Phyre2

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Description	RVBD3618_(-)_4058877_4060064
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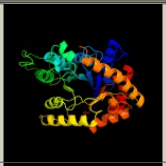
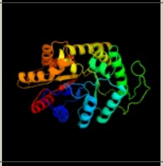
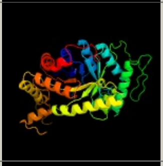
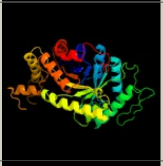
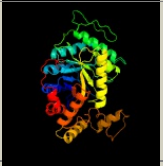
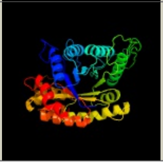
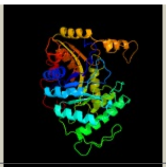
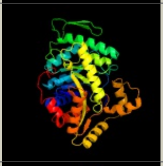
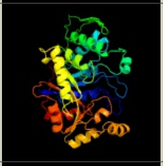
Unique Job ID	4b29a0ffa58394b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1luca_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
2	c2wgkA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3,6-diketocamphane 1,6 monooxygenase; **PDBTitle:** type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
3	c2i7gA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
4	d1lucb_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
5	c6friD_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alkanal monooxygenase beta chain; **PDBTitle:** structure of luxb from photobacterium leiognathi
6	c5tlcA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dibenzothiophene desulfurization enzyme a; **PDBTitle:** crystal structure of bdsa from bacillus subtilis wu-s2b
7	d1tvla_	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
8	c1tvlA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein ytnj; **PDBTitle:** structure of ytnj from bacillus subtilis
9	c3raoB_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative luciferase-like monooxygenase; **PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
10	c3sdoB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
11	d1ezwa_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases

12	c3b9nB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
13	c5w4zA_	Alignment		100.0	20	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**riboflavin lyase; **PDBTitle:** crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
14	c5dqpA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**edta monooxygenase; **PDBTitle:** edta monooxygenase (emoa) from chelativorans sp. bnc1
15	c1z69D_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)- **PDBTitle:** crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
16	d1nqka_	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
17	c5wanA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrimidine monooxygenase ruta; **PDBTitle:** crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
18	c6ak1B_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dimethyl-sulfide monooxygenase; **PDBTitle:** crystal structure of dmoa from hyphomicrobium sulfonivorans
19	d1f07a_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
20	c3c8nB_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable f420-dependent glucose-6-phosphate dehydrogenase **PDBTitle:** crystal structure of apo-fgd1 from mycobacterium tuberculosis
21	d1rhca_	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
22	c2b81D_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**luciferase-like monooxygenase; **PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
23	d1nfpa_	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	99.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
25	c4xkyC_	Alignment	not modelled	88.2	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
26	c2infB_	Alignment	not modelled	83.9	6	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
27	d1r3sa_	Alignment	not modelled	79.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
28	c4exqA_	Alignment	not modelled	78.8	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264

29	c2ejaB_	Alignment	not modelled	78.7	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
30	c3b4uB_	Alignment	not modelled	77.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
31	d1j93a_	Alignment	not modelled	74.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
32	c1jpkA_	Alignment	not modelled	73.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
33	c3cyvA_	Alignment	not modelled	72.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
34	c3qy6A_	Alignment	not modelled	72.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe; **PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
35	c4uxdC_	Alignment	not modelled	62.7	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- **PDBTitle:** 2-keto 3-deoxygluconate aldolase from picrophilus torridus
36	c3d0cB_	Alignment	not modelled	62.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
37	c2w1vA_	Alignment	not modelled	59.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
38	c4zr8B_	Alignment	not modelled	59.4	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
39	c5ud6B_	Alignment	not modelled	58.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dhdps from cyanidioschyzon merolae with lysine2 bound
40	c3lciA_	Alignment	not modelled	58.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
41	c3si9B_	Alignment	not modelled	56.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
42	c3vniC_	Alignment	not modelled	54.3	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**xylose isomerase domain protein tim barrel; **PDBTitle:** crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
43	d1xkya1	Alignment	not modelled	53.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	c6h4eB_	Alignment	not modelled	52.4	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative n-acetylneuraminate lyase; **PDBTitle:** proteus mirabilis n-acetylneuraminate lyase
45	c3cprB_	Alignment	not modelled	52.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
46	c3eb2A_	Alignment	not modelled	51.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
47	c1ypxA_	Alignment	not modelled	49.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative vitamin-b12 independent methionine synthase family **PDBTitle:** crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
48	c2a7nA_	Alignment	not modelled	48.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
49	c2yxgD_	Alignment	not modelled	48.6	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
50	c4i7vD_	Alignment	not modelled	48.4	11	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** agrobacterium tumefaciens dhdps with pyruvate
51	d1p4ca_	Alignment	not modelled	48.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
52	d1hl2a_	Alignment	not modelled	46.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
53	c5k9hA_	Alignment	not modelled	45.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**0940_gh29; **PDBTitle:** crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium

54	c3kwsB_	Alignment	not modelled	44.7	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
55	c3noeA_	Alignment	not modelled	44.0	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
56	c3lerA_	Alignment	not modelled	43.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
57	c2v9dB_	Alignment	not modelled	42.1	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
58	d1f74a_	Alignment	not modelled	39.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	c3pueA_	Alignment	not modelled	39.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
60	c4dppB_	Alignment	not modelled	37.3	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase 2, chloroplastic; **PDBTitle:** the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
61	c3ilvA_	Alignment	not modelled	36.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
62	c2ehhE_	Alignment	not modelled	36.5	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
63	c3s5oA_	Alignment	not modelled	36.1	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
64	c4ah7C_	Alignment	not modelled	35.2	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** structure of wild type stapylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
65	c3na8A_	Alignment	not modelled	35.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
66	c2wjeA_	Alignment	not modelled	34.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
67	c5afdA_	Alignment	not modelled	32.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** native structure of n-acetylneuramininate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
68	d1r46a2	Alignment	not modelled	32.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	c3e96B_	Alignment	not modelled	32.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
70	c3dz1A_	Alignment	not modelled	32.4	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
71	c4nq1B_	Alignment	not modelled	32.1	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**4-hydroxy-tetrahydrodipicolinate synthase; **PDBTitle:** legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
72	d1f89a_	Alignment	not modelled	32.0	11	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
73	c5c54D_	Alignment	not modelled	31.7	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase/n-acetylneuraminate lyase; **PDBTitle:** crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
74	c4ay8B_	Alignment	not modelled	31.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methylcobalamin\: coenzyme m methyltransferase; **PDBTitle:** semet-derivative of a methyltransferase from m. mazei
75	c3lmzA_	Alignment	not modelled	30.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
76	c3bh1A_	Alignment	not modelled	30.7	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
77	c4lsbA_	Alignment	not modelled	29.3	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lyase/mutase; **PDBTitle:** crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**f5/8 type c domain protein;

78	c4zrxA_	Alignment	not modelled	29.3	17	**PDBTitle:** crystal structure of a putative alpha-l-fucosidase (bacova_04357) from2 bacteroides ovatus atcc 8483 at 1.59 a resolution
79	c3dcpB_	Alignment	not modelled	28.6	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol-phosphatase; **PDBTitle:** crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
80	c4k3zA_	Alignment	not modelled	28.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-erythrulose 4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
81	c3fluD_	Alignment	not modelled	27.8	8	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
82	d1hl9a2	Alignment	not modelled	27.6	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
83	c3bi8A_	Alignment	not modelled	27.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
84	c3wqoB_	Alignment	not modelled	26.7	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj1311; **PDBTitle:** crystal structure of d-tagatose 3-epimerase-like protein
85	c2qw5B_	Alignment	not modelled	26.6	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
86	c6k0aC_	Alignment	not modelled	26.5	15	**PDB header:**rna binding protein/rna **Chain:** C: **PDB Molecule:**ribonuclease p protein component 3; **PDBTitle:** cryo-em structure of an archaeal ribonuclease p
87	d2a6na1	Alignment	not modelled	26.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
88	d1xxxa1	Alignment	not modelled	25.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
89	c6arhA_	Alignment	not modelled	25.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** crystal structure of human nal at a resolution of 1.6 angstrom
90	c1bplA_	Alignment	not modelled	25.2	13	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
91	c2yb1A_	Alignment	not modelled	25.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
92	c3h5dD_	Alignment	not modelled	24.7	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
93	c5ktlA_	Alignment	not modelled	23.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-tetrahydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
94	c3noyA_	Alignment	not modelled	23.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
95	d1goxa_	Alignment	not modelled	23.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
96	c3fkkA_	Alignment	not modelled	23.2	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
97	c3rpdB_	Alignment	not modelled	22.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methionine synthase (b12-independent); **PDBTitle:** the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
98	c4b5nA_	Alignment	not modelled	22.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
99	c2hmcA_	Alignment	not modelled	21.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
100	c4a3uB_	Alignment	not modelled	21.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadh\:flavin oxidoreductase/nadh oxidase; **PDBTitle:** x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
101	d1mkza_	Alignment	not modelled	20.9	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
102	c6mqhA_	Alignment	not modelled	20.6	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-tetrahydrodipicolinate synthase; **PDBTitle:** crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
103	d2f6ua1	Alignment	not modelled	20.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases

						Family:FMN-linked oxidoreductases
104	c4icnB_	Alignment	not modelled	20.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from shewanella benthica