Phyre^2

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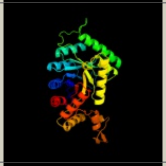
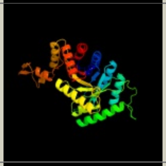
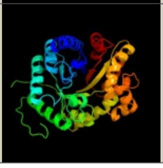
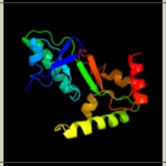
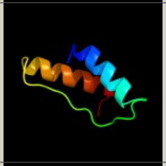
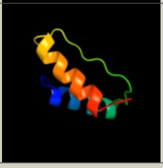
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1luca_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
2	d1lucb_	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
3	c2wgkA_	Alignment		100.0	17	**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
4	c2i7gA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
5	c3raoB_	Alignment		100.0	15	**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.
6	c1tvlA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein ytnj; **PDBTitle:** structure of ytnj from bacillus subtilis
7	d1tvla_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
8	c3sdoB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
9	d1ezwa_	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
10	d1f07a_	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
11	c1z69D_	Alignment		100.0	14	**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

12	d1nqka_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
13	d1rhca_	Alignment		100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
14	c3c8nB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable f420-dependent glucose-6-phosphate dehydrogenase **PDBTitle:** crystal structure of apo-fgd1 from mycobacterium tuberculosis
15	c2b81D_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**luciferase-like monooxygenase; **PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
16	c3b9nB_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
17	d1nfpa_	Alignment		99.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
18	d1fvpa_	Alignment		99.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
19	d1jpma1	Alignment		85.4	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
20	d1jdfa1	Alignment		79.7	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
21	c3qy6A_	Alignment	not modelled	77.6	27	**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
22	d1tzza1	Alignment	not modelled	77.2	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
23	c3d0cB_	Alignment	not modelled	76.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
24	c1ypxA_	Alignment	not modelled	75.0	6	**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
25	d1o5ka_	Alignment	not modelled	74.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
26	d1j93a_	Alignment	not modelled	72.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
27	c3rpdB_	Alignment	not modelled	71.9	19	**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.
28	c3na8A_	Alignment	not modelled	67.0	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase;

28	c3na8A_	Alignment	not modelled	67.0	12	**PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
29	c3e96B_	Alignment	not modelled	66.6	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
30	c2ehhE_	Alignment	not modelled	66.6	8	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
31	d1r3sa_	Alignment	not modelled	65.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
32	c1jpkA_	Alignment	not modelled	64.7	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
33	c2r8wB_	Alignment	not modelled	64.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
34	d1u1ha2	Alignment	not modelled	60.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
35	d1bqga1	Alignment	not modelled	60.7	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
36	c2yxgD_	Alignment	not modelled	59.3	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
37	d1liua2	Alignment	not modelled	58.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
38	c2infB_	Alignment	not modelled	57.7	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
39	c3si9B_	Alignment	not modelled	57.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
40	c2ejaB_	Alignment	not modelled	57.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
41	d1jpdx1	Alignment	not modelled	56.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
42	c3lerA_	Alignment	not modelled	56.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
43	c3pueA_	Alignment	not modelled	55.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dihydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
44	c3fkkA_	Alignment	not modelled	55.0	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
45	c2a7nA_	Alignment	not modelled	52.0	15	**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
46	d1a3xa2	Alignment	not modelled	50.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
47	c2oztA_	Alignment	not modelled	50.6	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tlr1174 protein; **PDBTitle:** crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
48	c3cprB_	Alignment	not modelled	50.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
49	c2vc6A_	Alignment	not modelled	49.7	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
50	c1jvnB_	Alignment	not modelled	48.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hisHF; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
51	d2a6na1	Alignment	not modelled	48.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
52	d2g50a2	Alignment	not modelled	48.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
53	c3hkxA_	Alignment	not modelled	47.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
						PDB header:lyase

54	c3g0sA_	Alignment	not modelled	47.9	11	**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
55	d1xxxa1	Alignment	not modelled	47.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
56	c3cyvA_	Alignment	not modelled	47.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
57	d1p4ca_	Alignment	not modelled	46.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
58	d2gdqa1	Alignment	not modelled	45.6	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
59	c2qddA_	Alignment	not modelled	44.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of a member of enolase superfamily from roseovarius2 nubinhibens ism
60	c1zfjA_	Alignment	not modelled	44.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
61	c3kwsB_	Alignment	not modelled	44.5	27	**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
62	c2v9dB_	Alignment	not modelled	43.2	14	**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
63	c3eb2A_	Alignment	not modelled	42.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
64	d1rvka1	Alignment	not modelled	42.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
65	d2d69a1	Alignment	not modelled	41.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
66	c2e28A_	Alignment	not modelled	40.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
67	d2noca1	Alignment	not modelled	40.0	17	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
68	c3eoeC_	Alignment	not modelled	39.8	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
69	c2nq5A_	Alignment	not modelled	39.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of methyltransferase from streptococcus2 mutans
70	c3bi8A_	Alignment	not modelled	38.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
71	c3e0vB_	Alignment	not modelled	38.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
72	d1uoka2	Alignment	not modelled	37.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c3fluD_	Alignment	not modelled	36.9	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
74	c3n2xB_	Alignment	not modelled	36.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
75	c2wjeA_	Alignment	not modelled	36.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
76	c3msyC_	Alignment	not modelled	36.5	2	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
77	c3ma8A_	Alignment	not modelled	36.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
78	c2vgbB_	Alignment	not modelled	35.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
79	c1a3wB_	Alignment	not modelled	35.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase;

						PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
80	c1u22A_	Alignment	not modelled	34.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
81	c1pklB_	Alignment	not modelled	33.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
82	c3noeA_	Alignment	not modelled	33.7	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
83	d1pkla2	Alignment	not modelled	33.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
84	c3lciA_	Alignment	not modelled	31.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
85	c1t5aB_	Alignment	not modelled	30.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
86	c2d69B_	Alignment	not modelled	30.7	8	**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)
87	c2qgyA_	Alignment	not modelled	30.3	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
88	d1pv8a_	Alignment	not modelled	30.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
89	c2rfgB_	Alignment	not modelled	30.0	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
90	c2rdxG_	Alignment	not modelled	29.7	13	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, putative; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from roseovarius nubinhibens ism
91	c1t7lA_	Alignment	not modelled	29.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of cobalamin-independent methionine2 synthase from t. maritima
92	d1f74a_	Alignment	not modelled	29.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
93	c3my9A_	Alignment	not modelled	29.0	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase; **PDBTitle:** crystal structure of a muconate cycloisomerase from azorhizobium2 caulinodans
94	d1m53a2	Alignment	not modelled	28.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	c3dcpB_	Alignment	not modelled	28.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol-phosphatase; **PDBTitle:** crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141.
96	c3k1dA_	Alignment	not modelled	28.5	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
97	c3cnyA_	Alignment	not modelled	28.4	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
98	c2gdqB_	Alignment	not modelled	27.4	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yitf; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from bacillus subtilis at 1.8 a resolution
99	c1bf2A_	Alignment	not modelled	27.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
100	c2r94B_	Alignment	not modelled	27.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
101	d1x7fa2	Alignment	not modelled	27.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
102	d1xkya1	Alignment	not modelled	26.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
103	c2yb1A_	Alignment	not modelled	26.1	21	**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.

104	d1uf5a_	Alignment	not modelled	26.0	18	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
105	c3e0fA_	Alignment	not modelled	26.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase; **PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
106	c1m7xC_	Alignment	not modelled	25.8	4	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
107	d1oyaa_	Alignment	not modelled	25.0	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
108	c2qdeA_	Alignment	not modelled	24.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
109	c2gq8A_	Alignment	not modelled	23.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, fmn-binding; **PDBTitle:** structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
110	c3daqB_	Alignment	not modelled	23.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
111	c1aqfB_	Alignment	not modelled	23.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
112	c3ucqA_	Alignment	not modelled	23.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
113	c3ik4A_	Alignment	not modelled	23.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
114	c2ze0A_	Alignment	not modelled	22.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
115	d1cgta4	Alignment	not modelled	22.8	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c3h5dD_	Alignment	not modelled	22.7	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
117	d1w3ia_	Alignment	not modelled	22.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
118	d1hl2a_	Alignment	not modelled	22.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
119	d1ykwa1	Alignment	not modelled	22.3	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
120	d1q45a_	Alignment	not modelled	21.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases