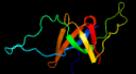
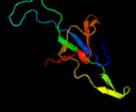
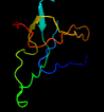
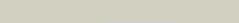
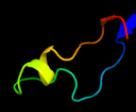
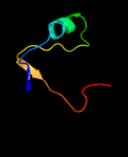
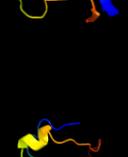
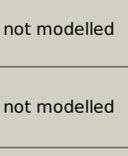


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3418c\_groES\_3837166\_3837468  
 Date Fri Aug 9 18:20:09 BST 2019  
 Unique Job ID 964c35b45a6b27c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1p3ha_</a>	 Alignment		100.0	100	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
2	<a href="#">d1aono_</a>	 Alignment		100.0	45	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
3	<a href="#">c4pj1V_</a>	 Alignment		100.0	34	<b>PDB header:</b> chaperone <b>Chain:</b> V; <b>PDB Molecule:</b> 10 kda heat shock protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the human mitochondrial chaperonin symmetrical2 'football' complex
4	<a href="#">d1we3o_</a>	 Alignment		100.0	59	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
5	<a href="#">d1lepa_</a>	 Alignment		99.9	98	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
6	<a href="#">c3nx6A_</a>	 Alignment		99.9	43	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> 10kda chaperonin; <b>PDBTitle:</b> crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
7	<a href="#">d1g31a_</a>	 Alignment		96.1	27	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
8	<a href="#">c1p82A_</a>	 Alignment		85.2	100	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> 10 kda chaperonin; <b>PDBTitle:</b> nmr structure of 1-25 fragment of mycobacterium2 tuberculosis cpn10
9	<a href="#">c5vm2A_</a>	 Alignment		80.8	31	<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
10	<a href="#">c1yqxB_</a>	 Alignment		79.7	43	<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
11	<a href="#">c4qi2B_</a>	 Alignment		78.5	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase

12	<a href="#">c4z6kD</a>	Alignment		76.6	48	<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
13	<a href="#">c5h81A</a>	Alignment		76.4	30	<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+
14	<a href="#">c1lluD</a>	Alignment		76.0	55	<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
15	<a href="#">c4a10A</a>	Alignment		75.6	50	<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.
16	<a href="#">c3m6iA</a>	Alignment		75.1	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinitol 4-dehydrogenase; <b>PDBTitle:</b> l-arabinitol 4-dehydrogenase
17	<a href="#">c1vj0B</a>	Alignment		75.1	28	<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
18	<a href="#">c2ejvA</a>	Alignment		74.9	42	<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+
19	<a href="#">c1rjwA</a>	Alignment		74.6	41	<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
20	<a href="#">c1kevB</a>	Alignment		74.5	44	<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
21	<a href="#">c1k0lA</a>	Alignment	not modelled	73.9	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of formaldehyde dehydrogenase
22	<a href="#">c2ouiB</a>	Alignment	not modelled	72.8	33	<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
23	<a href="#">d1luufa1</a>	Alignment	not modelled	72.5	42	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
24	<a href="#">c4eezB</a>	Alignment	not modelled	72.3	29	<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
25	<a href="#">c3ukoA</a>	Alignment	not modelled	71.7	46	<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
26	<a href="#">c2hcyD</a>	Alignment	not modelled	71.4	33	<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
27	<a href="#">c4gkvC</a>	Alignment	not modelled	71.2	38	<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
28	<a href="#">c4oagA</a>	Alignment	not modelled	70.7	48	<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

29	<a href="#">c1r37B</a>	Alignment	not modelled	70.7	30	<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
30	<a href="#">c2cf5A</a>	Alignment	not modelled	70.4	43	<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
31	<a href="#">c4cpdA</a>	Alignment	not modelled	70.4	44	<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
32	<a href="#">c2xaaC</a>	Alignment	not modelled	70.3	37	<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
33	<a href="#">c4ejmA</a>	Alignment	not modelled	70.3	35	<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
34	<a href="#">c3krtC</a>	Alignment	not modelled	70.2	38	<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)
35	<a href="#">c4ilkB</a>	Alignment	not modelled	70.1	26	<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
36	<a href="#">c4a2cB</a>	Alignment	not modelled	70.1	52	<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
37	<a href="#">c5vktB</a>	Alignment	not modelled	70.0	48	<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
38	<a href="#">c5kiaA</a>	Alignment	not modelled	69.6	26	<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
39	<a href="#">c4rquA</a>	Alignment	not modelled	69.5	44	<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
40	<a href="#">c1h2bA</a>	Alignment	not modelled	69.4	30	<b>PDB header:</b> oxidoreductase <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
41	<a href="#">c5k1sD</a>	Alignment	not modelled	68.9	30	<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
42	<a href="#">c1f8fA</a>	Alignment	not modelled	68.7	38	<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
43	<a href="#">c6c49A</a>	Alignment	not modelled	68.1	33	<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
44	<a href="#">c2eihA</a>	Alignment	not modelled	68.1	60	<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
45	<a href="#">c1e3jA</a>	Alignment	not modelled	68.0	45	<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
46	<a href="#">c1piwA</a>	Alignment	not modelled	67.4	35	<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
47	<a href="#">c4jbiB</a>	Alignment	not modelled	67.2	37	<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
48	<a href="#">c5fi5A</a>	Alignment	not modelled	66.9	38	<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
49	<a href="#">c2dphA</a>	Alignment	not modelled	66.9	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dismutase; <b>PDBTitle:</b> crystal structure of formaldehyde dismutase
50	<a href="#">c2lt1A</a>	Alignment	not modelled	65.2	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> card protein; <b>PDBTitle:</b> solution nmr structure of the 72-residue n-terminal domain of2 myxococcus xanthus card
51	<a href="#">c5ylnB</a>	Alignment	not modelled	64.8	35	<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
52	<a href="#">c1cdoB</a>	Alignment	not modelled	63.5	41	<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
53	<a href="#">c3uogB</a>	Alignment	not modelled	63.2	42	<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

54	<a href="#">c3cosD</a>	Alignment	not modelled	63.0	50	<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
55	<a href="#">c1ma0B</a>	Alignment	not modelled	63.0	42	<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
56	<a href="#">c1pl6A</a>	Alignment	not modelled	62.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> human sdh/nadh/inhibitor complex
57	<a href="#">c1uufA</a>	Alignment	not modelled	61.6	52	<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 yakh
58	<a href="#">c2dfvB</a>	Alignment	not modelled	61.4	48	<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
59	<a href="#">c6n7lB</a>	Alignment	not modelled	60.9	62	<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
60	<a href="#">c2lqkA</a>	Alignment	not modelled	60.2	31	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the cdnl protein2 from thermus thermophilus
61	<a href="#">c1p0fA</a>	Alignment	not modelled	59.7	33	<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
62	<a href="#">c1hf3A</a>	Alignment	not modelled	57.7	45	<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
63	<a href="#">c5tnxA</a>	Alignment	not modelled	55.8	38	<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
64	<a href="#">c3widC</a>	Alignment	not modelled	55.0	24	<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
65	<a href="#">d1p0fa1</a>	Alignment	not modelled	55.0	35	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
66	<a href="#">c4dviA</a>	Alignment	not modelled	51.9	41	<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
67	<a href="#">c3ip1C</a>	Alignment	not modelled	50.4	27	<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
68	<a href="#">d2eyqa1</a>	Alignment	not modelled	49.8	34	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> CarD-like <b>Family:</b> CarD-like
69	<a href="#">d1piwa1</a>	Alignment	not modelled	49.5	33	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
70	<a href="#">d1kola1</a>	Alignment	not modelled	46.1	29	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
71	<a href="#">c2lt4A</a>	Alignment	not modelled	45.2	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family; <b>PDBTitle:</b> cdnlnt from myxococcus xanthus
72	<a href="#">c3slkB</a>	Alignment	not modelled	44.5	22	<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
73	<a href="#">c4j6fB</a>	Alignment	not modelled	44.0	38	<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
74	<a href="#">d1pl8a1</a>	Alignment	not modelled	43.7	32	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
75	<a href="#">c4y0kA</a>	Alignment	not modelled	43.3	45	<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
76	<a href="#">c2cdaA</a>	Alignment	not modelled	41.9	20	<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
77	<a href="#">c2h6eA</a>	Alignment	not modelled	41.8	42	<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
78	<a href="#">c5x7nA</a>	Alignment	not modelled	39.5	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum

79	<a href="#">c2vnud3</a>	Alignment	not modelled	38.4	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
80	<a href="#">c2lwiA_</a>	Alignment	not modelled	37.5	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, card family; <b>PDBTitle:</b> nmr solution structure myxococcus xanthus cdnl
81	<a href="#">d1knwa1</a>	Alignment	not modelled	34.4	24	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
82	<a href="#">c4l5gA_</a>	Alignment	not modelled	34.0	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> card; <b>PDBTitle:</b> crystal structure of thermus thermophilus card
83	<a href="#">c3b70A_</a>	Alignment	not modelled	33.4	48	<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 (lovC) with bound nadp
84	<a href="#">c3n2bD_</a>	Alignment	not modelled	31.1	25	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
85	<a href="#">c2j8zA_</a>	Alignment	not modelled	30.4	37	<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)
86	<a href="#">c4jf7B_</a>	Alignment	not modelled	30.2	26	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin-neuraminidase; <b>PDBTitle:</b> structure of the parainfluenza virus 5 (piv5) hemagglutinin-2 neuraminidase (hn) ectodomain
87	<a href="#">c2fg0B_</a>	Alignment	not modelled	29.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cog0791: cell wall-associated hydrolases (invasion- <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
88	<a href="#">c1n9gF_</a>	Alignment	not modelled	29.0	31	<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
89	<a href="#">c6eowC_</a>	Alignment	not modelled	27.4	11	<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
90	<a href="#">c4b7cB_</a>	Alignment	not modelled	26.6	11	<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.
91	<a href="#">c2vnuD_</a>	Alignment	not modelled	26.3	19	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> exosome complex exonuclease rrp44; <b>PDBTitle:</b> crystal structure of sc rrp44
92	<a href="#">c4kbmB_</a>	Alignment	not modelled	25.9	33	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase-binding transcription factor card; <b>PDBTitle:</b> structure of the mtb card/rnap beta subunit b1-b2 domains complex
93	<a href="#">c3gazA_</a>	Alignment	not modelled	25.7	30	<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
94	<a href="#">c5fwhA_</a>	Alignment	not modelled	25.0	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> essc; <b>PDBTitle:</b> n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
95	<a href="#">d1kk1a2</a>	Alignment	not modelled	23.7	19	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
96	<a href="#">c3nfpB_</a>	Alignment	not modelled	23.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
97	<a href="#">d1jt8a_</a>	Alignment	not modelled	22.1	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
98	<a href="#">d1zq1a1</a>	Alignment	not modelled	21.5	24	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> GatD N-terminal domain-like <b>Family:</b> GatD N-terminal domain-like
99	<a href="#">c1z4xA_</a>	Alignment	not modelled	21.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin-neuraminidase; <b>PDBTitle:</b> parainfluenza virus 5 (sv5) hemagglutinin-neuraminidase (hn) with2 ligand sialyllactose (soaked with sialyllactose, ph8.0)
100	<a href="#">c2vvpA_</a>	Alignment	not modelled	21.4	37	<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.
101	<a href="#">c4fdyA_</a>	Alignment	not modelled	20.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family; <b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution