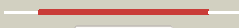
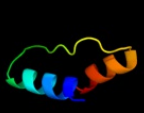


Phyre2

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Description	P80645
Date	Thu Jan 5 12:33:15 GMT 2012
Unique Job ID	5917a49f1847ac43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlnqka_	 Alignment		100.0	98	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
2	c3raoB_	 Alignment		100.0	29	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.
3	c3sdoB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
4	c3b9nB_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
5	d1tvla_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
6	c1tvla_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
7	d1ezwa_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
8	d1luca_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
9	c1z69D_	 Alignment		100.0	20	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
10	c2wgkA_	 Alignment		100.0	16	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
11	d1lucb_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)

12	dlrhca_	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
13	c2i7gA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
14	dlf07a_	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
15	c3c8nB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
16	c2b81D_	Alignment		100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus cereus
17	dlnfpa_	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
18	dlfvpa_	Alignment		99.3	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
19	dlmuma_	Alignment		91.5	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
20	clzlpA_	Alignment		91.4	19	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming 2 a thiohemiacetal adduct
21	c3fa4D_	Alignment	not modelled	91.3	28	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate 2 lyase superfamily member, triclinic crystal form
22	c3eool_	Alignment	not modelled	91.2	19	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from burkholderia pseudomallei
23	c3lyeA_	Alignment	not modelled	91.0	24	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
24	dlujqa_	Alignment	not modelled	90.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
25	c2ze3A_	Alignment	not modelled	89.9	17	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus fuscus
26	c3b8iF_	Alignment	not modelled	89.8	25	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
27	c2qiwa_	Alignment	not modelled	89.5	19	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at 1.80 a resolution
28	c3ih1A_	Alignment	not modelled	89.4	19	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase;

28	csm1A_	Alignment	not modelled	85.4	19	PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
29	d1s2wa_	Alignment	not modelled	83.1	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
30	c2hjpA_	Alignment	not modelled	78.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
31	c1rcxH_	Alignment	not modelled	65.0	13	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
32	d2d69a1	Alignment	not modelled	59.5	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
33	d1jpdx1	Alignment	not modelled	57.7	12	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
34	c1ydnA_	Alignment	not modelled	55.7	17	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
35	c3qy6A_	Alignment	not modelled	54.3	17	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
36	d1jpmal	Alignment	not modelled	52.4	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
37	d2fiqa1	Alignment	not modelled	50.4	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
38	c3bg5C_	Alignment	not modelled	50.0	14	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate2 carboxylase
39	c2ftpA_	Alignment	not modelled	48.5	17	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
40	c3ivuB_	Alignment	not modelled	46.5	17	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
41	c2cw6B_	Alignment	not modelled	40.9	9	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
42	d1ej7l1	Alignment	not modelled	40.6	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
43	c3ez4B_	Alignment	not modelled	40.1	16	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
44	c1rr2A_	Alignment	not modelled	38.2	7	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
45	d1tza1	Alignment	not modelled	35.8	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
46	c3cixA_	Alignment	not modelled	35.5	11	PDB header: adomet binding protein Chain: A: PDB Molecule: ifefe-hydrogenase maturase; PDBTitle: x-ray structure of the [ife]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
47	c1ydoC_	Alignment	not modelled	35.2	9	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
48	d7reqb2	Alignment	not modelled	33.6	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
49	d2gl5a1	Alignment	not modelled	33.2	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
50	d1m3ua_	Alignment	not modelled	33.0	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
51	c3bleA_	Alignment	not modelled	32.8	7	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
52	c3pueA_	Alignment	not modelled	32.6	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
						PDB header: hydrolase

53	c2wjeA	Alignment	not modelled	31.0	10	Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
54	c2nx9B	Alignment	not modelled	30.0	9	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
55	c3e02A	Alignment	not modelled	29.8	14	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
56	d1nvma2	Alignment	not modelled	29.5	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
57	d1xxa1	Alignment	not modelled	29.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	d2noca1	Alignment	not modelled	29.3	22	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
59	d1r3sa	Alignment	not modelled	29.1	7	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
60	c1jpkA	Alignment	not modelled	29.0	7	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
61	c1zfjA	Alignment	not modelled	28.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
62	d1uoka2	Alignment	not modelled	28.8	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
63	d1m53a2	Alignment	not modelled	28.1	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
64	c1rldB	Alignment	not modelled	27.8	12	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
65	d1o5ka	Alignment	not modelled	27.6	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
66	d1j93a	Alignment	not modelled	27.5	22	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
67	d8ruca1	Alignment	not modelled	27.5	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
68	c2d69B	Alignment	not modelled	27.0	13	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
69	d1ht6a2	Alignment	not modelled	25.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	d1bxna1	Alignment	not modelled	25.6	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
71	c2ejaB	Alignment	not modelled	24.5	12	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
72	d1geha1	Alignment	not modelled	24.4	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
73	d1lwha2	Alignment	not modelled	24.1	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
74	d1wdda1	Alignment	not modelled	24.1	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
75	c1bf2A	Alignment	not modelled	22.8	15	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
76	d1gxha	Alignment	not modelled	22.7	33	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
77	d1igwa	Alignment	not modelled	22.3	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
78	d2a6na1	Alignment	not modelled	21.8	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase;

79	c2hl2A_	Alignment	not modelled	21.2	17	PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
80	c2ekcA_	Alignment	not modelled	21.2	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
81	d1g5aa2	Alignment	not modelled	21.1	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	d1rbla1	Alignment	not modelled	21.0	9	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
83	c3noeA_	Alignment	not modelled	20.9	18	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
84	c1nvmG_	Alignment	not modelled	20.4	12	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
85	c3lerA_	Alignment	not modelled	20.3	13	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
86	c2infB_	Alignment	not modelled	19.9	12	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
87	d1jdfa1	Alignment	not modelled	19.8	23	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
88	d1veya1	Alignment	not modelled	19.7	18	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
89	c3cyvA_	Alignment	not modelled	19.4	15	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexneri: new insights into its catalytic3 mechanism
90	c3c6cA_	Alignment	not modelled	19.3	10	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
91	c2ze0A_	Alignment	not modelled	19.2	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
92	d1oyaa_	Alignment	not modelled	19.1	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
93	c3eegB_	Alignment	not modelled	19.0	18	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
94	c3chvA_	Alignment	not modelled	18.8	10	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
95	d2gjpa2	Alignment	not modelled	18.4	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	c2y7eA_	Alignment	not modelled	18.2	12	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
97	d1ua7a2	Alignment	not modelled	17.8	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	c3ewbX_	Alignment	not modelled	17.5	18	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
99	d1vjia_	Alignment	not modelled	16.9	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases