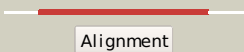

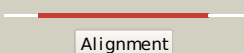

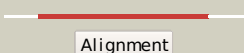

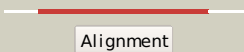

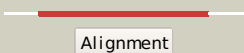

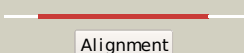

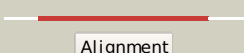

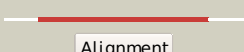

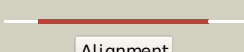

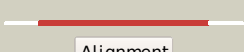

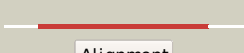








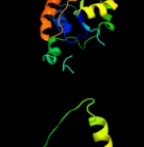
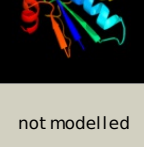


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ACZ2
Date	Thu Jan 5 11:19:29 GMT 2012
Unique Job ID	4ae300a7eeb240ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2fekA_</a>	 Alignment		100.0	56	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase <b>PDBTitle:</b> structure of a protein tyrosine phosphatase
2	<a href="#">c2wmyH_</a>	 Alignment		100.0	62	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> putative acid phosphatase wzb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
3	<a href="#">d1dg9a_</a>	 Alignment		100.0	32	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
4	<a href="#">c2gi4A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible phosphotyrosine protein phosphatase; <b>PDBTitle:</b> solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
5	<a href="#">d5pnta_</a>	 Alignment		100.0	32	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
6	<a href="#">c2cwwA_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight phosphotyrosine protein phosphatase; <b>PDBTitle:</b> crystal structure of tt1001 protein from thermus thermophilus hb8
7	<a href="#">d1p8aa_</a>	 Alignment		100.0	23	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
8	<a href="#">d1d1qa_</a>	 Alignment		100.0	27	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
9	<a href="#">c3rofA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase ptpa; <b>PDBTitle:</b> crystal structure of the s. aureus protein tyrosine phosphatase ptpa
10	<a href="#">c1zggA_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative low molecular weight protein-tyrosine- <b>PDBTitle:</b> solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
11	<a href="#">c3jviA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase; <b>PDBTitle:</b> product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica

12	<a href="#">c1u2pA_</a>	Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine- <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
13	<a href="#">c2l18A_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> an arsenate reductase in the phosphate binding state
14	<a href="#">d1jf8a_</a>	Alignment		100.0	22	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
15	<a href="#">d1jl3a_</a>	Alignment		100.0	20	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
16	<a href="#">d1y11a_</a>	Alignment		100.0	23	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
17	<a href="#">c3rh0A_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
18	<a href="#">c3t38B_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
19	<a href="#">c3fdfA_</a>	Alignment		97.3	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fr253; <b>PDBTitle:</b> crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
20	<a href="#">c3o2qB_</a>	Alignment		96.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii subunit a c-terminal domain phosphatase <b>PDBTitle:</b> crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
21	<a href="#">c3o2sB_</a>	Alignment	not modelled	96.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii subunit a c-terminal domain phosphatase <b>PDBTitle:</b> crystal structure of the human symplekin-ssu72 complex
22	<a href="#">c2f00A_</a>	Alignment	not modelled	94.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
23	<a href="#">c1gpiA_</a>	Alignment	not modelled	90.1	18	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
24	<a href="#">d1p3da1</a>	Alignment	not modelled	89.0	19	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
25	<a href="#">c1j6uA_</a>	Alignment	not modelled	87.5	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
26	<a href="#">d1pjqa1</a>	Alignment	not modelled	86.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
27	<a href="#">d1gpja2</a>	Alignment	not modelled	85.9	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
28	<a href="#">d1j6ua1</a>	Alignment	not modelled	82.5	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
						<b>PDB header:</b> transferase

29	<a href="#">c1vkrA</a>	Alignment	not modelled	81.0	30	<b>Chain:</b> A: <b>PDB Molecule:</b> mannitol-specific pts system enzyme iiabc components; <b>PDBTitle:</b> structure of iib domain of the mannitol-specific permease enzyme ii
30	<a href="#">d1vkra</a>	Alignment	not modelled	81.0	30	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
31	<a href="#">c3ggpA</a>	Alignment	not modelled	80.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
32	<a href="#">c1gqgA</a>	Alignment	not modelled	80.0	20	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
33	<a href="#">c1ml4A</a>	Alignment	not modelled	79.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate transcarbamoylase; <b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
34	<a href="#">c2rgwD</a>	Alignment	not modelled	79.6	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
35	<a href="#">d1tuga1</a>	Alignment	not modelled	77.0	16	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
36	<a href="#">c3eagA</a>	Alignment	not modelled	75.5	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitidis
37	<a href="#">c1tvmA</a>	Alignment	not modelled	75.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, galactitol-specific iib component; <b>PDBTitle:</b> nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
38	<a href="#">c3kcqA</a>	Alignment	not modelled	75.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
39	<a href="#">c3czcA</a>	Alignment	not modelled	74.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rmpb; <b>PDBTitle:</b> the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
40	<a href="#">c2bibA</a>	Alignment	not modelled	73.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> teichoic acid phosphorylcholine esterase/ choline binding <b>PDBTitle:</b> crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
41	<a href="#">d2jfga1</a>	Alignment	not modelled	72.2	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
42	<a href="#">d1vlva2</a>	Alignment	not modelled	71.5	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
43	<a href="#">c3ktdC</a>	Alignment	not modelled	70.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
44	<a href="#">c3hn7A</a>	Alignment	not modelled	69.6	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
45	<a href="#">c2eq8C</a>	Alignment	not modelled	69.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
46	<a href="#">c3dfzB</a>	Alignment	not modelled	68.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
47	<a href="#">c3l6dB</a>	Alignment	not modelled	64.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
48	<a href="#">d1u6ka1</a>	Alignment	not modelled	63.3	21	<b>Fold:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) <b>Superfamily:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) <b>Family:</b> F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
49	<a href="#">c3gt0A</a>	Alignment	not modelled	59.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
50	<a href="#">c3b1fA</a>	Alignment	not modelled	56.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from streptococcus2 mutans
51	<a href="#">d1cmca</a>	Alignment	not modelled	54.6	13	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Met repressor, MetJ (MetR)
						<b>PDB header:</b> structural genomics, unknown function

52	<a href="#">c1wv9B_</a>	Alignment	not modelled	54.3	17	<b>Chain:</b> B: <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
53	<a href="#">d1ljza_</a>	Alignment	not modelled	52.9	14	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
54	<a href="#">d1bala_</a>	Alignment	not modelled	51.8	17	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
55	<a href="#">c3i2vA_</a>	Alignment	not modelled	51.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase and sulfurtransferase mocs3; <b>PDBTitle:</b> crystal structure of human mocs3 rhodanese-like domain
56	<a href="#">c1e0cA_</a>	Alignment	not modelled	51.0	20	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
57	<a href="#">d1yt8a4</a>	Alignment	not modelled	50.1	13	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
58	<a href="#">d1w85i_</a>	Alignment	not modelled	50.0	19	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
59	<a href="#">c3d1pA_</a>	Alignment	not modelled	49.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase yor285w; <b>PDBTitle:</b> atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
60	<a href="#">c2rhoB_</a>	Alignment	not modelled	48.4	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
61	<a href="#">d1duvg2</a>	Alignment	not modelled	48.3	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
62	<a href="#">c2e85B_</a>	Alignment	not modelled	47.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 3 maturation protease; <b>PDBTitle:</b> crystal structure of the hydrogenase 3 maturation protease
63	<a href="#">d1w4ha1</a>	Alignment	not modelled	46.6	17	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
64	<a href="#">c2k0zA_</a>	Alignment	not modelled	46.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp1203; <b>PDBTitle:</b> solution nmr structure of protein hp1203 from helicobacter pylori2 26695, northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
65	<a href="#">d1ml4a2</a>	Alignment	not modelled	45.5	8	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
66	<a href="#">c2eq9C_</a>	Alignment	not modelled	45.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
67	<a href="#">c3ghyA_</a>	Alignment	not modelled	44.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
68	<a href="#">c1np3B_</a>	Alignment	not modelled	43.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxyhydroxy acid isomeroeductase from2 pseudomonas aeruginosa
69	<a href="#">d2fug21</a>	Alignment	not modelled	43.6	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
70	<a href="#">d2cyua1</a>	Alignment	not modelled	42.8	19	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
71	<a href="#">c3lxmC_</a>	Alignment	not modelled	42.7	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
72	<a href="#">c1zwvA_</a>	Alignment	not modelled	42.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched- <b>PDBTitle:</b> solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
73	<a href="#">c1m67A_</a>	Alignment	not modelled	41.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
74	<a href="#">c3ia7A_</a>	Alignment	not modelled	41.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin

					glycosyltransferase
75	<a href="#">d2vapa1</a>	Alignment	not modelled	40.7	18 <b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
76	<a href="#">d1u9ca</a>	Alignment	not modelled	40.5	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/PfpI
77	<a href="#">c1w5fA</a>	Alignment	not modelled	39.6	19 <b>PDB header:</b> cell division <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz, t7 mutated, domain swapped (t. maritima)
78	<a href="#">c1w3dA</a>	Alignment	not modelled	39.4	19 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
79	<a href="#">c2jtaA</a>	Alignment	not modelled	39.1	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phage shock protein e; <b>PDBTitle:</b> rhodanese from e.coli
80	<a href="#">d1iiba</a>	Alignment	not modelled	39.1	11 <b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
81	<a href="#">c3foja</a>	Alignment	not modelled	38.7	12 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
82	<a href="#">c3emeA</a>	Alignment	not modelled	38.6	19 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese-like domain protein; <b>PDBTitle:</b> crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
83	<a href="#">c2auvA</a>	Alignment	not modelled	38.0	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> potential nad-reducing hydrogenase subunit; <b>PDBTitle:</b> solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
84	<a href="#">c3k96B</a>	Alignment	not modelled	37.9	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
85	<a href="#">c2g5cD</a>	Alignment	not modelled	37.3	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus
86	<a href="#">c1w4kA</a>	Alignment	not modelled	37.1	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e2; <b>PDBTitle:</b> peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
87	<a href="#">c2eq7C</a>	Alignment	not modelled	36.8	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e2 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
88	<a href="#">c2coaA</a>	Alignment	not modelled	36.4	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipamide acyltransferase component of branched- <b>PDBTitle:</b> solution structure of the e3_binding domain of2 dihydrolipamide branched chaintransacylase
89	<a href="#">d1n1ea2</a>	Alignment	not modelled	36.2	23 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
90	<a href="#">c3nbmA</a>	Alignment	not modelled	36.0	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
91	<a href="#">d1cfza</a>	Alignment	not modelled	35.6	33 <b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> HybD-like <b>Family:</b> Hydrogenase maturing endopeptidase HybD
92	<a href="#">d1f37b</a>	Alignment	not modelled	35.5	13 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioredoxin-like 2Fe-2S ferredoxin
93	<a href="#">d1l1ca1</a>	Alignment	not modelled	34.8	15 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
94	<a href="#">c2imgA</a>	Alignment	not modelled	34.6	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 23; <b>PDBTitle:</b> crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
95	<a href="#">c2g6zB</a>	Alignment	not modelled	34.5	38 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity protein phosphatase 5; <b>PDBTitle:</b> crystal structure of human dusp5
96	<a href="#">c3triB</a>	Alignment	not modelled	33.9	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
97	<a href="#">d1ekxa2</a>	Alignment	not modelled	33.7	12 <b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
98	<a href="#">c3dv0I</a>	Alignment	not modelled	33.5	23 <b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2



						dehydrogenase multi-enzyme complex <b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
99	<a href="#">d1w85b2</a>	Alignment	not modelled	33.4	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase
100	<a href="#">c2eg4B_</a>	Alignment	not modelled	32.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
101	<a href="#">c1evjC_</a>	Alignment	not modelled	32.6	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Pce catalytic domain-like
102	<a href="#">d1wraa1</a>	Alignment	not modelled	32.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus
103	<a href="#">c3d0oA_</a>	Alignment	not modelled	32.1	12	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
104	<a href="#">d1dxha2</a>	Alignment	not modelled	31.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> m-phase inducer phosphatase 2; <b>PDBTitle:</b> protein phosphatase, new crystal form
105	<a href="#">c2uzqE_</a>	Alignment	not modelled	30.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein mth1747; <b>PDBTitle:</b> structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
106	<a href="#">c1i36A_</a>	Alignment	not modelled	30.6	18	<b>PDB header:</b> cell division <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz homolog 1; <b>PDBTitle:</b> ftsz dimer, empty (m. jannaschii)
107	<a href="#">c1w59B_</a>	Alignment	not modelled	30.6	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
108	<a href="#">d1hdoa_</a>	Alignment	not modelled	30.6	12	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
109	<a href="#">d1umdb2</a>	Alignment	not modelled	30.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase-like 15 isoform a; <b>PDBTitle:</b> crystal structure of dusp15
110	<a href="#">c1yz4A_</a>	Alignment	not modelled	30.4	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	<a href="#">d1zh8a1</a>	Alignment	not modelled	29.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase mitochondrial 1; <b>PDBTitle:</b> crystal structure of ptpmt1 in complex with pi(5)p
112	<a href="#">c3rgqA_</a>	Alignment	not modelled	29.6	19	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp/gtp binding protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
113	<a href="#">c3g5jA_</a>	Alignment	not modelled	29.3	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz pseudomonas aeruginosa gdp
114	<a href="#">c2vawA_</a>	Alignment	not modelled	29.3	22	<b>PDB header:</b> bacterial cell division inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> crystal structure of sula:fts from pseudomonas aeruginosa
115	<a href="#">c1ofuB_</a>	Alignment	not modelled	28.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase; <b>PDBTitle:</b> the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
116	<a href="#">c3c1oA_</a>	Alignment	not modelled	28.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	<a href="#">d1f0ya2</a>	Alignment	not modelled	28.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 14; <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 14
118	<a href="#">c2wgpA_</a>	Alignment	not modelled	27.7	29	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
119	<a href="#">d1okga2</a>	Alignment	not modelled	27.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
120	<a href="#">c3oj0A_</a>	Alignment	not modelled	27.0	19	