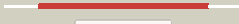



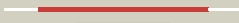



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3548c_(-)_3987561_3988475
Date	Fri Aug 9 18:20:22 BST 2019
Unique Job ID	85cb8c26cb966bab

Detailed template information


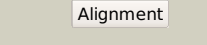
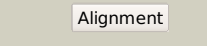





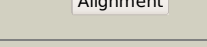
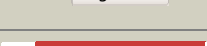





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3qljB_</a>	 Alignment		100.0	91	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 avium
2	<a href="#">c4kzpC_</a>	 Alignment		100.0	45	<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 a putative short chain dehydrogenase from2 mycobacterium smegmatis
3	<a href="#">c5jy1C_</a>	 Alignment		100.0	35	<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
4	<a href="#">c3tscB_</a>	 Alignment		100.0	29	<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
5	<a href="#">c2et6A_</a>	 Alignment		100.0	37	<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
6	<a href="#">d1yxma1</a>	 Alignment		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
7	<a href="#">c3t7cC_</a>	 Alignment		100.0	30	<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
8	<a href="#">d1w6ua_</a>	 Alignment		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
9	<a href="#">c3cxtA_</a>	 Alignment		100.0	29	<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
10	<a href="#">c3pgxB_</a>	 Alignment		100.0	30	<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 paratuberculosis bound to nicotinamide adenine3 dinucleotide
11	<a href="#">c5EpoD_</a>	 Alignment		100.0	26	<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

12	<a href="#">c3grkE_</a>	Alignment		100.0	18	<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
13	<a href="#">c6ci9D_</a>	Alignment		100.0	24	<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
14	<a href="#">c5jc8C_</a>	Alignment		100.0	29	<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
15	<a href="#">d1geea_</a>	Alignment		100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
16	<a href="#">c5jydA_</a>	Alignment		100.0	33	<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
17	<a href="#">c4cr8D_</a>	Alignment		100.0	30	<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
18	<a href="#">c4fc6B_</a>	Alignment		100.0	22	<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
19	<a href="#">c3uveC_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase ((+)-trans-carveol dehydrogenase); <b>PDBTitle:</b> crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
20	<a href="#">c4rgbB_</a>	Alignment		100.0	28	<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
21	<a href="#">c4iboA_</a>	Alignment	not modelled	100.0	28	<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)
22	<a href="#">c4g81A_</a>	Alignment	not modelled	100.0	29	<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
23	<a href="#">c4afnB_</a>	Alignment	not modelled	100.0	30	<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
24	<a href="#">c4j2hA_</a>	Alignment	not modelled	100.0	29	<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)
25	<a href="#">d1zema1</a>	Alignment	not modelled	100.0	28	<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="#">c4nqzF_</a>	Alignment	not modelled	100.0	17	<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
27	<a href="#">c3iccA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl carrier protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution

28	<a href="#">c5x8hA</a>	Alignment	not modelled	100.0	31	<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 of <i>Chryseobacterium</i> sp. ca49
29	<a href="#">c5h5xH</a>	Alignment	not modelled	100.0	28	<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 <i>Streptomyces</i> 2 coelicolor
30	<a href="#">c3wtcB</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2036
31	<a href="#">c3oecA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carveol dehydrogenase (mytha.01326.c, a0r518 homolog); <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from <i>Mycobacterium</i> 2 thermoresistibile
32	<a href="#">c3ek2D</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nah); <b>PDBTitle:</b> crystal structure of enoyl-(acyl carrier protein) reductase from <i>Burkholderia pseudomallei</i> 1719b
33	<a href="#">c3k31B</a>	Alignment	not modelled	100.0	17	<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 from <i>Anaplasma phagocytophilum</i> in complex with nad at 1.9a resolution
34	<a href="#">c4wuvB</a>	Alignment	not modelled	100.0	26	<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 from <i>Haemophilus influenzae</i> (avi_5165, target efi-513796) with bound nad
35	<a href="#">c4gh5B</a>	Alignment	not modelled	100.0	31	<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)
36	<a href="#">c2c07A</a>	Alignment	not modelled	100.0	32	<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 <i>Plasmodium falciparum</i>
37	<a href="#">d2c07a1</a>	Alignment	not modelled	100.0	32	<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="#">c3imfA</a>	Alignment	not modelled	100.0	30	<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 <i>Bacillus anthracis</i> str. 'ames ancestor'
39	<a href="#">c3r3sD</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from <i>Salmonella enterica</i>
40	<a href="#">c6ds1C</a>	Alignment	not modelled	100.0	24	<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+
41	<a href="#">c4nbvA</a>	Alignment	not modelled	100.0	35	<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 <i>Cupriavidus taiwanensis</i>
42	<a href="#">c4urfB</a>	Alignment	not modelled	100.0	35	<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 <i>Aromatoleum aromaticum</i> ebn1
43	<a href="#">c3itdA</a>	Alignment	not modelled	100.0	31	<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 <i>Cochliobolus lunatus</i>
44	<a href="#">c2jyD</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of <i>Francisella tularensis</i> enoyl reductase2 (ftfab) with bound nad
45	<a href="#">d2ae2a</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
46	<a href="#">c4lvuB</a>	Alignment	not modelled	100.0	27	<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 from <i>Burkholderia thailandensis</i>
47	<a href="#">c4z9yA</a>	Alignment	not modelled	100.0	29	<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 from <i>Pectobacterium carotovorum</i>
48	<a href="#">c3afnC</a>	Alignment	not modelled	100.0	25	<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
49	<a href="#">c4trrH</a>	Alignment	not modelled	100.0	29	<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 <i>Burkholderia cenocepacia</i> j2315
50	<a href="#">c4imrA</a>	Alignment	not modelled	100.0	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 3-oxoacyl (acyl-carrier-protein) reductase2 (target efi-506442) from <i>Agrobacterium tumefaciens</i> c58 with nadp3 bound <b>PDB header:</b> oxidoreductase

51	<a href="#">c3lf2B_</a>	Alignment	not modelled	100.0	28	<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
52	<a href="#">c3lylB_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
53	<a href="#">c4egfA_</a>	Alignment	not modelled	100.0	32	<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
54	<a href="#">c3toxG_</a>	Alignment	not modelled	100.0	32	<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
55	<a href="#">d1ae1a_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
56	<a href="#">c4nimA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> versicolorin reductase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from brucella2 melitensis
57	<a href="#">c4m87B_</a>	Alignment	not modelled	100.0	18	<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+
58	<a href="#">c5u9pB_</a>	Alignment	not modelled	100.0	28	<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
59	<a href="#">c2uvdE_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> the crystal structure of a 3-oxoacyl-(acyl carrier protein) reductase2 from bacillus anthracis (ba3989)
60	<a href="#">c3svtA_</a>	Alignment	not modelled	100.0	24	<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
61	<a href="#">d2ew8a1</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
62	<a href="#">d1ja9a_</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
63	<a href="#">c4zjuA_</a>	Alignment	not modelled	100.0	18	<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
64	<a href="#">d2pd4a1</a>	Alignment	not modelled	100.0	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
65	<a href="#">d1iy8a_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
66	<a href="#">c4gloC_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase homolog (target efi-2 505321) from burkholderia multivorans, with bound nad
67	<a href="#">c3o38D_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
68	<a href="#">c5er6C_</a>	Alignment	not modelled	100.0	33	<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
69	<a href="#">c3rihB_</a>	Alignment	not modelled	100.0	27	<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
70	<a href="#">c5o30A_</a>	Alignment	not modelled	100.0	18	<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 hheg
71	<a href="#">c5k9zB_</a>	Alignment	not modelled	100.0	31	<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
72	<a href="#">c4mowB_</a>	Alignment	not modelled	100.0	35	<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
73	<a href="#">c3tzqD_</a>	Alignment	not modelled	100.0	27	<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
74	<a href="#">c3awdD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase; <b>PDBTitle:</b> crystal structure of gox2181
75	<a href="#">c4jroC_</a>	Alignment	not modelled	100.0	35	<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+
76	<a href="#">c2zatC_</a>	Alignment	not modelled	100.0	24	<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
77	<a href="#">c2q2qG_</a>	Alignment	not modelled	100.0	37	<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
78	<a href="#">d2rhca1</a>	Alignment	not modelled	100.0	32	<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="#">c6d9yB_</a>	Alignment	not modelled	100.0	30	<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
80	<a href="#">c1w4zA_</a>	Alignment	not modelled	100.0	32	<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
81	<a href="#">c5un1A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-acp reductase; <b>PDBTitle:</b> crystal structure of a d-beta-hydroxybutyrate dehydrogenase from2 burkholderia multivorans
82	<a href="#">d1xhla_</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
83	<a href="#">c3jirF_</a>	Alignment	not modelled	100.0	26	<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+
84	<a href="#">d1fmca_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
85	<a href="#">d1zbqa1</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
86	<a href="#">c4iiuB_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-[acyl-carrier2 protein]reductase from escherichia coli strain cft073 complexed with3 nadp+ at 2.1 a resolution
87	<a href="#">c4fn4A_</a>	Alignment	not modelled	100.0	31	<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 sulfobolus2 acidocaldarius
88	<a href="#">c1zbqB_</a>	Alignment	not modelled	100.0	40	<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
89	<a href="#">c4kwhA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> reductase homolog; <b>PDBTitle:</b> the crystal structure of angucycline c-6 ketoreductase lanv with bound2 nadp
90	<a href="#">d1nffa_</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
91	<a href="#">c2p68A_</a>	Alignment	not modelled	100.0	30	<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
92	<a href="#">c3ai3A_</a>	Alignment	not modelled	100.0	23	<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
93	<a href="#">d1hdca_</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
94	<a href="#">c3om1A_</a>	Alignment	not modelled	100.0	40	<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
95	<a href="#">c5itvC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroantcapsin 7-dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus subtilis bacc dihydroantcapsin 7-2 dehydrogenase in complex with nadh
96	<a href="#">c3emkA_</a>	Alignment	not modelled	100.0	34	<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
97	<a href="#">c4weoD_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acetoin(diacetyl) reductase; <b>PDBTitle:</b> crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
98	<a href="#">c4dmmA_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> 3-oxoacyl-[acyl-carrier-protein] reductase from synechococcus2 elongatus pcc 7942 in complex with nadp
99	<a href="#">d1g0oa_</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
100	<a href="#">c2cfcB_</a>	Alignment	not modelled	100.0	28	<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

101	<a href="#">c5ojgB</a>	 Alignment	not modelled	100.0	24	<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
102	<a href="#">c6oz7A</a>	 Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase yohf; <b>PDBTitle:</b> putative oxidoreductase from escherichia coli str. k-12
103	<a href="#">c4npcA</a>	 Alignment	not modelled	100.0	30	<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
104	<a href="#">c5g4kB</a>	 Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family <b>PDBTitle:</b> phloroglucinol reductase from clostridium sp. apo-form
105	<a href="#">c3uf0A</a>	 Alignment	not modelled	100.0	33	<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)
106	<a href="#">c4ni5A</a>	 Alignment	not modelled	100.0	33	<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
107	<a href="#">c4nk4E</a>	 Alignment	not modelled	100.0	16	<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 fabi from candidatus liberibacter asiaticus
108	<a href="#">d1qsga</a>	 Alignment	not modelled	100.0	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
109	<a href="#">c5ff9C</a>	 Alignment	not modelled	100.0	23	<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
110	<a href="#">c4nbwA</a>	 Alignment	not modelled	100.0	34	<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
111	<a href="#">c4tkmA</a>	 Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-dependent reductase for 4-deoxy-l-erythro-5- <b>PDBTitle:</b> crystal structure of nadh-dependent reductase a1-r' complexed with nad
112	<a href="#">c3ftpD</a>	 Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 burkholderia pseudomallei at 2.05 a resolution
113	<a href="#">d1k2wa</a>	 Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
114	<a href="#">c3pk0B</a>	 Alignment	not modelled	100.0	29	<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
115	<a href="#">c4dqxB</a>	 Alignment	not modelled	100.0	33	<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
116	<a href="#">c5idxB</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 an oxidoreductase from burkholderia vietnamiensis
117	<a href="#">c3nugA</a>	 Alignment	not modelled	100.0	32	<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
118	<a href="#">c3v2gA</a>	 Alignment	not modelled	100.0	35	<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
119	<a href="#">c5koiH</a>	 Alignment	not modelled	100.0	20	<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
120	<a href="#">d2bgka1</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