Phyre^2

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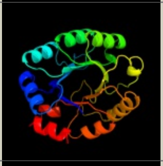
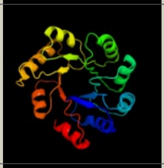
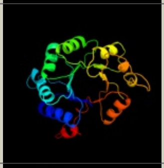
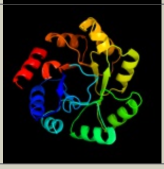
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cu2A_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
2	c3qc3B_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
3	c3ct7E_	Alignment		100.0	29	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
4	d1rpxa_	Alignment		100.0	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
5	d2flia1	Alignment		100.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
6	d1h1ya_	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
7	d1tqja_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
8	d1tqxa_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
9	c3inpA_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
10	d1qopa_	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
11	d1rd5a_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes

12	d1vc4a_	Alignment		100.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
13	c3thaB_	Alignment		99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
14	c3ajxA_	Alignment		99.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hexulose-6-phosphate synthase; **PDBTitle:** crystal structure of 3-hexulose-6-phosphate synthase
15	c3qjaA_	Alignment		99.9	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
16	d1a53a_	Alignment		99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
17	c3f4wA_	Alignment		99.9	12	**PDB header:**synthase, lyase **Chain:** A: **PDB Molecule:**putative hexulose 6 phosphate synthase; **PDBTitle:** the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
18	c3navB_	Alignment		99.9	14	**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
19	d1piia2	Alignment		99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
20	d1geqa_	Alignment		99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
21	d1q6oa_	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
22	c2ekcA_	Alignment	not modelled	99.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
23	d1j5ta_	Alignment	not modelled	99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
24	d1i4na_	Alignment	not modelled	99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
25	c1piiA_	Alignment	not modelled	99.9	13	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
26	c3jr2D_	Alignment	not modelled	99.9	13	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh; **PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
27	c2c3zA_	Alignment	not modelled	99.9	14	**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
						Fold:TIM beta/alpha-barrel

28	d1ujpa_	Alignment	not modelled	99.9	18	**Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
29	d1xcfa_	Alignment	not modelled	99.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
30	c2y85D_	Alignment	not modelled	99.9	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
31	c3ru6C_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
32	c3exsB_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**rmpd (hexulose-6-phosphate synthase); **PDBTitle:** crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
33	d2czda1	Alignment	not modelled	99.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
34	d1wbha1	Alignment	not modelled	99.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	d1wa3a1	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
36	d1h5ya_	Alignment	not modelled	99.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
37	d1km4a_	Alignment	not modelled	99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
38	d1thfd_	Alignment	not modelled	99.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
39	d1eixa_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
40	d2tpsa_	Alignment	not modelled	99.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
41	d1dvja_	Alignment	not modelled	99.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
42	c3nm3D_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
43	d1xi3a_	Alignment	not modelled	99.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
44	d1ka9f_	Alignment	not modelled	99.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
45	d1yxya1	Alignment	not modelled	99.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
46	d1vhca_	Alignment	not modelled	99.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
47	c3tfxB_	Alignment	not modelled	99.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
48	c2v82A_	Alignment	not modelled	99.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
49	c2bdqA_	Alignment	not modelled	99.8	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
50	d1mxsa_	Alignment	not modelled	99.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
51	d1y0ea_	Alignment	not modelled	99.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
52	c3o63B_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
53	d1vzwa1	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
						PDB header:isomerase

54	c3q58A_	Alignment	not modelled	99.8	17	**Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
55	c1yadD_	Alignment	not modelled	99.8	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
56	c3igsB_	Alignment	not modelled	99.8	14	**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
57	c3labA_	Alignment	not modelled	99.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
58	d1vqta1	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
59	c1znnF_	Alignment	not modelled	99.8	12	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
60	c3ldvB_	Alignment	not modelled	99.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** 1.77 angstrom resolution crystal structure of orotidine 5'-2 phosphate decarboxylase from vibrio cholerae o1 biovar3 eltor str. n16961
61	c3tr2A_	Alignment	not modelled	99.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** structure of a orotidine 5'-phosphate decarboxylase (pyrf) from2 coxiella burnetii
62	d1znna1	Alignment	not modelled	99.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
63	d1w0ma_	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
64	c2yytA_	Alignment	not modelled	99.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
65	c2yw3E_	Alignment	not modelled	99.7	19	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
66	d1losc_	Alignment	not modelled	99.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
67	d1hg3a_	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
68	c2w6rA_	Alignment	not modelled	99.7	13	**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
69	c3ceuA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
70	c2h6rG_	Alignment	not modelled	99.7	10	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
71	d1jvna1	Alignment	not modelled	99.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
72	d1dbta_	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
73	d1qo2a_	Alignment	not modelled	99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
74	c1jvnB_	Alignment	not modelled	99.6	10	**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
75	c2agkA_	Alignment	not modelled	99.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) **PDBTitle:** structure of s. cerevisiae his6 protein
76	d1viza_	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
77	d2f6ua1	Alignment	not modelled	99.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
						Fold:TIM beta/alpha-barrel

78	d1wv2a_	Alignment	not modelled	99.4	9	**Superfamily:**ThiG-like **Family:**ThiG-like
79	d1twda_	Alignment	not modelled	99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
80	c1gthD_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
81	c2htmB_	Alignment	not modelled	99.3	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
82	c2qcnA_	Alignment	not modelled	99.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uridine 5'-monophosphate synthase; **PDBTitle:** covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump
83	c3bvjA_	Alignment	not modelled	99.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uridine 5'-monophosphate synthase; **PDBTitle:** crystal structure of human orotidine 5'-monophosphate decarboxylase2 complexed with xmp
84	d1ojxa_	Alignment	not modelled	99.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
85	d1o4ua1	Alignment	not modelled	99.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
86	d1xm3a_	Alignment	not modelled	99.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
87	c3gndC_	Alignment	not modelled	99.2	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
88	d1dqwa_	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
89	c2gjlA_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
90	c2z6jB_	Alignment	not modelled	99.2	20	**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
91	c1zfjA_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
92	c3iwpK_	Alignment	not modelled	99.2	14	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
93	c3b0vD_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
94	d1gtea2	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
95	c2qjhH_	Alignment	not modelled	99.1	12	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
96	c3bo9B_	Alignment	not modelled	99.1	19	**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
97	d1vhna_	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	d1tb3a1	Alignment	not modelled	99.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
99	c2e77B_	Alignment	not modelled	99.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
100	d1d3ga_	Alignment	not modelled	99.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
101	c3qw3B_	Alignment	not modelled	99.0	15	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**orotidine-5-phosphate decarboxylase/orotate **PDBTitle:** structure of leishmania donovani omp decarboxylase
102	d1qpoa1	Alignment	not modelled	99.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
103	d1goxa_	Alignment	not modelled	98.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
104	d1kbia1	Alignment	not modelled	98.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases

						Family:FMN-linked oxidoreductases
105	c3khjE_	Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
106	c3oixA_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
107	c2a7nA_	Alignment	not modelled	98.9	17	**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
108	d1p0ka_	Alignment	not modelled	98.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
109	d1p4ca_	Alignment	not modelled	98.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
110	c3r2gA_	Alignment	not modelled	98.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
111	c2fptA_	Alignment	not modelled	98.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase, mitochondrial; **PDBTitle:** dual binding mode of a novel series of dhodh inhibitors
112	c3bw2A_	Alignment	not modelled	98.9	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
113	c2zrvC_	Alignment	not modelled	98.9	14	**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.
114	c3gr7A_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
115	c1kbiB_	Alignment	not modelled	98.8	18	**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
116	d1juba_	Alignment	not modelled	98.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
117	c2nv2U_	Alignment	not modelled	98.8	16	**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
118	d1uuma_	Alignment	not modelled	98.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
119	d1qapa1	Alignment	not modelled	98.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
120	c2zbtB_	Alignment	not modelled	98.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8