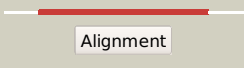

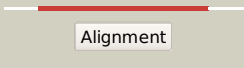

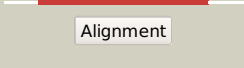

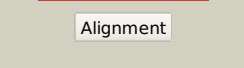

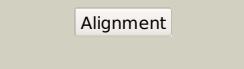

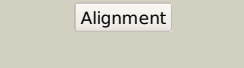

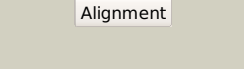

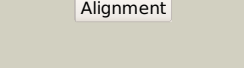
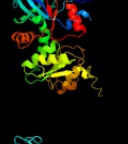
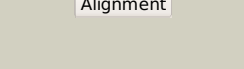

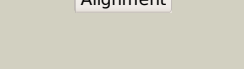
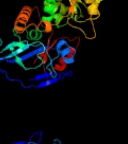
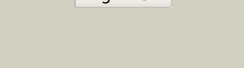




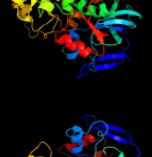
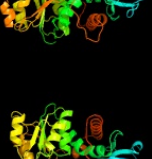
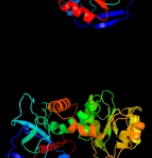


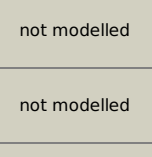


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3777_(- )_4222872_4223858
Date	Fri Aug 9 18:20:48 BST 2019
Unique Job ID	984d69805ff90120

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3krtC_</a>			100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> crotonyl coa reductase; <b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
2	<a href="#">c2j8zA_</a>			100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of human p53 inducible oxidoreductase (2 tp53i3.pig3)
3	<a href="#">c4gi2B_</a>			100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase
4	<a href="#">c3qwbC_</a>			100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae zeta-crystallin-like2 quinone oxidoreductase zta1 complexed with nadph
5	<a href="#">c4a10A_</a>			100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> octenoyl-coa reductase/carboxylase; <b>PDBTitle:</b> apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
6	<a href="#">c3ukoA_</a>			100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase class-3; <b>PDBTitle:</b> crystal structure of s-nitrosoglutathione reductase from arabidopsis2 thaliana, complex with nadh
7	<a href="#">c3uogB_</a>			100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021
8	<a href="#">c4y0kA_</a>			100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ante; <b>PDBTitle:</b> structure of crotonyl-coa carboxylase/reductase ante in complex with2 nadp
9	<a href="#">c1f8fA_</a>			100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> benzyl alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus
10	<a href="#">c2vcyA_</a>			100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of 2-enoyl thioester reductase of human fas ii
11	<a href="#">c1ma0B_</a>			100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione-dependent formaldehyde dehydrogenase; <b>PDBTitle:</b> ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid

12	<a href="#">c2eihA</a>	Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent alcohol dehydrogenase
13	<a href="#">c4rquA</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase crystal structure in complex with nad
14	<a href="#">c1cdoB</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase (ch-oh(d)-nad(a)) <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc
15	<a href="#">c3jynA</a>	Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structures of pseudomonas syringae pv. tomato dc30002 quinone oxidoreductase complexed with nadph
16	<a href="#">c5tnxA</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase zinc-binding domain protein; <b>PDBTitle:</b> crystal structure of alcohol dehydrogenase zinc-binding domain protein2 from burkholderia ambifaria
17	<a href="#">c3gmsA</a>	Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadph:quinone reductase; <b>PDBTitle:</b> crystal structure of putative nadph:quinone reductase from bacillus2 thuringiensis
18	<a href="#">c4rvsA</a>	Alignment		100.0	31	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable quinone reductase qor (nadph:quinone reductase) <b>PDBTitle:</b> the native structure of mycobacterial quinone oxidoreductase rv154c.
19	<a href="#">c1hf3A</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase e chain; <b>PDBTitle:</b> atomic x-ray structure of liver alcohol dehydrogenase containing2 cadmium and a hydroxide adduct to nadh
20	<a href="#">c3cosD</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn
21	<a href="#">c1pl6A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> human sdh/nadh/inhibitor complex
22	<a href="#">c5zxnA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of cura from vibrio vulnificus
23	<a href="#">c1wlyA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-haloacrylate reductase; <b>PDBTitle:</b> crystal structure of 2-haloacrylate reductase
24	<a href="#">c4gkvC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase, propanol-preferring; <b>PDBTitle:</b> structure of escherichia coli adhP (ethanol-inducible dehydrogenase)2 with bound nad
25	<a href="#">c1yb5A</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of human zeta-crystallin with bound nadp
26	<a href="#">c2c0cB</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> zinc binding alcohol dehydrogenase, domain containing 2; <b>PDBTitle:</b> structure of the mgc45594 gene product
27	<a href="#">c4dvjA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc-dependent alcohol dehydrogenase protein; <b>PDBTitle:</b> crystal structure of a putative zinc-dependent alcohol dehydrogenase2 protein from rhizobium etli cfn 42
28	<a href="#">c3b70A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl reductase; <b>PDBTitle:</b> crystal structure of aspergillus terreus trans-acting

					lovastatin2 polyketide enoyl reductase (lov) with bound nadp <b>PDB header:</b> oxidoreductase
29	<a href="#">c3pi7A_</a>	Alignment	not modelled	100.0	19 <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph:quinone reductase (ml13093) from2 mesorhizobium loti at 1.71 a resolution
30	<a href="#">c4j6fB_</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021, nysgrc-target 012230
31	<a href="#">c1y9eB_</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein yhfj; <b>PDBTitle:</b> crystal structure of bacillus subtilis protein yhfj with nad bound
32	<a href="#">c5k1sD_</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, zinc-binding dehydrogenase family; <b>PDBTitle:</b> crystal structure of aibc
33	<a href="#">c1r37B_</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol
34	<a href="#">c2hcyD_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 1; <b>PDBTitle:</b> yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme
35	<a href="#">c1o89A_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yhdh; <b>PDBTitle:</b> crystal structure of e. coli k-12 yhdh
36	<a href="#">c4eezB_</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactococcus lactis alcohol dehydrogenase variant2 re1
37	<a href="#">c5kiaA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of l-threonine 3-dehydrogenase from burkholderia2 thailandensis
38	<a href="#">c2dphA_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dismutase; <b>PDBTitle:</b> crystal structure of formaldehyde dismutase
39	<a href="#">c1qorA_</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of escherichia coli quinone oxidoreductase complexed2 with nadph
40	<a href="#">c5ylnB_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> zinc dependent alcohol dehydrogenase 2 from streptococcus pneumonia -2 apo form
41	<a href="#">c5gxeA_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acrylyl-coa reductase acui; <b>PDBTitle:</b> crystal structure of acryloyl-coa reductase acui in complex with nadph
42	<a href="#">c3fbgA_</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative arginate lyase; <b>PDBTitle:</b> crystal structure of a putative arginate lyase from staphylococcus2 haemolyticus
43	<a href="#">c4b7cB_</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of hypothetical protein pa1648 from2 pseudomonas aeruginosa.
44	<a href="#">c4a2cB_</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> galactitol-1-phosphate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of galactitol-1-phosphate dehydrogenase from2 escherichia coli
45	<a href="#">c2cf5A_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cinnamyl alcohol dehydrogenase; <b>PDBTitle:</b> crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5
46	<a href="#">c4cpdA_</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase tadh from thermus sp. atn1
47	<a href="#">c4z6kD_</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from the antarctic psychrophile moraxella sp.2 tae 123
48	<a href="#">c3gazA_</a>	Alignment	not modelled	100.0	31 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase superfamily protein; <b>PDBTitle:</b> crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans
49	<a href="#">c4ilkB_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> starvation sensing protein rspb; <b>PDBTitle:</b> crystal structure of short chain alcohol dehydrogenase (rspb) from e.2 coli cft073 (efi target efi-506413) complexed with cofactor nadh
50	<a href="#">c4oaqA_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> r-specific carbonyl reductase; <b>PDBTitle:</b> crystal structure of the r-specific carbonyl reductase from candida2 parapsilosis atcc 7330
51	<a href="#">c1p0fA_</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp
52	<a href="#">c1vj0B_</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> crystal structure of alcohol dehydrogenase (tm0436) from thermotoga2 maritima at 2.00 a resolution
53	<a href="#">c1n9gF_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> mitochondrial 2-enoyl thioester reductase etr1p/etr2p heterodimer from2 candida tropicalis

54	<a href="#">c1lluD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate
55	<a href="#">c1kolA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of formaldehyde dehydrogenase
56	<a href="#">c2j3iB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent oxidoreductase p1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana double bond2 reductase (at5g16970)-binary complex
57	<a href="#">c1yqxB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sinapyl alcohol dehydrogenase; <b>PDBTitle:</b> sinapyl alcohol dehydrogenase at 2.5 angstrom resolution
58	<a href="#">c4a27A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> synaptic vesicle membrane protein vat-1 homolog-like; <b>PDBTitle:</b> crystal structure of human synaptic vesicle membrane protein vat-12 homolog-like protein
59	<a href="#">c4ejmA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc-binding dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative zinc-binding dehydrogenase (target2 psi-012003) from sinorhizobium meliloti 1021 bound to nadp
60	<a href="#">c6n7iB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of an alcohol dehydrogenase from elizabethkingia2 anophelis nuhp1
61	<a href="#">c6c49A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of alcohol dehydrogenase from acinetobacter2 baumannii
62	<a href="#">c5a3iF_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative quinone-oxidoreductase homolog, chloroplastic; <b>PDBTitle:</b> crystal structure of the chloroplastic gamma-ketol reductase from2 arabidopsis thaliana bound to 13-oxo-9(z),11(e),15(z)-3 octadecatrienoic acid.
63	<a href="#">c5fi5A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydroalstonine synthase; <b>PDBTitle:</b> heteroyohimbine synthase thas1 from catharanthus roseus - apo form
64	<a href="#">c2dfvB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable l-threonine 3-dehydrogenase; <b>PDBTitle:</b> hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii
65	<a href="#">c4jbiB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase (zinc); <b>PDBTitle:</b> 2.35a resolution structure of nadph bound thermostable alcohol2 dehydrogenase from pyrobaculum aerophilum
66	<a href="#">c2ouiB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
67	<a href="#">c2ejvA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of threonine 3-dehydrogenase complexed with nad+
68	<a href="#">c5vm2A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of eck1772, an oxidoreductase/dehydrogenase of2 unknown specificity involved in membrane biogenesis from escherichia3 coli
69	<a href="#">c4jxkA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase rop_24000 (target efi-506400) from2 rhodococcus opacus b4
70	<a href="#">c5vktB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cinnamyl alcohol dehydrogenases (sbcad4); <b>PDBTitle:</b> cinnamyl alcohol dehydrogenases (sbcad4) from sorghum bicolor (l.)2 moench
71	<a href="#">c3ip1C_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> structure of putative alcohol dehydrogenase (tm_042) from thermotoga2 maritima
72	<a href="#">c2xaaC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> secondary alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol
73	<a href="#">c2w4qA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin reductase 2; <b>PDBTitle:</b> crystal structure of human zinc-binding alcohol2 dehydrogenase 1 (zadh1) in ternary complex with nadp and3 18beta-glycyrrhetic acid
74	<a href="#">c1rjwA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r
75	<a href="#">c1e3iA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp(h)-dependent ketose reductase; <b>PDBTitle:</b> ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly
76	<a href="#">c1xa0B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph dependent oxidoreductases; <b>PDBTitle:</b> crystal structure of mcsg target apc35536 from bacillus2 stearothermophilus
77	<a href="#">c1kevB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> structure of nadp-dependent alcohol dehydrogenase
						<b>PDB header:</b> oxidoreductase

78	<a href="#">c1h2bA</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a resolution
79	<a href="#">c4mkrC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> zingiber officinale double bond reductase; <b>PDBTitle:</b> structure of the apo form of a zingiber officinale double bond2 reductase
80	<a href="#">c1piwA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical zinc-type alcohol dehydrogenase- <b>PDBTitle:</b> apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae
81	<a href="#">c5dp1A</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> curk; <b>PDBTitle:</b> crystal structure of curk enoyl reductase
82	<a href="#">c1zsvB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent leukotriene b4 12- <b>PDBTitle:</b> crystal structure of human nadp-dependent leukotriene b4 12-2 hydroxydehydrogenase
83	<a href="#">c4eyeA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase from mycobacterium2 abscessus solved by iodide ion sad
84	<a href="#">c6dkhC</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> l-idonate 5-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> the crystal structure of l-idonate 5-dehydrogenase from escherichia2 coli str. k-12 substr. mg1655
85	<a href="#">c4dupB</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of a quinone oxidoreductase from rhizobium etli cfn2 42
86	<a href="#">c2cdaA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> sulfolobus solfataricus glucose dehydrogenase 1 in complex with nadp
87	<a href="#">c5h81A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heteroyohimbine synthase thas2; <b>PDBTitle:</b> heteroyohimbine synthase thas2 from catharanthus roseus - complex with2 nadp+
88	<a href="#">c1uufA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-type alcohol dehydrogenase-like protein <b>PDBTitle:</b> crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk
89	<a href="#">c3tqhA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> structure of the quinone oxidoreductase from coxiella burnetii
90	<a href="#">c3iupB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph:quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
91	<a href="#">c3gohA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> crystal structure of alcohol dehydrogenase superfamily protein2 (np_718042.1) from shewanella oneidensis at 1.55 a resolution
92	<a href="#">c5dp2A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> curf; <b>PDBTitle:</b> curf er cyclopropanase from curacin a biosynthetic pathway
93	<a href="#">c2vvpA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> haloferax mediterranei glucose dehydrogenase in complex with nadph and2 zn.
94	<a href="#">c6eowC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ketone/zingerone synthase 1; <b>PDBTitle:</b> structure of raspberry ketone synthase with hydroxybenzalacetone
95	<a href="#">c5dovB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> jamj; <b>PDBTitle:</b> crystal structure of jamj enoyl reductase (apo form)
96	<a href="#">c3m6iA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinitol 4-dehydrogenase; <b>PDBTitle:</b> l-arabinitol 4-dehydrogenase
97	<a href="#">c3widC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose 1-dehydrogenase; <b>PDBTitle:</b> structure of a glucose dehydrogenase t277f mutant in complex with nadp
98	<a href="#">c2vn8B</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> receptor inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> reticulon-4-interacting protein 1; <b>PDBTitle:</b> crystal structure of human reticulon 4 interacting protein 1 in2 complex with nadph
99	<a href="#">c2h6eA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-arabinose 1-dehydrogenase; <b>PDBTitle:</b> crystal structure of the d-arabinose dehydrogenase from sulfolobus2 solfataricus
100	<a href="#">c4idbA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ripening-induced protein; <b>PDBTitle:</b> structure of the fragaria x ananassa enone oxidoreductase in complex2 with nadp+
101	<a href="#">c1iz0A</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinone oxidoreductase; <b>PDBTitle:</b> crystal structures of the quinone oxidoreductase from2 thermus thermophilus hb8 and its complex with nadph
102	<a href="#">c3slkB</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase extender module 2; <b>PDBTitle:</b> structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase <b>PDB header:</b> transferase

103	<a href="#">c6fn6A_</a>	Alignment	not modelled	99.9	25	<b>Chain:</b> A; <b>PDB Molecule:</b> fatty acid synthase 1, isoform a; <b>PDBTitle:</b> modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
104	<a href="#">d1pl8a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
105	<a href="#">d1uufa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
106	<a href="#">d1p0fa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
107	<a href="#">d1f8fa1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
108	<a href="#">d1gu7a1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
109	<a href="#">d1piwa1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
110	<a href="#">d1cdoa1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
111	<a href="#">d1kola1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
112	<a href="#">d1jqba1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
113	<a href="#">d1u3wa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
114	<a href="#">d1o89a1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
115	<a href="#">d1d1ta1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
116	<a href="#">d1u3ta1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
117	<a href="#">d1xa0a1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
118	<a href="#">d2fzwa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
119	<a href="#">d1ykfa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
120	<a href="#">d1llua1</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain