nugA_</a>	Alignment	not modelled	100.0	21	<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 wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
72	<a href="#">c5k9zB_</a>	Alignment	not modelled	100.0	24	<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
73	<a href="#">c5o30A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of the novel halohydrin dehalogenase hhcg
74	<a href="#">d2pd4a1</a>	Alignment	not modelled	100.0	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
75	<a href="#">d1geea_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
76	<a href="#">c4hp8A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-deoxy-d-gluconate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative 2-deoxy-d-gluconate 3-

					dehydrogenase2 from agrobacterium tumefaciens (target efi-506435) with bound nadp
77	<a href="#">c4fn4A_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolbus2 acidocaldarius
78	<a href="#">d1xkqa_</a>	Alignment	not modelled	100.0	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
79	<a href="#">d1h5qa_</a>	Alignment	not modelled	100.0	33 <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="#">c4lvuB_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia thailandensis
81	<a href="#">c4m8sB_</a>	Alignment	not modelled	100.0	25 <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
82	<a href="#">d1q7ba_</a>	Alignment	not modelled	100.0	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
83	<a href="#">c4gh5B_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)
84	<a href="#">c5jc8C_</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
85	<a href="#">c3jirF_</a>	Alignment	not modelled	100.0	19 <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+
86	<a href="#">c4dqxB_</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from rhizobium etli2 cfn 42
87	<a href="#">c2pd6D_</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> estradiol 17-beta-dehydrogenase 8; <b>PDBTitle:</b> structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
88	<a href="#">c2wdzD_</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
89	<a href="#">d1vl8a_</a>	Alignment	not modelled	100.0	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
90	<a href="#">c3tscB_</a>	Alignment	not modelled	100.0	27 <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
91	<a href="#">c5ff9C_</a>	Alignment	not modelled	100.0	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> noroxomaritidine/norcraugsodine reductase; <b>PDBTitle:</b> noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
92	<a href="#">c5er6C_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from brucella ovis
93	<a href="#">d1zema1</a>	Alignment	not modelled	100.0	19 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
94	<a href="#">d1ja9a_</a>	Alignment	not modelled	100.0	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
95	<a href="#">d2c07a1</a>	Alignment	not modelled	100.0	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
96	<a href="#">c2c07A_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> oxoacyl-acyl reductase of plasmodium falciparum
97	<a href="#">c4jroC_</a>	Alignment	not modelled	100.0	31 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> fabg protein; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein]reductase (fabg)2 from listeria monocytogenes in complex with nadp+
98	<a href="#">c4xgnD_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with2 nad from burkholderia thailandensis
99	<a href="#">d1bdba_</a>	Alignment	not modelled	100.0	19 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
100	<a href="#">d1cyda_</a>	Alignment	not modelled	100.0	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

101	<a href="#">c4h15B_</a>	Alignment	not modelled	100.0	23	<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
102	<a href="#">d1zk4a1</a>	Alignment	not modelled	100.0	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
103	<a href="#">c2b4qB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] <b>PDBTitle:</b> pseudomonas aeruginosa rhlg/nadp active-site complex
104	<a href="#">c3emkA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase; <b>PDBTitle:</b> 2.5a crystal structure of glucose/ribitol dehydrogenase from brucella2 melitensis
105	<a href="#">c2yz7B_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-3-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> x-ray analyses of 3-hydroxybutyrate dehydrogenase from2 alcaligenes faecalis
106	<a href="#">c3imfA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
107	<a href="#">d1hxha_</a>	Alignment	not modelled	100.0	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
108	<a href="#">c4mowB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative glucose 1-dehydrogenase from2 burkholderia cenocepacia j2315
109	<a href="#">c4nqzF_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh] fabi; <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa enoyl-acyl carrier2 protein reductase (fabi) in apo form
110	<a href="#">d1o5ia_</a>	Alignment	not modelled	100.0	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
111	<a href="#">c3afnC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of aldose reductase a1-r complexed with nadp
112	<a href="#">c5jydA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
113	<a href="#">c3grkE_</a>	Alignment	not modelled	100.0	24	<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
114	<a href="#">c6f9qC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> 7s-cis-cis-nepetalactol cyclase; <b>PDBTitle:</b> binary complex of a 7s-cis-cis-nepetalactol cyclase from nepeta2 mussinii with nad+
115	<a href="#">c2p68A_</a>	Alignment	not modelled	100.0	21	<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 aq_1716 from aquifex aeolicus vf5
116	<a href="#">c4zjuA_</a>	Alignment	not modelled	100.0	22	<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-acp reductase from acinetobacter2 baumannii in complex with nad
117	<a href="#">c5jlaB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase from brucella2 melitensis 16m
118	<a href="#">d1nffa_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
119	<a href="#">c5tt0A_</a>	Alignment	not modelled	100.0	28	<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 an oxidoreductase (short chain2 dehydrogenase/reductase family) from burkholderia thailandensis
120	<a href="#">c5koiH_</a>	Alignment	not modelled	100.0	24	<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