Phyre2

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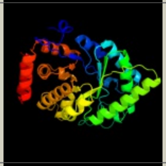
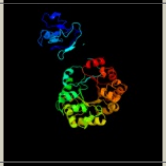
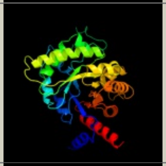
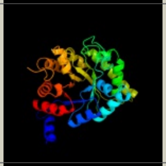
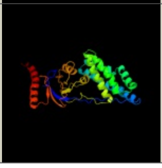
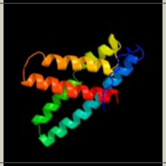
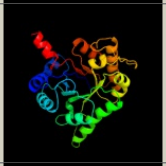
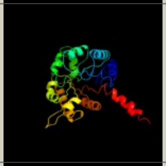
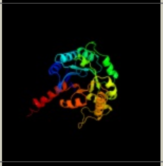
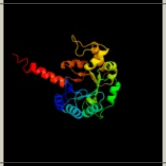
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hwgA_	Alignment		100.0	97	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
2	c2hroA_	Alignment		100.0	52	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
3	c1h6zA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
4	c1kblA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
5	c2bg5C_	Alignment		100.0	58	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
6	c1vbhA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
7	c2olsA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
8	d1h6za1	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
9	d1vbga1	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
10	d1kbla1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
11	c1ezaA_	Alignment		100.0	100	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure

12	d1zyma2		Alignment		99.9	96	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
13	d1zyma1		Alignment		99.9	100	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
14	d1dxea_		Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
15	c3qz6A_		Alignment		99.9	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
16	d1izca_		Alignment		99.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
17	c1izcA_		Alignment		99.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
18	d1vbga2		Alignment		99.8	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
19	c2v5jB_		Alignment		99.8	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
20	d1h6za2		Alignment		99.8	23	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
21	d1kbla2		Alignment	not modelled	99.8	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
22	c2vwtA_		Alignment	not modelled	99.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
23	c3t07D_		Alignment	not modelled	99.5	18	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
24	c2e28A_		Alignment	not modelled	99.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
25	c3qqwC_		Alignment	not modelled	99.4	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**putative citrate lyase; **PDBTitle:** crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
26	c1sgjB_		Alignment	not modelled	99.3	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
27	d1sgja_		Alignment	not modelled	99.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
28	d1e0ta2		Alignment	not modelled	99.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
							Fold:TIM beta/alpha-barrel

29	d2g50a2	Alignment	not modelled	99.2	16	**Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
30	d1a3xa2	Alignment	not modelled	99.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
31	d1pkla2	Alignment	not modelled	99.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
32	c3r4iB_	Alignment	not modelled	99.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
33	d1liua2	Alignment	not modelled	99.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
34	c1u5vA_	Alignment	not modelled	99.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
35	d1u5ha_	Alignment	not modelled	99.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
36	c3cuzA_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase a; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
37	c3qllB_	Alignment	not modelled	98.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of ripc from yersinia pestis
38	c3cuxA_	Alignment	not modelled	98.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
39	c2vgbB_	Alignment	not modelled	98.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
40	c3ma8A_	Alignment	not modelled	98.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
41	c3eoeC_	Alignment	not modelled	98.1	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
42	c3pugA_	Alignment	not modelled	97.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
43	c1e0tD_	Alignment	not modelled	97.9	15	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
44	c1aqfB_	Alignment	not modelled	97.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
45	c1t5aB_	Alignment	not modelled	97.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
46	c3e0vB_	Alignment	not modelled	97.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
47	c1a3wB_	Alignment	not modelled	97.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
48	c1pklB_	Alignment	not modelled	97.6	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
49	d1d8ca_	Alignment	not modelled	97.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
50	c3khdC_	Alignment	not modelled	96.7	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
51	c2zbtB_	Alignment	not modelled	95.3	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
52	c2nv2U_	Alignment	not modelled	94.8	23	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
53	c3femB_	Alignment	not modelled	94.6	22	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
54	d1eepa_	Alignment	not modelled	94.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
55	c2a7rD_	Alignment	not modelled	93.6	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2;

		Alignment	not modelled			**PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
56	d1vrda1	Alignment	not modelled	92.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
57	d1jr1a1	Alignment	not modelled	92.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
58	c3odmE_	Alignment	not modelled	92.0	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
59	d1n8ia_	Alignment	not modelled	91.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
60	d2hi6a1	Alignment	not modelled	91.7	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
61	c3r2gA_	Alignment	not modelled	91.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
62	c1vrdA_	Alignment	not modelled	90.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
63	d1zfja1	Alignment	not modelled	89.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
64	c3khjE_	Alignment	not modelled	88.5	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
65	c1jcnA_	Alignment	not modelled	87.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase i; **PDBTitle:** binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
66	d1tb3a1	Alignment	not modelled	87.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
67	c3qjaA_	Alignment	not modelled	86.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
68	d1pvna1	Alignment	not modelled	86.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
69	c3pm6B_	Alignment	not modelled	86.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
70	d1jcna1	Alignment	not modelled	83.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
71	c2yzrB_	Alignment	not modelled	82.9	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
72	c2vc6A_	Alignment	not modelled	82.3	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
73	d2cu0a1	Alignment	not modelled	79.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
74	d2gp4a1	Alignment	not modelled	77.4	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
75	c1ypfB_	Alignment	not modelled	77.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
76	c2e77B_	Alignment	not modelled	75.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
77	c2zrvC_	Alignment	not modelled	74.9	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
78	d1goxa_	Alignment	not modelled	74.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
79	d1o5ka_	Alignment	not modelled	74.5	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
						PDB header:transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative;

80	c2f7iA_	Alignment	not modelled	73.7	17	**PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
81	c2rduA_	Alignment	not modelled	72.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
82	c2gp4A_	Alignment	not modelled	71.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
83	c3n2xB_	Alignment	not modelled	70.9	15	**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
84	d1j93a_	Alignment	not modelled	70.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
85	c2qr6A_	Alignment	not modelled	69.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase; **PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
86	c1me9A_	Alignment	not modelled	68.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
87	c3s5oA_	Alignment	not modelled	68.6	14	**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
88	c3lerA_	Alignment	not modelled	68.5	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
89	d1a53a_	Alignment	not modelled	68.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
90	c3pueA_	Alignment	not modelled	68.3	21	**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
91	d1qapa1	Alignment	not modelled	67.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
92	c2cu0B_	Alignment	not modelled	66.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
93	c3lciA_	Alignment	not modelled	64.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
94	c2ehhE_	Alignment	not modelled	63.8	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
95	d1hl2a_	Alignment	not modelled	62.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
96	c3na8A_	Alignment	not modelled	62.5	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
97	c2a7nA_	Alignment	not modelled	61.5	19	**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
98	c3dz1A_	Alignment	not modelled	60.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
99	c2c3zA_	Alignment	not modelled	60.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
100	c2pkpA_	Alignment	not modelled	60.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
101	c3cprB_	Alignment	not modelled	58.7	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
102	d1xxxa1	Alignment	not modelled	58.1	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
103	c3iz5H_	Alignment	not modelled	57.9	34	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l7a (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
104	d1qpoa1	Alignment	not modelled	57.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like

						Family: NadC C-terminal domain-like
105	c2rfgB_	Alignment	not modelled	57.2	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
106	c2r8wB_	Alignment	not modelled	56.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
107	c2v9dB_	Alignment	not modelled	56.4	15	**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
108	c3daqB_	Alignment	not modelled	55.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
109	c1zfjA_	Alignment	not modelled	55.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
110	d1v7la_	Alignment	not modelled	55.0	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
111	c1kbiB_	Alignment	not modelled	54.6	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome b2; **PDBTitle:** crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
112	c3ke8A_	Alignment	not modelled	54.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
113	c2yxgD_	Alignment	not modelled	54.1	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
114	c2cdh1_	Alignment	not modelled	54.0	18	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
115	c2zkrf_	Alignment	not modelled	54.0	29	**PDB header:**ribosomal protein/rna **Chain:** F: **PDB Molecule:**rna expansion segment es7 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
116	c1x1oC_	Alignment	not modelled	52.5	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
117	c2vy9A_	Alignment	not modelled	52.4	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
118	c3noeA_	Alignment	not modelled	52.1	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
119	d1o4ua1	Alignment	not modelled	50.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
120	c3izcH_	Alignment	not modelled	50.1	29	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein rpl8 (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome