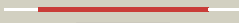












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3192_(-)_3559560_3560021
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	575d3451283a2e15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1lucb_</a>	 Alignment		100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
2	<a href="#">c6friD_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alkanal monooxygenase beta chain; <b>PDBTitle:</b> structure of luxb from photobacterium leiognathi
3	<a href="#">c2b81D_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
4	<a href="#">c3raoB_</a>	 Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
5	<a href="#">d1nqka_</a>	 Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
6	<a href="#">d1luca_</a>	 Alignment		100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
7	<a href="#">c2i7gA_</a>	 Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
8	<a href="#">c3sdoB_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
9	<a href="#">d1ezwa_</a>	 Alignment		100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
10	<a href="#">c1z69D_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> coenzyme f420-dependent n(5),n(10)- <b>PDBTitle:</b> crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
11	<a href="#">c5tlcA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme a; <b>PDBTitle:</b> crystal structure of bdsa from bacillus subtilis wu-s2b

12	<a href="#">c5dqpA</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> edta monoxygenase; <b>PDBTitle:</b> edta monoxygenase (emoa) from chelativorans sp. bnc1
13	<a href="#">c2wgkA</a>	Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monoxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monoxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monoxygenase from3 pseudomonas putida
14	<a href="#">c1tvIA</a>	Alignment		100.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
15	<a href="#">d1tvIA</a>	Alignment		100.0	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monoxygenases
16	<a href="#">d1rhca</a>	Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
17	<a href="#">c5wanA</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monoxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
18	<a href="#">d1f07a</a>	Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
19	<a href="#">c3b9nB</a>	Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monoxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monoxygenase (lada)
20	<a href="#">c3c8nB</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable f420-dependent glucose-6-phosphate dehydrogenase <b>PDBTitle:</b> crystal structure of apo-fgd1 from mycobacterium tuberculosis
21	<a href="#">c5w4zA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin lyase; <b>PDBTitle:</b> crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
22	<a href="#">c6ak1B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monoxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans
23	<a href="#">d1nfpa</a>	Alignment	not modelled	93.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
24	<a href="#">c5i4rA</a>	Alignment	not modelled	40.1	19	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> contact-dependent inhibitor a; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
25	<a href="#">d1oyaa</a>	Alignment	not modelled	39.6	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
26	<a href="#">c4tmcB</a>	Alignment	not modelled	38.8	9	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> old yellow enzyme; <b>PDBTitle:</b> crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
27	<a href="#">c3fa4D</a>	Alignment	not modelled	37.1	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
28	<a href="#">c4ot7A</a>	Alignment	not modelled	37.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of a variant of ncr from zymomonas mobilis
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3gr7A_</a>	Alignment	not modelled	36.2	18	<b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal crystal form
30	<a href="#">c4jicB_</a>	Alignment	not modelled	35.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gtn reductase; <b>PDBTitle:</b> glycerol trinitrate reductase nera from agrobacterium radiobacter
31	<a href="#">c2yb1A_</a>	Alignment	not modelled	33.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
32	<a href="#">d1icpa_</a>	Alignment	not modelled	32.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
33	<a href="#">c4lsbA_</a>	Alignment	not modelled	32.6	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
34	<a href="#">c5dxxA_</a>	Alignment	not modelled	32.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> artemisinic aldehyde delta(11(13)) reductase; <b>PDBTitle:</b> crystal structure of dbr2
35	<a href="#">c2gq8A_</a>	Alignment	not modelled	31.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
36	<a href="#">c1zlpA_</a>	Alignment	not modelled	29.9	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
37	<a href="#">c4a3uB_</a>	Alignment	not modelled	29.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
38	<a href="#">d1vjia_</a>	Alignment	not modelled	29.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
39	<a href="#">c3ih1A_</a>	Alignment	not modelled	29.4	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
40	<a href="#">c2h90A_</a>	Alignment	not modelled	29.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
41	<a href="#">d1z41a1</a>	Alignment	not modelled	28.8	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
42	<a href="#">c2ze3A_</a>	Alignment	not modelled	28.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
43	<a href="#">d1s2wa_</a>	Alignment	not modelled	27.1	5	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
44	<a href="#">d1djqa1</a>	Alignment	not modelled	26.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
45	<a href="#">c4df2A_</a>	Alignment	not modelled	26.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> p. stiptitis oye2.6 complexed with p-chlorophenol
46	<a href="#">c2vwtA_</a>	Alignment	not modelled	26.1	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
47	<a href="#">c4b5nA_</a>	Alignment	not modelled	25.4	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
48	<a href="#">d1vyra_</a>	Alignment	not modelled	25.3	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
49	<a href="#">d1gwja_</a>	Alignment	not modelled	24.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
50	<a href="#">d1q45a_</a>	Alignment	not modelled	24.5	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
51	<a href="#">d1oy0a_</a>	Alignment	not modelled	23.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
52	<a href="#">d1ujqa_</a>	Alignment	not modelled	23.7	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
53	<a href="#">c4qnwA_</a>	Alignment	not modelled	23.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chanoclavine-i aldehyde reductase; <b>PDBTitle:</b> crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
54	<a href="#">c3qy6A_</a>	Alignment	not modelled	23.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe; <b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases <b>PDB header:</b> oxidoreductase

55	<a href="#">c3kruC</a>	Alignment	not modelled	21.6	15	<b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from <i>Thermoanaerobacter pseudethanolicus</i> e39
56	<a href="#">d1muma</a>	Alignment	not modelled	20.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
57	<a href="#">c3lyeA</a>	Alignment	not modelled	20.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
58	<a href="#">c3l5aA</a>	Alignment	not modelled	20.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh/flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of a probable nadh-dependent flavin oxidoreductase2 from <i>Staphylococcus aureus</i>
59	<a href="#">c6mywA</a>	Alignment	not modelled	20.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> gluconobacter ene-reductase (gluer) mutant - t36a
60	<a href="#">c4tv6A</a>	Alignment	not modelled	20.1	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyglucarate aldolase; <b>PDBTitle:</b> crystal structure of citrate synthase variant sbng e151q
61	<a href="#">c4mg4G</a>	Alignment	not modelled	19.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from <i>Burkholderia</i> 2 cenocepacia j2315
62	<a href="#">c4rnvD</a>	Alignment	not modelled	19.6	10	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> nadh dehydrogenase 1; <b>PDBTitle:</b> g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
63	<a href="#">c2i6dA</a>	Alignment	not modelled	19.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rna methyltransferase, trmh family; <b>PDBTitle:</b> the structure of a putative rna methyltransferase of the trmh family2 from <i>Porphyromonas gingivalis</i> .
64	<a href="#">c5uncB</a>	Alignment	not modelled	18.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> the crystal structure of phosphoenolpyruvate phosphomutase from <i>Streptomyces platensis</i> subsp. <i>rosaceus</i>
65	<a href="#">c2qiwa</a>	Alignment	not modelled	18.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncg11015, cgl1060) from <i>Corynebacterium glutamicum</i> atcc 13032 at 3.1.80 a resolution
66	<a href="#">c6dvhF</a>	Alignment	not modelled	18.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> lactate 2-monooxygenase; <b>PDBTitle:</b> lactate monooxygenase from <i>Mycobacterium smegmatis</i> - c203a mutant
67	<a href="#">c2hjpA</a>	Alignment	not modelled	17.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with 2 phosphonopyruvate and mg++
68	<a href="#">c1x7pB</a>	Alignment	not modelled	17.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rrna methyltransferase; <b>PDBTitle:</b> crystal structure of the <i>Spo</i> methyltransferase avirb from <i>Streptomyces viridochromogenes</i> in complex with the cofactor adomet
69	<a href="#">d1qk1a2</a>	Alignment	not modelled	17.1	12	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Guanido kinase catalytic domain
70	<a href="#">c6ahuJ</a>	Alignment	not modelled	16.9	21	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p protein subunit p30; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p with mature trna
71	<a href="#">c3i4eA</a>	Alignment	not modelled	16.7	7	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> crystal structure of isocitrate lyase from <i>Burkholderia</i> 2 pseudomallei
72	<a href="#">c3hf3A</a>	Alignment	not modelled	16.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from <i>Thermus scotoductus</i> sa-01
73	<a href="#">c3gkaB</a>	Alignment	not modelled	16.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from <i>Burkholderia pseudomallei</i>
74	<a href="#">d1ps9a1</a>	Alignment	not modelled	16.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
75	<a href="#">c4rnxA</a>	Alignment	not modelled	16.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase 1; <b>PDBTitle:</b> k154 circular permutation of old yellow enzyme
76	<a href="#">c5epdA</a>	Alignment	not modelled	16.1	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol trinitrate reductase; <b>PDBTitle:</b> crystal structure of glycerol trinitrate reductase xdpb from <i>Agrobacterium</i> sp. r89-1 (apo form)
77	<a href="#">c3bh1A</a>	Alignment	not modelled	15.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0371 protein dip2346; <b>PDBTitle:</b> crystal structure of protein dip2346 from <i>Corynebacterium diphtheriae</i>
78	<a href="#">c4mf4F</a>	Alignment	not modelled	15.5	13	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> hpch/hpai aldolase/citrate lyase family protein; <b>PDBTitle:</b> crystal structure of a hpch/hpai aldolase/citrate lyase family protein2 from <i>Burkholderia cenocepacia</i> j2315
79	<a href="#">c5ocsB</a>	Alignment	not modelled	15.5	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-dependent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from <i>Ralstonia (Cupriavidus) metallidurans</i>
80	<a href="#">d3c7bb2</a>	Alignment	not modelled	15.4	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like

						<b>Family:</b> DsrA/DsrB N-terminal-domain-like
81	<a href="#">c6ei9A_</a>	Alignment	not modelled	15.4	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase b; <b>PDBTitle:</b> crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
82	<a href="#">c5kzkA_</a>	Alignment	not modelled	15.4	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna methyltransferase, trmh family; <b>PDBTitle:</b> crystal structure of rna methyltransferase from sinorhizobium2 meliloti
83	<a href="#">c3ffsC_</a>	Alignment	not modelled	15.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
84	<a href="#">c6de6B_</a>	Alignment	not modelled	15.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9
85	<a href="#">c3e5bB_</a>	Alignment	not modelled	15.0	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> 2.4 a crystal structure of isocitrate lyase from brucella melitensis
86	<a href="#">c2v5jB_</a>	Alignment	not modelled	14.6	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
87	<a href="#">c1izcA_</a>	Alignment	not modelled	14.3	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophomate synthase intermolecular diels-alderase; <b>PDBTitle:</b> crystal structure analysis of macrophomate synthase
88	<a href="#">d1izca_</a>	Alignment	not modelled	14.3	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Hpch/Hpai aldolase
89	<a href="#">c3qz6A_</a>	Alignment	not modelled	14.2	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
90	<a href="#">c2wjeA_</a>	Alignment	not modelled	14.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
91	<a href="#">c6daqA_</a>	Alignment	not modelled	14.1	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phdj; <b>PDBTitle:</b> phdj bound to substrate intermediate
92	<a href="#">c3dcpB_</a>	Alignment	not modelled	13.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
93	<a href="#">c2a7nA_</a>	Alignment	not modelled	13.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l(+)-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
94	<a href="#">d1p4ca_</a>	Alignment	not modelled	13.0	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
95	<a href="#">d1igwa_</a>	Alignment	not modelled	13.0	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
96	<a href="#">d1crka2</a>	Alignment	not modelled	12.5	10	<b>Fold:</b> Glutamine synthetase/guanido kinase <b>Superfamily:</b> Glutamine synthetase/guanido kinase <b>Family:</b> Guanido kinase catalytic domain
97	<a href="#">c4e38A_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate <b>PDBTitle:</b> crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
98	<a href="#">d1zj8a1</a>	Alignment	not modelled	12.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
99	<a href="#">c1apyA_</a>	Alignment	not modelled	12.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartylglucosaminidase; <b>PDBTitle:</b> human aspartylglucosaminidase