Phyre^2

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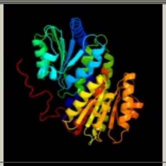
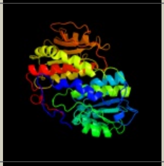
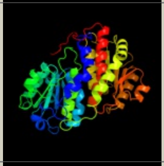
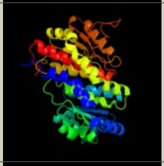
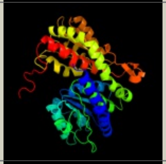
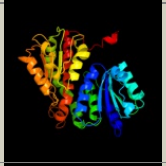
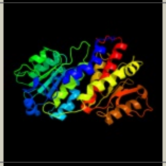
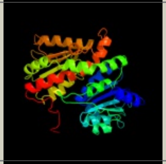
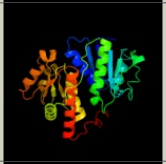
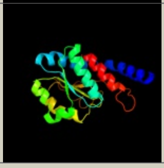
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3odpA_	Alignment		100.0	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
2	c3c3jA_	Alignment		100.0	98	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
3	c3i0zB_	Alignment		100.0	42	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
4	c1jxaA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
5	c2zj3A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
6	c2amlB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
7	d1moqa_	Alignment		100.0	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
8	c3tbfA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
9	c3fj1A_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
10	c3g68A_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
11	c2decA_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3

12	d1j5xa_	Alignment		100.0	22	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
13	c2a3nA_	Alignment		100.0	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
14	c3euaD_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
15	c2puwA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
16	c3fkjA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
17	c3knzA_	Alignment		100.0	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
18	c3hbaA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
19	d1x9ia_	Alignment		100.0	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
20	c2xhzC_	Alignment		99.8	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
21	c3etnD_	Alignment	not modelled	99.8	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
22	c1nriA_	Alignment	not modelled	99.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
23	d1nria_	Alignment	not modelled	99.8	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
24	c3fxaA_	Alignment	not modelled	99.8	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
25	d1vima_	Alignment	not modelled	99.7	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
26	c3shoA_	Alignment	not modelled	99.7	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
27	d1tk9a_	Alignment	not modelled	99.7	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
28	d1x94a_	Alignment	not modelled	99.7	16	**Fold:**SIS domain **Superfamily:**SIS domain

						Family:mono-SIS domain
29	d1m3sa_	Alignment	not modelled	99.6	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
30	c2x3yA_	Alignment	not modelled	99.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
31	c3cvjB_	Alignment	not modelled	99.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
32	d1x92a_	Alignment	not modelled	99.5	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
33	c3trjC_	Alignment	not modelled	99.5	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
34	d1jeoa_	Alignment	not modelled	99.5	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
35	c2yvaB_	Alignment	not modelled	99.5	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
36	c1zzgB_	Alignment	not modelled	98.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
37	c2q8nB_	Alignment	not modelled	98.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
38	d1c7qa_	Alignment	not modelled	98.2	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
39	c3ff1B_	Alignment	not modelled	98.1	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
40	c3hjbA_	Alignment	not modelled	98.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
41	d1gzda_	Alignment	not modelled	98.0	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
42	c3ljkA_	Alignment	not modelled	98.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
43	c2wu8A_	Alignment	not modelled	98.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
44	d1u0fa_	Alignment	not modelled	98.0	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
45	c3pr3B_	Alignment	not modelled	98.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
46	c3ujhB_	Alignment	not modelled	98.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
47	c2o2cB_	Alignment	not modelled	97.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
48	d1iata_	Alignment	not modelled	97.9	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
49	d1hm5a_	Alignment	not modelled	97.9	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
50	c1t10A_	Alignment	not modelled	97.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
51	d1q50a_	Alignment	not modelled	97.8	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
52	c3nbuC_	Alignment	not modelled	97.8	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
53	d1wiwa_	Alignment	not modelled	92.8	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
54	d1pjza_	Alignment	not modelled	82.7	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family: Thiopurine S-methyltransferase
55	c3iabB_	Alignment	not modelled	76.3	13	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonucleases p/mrp protein subunit pop7; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
56	d2bzga1	Alignment	not modelled	75.6	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
57	c3bgdB_	Alignment	not modelled	69.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
58	d2ieaa3	Alignment	not modelled	64.9	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
59	d2dw4a2	Alignment	not modelled	60.4	28	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
60	d1w6ta1	Alignment	not modelled	57.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
61	d1pkla3	Alignment	not modelled	54.2	27	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
62	c2bi8A_	Alignment	not modelled	52.8	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
63	c3otrC_	Alignment	not modelled	51.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase; **PDBTitle:** 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii
64	d2ptza1	Alignment	not modelled	50.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
65	d1a9xa4	Alignment	not modelled	49.8	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
66	d1e0ta3	Alignment	not modelled	49.7	32	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
67	d2bkwa1	Alignment	not modelled	49.6	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
68	d1xjca_	Alignment	not modelled	49.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
69	c2e1mA_	Alignment	not modelled	48.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
70	c2bpoA_	Alignment	not modelled	47.8	13	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
71	c1kjjA_	Alignment	not modelled	47.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
72	c3rhtB_	Alignment	not modelled	45.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
73	d1iyxa1	Alignment	not modelled	45.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
74	c1sezA_	Alignment	not modelled	43.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
75	c1vkrA_	Alignment	not modelled	43.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
76	d1vkra_	Alignment	not modelled	43.6	25	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
77	c2xagA_	Alignment	not modelled	43.4	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
78	c2v1dA_	Alignment	not modelled	43.4	28	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
79	c2hkoA_	Alignment	not modelled	43.4	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
80	d1a3xa3	Alignment	not modelled	43.0	19	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like

						Family: Pyruvate kinase, C-terminal domain
81	d1a7ja_	Alignment	not modelled	40.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
82	c3fpjA_	Alignment	not modelled	40.8	10	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
83	d1reoa1	Alignment	not modelled	39.4	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
84	d2g50a3	Alignment	not modelled	39.3	17	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
85	d1pdza1	Alignment	not modelled	38.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
86	c2yxbA_	Alignment	not modelled	36.5	5	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
87	c1xx6B_	Alignment	not modelled	35.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
88	c3khdC_	Alignment	not modelled	35.5	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
89	c2jb1B_	Alignment	not modelled	35.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
90	c1f8sA_	Alignment	not modelled	35.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
91	c3q2oB_	Alignment	not modelled	35.4	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
92	c1a3wB_	Alignment	not modelled	34.9	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
93	c2hcuA_	Alignment	not modelled	34.5	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
94	c2vgbB_	Alignment	not modelled	33.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
95	c3allA_	Alignment	not modelled	33.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
96	c2z2uA_	Alignment	not modelled	32.8	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
97	c2z9wA_	Alignment	not modelled	32.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
98	c3eoeC_	Alignment	not modelled	32.2	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
99	c1e0tD_	Alignment	not modelled	32.1	32	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
100	c3kpgA_	Alignment	not modelled	31.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative; **PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
101	d1v8ba2	Alignment	not modelled	31.5	12	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
102	c3h5jA_	Alignment	not modelled	31.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
103	c3lovA_	Alignment	not modelled	31.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
104	d1ycga1	Alignment	not modelled	31.1	4	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
						PDB header:flavoprotein

105	c3edoA_	Alignment	not modelled	30.1	17	**Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
106	c1dl5A_	Alignment	not modelled	30.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** protein-l-isoaspartate o-methyltransferase
107	d2bfdb2	Alignment	not modelled	29.7	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
108	d1v8da_	Alignment	not modelled	29.4	24	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679
109	c3b2nA_	Alignment	not modelled	29.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
110	d7reqa2	Alignment	not modelled	28.9	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
111	d2b3ya1	Alignment	not modelled	28.8	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
112	c2pxxA_	Alignment	not modelled	28.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mgc2408; **PDBTitle:** human putative methyltransferase mgc2408
113	d2bi7a1	Alignment	not modelled	28.3	32	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
114	c3uvzB_	Alignment	not modelled	28.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
115	d1ka9h_	Alignment	not modelled	28.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
116	d2al1a1	Alignment	not modelled	28.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
117	c3q3wB_	Alignment	not modelled	28.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
118	c3i9fB_	Alignment	not modelled	27.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative type 11 methyltransferase; **PDBTitle:** crystal structure of a putative type 11 methyltransferase2 from sulfolobus solfataricus
119	c1l8pC_	Alignment	not modelled	26.5	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
120	c1v0jB_	Alignment	not modelled	26.5	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from mycobacterium tuberculosis