Phyre2

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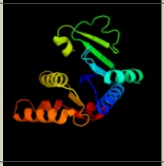
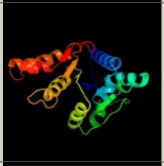
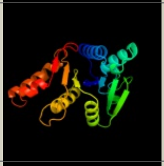
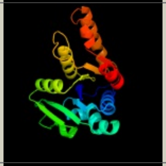
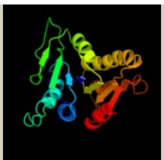
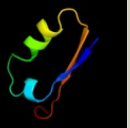
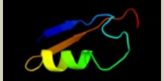
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bq9A_	Alignment		100.0	62	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
2	c3gh1A_	Alignment		100.0	68	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted nucleotide-binding protein; **PDBTitle:** crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
3	d1weka_	Alignment		100.0	25	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
4	d1t35a_	Alignment		100.0	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
5	c2q4dB_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
6	d1ydha_	Alignment		100.0	19	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
7	c3quaA_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
8	c3sbxC_	Alignment		100.0	20	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
9	d2q4oa1	Alignment		100.0	22	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
10	c2q4oA_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
11	d1weha_	Alignment		100.0	21	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like

12	c1rcuB_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
13	d1rcua_	Alignment		99.9	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
14	c2iz6A_	Alignment		99.9	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
15	c3majA_	Alignment		96.4	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
16	d1o1xa_	Alignment		82.8	23	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
17	d1e19a_	Alignment		80.8	29	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
18	c3c5yD_	Alignment		77.3	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
19	c2ppwA_	Alignment		75.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
20	c3kzfC_	Alignment		74.4	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
21	c2fzvC_	Alignment	not modelled	71.4	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
22	c3l86A_	Alignment	not modelled	69.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
23	c3he8A_	Alignment	not modelled	67.8	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
24	c2e9yA_	Alignment	not modelled	60.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
25	d1b7ba_	Alignment	not modelled	59.0	27	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
26	d2btya1	Alignment	not modelled	58.9	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
27	d2bufa1	Alignment	not modelled	58.1	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
28	c2rd5A_	Alignment	not modelled	55.3	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acetylglutamate kinase-like protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
						Fold: Carbamate kinase-like

29	d2ij9a1	Alignment	not modelled	53.9	18	**Superfamily:**Carbamate kinase-like **Family:**PyrH-like
30	c2ogxB_	Alignment	not modelled	53.7	28	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**molybdenum storage protein subunit beta; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
31	d2nu7b1	Alignment	not modelled	50.8	7	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
32	c2w21A_	Alignment	not modelled	50.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
33	c3nwyB_	Alignment	not modelled	49.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
34	c2ekcA_	Alignment	not modelled	49.5	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
35	c3ek5A_	Alignment	not modelled	49.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
36	d2akoa1	Alignment	not modelled	48.5	27	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
37	d1vhqa_	Alignment	not modelled	45.1	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
38	c2l5aA_	Alignment	not modelled	45.1	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
39	c2jjxC_	Alignment	not modelled	44.4	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
40	d2ocda1	Alignment	not modelled	44.0	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
41	d1z9da1	Alignment	not modelled	43.0	10	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
42	d1ikta_	Alignment	not modelled	41.9	9	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
43	c3bn8A_	Alignment	not modelled	41.3	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative sterol carrier protein 2; **PDBTitle:** crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
44	c3o8nA_	Alignment	not modelled	40.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
45	c3qd5B_	Alignment	not modelled	39.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
46	c2egxA_	Alignment	not modelled	39.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
47	d2fzva1	Alignment	not modelled	38.9	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
48	c2j5gL_	Alignment	not modelled	38.6	15	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**alr4455 protein; **PDBTitle:** the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
49	c3onoA_	Alignment	not modelled	37.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
50	c2jzcA_	Alignment	not modelled	36.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
51	c2j5tF_	Alignment	not modelled	35.5	17	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
52	d1oaoa_	Alignment	not modelled	35.3	11	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
53	d2brxa1	Alignment	not modelled	34.2	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
						PDB header:biosynthetic protein

54	c3l3bA_	Alignment	not modelled	33.6	24	**Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
55	d1qopa_	Alignment	not modelled	33.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
56	c3lo3E_	Alignment	not modelled	32.9	13	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
57	c3m1pA_	Alignment	not modelled	32.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
58	c3k7pA_	Alignment	not modelled	32.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
59	c2jbwB_	Alignment	not modelled	32.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
60	c2hihB_	Alignment	not modelled	31.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase 46 kda form; **PDBTitle:** crystal structure of staphylococcus hyicus lipase
61	c3l76B_	Alignment	not modelled	30.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
62	c2va1A_	Alignment	not modelled	28.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
63	d1nn4a_	Alignment	not modelled	28.3	26	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
64	c2ogxA_	Alignment	not modelled	28.0	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
65	d2jbwa1	Alignment	not modelled	28.0	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
66	c3ab4K_	Alignment	not modelled	27.5	12	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
67	c3pm6B_	Alignment	not modelled	27.4	14	**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
68	c2j4kC_	Alignment	not modelled	27.3	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
69	d1ojta1	Alignment	not modelled	27.3	38	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
70	d1qvwa_	Alignment	not modelled	27.2	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
71	d1q1ra2	Alignment	not modelled	25.1	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
72	c1ibtC_	Alignment	not modelled	24.8	38	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase beta chain; **PDBTitle:** structure of the d53,54n mutant of histidine decarboxylase at-170 c
73	c2l8kA_	Alignment	not modelled	24.7	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
74	d2fiua1	Alignment	not modelled	24.6	26	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
75	d1djqa3	Alignment	not modelled	23.5	38	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
76	d1lvla1	Alignment	not modelled	23.5	38	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
77	c3nquA_	Alignment	not modelled	23.2	34	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein a; **PDBTitle:** crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
78	d1hbnb1	Alignment	not modelled	23.1	16	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain

79	d4pgaa_	Alignment	not modelled	22.6	29	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
80	d2pq6a1	Alignment	not modelled	22.6	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
81	c3ll9A_	Alignment	not modelled	22.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
82	d3lada1	Alignment	not modelled	22.3	46	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
83	d1mqsa_	Alignment	not modelled	22.0	21	**Fold:**Sec1/munc18-like (SM) proteins **Superfamily:**Sec1/munc18-like (SM) proteins **Family:**Sec1/munc18-like (SM) proteins
84	c3opyB_	Alignment	not modelled	22.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
85	c3opyH_	Alignment	not modelled	22.0	21	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
86	c3navB_	Alignment	not modelled	21.8	16	**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
87	d1id3a_	Alignment	not modelled	21.4	30	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
88	d2j0wa1	Alignment	not modelled	21.1	16	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
89	c1jqkE_	Alignment	not modelled	21.1	11	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase; **PDBTitle:** crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
90	d1jqka_	Alignment	not modelled	21.1	11	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
91	d1onfa1	Alignment	not modelled	21.0	46	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
92	d1acoa2	Alignment	not modelled	20.5	14	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
93	d1vdca1	Alignment	not modelled	20.3	36	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
94	d2bona1	Alignment	not modelled	20.3	26	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
95	d2bnea1	Alignment	not modelled	20.2	10	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
96	d2jgra1	Alignment	not modelled	20.2	30	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
97	c1z6gA_	Alignment	not modelled	20.2	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from plasmodium falciparum
98	c2vvyC_	Alignment	not modelled	19.9	19	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein b15; **PDBTitle:** structure of vaccinia virus protein b14
99	d2vvpa1	Alignment	not modelled	19.8	18	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB