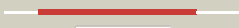























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3072c_(-)_3435795_3436319
Date	Thu Aug 8 16:20:24 BST 2019
Unique Job ID	4fbb415e953a4ae8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3sdoB_</a>	 Alignment		99.9	18	<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
2	<a href="#">c1tvIA_</a>	 Alignment		99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
3	<a href="#">d1tvIA_</a>	 Alignment		99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
4	<a href="#">c5tlcA_</a>	 Alignment		99.9	20	<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
5	<a href="#">c2b81D_</a>	 Alignment		99.9	24	<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
6	<a href="#">c3raoB_</a>	 Alignment		99.9	29	<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.
7	<a href="#">c5w4zA_</a>	 Alignment		99.9	19	<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
8	<a href="#">c3b9nB_</a>	 Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monooxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monooxygenase (lada)
9	<a href="#">d1lucb_</a>	 Alignment		99.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
10	<a href="#">c2i7gA_</a>	 Alignment		99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
11	<a href="#">c5dqpA_</a>	 Alignment		99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> edta monooxygenase; <b>PDBTitle:</b> edta monooxygenase (emoa) from chelativorans sp. bnc1

12	<a href="#">d1luca_</a>	Alignment		99.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
13	<a href="#">d1rhca_</a>	Alignment		99.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
14	<a href="#">c2wgkA_</a>	Alignment		99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monooxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
15	<a href="#">c6friD_</a>	Alignment		99.9	23	<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
16	<a href="#">d1ezwa_</a>	Alignment		99.9	25	<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		99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monooxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
18	<a href="#">c6ak1B_</a>	Alignment		99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monooxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans
19	<a href="#">c3c8nB_</a>	Alignment		99.9	23	<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
20	<a href="#">c1z69D_</a>	Alignment		99.9	25	<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
21	<a href="#">d1f07a_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
22	<a href="#">d1nqka_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
23	<a href="#">c3qy6A_</a>	Alignment	not modelled	67.1	32	<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
24	<a href="#">d1oy0a_</a>	Alignment	not modelled	53.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
25	<a href="#">d1oyaa_</a>	Alignment	not modelled	44.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
26	<a href="#">c2ze3A_</a>	Alignment	not modelled	44.8	19	<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
27	<a href="#">c6ei9A_</a>	Alignment	not modelled	43.9	23	<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)
28	<a href="#">c3bwwA_</a>	Alignment	not modelled	43.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf692/cog3220; <b>PDBTitle:</b> crystal structure of a duf692 family protein (hs 1138)

						from2 haemophilus somnus 129pt at 2.20 a resolution
29	<a href="#">c1zlpA</a>	Alignment	not modelled	43.4	27	<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
30	<a href="#">c5dxxA</a>	Alignment	not modelled	43.0	20	<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
31	<a href="#">d1e8ca2</a>	Alignment	not modelled	41.9	13	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
32	<a href="#">c3e96B</a>	Alignment	not modelled	41.8	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
33	<a href="#">d1z41a1</a>	Alignment	not modelled	41.2	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
34	<a href="#">c4b5nA</a>	Alignment	not modelled	40.8	15	<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 (sy4)
35	<a href="#">c3b0vD</a>	Alignment	not modelled	40.6	23	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
36	<a href="#">c3dcpB</a>	Alignment	not modelled	40.3	24	<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 hsk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
37	<a href="#">c4lsbA</a>	Alignment	not modelled	40.1	24	<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
38	<a href="#">c2h90A</a>	Alignment	not modelled	39.2	25	<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
39	<a href="#">c3lyeA</a>	Alignment	not modelled	38.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
40	<a href="#">d1s2wa</a>	Alignment	not modelled	38.5	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
41	<a href="#">c2wjwA</a>	Alignment	not modelled	38.0	16	<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 steptococcus pneumoniae tigr4.
42	<a href="#">c4a3uB</a>	Alignment	not modelled	37.8	20	<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)
43	<a href="#">c4tmcB</a>	Alignment	not modelled	37.3	20	<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
44	<a href="#">d1vjia</a>	Alignment	not modelled	36.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
45	<a href="#">d1gwja</a>	Alignment	not modelled	36.6	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
46	<a href="#">c2qiwa</a>	Alignment	not modelled	35.8	31	<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 corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
47	<a href="#">c3l5aA</a>	Alignment	not modelled	35.0	15	<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 staphylococcus aureus
48	<a href="#">c3fa4D</a>	Alignment	not modelled	35.0	33	<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
49	<a href="#">c2gq8A</a>	Alignment	not modelled	34.9	25	<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
50	<a href="#">d1muma</a>	Alignment	not modelled	34.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
51	<a href="#">c2yb1A</a>	Alignment	not modelled	34.7	24	<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.
52	<a href="#">d1q45a</a>	Alignment	not modelled	34.2	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
53	<a href="#">d1vyra</a>	Alignment	not modelled	34.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
						<b>PDB header:</b> lyase

54	<a href="#">c5n2pA_</a>	Alignment	not modelled	33.2	17	<b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> sulfobolus solfataricus tryptophan synthase a
55	<a href="#">c4jicB_</a>	Alignment	not modelled	32.7	28	<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
56	<a href="#">c2fptA_</a>	Alignment	not modelled	32.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotate dehydrogenase, mitochondrial; <b>PDBTitle:</b> dual binding mode of a novel series of dhodh inhibitors
57	<a href="#">c4rnxA_</a>	Alignment	not modelled	30.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase 1; <b>PDBTitle:</b> k154 circular permutation of old yellow enzyme
58	<a href="#">d1icpa_</a>	Alignment	not modelled	30.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
59	<a href="#">c3d0cB_</a>	Alignment	not modelled	30.2	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
60	<a href="#">c3gr7A_</a>	Alignment	not modelled	29.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal crystal form
61	<a href="#">c3eooL_</a>	Alignment	not modelled	28.9	27	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
62	<a href="#">c3b8iF_</a>	Alignment	not modelled	28.8	40	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
63	<a href="#">c5uncB_</a>	Alignment	not modelled	28.8	33	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
64	<a href="#">d1m3ua_</a>	Alignment	not modelled	28.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
65	<a href="#">c4rnvD_</a>	Alignment	not modelled	28.3	10	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> nadph dehydrogenase 1; <b>PDBTitle:</b> g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
66	<a href="#">c3kruC_</a>	Alignment	not modelled	28.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
67	<a href="#">c3gkaB_</a>	Alignment	not modelled	28.0	30	<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 from2 burkholderia pseudomallei
68	<a href="#">d1o5ka_</a>	Alignment	not modelled	27.7	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
69	<a href="#">d1djqa1</a>	Alignment	not modelled	27.6	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
70	<a href="#">c6ahuj_</a>	Alignment	not modelled	27.6	19	<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="#">c3na8A_</a>	Alignment	not modelled	27.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
72	<a href="#">c4qnwA_</a>	Alignment	not modelled	26.6	25	<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
73	<a href="#">c6daqA_</a>	Alignment	not modelled	26.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phdj; <b>PDBTitle:</b> phdj bound to substrate intermediate
74	<a href="#">c4df2A_</a>	Alignment	not modelled	26.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dehydrogenase; <b>PDBTitle:</b> p. stiptitis oye2.6 complexed with p-chlorophenol
75	<a href="#">c3w9zA_</a>	Alignment	not modelled	25.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
76	<a href="#">c4ot7A_</a>	Alignment	not modelled	24.9	21	<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
77	<a href="#">d3d1ma1</a>	Alignment	not modelled	24.6	25	<b>Fold:</b> Hedgehog/DD-peptidase <b>Superfamily:</b> Hedgehog/DD-peptidase <b>Family:</b> Hedgehog (development protein), N-terminal signaling domain
78	<a href="#">d1m65a_</a>	Alignment	not modelled	24.5	14	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
79	<a href="#">c6k0aC_</a>	Alignment	not modelled	22.9	0	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease p protein component 3; <b>PDBTitle:</b> cryo-em structure of an archaeal ribonuclease p
80	<a href="#">d1ps9a1</a>	Alignment	not modelled	22.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases

					Family:FMN-linked oxidoreductases
81	<a href="#">c3ih1A_</a>	Alignment	not modelled	22.8	16 <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
82	<a href="#">c3m1nB_</a>	Alignment	not modelled	22.5	25 <b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> sonic hedgehog protein; <b>PDBTitle:</b> crystal structure of human sonic hedgehog n-terminal domain
83	<a href="#">c3bh1A_</a>	Alignment	not modelled	22.5	45 <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 corynebacterium diphtheriae
84	<a href="#">c3i4eA_</a>	Alignment	not modelled	21.2	13 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> crystal structure of isocitrate lyase from burkholderia2 pseudomallei
85	<a href="#">c6agzA_</a>	Alignment	not modelled	20.8	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> old yellow enzyme; <b>PDBTitle:</b> crystal structure of old yellow enzyme from pichia sp. aku4542
86	<a href="#">d1o66a_</a>	Alignment	not modelled	20.7	37 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
87	<a href="#">c6mywA_</a>	Alignment	not modelled	20.7	20 <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
88	<a href="#">d2ibge1</a>	Alignment	not modelled	20.4	25 <b>Fold:</b> Hedgehog/DD-peptidase <b>Superfamily:</b> Hedgehog/DD-peptidase <b>Family:</b> Hedgehog (development protein), N-terminal signaling domain
89	<a href="#">c6de6B_</a>	Alignment	not modelled	20.4	15 <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
90	<a href="#">c1ydnA_</a>	Alignment	not modelled	20.3	17 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
91	<a href="#">c5epdA_</a>	Alignment	not modelled	19.8	20 <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 from2 agrobacterium sp. r89-1 (apo form)
92	<a href="#">d1yxya1</a>	Alignment	not modelled	19.8	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> NanE-like
93	<a href="#">c2w9mB_</a>	Alignment	not modelled	19.3	24 <b>PDB header:</b> dna replication <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from deinococcus2 radiodurans
94	<a href="#">c3eb2A_</a>	Alignment	not modelled	18.5	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
95	<a href="#">c3e0fA_</a>	Alignment	not modelled	18.3	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphoesterase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
96	<a href="#">c3vsjA_</a>	Alignment	not modelled	18.1	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-5-chlorophenol 1,6-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
97	<a href="#">c3hf3A_</a>	Alignment	not modelled	18.1	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
98	<a href="#">c5ocsB_</a>	Alignment	not modelled	17.8	22 <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 ralstonia (cupriavidus) metallidurans
99	<a href="#">c4gx9A_</a>	Alignment	not modelled	17.6	14 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii <b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon chimera