Phyre^2

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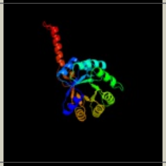
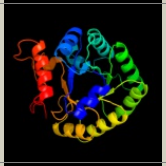
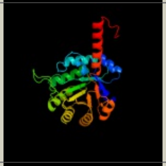
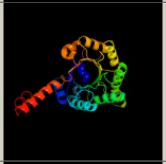
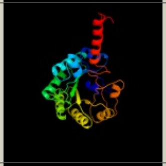
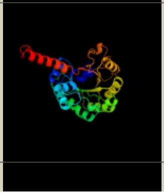
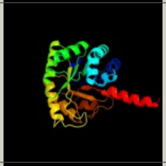
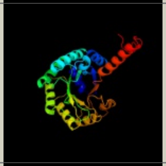
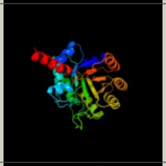
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m3ua_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
2	d1o66a_	Alignment		100.0	51	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
3	d1oy0a_	Alignment		100.0	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
4	c3ez4B_	Alignment		100.0	54	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
5	c1zlpA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
6	d1muma_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
7	d1ujqa_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
8	c2ze3A_	Alignment		100.0	16	**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 ficus
9	c3eooL_	Alignment		100.0	14	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
10	c3ih1A_	Alignment		100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
11	c2hjpA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++

12	c3b8iF_	Alignment		100.0	18	**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+.
13	c2qiwA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
14	c3fa4D_	Alignment		100.0	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
15	c3lyeA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
16	d1s2wa_	Alignment		100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
17	d1f61a_	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
18	c3e5bB_	Alignment		100.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
19	d1igwa_	Alignment		99.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
20	d1dqua_	Alignment		99.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
21	d1xcfa_	Alignment	not modelled	98.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	d2p10a1	Alignment	not modelled	98.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
23	c2p10D_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
24	d1gvfa_	Alignment	not modelled	97.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
25	c3navB_	Alignment	not modelled	97.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
26	c2z6jB_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trans-2-enoyl-acp reductase ii; **PDBTitle:** crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
27	d1qopa_	Alignment	not modelled	97.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
28	d1xm3a_	Alignment	not modelled	97.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
						PDB header:isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin

29	c2eq5D_	Alignment	not modelled	97.1	17	racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
30	c2gjlA_	Alignment	not modelled	97.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
31	c3pm6B_	Alignment	not modelled	97.1	17	**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
32	d1rd5a_	Alignment	not modelled	97.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
33	c3igsB_	Alignment	not modelled	96.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
34	c3q94B_	Alignment	not modelled	96.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
35	c3bw2A_	Alignment	not modelled	96.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
36	d1rvga_	Alignment	not modelled	96.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
37	c2iswB_	Alignment	not modelled	96.7	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
38	c2h90A_	Alignment	not modelled	96.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
39	c2htmB_	Alignment	not modelled	96.6	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
40	d1jpma1	Alignment	not modelled	96.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
41	d1vzwa1	Alignment	not modelled	96.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
42	d1wv2a_	Alignment	not modelled	96.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
43	c1zfjA_	Alignment	not modelled	96.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
44	c1jvnB_	Alignment	not modelled	96.3	23	**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
45	c3elfA_	Alignment	not modelled	96.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
46	c3lerA_	Alignment	not modelled	96.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
47	c2rfgB_	Alignment	not modelled	96.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
48	d1h5ya_	Alignment	not modelled	96.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
49	c3hf3A_	Alignment	not modelled	96.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
50	c3ffsC_	Alignment	not modelled	96.1	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
51	c3qm3C_	Alignment	not modelled	96.1	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
52	c3c52B_	Alignment	not modelled	96.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
53	c2r94B_	Alignment	not modelled	96.0	25	**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

54	d1gwja_	Alignment	not modelled	96.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
55	c3bo9B_	Alignment	not modelled	95.9	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase; **PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
56	c3daqB_	Alignment	not modelled	95.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
57	c1jcnA_	Alignment	not modelled	95.9	19	**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
58	c2qjhH_	Alignment	not modelled	95.8	14	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
59	d1dosa_	Alignment	not modelled	95.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
60	d1vyra_	Alignment	not modelled	95.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
61	c3n2xB_	Alignment	not modelled	95.7	20	**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
62	d1zfja1	Alignment	not modelled	95.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
63	c2vlbC_	Alignment	not modelled	95.6	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
64	c2y85D_	Alignment	not modelled	95.6	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
65	d1jfla1	Alignment	not modelled	95.5	31	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
66	c3b0vD_	Alignment	not modelled	95.5	18	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
67	c3gr7A_	Alignment	not modelled	95.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
68	c3gkaB_	Alignment	not modelled	95.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
69	d1vjia_	Alignment	not modelled	95.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
70	d1f76a_	Alignment	not modelled	95.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
71	c2hmcA_	Alignment	not modelled	95.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
72	c1ps9A_	Alignment	not modelled	95.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
73	c2gq8A_	Alignment	not modelled	95.2	20	**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
74	c3q58A_	Alignment	not modelled	95.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
75	d1rvka1	Alignment	not modelled	95.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
76	d1ps9a1	Alignment	not modelled	95.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
77	c2v9dB_	Alignment	not modelled	95.0	13	**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
78	d1ojxa_	Alignment	not modelled	95.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
79	c3qvjB_	Alignment	not modelled	95.0	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae

80	d1ykwa1	Alignment	not modelled	94.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
81	d1o5ka_	Alignment	not modelled	94.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
82	d1ka9f_	Alignment	not modelled	94.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
83	c3e96B_	Alignment	not modelled	94.6	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
84	c1ypfB_	Alignment	not modelled	94.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
85	d1y0ea_	Alignment	not modelled	94.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
86	c2vc6A_	Alignment	not modelled	94.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
87	c3nwrA_	Alignment	not modelled	94.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
88	d1goxa_	Alignment	not modelled	94.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
89	d1pv8a_	Alignment	not modelled	94.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
90	c1vrdA_	Alignment	not modelled	94.2	15	**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
91	c2w6rA_	Alignment	not modelled	94.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
92	d1pvna1	Alignment	not modelled	94.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
93	d1p4ca_	Alignment	not modelled	94.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	c3fokH_	Alignment	not modelled	94.0	19	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
95	c3fluD_	Alignment	not modelled	94.0	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
96	c3s5oA_	Alignment	not modelled	94.0	16	**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
97	c3noeA_	Alignment	not modelled	93.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
98	c3obkH_	Alignment	not modelled	93.9	19	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
99	c2xecD_	Alignment	not modelled	93.9	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
100	d1z41a1	Alignment	not modelled	93.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
101	d1jr1a1	Alignment	not modelled	93.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
102	c2vwtA_	Alignment	not modelled	93.8	15	**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
103	d1tzza1	Alignment	not modelled	93.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
104	c3ojcD_	Alignment	not modelled	93.7	29	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis

105	c2jfzB_	Alignment	not modelled	93.7	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
106	c2zskA_	Alignment	not modelled	93.6	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
107	c3jrkG_	Alignment	not modelled	93.6	17	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
108	c2ps2A_	Alignment	not modelled	93.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of putative mandelate racemase/muconate2 lactonizing enzyme from aspergillus oryzae
109	c1telA_	Alignment	not modelled	93.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
110	d2mnra1	Alignment	not modelled	93.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
111	c3stgA_	Alignment	not modelled	93.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
112	c1b74A_	Alignment	not modelled	93.5	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
113	d1geqa_	Alignment	not modelled	93.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
114	d2tpsa_	Alignment	not modelled	93.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
115	d2c1ha1	Alignment	not modelled	93.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
116	c2nuxB_	Alignment	not modelled	93.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
117	c3fkkA_	Alignment	not modelled	93.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
118	c3s81A_	Alignment	not modelled	93.2	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
119	c3pueA_	Alignment	not modelled	93.2	19	**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
120	d1geha1	Alignment	not modelled	93.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain