Phyre2

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Description	RVBD0573c_(-)_665854_667245
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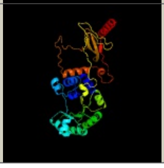
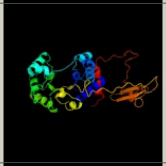
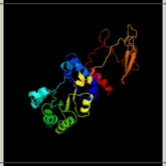
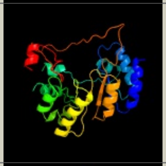
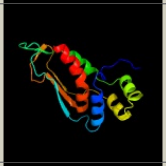
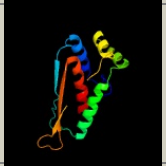
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f7fA_	Alignment		100.0	39	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase, putative; **PDBTitle:** crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
2	c4yubB_	Alignment		100.0	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of human nicotinic acid phosphoribosyltransferase
3	c4hl7A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
4	c1yirA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
5	c1vlpA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
6	c2im5C_	Alignment		100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase from2 porphyromonas gingivalis
7	c3os4A_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
8	c1ybeA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase
9	c2e5cA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinamide phosphoribosyltransferase; **PDBTitle:** crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
10	c2i14B_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
11	d2f7fa1	Alignment		100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like

12	c1ytkA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase from thermoplasma **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
13	d2i14a1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
14	d1ytda1	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
15	d1yira1	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
16	d1ybea1	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
17	d1vlpa2	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
18	d2f7fa2	Alignment		100.0	38	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
19	d1vlpa1	Alignment		100.0	15	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
20	d1yira2	Alignment		100.0	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
21	d1ybea2	Alignment	not modelled	100.0	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
22	c2b7pA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
23	c1x1oC_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
24	c1qpoA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
25	c3l0gD_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
26	c2jbmA_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
27	c3pajA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961

28	c5huoH_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** H: **PDB Molecule:**nicotinate-nucleotide diphosphorylase (carboxylating); **PDBTitle:** crystal structure of nadc deletion mutant in c2221 space group
29	c1o4uA_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
30	c1qapA_	Alignment	not modelled	100.0	21	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
31	c3tqvA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
32	c3gnnA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
33	c3c2vA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of the quinolinate phosphoribosyl transferase (bna6)2 from saccharomyces cerevisiae complexed with prpp and the inhibitor3 phthalate
34	d2i14a2	Alignment	not modelled	100.0	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
35	d1ytda2	Alignment	not modelled	100.0	27	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
36	d1qapa1	Alignment	not modelled	99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
37	d1qpoa1	Alignment	not modelled	99.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
38	d1o4ua1	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
39	d1qpoa2	Alignment	not modelled	97.7	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
40	d1qapa2	Alignment	not modelled	97.4	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
41	d1o4ua2	Alignment	not modelled	96.9	16	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
42	c6oviA_	Alignment	not modelled	93.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**keto-deoxy-phosphogluconate aldolase; **PDBTitle:** crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
43	c3cu2A_	Alignment	not modelled	90.8	14	**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
44	d7reqa2	Alignment	not modelled	90.6	20	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
45	c1e1cA_	Alignment	not modelled	89.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
46	d2flia1	Alignment	not modelled	88.1	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
47	c5umfB_	Alignment	not modelled	88.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribulose-phosphate 3-epimerase; **PDBTitle:** crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
48	c3tsmB_	Alignment	not modelled	87.6	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
49	d1xi3a_	Alignment	not modelled	87.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
50	d1tqxa_	Alignment	not modelled	87.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
51	c4bk9B_	Alignment	not modelled	86.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo **PDBTitle:** crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
52	c4qccA_	Alignment	not modelled	86.2	28	**PDB header:**structural protein, lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- **PDBTitle:** structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains

53	d1rpxa_	Alignment	not modelled	85.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
54	d1ea0a2	Alignment	not modelled	84.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
55	c5aheA_	Alignment	not modelled	83.8	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:** **PDBTitle:** crystal structure of salmonella enterica hisa
56	c3inpA_	Alignment	not modelled	83.8	12	**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.
57	d1hg3a_	Alignment	not modelled	83.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
58	c3o63B_	Alignment	not modelled	82.5	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
59	d1vhca_	Alignment	not modelled	82.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
60	c2v82A_	Alignment	not modelled	81.9	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
61	c4e38A_	Alignment	not modelled	81.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate **PDBTitle:** crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
62	d2tpsa_	Alignment	not modelled	81.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
63	d1a53a_	Alignment	not modelled	81.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
64	c3labA_	Alignment	not modelled	80.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
65	d1ofda2	Alignment	not modelled	80.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
66	c1yadD_	Alignment	not modelled	80.3	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
67	d1wbha1	Alignment	not modelled	80.2	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
68	c2h6rG_	Alignment	not modelled	79.8	18	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
69	c2c3zA_	Alignment	not modelled	79.0	20	**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
70	c3qjaA_	Alignment	not modelled	75.6	20	**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
71	d1wa3a1	Alignment	not modelled	75.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
72	c4utwB_	Alignment	not modelled	73.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfingens
73	c3qc3B_	Alignment	not modelled	73.6	13	**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
74	c4nu7C_	Alignment	not modelled	72.6	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
75	c3ceuA_	Alignment	not modelled	72.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase (bt_0647)2 from bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr268
76	d1tqja_	Alignment	not modelled	71.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
77	c5n2pA_	Alignment	not modelled	70.9	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** sulfolobus solfataricus tryptophan synthase a
78	c6hmaA	Alignment	not modelled	70.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;

78	[illegible]	Alignment	not modelled	70.8	21	**PDBTitle:** the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
79	d1mxsa_	Alignment	not modelled	69.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
80	c3ct7E_	Alignment	not modelled	67.2	21	**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
81	d1rd5a_	Alignment	not modelled	67.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
82	d1ccwa_	Alignment	not modelled	67.1	20	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
83	d1vzwa1	Alignment	not modelled	66.9	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
84	d1h5ya_	Alignment	not modelled	66.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
85	d1w0ma_	Alignment	not modelled	66.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
86	d1thfd_	Alignment	not modelled	66.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
87	c3igsB_	Alignment	not modelled	65.9	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
88	c4n6eA_	Alignment	not modelled	64.8	15	**PDB header:**lyase/biosynthetic protein **Chain:** A: **PDB Molecule:**putative thiosugar synthase; **PDBTitle:** crystal structure of amycolatopsis orientalis bexx/cyso complex
89	d1jgta1	Alignment	not modelled	64.7	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
90	c5cssA_	Alignment	not modelled	64.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate
91	c3gr7A_	Alignment	not modelled	63.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal crystal form
92	d1h1ya_	Alignment	not modelled	63.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
93	c5zknA_	Alignment	not modelled	62.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
94	c4x2rA_	Alignment	not modelled	61.9	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) **PDBTitle:** crystal structure of pria from actinomyces urogenitalis
95	c3f4wA_	Alignment	not modelled	60.6	18	**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
96	d1qopa_	Alignment	not modelled	59.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
97	c4g1kB_	Alignment	not modelled	58.8	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
98	c5zjnB_	Alignment	not modelled	57.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
99	c4axkB_	Alignment	not modelled	57.2	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) **PDBTitle:** crystal structure of subhisa from the thermophile corynebacterium2 efficiens
100	c3absD_	Alignment	not modelled	56.2	26	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
101	d1xcfa_	Alignment	not modelled	55.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
102	d1yxya1	Alignment	not modelled	55.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
103	d1ka9f_	Alignment	not modelled	55.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family: Histidine biosynthesis enzymes
104	c5b69A_	Alignment	not modelled	54.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**geranylgeranylglyceryl phosphate synthase; **PDBTitle:** crystal structure of geranylgeranylglyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
105	c2bdqA_	Alignment	not modelled	54.2	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast strucural genomics target sar15.
106	d1geqa_	Alignment	not modelled	54.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
107	c4ml9A_	Alignment	not modelled	54.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsebaldella termitidis
108	c3tdmD_	Alignment	not modelled	53.8	25	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
109	c1znnF_	Alignment	not modelled	53.7	20	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
110	d1znna1	Alignment	not modelled	53.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
111	c6nkeA_	Alignment	not modelled	53.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**geranylgeranylglyceryl phosphate synthase; **PDBTitle:** wild-type gggps from thermoplasma volcanium
112	c2yw3E_	Alignment	not modelled	53.3	20	**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
113	c3bicA_	Alignment	not modelled	51.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase, mitochondrial precursor; **PDBTitle:** crystal structure of human methylmalonyl-coa mutase
114	c6bkaA_	Alignment	not modelled	51.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitronate monooxygenase; **PDBTitle:** crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
115	c3tdnB_	Alignment	not modelled	50.7	25	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**flr symmetric alpha-beta tim barrel; **PDBTitle:** computationally designed two-fold symmetric tim-barrel protein, flr
116	d1gwja_	Alignment	not modelled	50.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
117	d1vc4a_	Alignment	not modelled	49.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
118	c2e18B_	Alignment	not modelled	48.4	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
119	c5ocsB_	Alignment	not modelled	46.5	14	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**putative nadh-depentdent flavin oxidoreductase; **PDBTitle:** ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
120	c2jgqB_	Alignment	not modelled	45.5	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori