

AD _____

Award Number: W81XWH-09-2-0096

TITLE: Using Computer Models to Identify Common Therapeutic Targets in Host-adapted Bacterial Threat Agents

PRINCIPAL INVESTIGATOR: Simon Daefler, M.D., Ph.D.

CONTRACTING ORGANIZATION: Mount Sinai School of Medicine
New York, NY 10029

REPORT DATE: August 2011

TYPE OF REPORT: Final

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release;
Distribution Unlimited

The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army position, policy or decision unless so designated by other documentation.

REPORT DOCUMENTATION PAGE				<i>Form Approved</i> <i>OMB No. 0704-0188</i>	
Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing this collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to Department of Defense, Washington Headquarters Services, Directorate for Information Operations and Reports (0704-0188), 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302. Respondents should be aware that notwithstanding any other provision of law, no person shall be subject to any penalty for failing to comply with a collection of information if it does not display a currently valid OMB control number. PLEASE DO NOT RETURN YOUR FORM TO THE ABOVE ADDRESS.					
1. REPORT DATE August 2011		2. REPORT TYPE Final		3. DATES COVERED 27 July 2010 – 26 July 2011	
4. TITLE AND SUBTITLE Using Computer Models to Identify Common Therapeutic Targets in Host-adapted Bacterial Threat Agents				5a. CONTRACT NUMBER	
				5b. GRANT NUMBER W81XWH-09-2-0096	
				5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S) Simon Daepler E-Mail: simon.daepler@mssm.edu				5d. PROJECT NUMBER	
				5e. TASK NUMBER	
				5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Mount Sinai School of Medicine New York, NY 10029				8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012				10. SPONSOR/MONITOR'S ACRONYM(S)	
				11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION / AVAILABILITY STATEMENT Approved for Public Release; Distribution Unlimited					
13. SUPPLEMENTARY NOTES					
14. ABSTRACT This proposal seeks to develop computer algorithms for the evaluation of metabolic pathways in bacterial biothreat agents that can be exploited as therapeutic targets. We have completed genome-scale metabolic models for Francisella Schu4 (type A strain, Francisella LVS (type B), Burkholderia mallei, and Burkholderia pseudomallei. Some models were validated by metabolic assays, growth experiments in defined media, and transcriptomic data. Algorithms were developed and implemented for genome scale in silico simulation to identify single and synthetic lethals (double, triple, and quadruple). Identification of gene products that cause lethality leads to potential suitable therapeutic targets. The suitability of this approach starting from genomic data of an unknown Francisella strain was successfully tested. with a 24h turn-around time for each strain. This demonstrates the feasibility of this methodology and underlines its importance for evaluation of potentially modified or emerging bacterial pathogens.					
15. SUBJECT TERMS systems biology, computer modeling, therapeutic targets, Francisella, Burkholderia					
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT UU	18. NUMBER OF PAGES 56	19a. NAME OF RESPONSIBLE PERSON USAMRMC
a. REPORT U	b. ABSTRACT U	c. THIS PAGE U			19b. TELEPHONE NUMBER (include area code)

Table of Contents

	<u>Page</u>
Introduction.....	5
Body.....	5
Key Research Accomplishments.....	11
Reportable Outcomes.....	12
Conclusion.....	12
References.....	12
Appendices.....	13

Introduction

The potential introduction of novel or modified bacterial biothreat agents poses significant risks to the population. Once such pathogens have been identified and characterized by high-throughput techniques there is a need for novel suitable methodologies to identify vulnerable metabolic pathways and therapeutic targets within a short time frame.

The pipeline of novel targets for antimicrobial drugs is stagnating. Genomics, genomic screens, and high-throughput technologies have not yielded the expected success [1]. Previous investigations have addressed the metabolic capacities of *Salmonella* by extensive in-vivo analysis and network analysis [2]. The sobering result was that there are limited novel metabolic targets due to the robustness of the metabolic networks and the availability of many nutrients in the pathogen's environment. Most of the targets identified had already been considered for development of new antimicrobials. However, it became clear that the large datasets generated by such experiments and other comprehensive investigations suggest a complexity of metabolic networks that cannot be intuitively explained and explored by manual analysis. This situation is amplified in a situation of a potential release of an emerging or modified biothreat agent, where a fast response is required and where genomic data might be available.

Metabolic genome-scale models of bacteria have provided a computational framework for *in silico* simulations of single or double gene deletions under a wide variety of growth conditions [3]. The feasibility of antimicrobial hit discovery from flux-balance analysis of metabolic networks has recently been demonstrated for single targets [4]. *In silico* simulation of genome scale metabolic models also provides system-level understanding, might be used to assess the complex effects of inactivation of metabolic reactions and its compensatory mechanisms, correlate them with a phenotype, and enables us to interrogate a large number of possible target combinations.

The goal of this proposal is to develop genome-scale metabolic models of the biothreat agents *Francisella* and *Burkholderia* and validate these models with metabolic and genome experimental data. Algorithms will be developed that will allow fast modeling of related novel strains and the prediction of suitable novel therapeutic targets..

Body/ Results

Models for *Francisella*

We have completed the constraints-based model for the *Francisella tularensis* *subsp. tularensis* vaccine strain (Francisella LVS, type B strain). The essential features of this model are summarized in Figure 1. This model predicts single and double synthetic lethals, which are immediate targets for potential novel antibiotics. This model has been validated by metabolomic data and partial transcriptomic analysis. Our model also describes the physiologic intracellular behaviour of *Francisella* and its switch from oxidative metabolism. These findings had been included in our previous annual report and have been published in part in BMC Systems Biology. and has been added to this report in the appendix section. Additional files of this manuscript also contain the complete set of metabolic reactions that are incorporated in this model. SBML files of this model will be made available for the Repository.

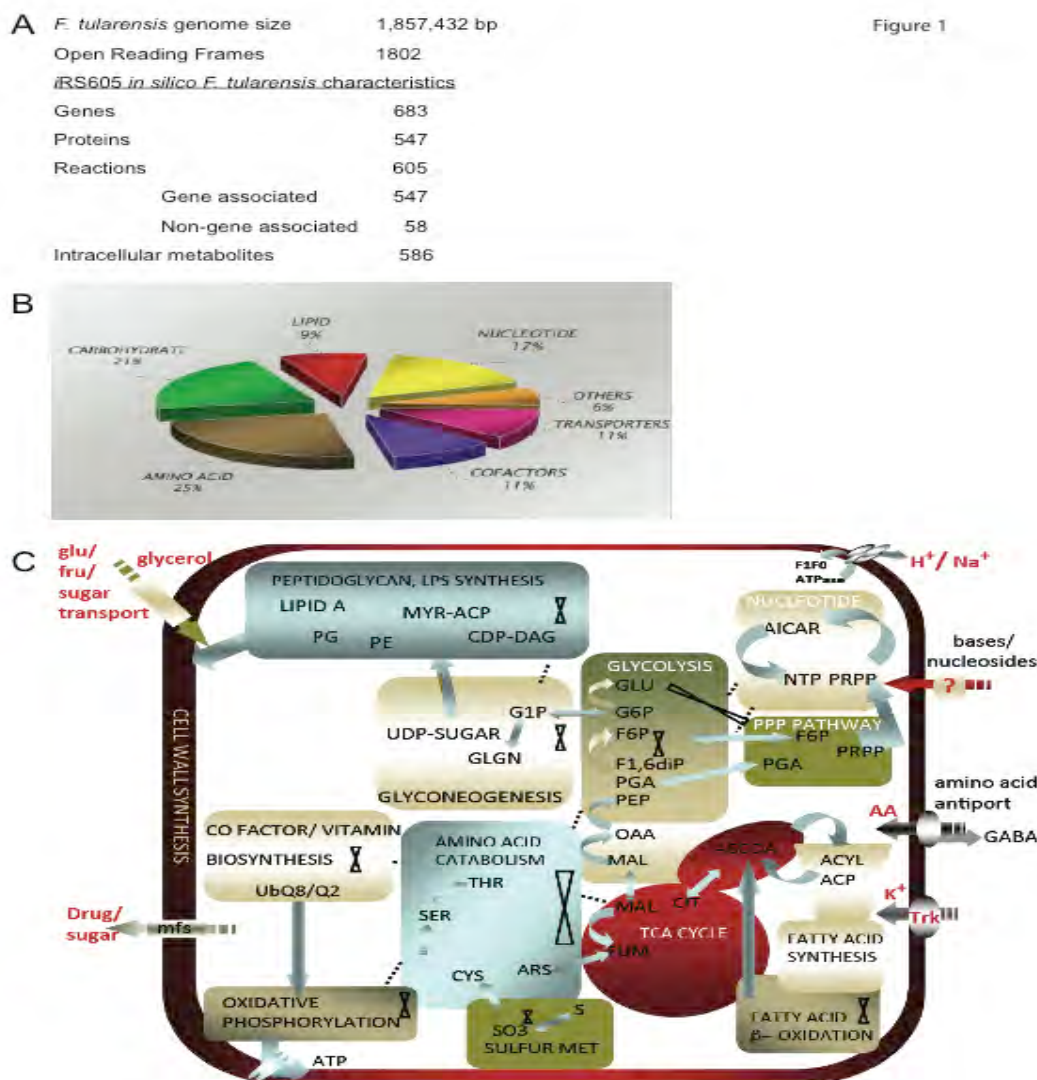


Figure 1

Figure 1: Reconstruction characteristics for constraints-based model of *Francisella tularensis* LVS. A. Statistics of the *Francisella tularensis* subspecies *holarctica* vaccine strain (*F. tularensis* LVS) genome and its *in silico* reconstruction *iRS605*. B. Functional classification of genes that are included in the model. C. Overview of metabolism in *Francisella*. Significant interconnections between pathways are shown. Pathways with missing genes are indicated by cross symbols.

A genome-scale metabolic model was also completed for *Francisella tularensis* Schu4 (type A *Francisella* strain) with integration of metabolomic and transcriptomic data. Based on these prototypic type A and B strains we developed models for 28 different type A and type B strains of *Francisella* for which we had genomic data (Dr. D. Rozack and J.Craig Venter Institute (JCVI)). Findings and analysis had been presented in the previous annual report.

We pursued further computational analysis of the *Francisella* models as follows. For *Francisella tularensis* LVS in a glucose minimal medium we identified a total of 101 essential reactions (13.5% of the reactions in the model) and 113 essential genes. Essential genes (or reactions) consist of genes (or reactions) whose individual deletion is lethal (i.e. no biomass formation) under a specific environment (e.g. glucose minimal medium). Of these genes there were 10 COG ontologies: 3 were category C (energy production and conversion), 26 were category E (amino acid transport and metabolism), 20 were category F (nucleotide transport and metabolism), 7 were category G (carbohydrate transport and metabolism), 6 were category H (coenzyme transport and metabolism), 9 were category I (lipid transport and metabolism), 20 of category M (cell wall/membrane/envelope biogenesis), 1 of category O (post-translational modification,

protein turnover, chaperons), 1 of category P (inorganic ion transport and metabolism), 4 of category R (general function prediction only). We found no essential genes in category L (replication, replication and repair). Gene ontology shows that the essential reactions are in 21 categories including amino acid biosynthesis, nucleotide salvage, cell wall biosynthesis, transport, anaplerotic reactions, and oxidative phosphorylation. We found 42 synthetic lethal pairs, with a total of 50 genes, of which 20 pairs have the same COG terms. For category C, there are 3 intra-category pairs and 2 pairs with the same category. There are ten pairs consisting of category H and M, and four consisting of category E and M. This shows that intra-lethality is not necessary for pairs with category M in contrast to what was found by Suthers et.al. for E. coli. Also for category G, there was a pair consisting of category G and category I, and a pair consisting of category G and category E also in contrast to Suthers et. al. The intra-lethal pairs consisted of 9 EE pairs, 6 GG pairs, 2 CC pairs, 2 FF pairs, and 1 MM pair. There were no pairs with category P. In addition there are 83 synthetic lethal triples with a total of 49 genes. Among these triples there was intra-lethality for category G, F and H. There were 18 GGG, 10 HHH and 3 FFF triples. The other triples were as follows: 20 EHH, 7 FGG, 6 GGE, 6 GGC, 2 CCE, 2 EEF, 2 EFM, 1 GCC, 1 CRF, 1 EFH, 1 REH, 1 REE, 1 REH, and 1 RCG. There were no triples with category O, P or I.

Finally there were 88 synthetic lethal quadruples, with a total of 61 genes. For the quadruples, there was intra-lethality for category C and category H, with 23 CCCC and 1 HHHH. The other quadruples were as follows: 11 CCCE, 8 CCCM, 7 CCCH, 4 CCCG, 7 FFHH, 2 FFCC, 5 CCME, 3 FFCH, 2 CCFG, 2 FFMG, 1 FFHE, 1 CCMR, 1 CCGR, 1 CCGH, 1 CCMF, 1 CGHE. In total there were 218 genes which had degree of essentiality less than or equal to 4. The degree of essentiality is defined as the size of the smallest synthetic lethal that the gene or reaction is a member of. We calculated the degree of essentiality for all of the genes in these lists. We found that there were 119 genes of degree 1, 50 of degree 2, 30 of degree 3 and 19 of degree 4. We also found among the genes of degree greater than 1, that there were 28 genes in category C, 28 in category E, 7 in category F, 13 in category G, 1 in category I, 6 in category H, 3 in category M, 2 in category O and 7 in category R. Out of these, for genes with degree of essentiality 2, there were 8 in category C, 21 in category E, 3 in category F, 8 in category G, 5 in category H, 1 in category I, 3 in category M and 2 in category O. For genes with degree of essentiality 3, 9 were in category C, 5 in category E, 5 in category F, 6 in category G, 2 in category H and 3 in category R. For genes with degree of essentiality 4, 11 were in category C, 3 in category E and 4 in category R.

Gene	COG Class	Degree of Essentiality
AceE	E	4
AceF	E	4
Acs	I	2
Apt	E	3
AspC1	E	2
AspC2	E	2
AtpA	C	4
AtpB	C	4
AtpF	C	4
AtpG	C	4
AtpH	C	4
CydA	O	2
CydB	O	2
DctA	C	2
DeoB	G	3
DeoC	F	3
DeoD	F	3
Dut	F	3
Eno	G	2

FbaB	G	2
Fdh	C	3
FumA	C	2
GalP1	G	3
GalT	C	2
GalU	M	2
GapA	G	2
GcvH1	E	2
GcvH2	E	2
GcvP1	E	2
GcvP2	E	2
GcvT	E	2
Gdh	E	4
Glk1	G	3
GlpX	E	2
GltA	C	3
GlyA	E	2
GpmI	G	2
Idh	C	3

Gene	COG Category	Degree of Essentiality
------	--------------	------------------------

Kbl	E	2
Lpd	EH	4
LpxB	M	2
LpxK	M	2
LysA1	E	2
MaeA	G	3
Mdh	C	3
MetK	H	2
NadA	H	2
NadB	H	2
NadC	H	2
NadE	H	2
PckA	C	3
PdpB2	R	3
Pgi	G	2
Pgk	G	2
PpdK	G	3
PpnK	H	3
Pta	E	2
PtsN	G	3
PurN	F	2
PurT	F	2
PutA	E	3
PutP	E	2
PyrH	F	3
SdaC2	E	2
SdhA	C	3
SdhB	C	3
SdhC	C	3

SdhD	C	3
SerA	EH	2
SerC	E	2
SpeE	E	2
SpeH	E	2
SucA	C	2
SucB	C	2
SucC	C	2
SucD	C	2
TdcD	G	2
Tdh	E	2
TpiA	G	2

Gene	COG category	Degree of Essentiality
Udp	F	3
Upp	F	2
FTT0207	R	4
FTT0208	R	4
FTT0209	R	4
FTT0361	E	3
FTT0598c	C	2
FTT0804	E	2
FTT0948c	R	3
FTT0979	E	3
FTT1248	R	3
FTT1333c	R	4
FTT1541c	C	4
FTT1633	E	2

For *Francisella tularensis* in vivo, there were 89 essential reactions, and 98 essential genes. The genes which are no longer essential in vivo, which are essential in glucose minimal medium are PyrD, dihydroorotate dehydrogenase (COG category F), FolD, methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase putative bifunctional protein (F), PyrB, aspartate carbamoyltransferase (E), CarA and CarB, carbamoyl-phosphate synthase (E), PyrE, orotate phosphoribosyltransferase (F), Alr, alanine racemase (M), FoaA, dihydrofolate reductase type I (H), SpeA, putative arginine decarboxylase (E), PyrC, dihydroorotase, adenylosuccinate synthetase (F), ThyA thymidylate synthase (F), DdlB, D-alanine—D-alanine ligase B (M). There are 48 synthetic lethal pairs in vivo consisting of 62 genes.

A number of genes with degree of essentiality 1 in glucose minimal medium become genes with degree of essentiality 2: DdlB, Alr, PyrB, PyrD, PyrC, CarA, CarB, FolD, and ThyA. Some genes which do not have degree of essentiality less than or equal to 4 in glucose have degree of essentiality 2 in vivo: FTT1651 (COG category M), Tet (COG category V: Defense mechanisms), FTT0794 (E), Pgm (G), GalE (M), WbtF (M), TdcD (R), NupC1 (F), and YbhO (I). Other genes have a higher degree of essentiality in vivo than in glucose: GcvH1, GcvH2, GcvP1, GcvP2, GcvT, MetK, Upp, SpeH, SpeE, GalU, CydA, and CydB. The intra-lethal pairs are as follows: 7 EE, 6 GG, 4 FF, 3 CC, and 3 MM. There are 8 MH pairs, 3 FG, 2 IM, 2 FH, 2 CG, 2 EG, 1 CE, 1 CM, 1MG, 1 IE, 1 RG, 1 HV.

We further validated our models by measuring amino acid and carbohydrate concentrations in defined growth media by HPLC. This analysis did not detect any differences in amino acid utilization by *Francisella* strains and it did not demonstrate selective or preferential utilization of certain amino acids or

carbon sources. This might be due to the insufficient sensitivity of our method employed to accurately and reproducibly determine small quantitative differences. More likely, however, these findings can be attributed to growing cells in saturating concentrations of defined compounds and to insufficient resolution of growth parameters over time (only one time-point was analyzed).

We participated in a TMTI exercise in which we received (incomplete) genomic data of an unknown *Francisella* strain. We were able to generate a genome scale metabolic model for this strain and predict potential therapeutic targets within seven days based on our pre-existing models for *Francisella* and using our established algorithms for in-silico analysis. A validation of those predicted targets is ongoing.

This exercise demonstrated the usefulness of our approach and the application of our methods to an unknown strain within a very short time frame.

Models for *Burkholderia*

We have completed genome-scale models with selected gene-protein reactions for the *Burkholderia mallei* China 7 (ATCC23344) and for *Burkholderia pseudomallei* K96243. The key characteristics of these models are summarized in Figure 2 and Figure 3.

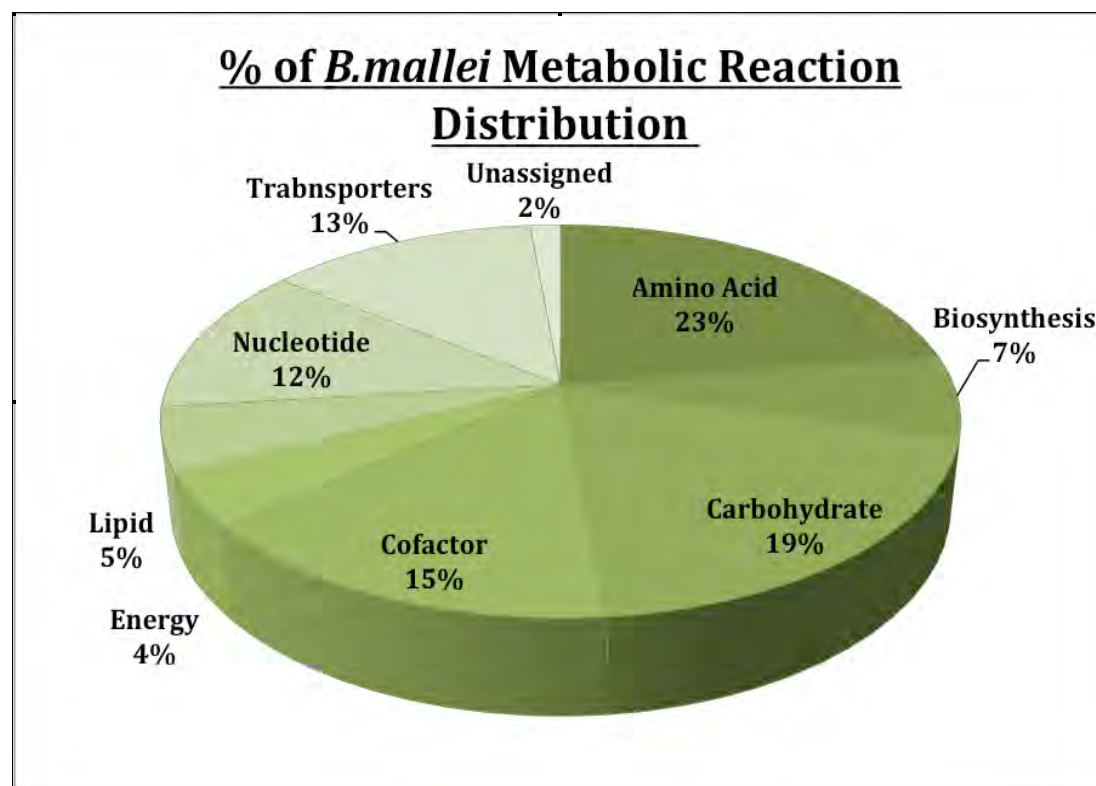


Figure 2: Reconstruction characteristics for constraints-based model of *Burkholderia mallei*. Tabulated reactions can be found in Appendices.

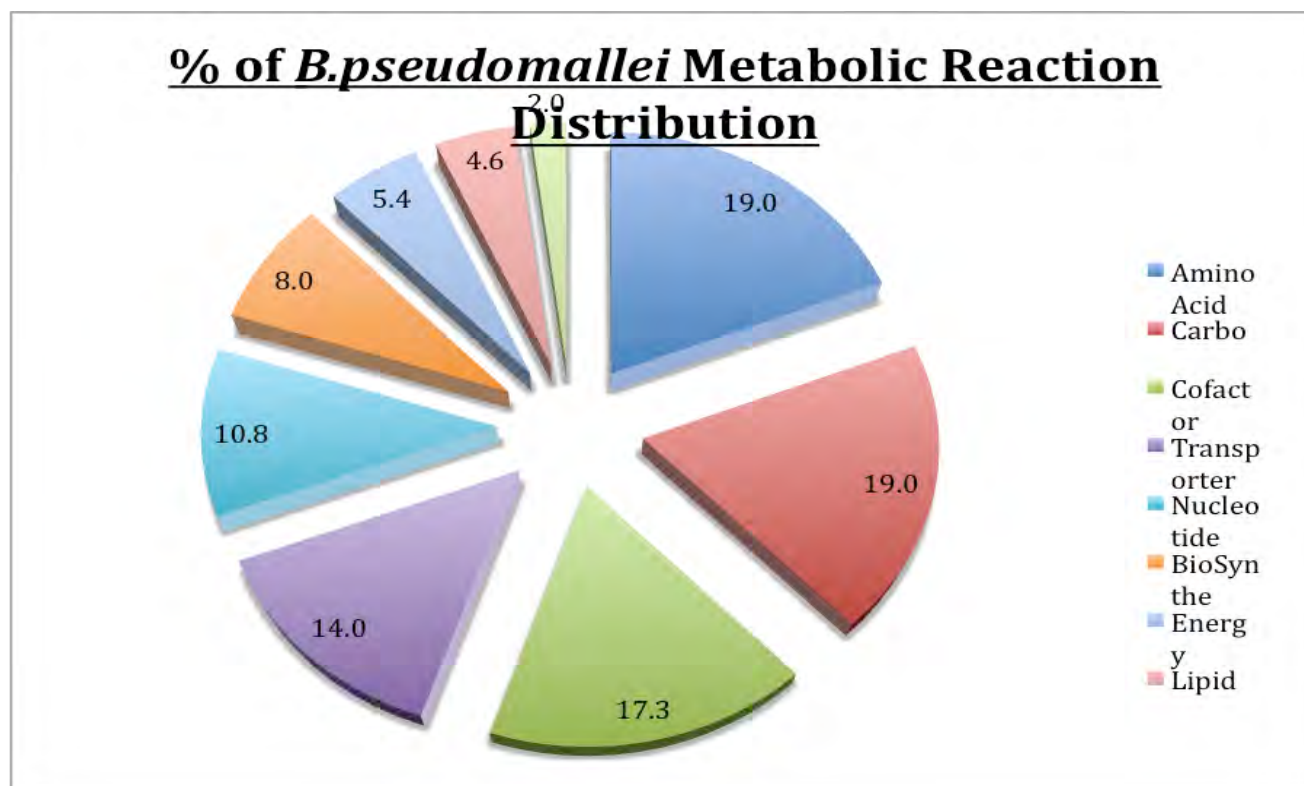


Figure 3: Reconstruction characteristics for constraints-based model of *Burkholderia pseudomallei*. Tabulated reactions can be found in Appendices.

The models for *B. mallei* and *B. pseudomallei* have been curated using existing databases and literature mining. As one might expect, the available literature is not extensive, so that many reactions had to be counted as reactions with low confidence levels. However, both models produce biomass, indicating that we have been able to include all reactions required for growth of the bacteria. The list of gene-proteins and their reactions are listed in detail in the Appendix.

In-silico simulations were performed to calculate single and synthetic lethals for *B. mallei* and *pseudomallei*. We present such an analysis in the Appendix for *B. mallei* under in-vivo conditions.

Future plans

Our project has met all milestones outlined in our proposal. As the group of Drs. K. Amemiya and D. Rozak will continue to validate our in-silico simulations, we will re-iteratively integrate new data into our models.

Key Research Accomplishments

Genome-scale metabolic models for the prototypic *Francisella* Schu4 (typeA) and *Francisella* LVS (typeB) strains have been completed.

Genome-scale metabolic models for the 28 different typeA and type B *Francisella* strains have been derived.

Genome-scale metabolic models for *Burkholderia mallei* and *Burkholderia pseudomallei* have been completed.

Algorithms have been established for calculation of single and synthetic lethals, which provide potential novel targets for therapeutic interventions.

Reportable Outcomes

Findings for *Francisella* have in part been published (BMC Syst Biol 4:118, 2010)

SBML files that contain metabolic reactions with fluxes have been created for 30 *Francisella* strains and for *Burkholderia mallei* and *Burkholderia pseudomallei*.

Conclusion

We have successfully developed and implemented genome-scale modeling of *Francisella* typeA and typeB strains and for *Burkholderia mallei* and *Burkholderia pseudomallei*. The development of suitable algorithms enables the prediction of single and synthetic lethals as therapeutic targets within a short time frame. This provides an important methodology for evaluating and utilizing data from ‘omics’ pipelines.

The application of our modeling efforts to ‘unknown’ strains for which genomic re-sequencing data had been obtained underlined the usefulness of our approach. We could also demonstrate that our model can be applied to calculating potential novel targets for therapeutic interventions for related unknown strains within a short time frame.

The limitations of our modeling approach are given by the incomplete annotation and experimental validation of bacterial genomes and by a lack of systematic validation of predicted lethals.

The knowledge gained by our approach provides an expandable platform for practical interrogation of genomic data and further in-depth research of a particular biothreat agent such as *Francisella*, but can also be adapted to other pathogens. This provides important insights into how one can integrate and analyze ‘-omics’ data as they might become available from a bacterial isolate that might have been released into the population and can generate a list of potential novel antimicrobial targets within a short time, as might be required for an adequate response to a pathogen that might carry resistance to multiple antibiotics.

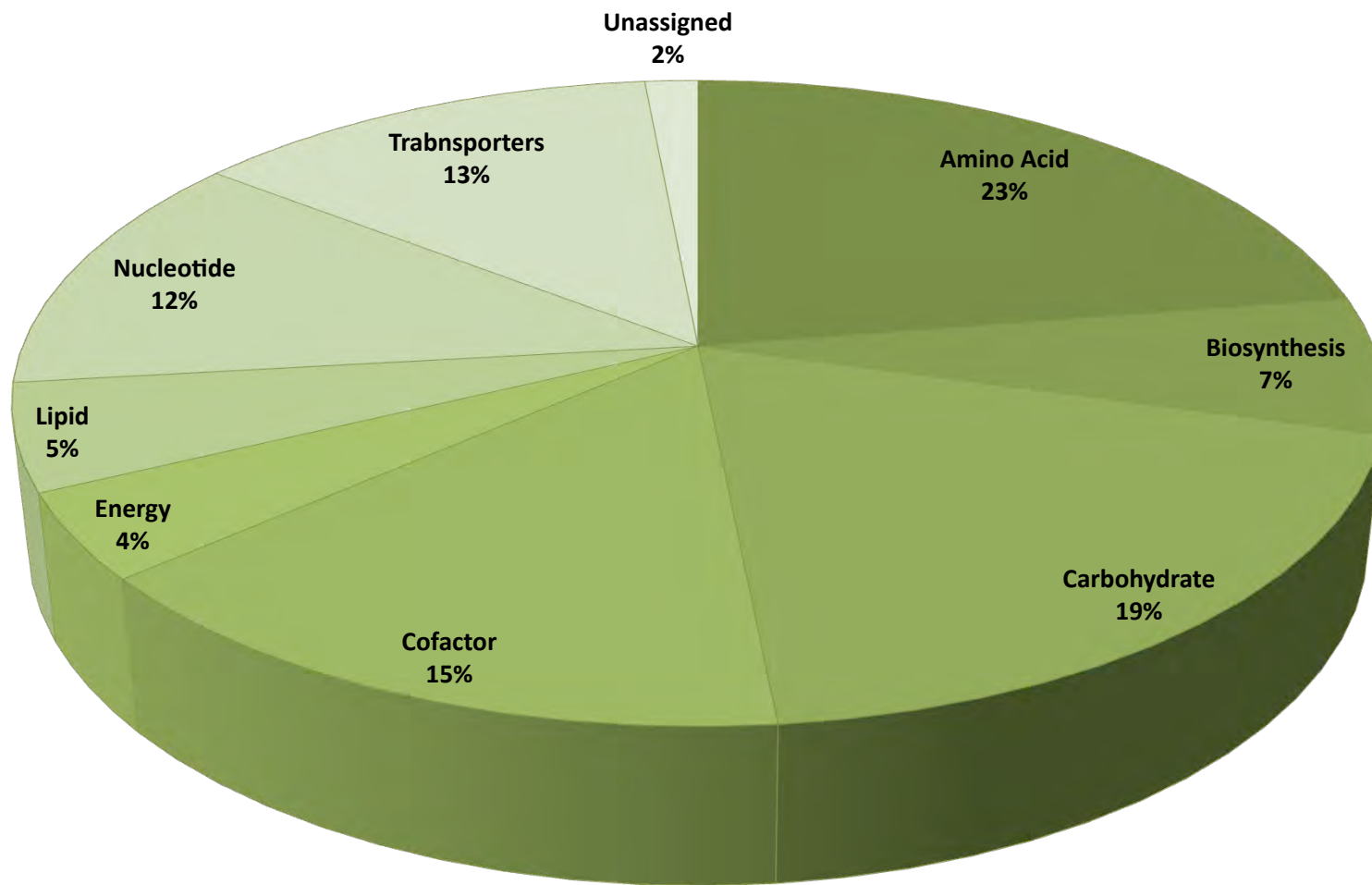
References

1. Payne DJ, Gwynn MN, Holmes DJ, Pompliano DL: **Drugs for bad bugs: confronting the challenges of antibacterial discovery.** *Nat Rev Drug Discov* 2007, **6**:29-40.
2. Becker D, Selbach M, Rollenhagen C, Ballmaier M, Meyer TF, Mann M, Bumann D: **Robust *Salmonella* metabolism limits possibilities for new antimicrobials.** *Nature* 2006, **440**:303-307.
3. Feist AM, Herrgard MJ, Thiele I, Reed JL, Palsson BO: **Reconstruction of biochemical networks in microorganisms.** *Nat Rev Microbiol* 2009, **7**:129-143.
4. Shen Y, Liu J, Estiu G, Isin B, Ahn YY, Lee DS, Barabasi AL, Kapatral V, Wiest O, Oltvai ZN: **Blueprint for antimicrobial hit discovery targeting metabolic networks.** *Proc Natl Acad Sci U S A* 2010,
5. Suthers PF, Zomorodi A, Maranas CD: **Genome-scale gene/reaction essentiality and synthetic lethality analysis.** *Mol Syst Biol* 2009, **5**:301.
6. Lun DS, Rockwell G, Guido NJ, Baym M, Kelner JA, Berger B, Galagan JE, Church GM: **Large-scale identification of genetic design strategies using local search.** *Mol Syst Biol* 2009, **5**:296.

Appendices

Gene-protein reactions for *B.mallei* and *B. pseudomallei* have been listed.

Burkholderia mallei: Gene-protein reactions



B.mallei r

Pathway	Number of reactions
Amino Acid	152
Biosynthesis	46
Carbohydrate	129
Cofactor	102
Energy	29
Lipid	36
Nucleotide	83
Trabnsporters	88
Unassigned	10

Model Contents	#
Reaction	675
Gene	777
Protein	587

metabolic Reaction Distribution

% of B.mallei metabolic reaction distribution
22.5
6.8
19.1
15.1
4.3
5.3
12.3
13.0
1.5

Abbreviation	Name	Equation	Subsystem	Gene	Protein	Protein Class
ASNN	L-asparagin [c] : asn-L + Alanine and aspartate metabolism	aa	BMA_1413	AnsB	EC-3.5.1.1	
ASNS1	asparagine [c] : asp-L + Alanine and aspartate metabolism	aa	BMA_A1158, BMA_0234, BMA_A1921	AsnB	EC-6.3.5.4	
DAAD	D-Amino ac [c] : ala-D + Alanine and aspartate metabolism	aa	BMA_A1933, BMA_0408	DadA	EC-1.4.99.1	
2DGLCNRx	2-dehydro-l [c] : 2dhglc Alternate Carbon Metabolism	car	BMA_0963	YiaE		
2DGLCNRy	2-dehydro-l [c] : 2dhglc Alternate Carbon Metabolism	car	BMA_0963	YiaE	EC-1.1.1.21	
2DGULRx	2-dehydro-l [c] : 2dhgul Alternate Carbon Metabolism	car	BMA_0963	YiaE		
2DGULRy	2-dehydro-l [c] : 2dhgul Alternate Carbon Metabolism	car	BMA_0963	YiaE		
3HCINNMH	3-hydroxyci [c] : 3hcinn Alternate Carbon Metabolism	car	BMA_2059, BMA_0452	MhpA		
3HPPPNH	3-(3-hydrox [c] : 3hpppr Alternate Carbon Metabolism	car	BMA_2059, BMA_0452	MhpA		
AGDC	N-acetylglu [c] : acgamf Alternate Carbon Metabolism	car	BMA_3168.1	NagA	EC-3.5.1.25	
ALDD25x	aldehyde di [c] : h2o + r Alternate Carbon Metabolism	car	BMA_A1365	FeaB	EC-1.2.1.39	
ALDD2x	aldehyde di [c] : acald + Alternate Carbon Metabolism	car	BMA_A1138	AldH	EC-1.2.1.3	
AMALT1	Amylomalt; [c] : malt + Alternate Carbon Metabolism	car	BMA_0817	MalQ	EC-2.4.1.25	
AMALT2	Amylomalt; [c] : malt + Alternate Carbon Metabolism	car	BMA_0817	MalQ	EC-2.4.1.25	
AMALT3	Amylomalt; [c] : malt + Alternate Carbon Metabolism	car	BMA_0817	MalQ	EC-2.4.1.25	
AMALT4	Amylomalt; [c] : malt + Alternate Carbon Metabolism	car	BMA_0817	MalQ	EC-2.4.1.25	
DDPGALA	2-dehydro-; [c] : 2dh3d; Alternate Carbon Metabolism	car	BMA_2488	DgoA	EC-4.1.2.21	
DHAPT	Dihydroxyar [c] : dha + r Alternate Carbon Metabolism	car	BMA_3211, BMA_A1809, BMA_1001, BM	DhaK+DhaL+PtsH+PtsI		
DKGLCNR2)	2,5-diketo-l [c] : 25dkgl Alternate Carbon Metabolism	car	BMA_0963	YiaE		
DKGLCNR2)	2,5-diketo-l [c] : 25dkgl Alternate Carbon Metabolism	car	BMA_0963	YiaE		
DRPA	deoxyribos; [c] : 2dr5p - Alternate Carbon Metabolism	car	BMA_A0110	DeoC	EC-4.1.2.4	
FAO4	fatty acid o; [c] : btcoa + Alternate Carbon Metabolism	car	BMA_3234	FadB		
FCLPA	L-fucose 1 [c] : fc1p <= Alternate Carbon Metabolism	car	BMA_A0575, BMA_1957	FucA, YgbL	EC-4.1.2.17	
G3PD2	glycerol-3-; [c] : glyc3p Alternate Carbon Metabolism	car	BMA_3204	GpsA	EC-1.1.1.94	
GALCTND	galactonate [c] : galctn- Alternate Carbon Metabolism	car	BMA_0254	DgoD	EC-4.2.1.6	
GALU	UTP-glucos; [c] : g1p + h Alternate Carbon Metabolism	car	BMA_A1702, BMA_0926	GalUec	EC-2.7.7.9	
GLCRAL	5-dehydro-; [c] : 5d4dgl Alternate Carbon Metabolism	car	BMA_0156	GarL	EC-4.1.2.20	
GLYCTO2	Glycolate o; [c] : glyclt + Alternate Carbon Metabolism	car	BMA_2415+BMA_A0959, BMA_2412+BM	GlcDF		
GLYCTO3	Glycolate o; [c] : glyclt + Alternate Carbon Metabolism	car	BMA_2415+BMA_A0959, BMA_2412+BM	GlcDF		
GLYCTO4	Glycolate o; [c] : 2dmm; Alternate Carbon Metabolism	car	BMA_2415+BMA_A0959, BMA_2412+BM	GlcDF		
GLYK	glycerol kin [c] : atp + g Alternate Carbon Metabolism	car	BMA_0240	GlpK	EC-2.7.1.30	
GNK	gluconokin; [c] : atp + g Alternate Carbon Metabolism	car	BMA_1194, BMA_2443	CarK, GntK	EC-2.7.1.12	
HPYRRx	hydroxypyr [c] : h + hpy Alternate Carbon Metabolism	car	BMA_0963	YiaE	EC-1.1.1.81	
HPYRRy	hydroxypyr [c] : h + hpy Alternate Carbon Metabolism	car	BMA_0963	YiaE	EC-1.1.1.81	
LCAD	lactaldehyd [c] : h2o + l; Alternate Carbon Metabolism	car	BMA_A1138	AldH	EC-1.2.1.22	

MANAO	Mannonate [c] : mana + Alternate Carbon Metabolism	car	BMA_A0768	UxuB	EC-1.1.1.57
MCITD	2-methylcit [c] : 2mcit - Alternate Carbon Metabolism	car	BMA_A1754	PrpD	EC-4.2.1.79
MCITS	2-methylcit [c] : h2o + c Alternate Carbon Metabolism	car	BMA_A1869	PrpC	EC-4.1.3.31
MICITL	methylisoci [c] : micit < Alternate Carbon Metabolism	car	BMA_A1870, BMA_A1768	PrpB	EC-4.1.3.30
OP4ENH	2-oxopent-4 [c] : 2h24pc Alternate Carbon Metabolism	car	BMA_A1135	MhpD	EC-4.2.1.80
PACCOAL	phenylacet [c] : atp + c Alternate Carbon Metabolism	car	BMA_A0539	PaaK	EC-6.2.1.30
PGLYCP	phosphogly [c] : 2pglyc Alternate Carbon Metabolism	car	BMA_A0534, BMA_0438	Gph	EC-3.1.3.18
PMANM	phosphomane [c] : man1p Alternate Carbon Metabolism	car	BMA_2191	CpsG	EC-5.4.2.8
PPC SCT	Propanoyl- [c] : pppcoa - Alternate Carbon Metabolism	car	BMA_A1763	YgfH	
TAUDO	taurine dio [c] : akg + o Alternate Carbon Metabolism	car	BMA_A2043	TauD	EC-1.14.11.1
TRE6PH	trehalose-6 [c] : h2o + t Alternate Carbon Metabolism	car	BMA_0821	TreC	EC-3.2.1.93
TRE6PP	trehalose-p [c] : h2o + t Alternate Carbon Metabolism	car	BMA_0565	OtsB	EC-3.1.3.12
TRE6PS	alpha, alpha [c] : g6p + u Alternate Carbon Metabolism	car	BMA_3010, BMA_0566	OtsA	EC-2.4.1.15
TREHe	alpha, alpha [e] : h2o + t Alternate Carbon Metabolism	car	BMA_A1166	TreA	EC-3.2.1.28
UDPG4E	UDPglucose [c] : udpg < Alternate Carbon Metabolism	car	BMA_2195	GalE	EC-5.1.3.2
XYLK	xylulokinase [c] : atp + x Alternate Carbon Metabolism	car	BMA_0343+BMA_A1079	XylB	EC-2.7.1.17
ICL	Isocitrate ly [c] : icit --> Anaplerotic reactions	car	BMA_1586	AceA	EC-4.1.3.1
ME2	malic enzyme [c] : mal-L + Anaplerotic reactions	car	BMA_2586, BMA_2477	Mae	EC-1.1.1.40
PPA	inorganic di [c] : h2o + p Anaplerotic reactions	car	BMA_0736	Ppa	EC-3.6.1.1
PPC	phosphoen [c] : co2 + h Anaplerotic reactions	car	BMA_0729	Ppc	EC-4.1.1.31
ABTA	4-aminobut [c] : 4abut + Arginine and Proline Metabolism	aa	BMA_A1480	GabT	EC-2.6.1.19
ACODA	acetylornith [c] : acorn + Arginine and Proline Metabolism	aa	BMA_1493	ArgE	EC-3.5.1.16
AGMT	agmatinase [c] : agm + l Arginine and Proline Metabolism	aa	BMA_A1597	SpeB	EC-3.5.3.11
AGPR	N-acetyl-g- [c] : acg5sa Arginine and Proline Metabolism	aa	BMA_2590	ArgC	EC-1.2.1.38
ARGDC	arginine de [c] : arg-L + Arginine and Proline Metabolism	aa	BMA_0715	AdiA	EC-4.1.1.19
ARGSL	argininosuc [c] : argsuc Arginine and Proline Metabolism	aa	BMA_1620, BMA_0718	ArgH	EC-4.3.2.1
ARGSS	argininosuc [c] : asp-L + Arginine and Proline Metabolism	aa	BMA_3363	ArgG	EC-6.3.4.5
AST	Arginine su [c] : arg-L + Arginine and Proline Metabolism	aa	BMA_0593, BMA_0592	AstA	EC-2.3.1.101
CBPS	carbamoyl- [c] : (2) atp Arginine and Proline Metabolism	aa	BMA_0770+BMA_0772	Car	EC-6.3.5.5
G5SD	glutamate- [c] : glu5p + Arginine and Proline Metabolism	aa	BMA_2450	ProA	EC-1.2.1.41
GLU5K	glutamate [c] : atp + g Arginine and Proline Metabolism	aa	BMA_2520	ProB	EC-2.7.2.11
NACODA	N-acetylorn [c] : acg5sa Arginine and Proline Metabolism	aa	BMA_1493	ArgE	
OCBT	ornithine c [c] : cbp + o Arginine and Proline Metabolism	aa	BMA_1146, BMA_0375	ArgI	EC-2.1.3.3
ORNTA	ornithine tr [c] : akg + o Arginine and Proline Metabolism	aa	BMA_A2094, BMA_A1364	YgjG	EC-2.6.1.13
P5CD	1-pyrroline- [c] : 1pyr5c Arginine and Proline Metabolism	aa	BMA_2965	PutAec	EC-1.5.1.12
P5CR	pyrroline-5- [c] : 1pyr5c Arginine and Proline Metabolism	aa	BMA_2410	ProC	EC-1.5.1.2

PRO1z	proline oxic [c] : fad + p Arginine and Proline Metabolism	aa	BMA_2965	PutAec	EC-1.5.99.8
SGDS	Succinylglut [c] : h2o + s Arginine and Proline Metabolism	aa	BMA_0596	AstE	
SGSAD	Succinylglut [c] : h2o + r Arginine and Proline Metabolism	aa	BMA_0594	AstD	
SOTA	Succinylorn [c] : akc + s Arginine and Proline Metabolism	aa	BMA_0595	AstB	
SPMS	spermidine [c] : ametar Arginine and Proline Metabolism	aa	BMA_2470	SpeE	EC-2.5.1.16
SSALy	succinate-s [c] : h2o + r Arginine and Proline Metabolism	aa	BMA_A1481	GabD	EC-1.2.1.16
AGMHE	ADP-D-glyc [c] : adphec Cell Envelope Biosynthesis	Biosynth	BMA_0421	RfaD	EC-5.1.3.20
ALAALA	D-alanine-C [c] : (2) ala- Cell Envelope Biosynthesis	Biosynth	BMA_2549	DdlB	EC-6.3.2.4
DAGK_EC	Diacylglycer [c] : (0.02) 1 Cell Envelope Biosynthesis	Biosynth	BMA_1856	DgkA	EC-2.7.1.10
EDTXS1	Endotoxin S [c] : ddcaAC Cell Envelope Biosynthesis	Biosynth	BMA_3261	LpxL	
ETHAAL	ethanolami [c] : etha --: Cell Envelope Biosynthesis	Biosynth	BMA_2983+BMA_2984	EutBC	EC-4.3.1.7
G1PACT	glucosamin [c] : accoa + Cell Envelope Biosynthesis	Biosynth	BMA_3380	GlmUec	EC-2.3.1.15
G1PTMT	glucose-1-p [c] : dttp + 1 Cell Envelope Biosynthesis	Biosynth	BMA_1989	RfbA	EC-2.7.7.24
GALUi	UTP-glucos [c] : g1p + h Cell Envelope Biosynthesis	Biosynth	BMA_A1702, BMA_0926	GalUec	EC-2.7.7.9
GDPMD	GDPmanno [c] : gdpma Cell Envelope Biosynthesis	Biosynth	BMA_2297, BMA_A1709	Gmd	EC-4.2.1.47
GF6PTA	glutamine-f [c] : f6p + g Cell Envelope Biosynthesis	Biosynth	BMA_3379, BMA_3059	GlmS	EC-2.6.1.16
GLUR	glutamate r [c] : glu-D < Cell Envelope Biosynthesis	Biosynth	BMA_A1799	MurI	EC-5.1.1.3
GMHEPAT	D-glycero-D [c] : atp + g Cell Envelope Biosynthesis	Biosynth	BMA_0422, BMA_0072	RfaEec	
GMHEPK	D-glycero-D [c] : atp + g Cell Envelope Biosynthesis	Biosynth	BMA_0422, BMA_0072	RfaEec	
GMHEPPA	D-glycero-D [c] : gmh17 Cell Envelope Biosynthesis	Biosynth	BMA_2293, BMA_0217, BMA_A1990	GmhB	
GPDDA1	Glyceropho [c] : g3pc + Cell Envelope Biosynthesis	Biosynth	BMA_2022	GlpQ	EC-3.1.4.46
GPDDA2	Glyceropho [c] : g3pe + Cell Envelope Biosynthesis	Biosynth	BMA_2022	GlpQ	EC-3.1.4.46
GPDDA3	Glyceropho [c] : g3ps + Cell Envelope Biosynthesis	Biosynth	BMA_2022	GlpQ	EC-3.1.4.46
GPDDA4	Glyceropho [c] : g3pg + Cell Envelope Biosynthesis	Biosynth	BMA_2022	GlpQ	EC-3.1.4.46
GPDDA5	Glyceropho [c] : g3pi + l Cell Envelope Biosynthesis	Biosynth	BMA_2022	GlpQ	EC-3.1.4.46
KDOPS	2-dehydro- [c] : ara5p + Cell Envelope Biosynthesis	Biosynth	BMA_1690	KdsA	EC-4.1.2.16
LPADSS	Lipid A disa [c] : lipidX + Cell Envelope Biosynthesis	Biosynth	BMA_1542	LpxB	EC-2.4.1.18
LPSSYN_EC	Lipopolysac [c] : (3) adp Cell Envelope Biosynthesis	Biosynth	BMA_0291, BMA_2108, BMA_2190	RfaC+RfaF	
MAN1PT2	mannose-1 [c] : gdp + h Cell Envelope Biosynthesis	Biosynth	BMA_0029, BMA_2310	ManC	EC-2.7.7.22
MI1PP	myo-inositc [c] : h2o + r Cell Envelope Biosynthesis	Biosynth	BMA_1664	SuhB	EC-3.1.3.25
MOAT	3-deoxy-D-i [c] : ckdo + Cell Envelope Biosynthesis	Biosynth	BMA_2188	KdtA	
MOAT2	3-deoxy-D-i [c] : ckdo + Cell Envelope Biosynthesis	Biosynth	BMA_2188	KdtA	
PAPPT3	phospho-N- [c] : udcpp Cell Envelope Biosynthesis	Biosynth	BMA_2554	MraY	EC-2.7.8.13
PGAMT	phosphoglu [c] : gam1p Cell Envelope Biosynthesis	Biosynth	BMA_0779	MrsA	EC-5.4.2.10
S7PI	sedoheptul [c] : s7p <== Cell Envelope Biosynthesis	Biosynth	BMA_2295	GmhA	
TDPDRE	dTDP-4-de [c] : dtdpdd Cell Envelope Biosynthesis	Biosynth	BMA_1988	RfbC	EC-5.1.3.13

TDPDRR	dTDP-4-deh [c] : dtdprrr Cell Envelope Biosynthesis	Biosynth BMA_1987	RfbD	EC-1.1.1.13
TDPGDH	dTDPglucos [c] : dtdpglc Cell Envelope Biosynthesis	Biosynth BMA_1983, BMA_1990	RfbB	EC-4.2.1.46
TDSK	Tetraacyldis [c] : atp + li Cell Envelope Biosynthesis	Biosynth BMA_2273	LpxK	EC-2.7.1.13
U23GAAT	UDP-3-O-(3 [c] : 3htdAC Cell Envelope Biosynthesis	Biosynth BMA_1545	LpxD	
UAAGDS	UDP-N-acet [c] : 26dap- Cell Envelope Biosynthesis	Biosynth BMA_2556	MurEec	EC-6.3.2.13
UAGAAT	UDP-N-acet [c] : 3htdAC Cell Envelope Biosynthesis	Biosynth BMA_1543	LpxA	EC-2.3.1.12
UAGCVT	UDP-N-acet [c] : pep + l Cell Envelope Biosynthesis	Biosynth BMA_A1237, BMA_2716	MurA	EC-2.5.1.7
UAGDP	UDP-N-acet [c] : acgam Cell Envelope Biosynthesis	Biosynth BMA_3380	GlmUec	EC-2.7.7.23
UAGPT3	UDP-N-acet [c] : uacgan Cell Envelope Biosynthesis	Biosynth BMA_2551	MurGec	
UAMAGS	UDP-N-acet [c] : atp + gl Cell Envelope Biosynthesis	Biosynth BMA_2553	MurD	EC-6.3.2.9
UAMAS	UDP-N-acet [c] : ala-L + Cell Envelope Biosynthesis	Biosynth BMA_2550	MurC	EC-6.3.2.8
UAPGR	UDP-N-acet [c] : h + nac Cell Envelope Biosynthesis	Biosynth BMA_0374	MurB	EC-1.1.1.15
UDPGD	UDPgucose [c] : h2o + (Cell Envelope Biosynthesis	Biosynth BMA_0423	Ugd	EC-1.1.1.22
UGMDDS	UDP-N-acet [c] : alaala + Cell Envelope Biosynthesis	Biosynth BMA_2555	MurFec	EC-6.3.2.15
UHGADA	UDP-3-O-ac [c] : h2o + l Cell Envelope Biosynthesis	Biosynth BMA_2543, BMA_2288	LpxC	
ACONT	aconitase [c] : cit <=> Citrate Cycle (TCA)	car BMA_A1755, BMA_A1868	AcnA	EC-4.2.1.3
CITL	Citrate lyase [c] : cit --> Citrate Cycle (TCA)	car BMA_A1653+BMA_A1752+BMA_A1951	CitDEF	EC-4.1.3.6
CS	citrate synthase [c] : accoa + Citrate Cycle (TCA)	car BMA_2258, BMA_A1744	GltA	
FUM	fumarate hydratase [c] : fum + l Citrate Cycle (TCA)	car BMA_A1797, BMA_0493	FumCec, FumC	EC-4.2.1.2
ICDHγ	isocitrate dehydrogenase [c] : icit + n Citrate Cycle (TCA)	car BMA_0486	Icd	EC-1.1.1.42
SUCD1i	succinate dehydrogenase [c] : fad + si Citrate Cycle (TCA)	car BMA_A1747+BMA_A1748+BMA_A1749+	Sdh	EC-1.3.99.1
SUCOAS	succinyl-CoA synthetase [c] : atp + ci Citrate Cycle (TCA)	car BMA_0275+BMA_0276	SucC	EC-6.2.1.5
4HTHRS	4-Hydroxy-lipoate synthase [c] : h2o + r Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_1384	ThrC	EC-4.2.3.1
ACBIPGT	Adenosyl carrier [c] : adcoba Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0696	CobU	
ACPS1	acyl-carrier protein [c] : apoACI Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0547	AcpS	EC-2.7.8.7
ADCOBAK	Adenosyl carrier [c] : adcoba Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0696	CobU	
ADCS	4-amino-4-hydroxy-lipoate synthase [c] : chor + r Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_2324	ChoM	
AMAOT	adenosyl carrier [c] : 8aonn Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0100	BioAec	EC-2.6.1.62
AMMQT8_	S-adenosyl carrier [c] : 2dmm Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_1593	MenG	
AMPMS	4-amino-2-hydroxy-lipoate synthase [c] : air + h2 Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_3090	ThiC	
AOXS	8-amino-7-hydroxy-lipoate synthase [c] : ala-L + Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0101	BioF	EC-2.3.1.47
APRAUR	5-amino-6-hydroxy-lipoate synthase [c] : 5apru Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_2143	RibDec	EC-1.1.1.19
ASP1DC	aspartate 1 [c] : asp-L + Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_0700	PanD	EC-4.1.1.11
ASPO3	L-aspartate [c] : asp-L + Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_2233	NadB	
ASPO4	L-aspartate [c] : asp-L + Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_2233	NadB	
ASPO5	L-aspartate [c] : asp-L + Cofactor and Prosthetic Group Biosynthesis	Cofactor BMA_2233	NadB	

ASPO6	L-aspartate [c] : asp-L + Cofactor and Prosthetic Group Biosyl Cofactor BMA_2233	NadB
BTS2	biotin synth [c] : cys-L + Cofactor and Prosthetic Group Biosyl Cofactor BMA_0103	BioBec
CBIAT	Cobinamide [c] : atp + cl Cofactor and Prosthetic Group Biosyl Cofactor BMA_1175	BtuR EC-2.5.1.17
CBL1abc	Cob(1)alam atp[c] + cbl Cofactor and Prosthetic Group Biosyl Cofactor BMA_0685, BMA_0693, BMA_A1829	BtuB+BtuC+BtuF
CBLAT	cob(l)alami [c] : atp + cl Cofactor and Prosthetic Group Biosyl Cofactor BMA_1175	BtuR EC-2.5.1.17
CDPMEK	4-(cytidine [c] : 4c2me Cofactor and Prosthetic Group Biosyl Cofactor BMA_3118	IspE
CPPPGO	coproporph [c] : cpppg3 Cofactor and Prosthetic Group Biosyl Cofactor BMA_1886	HemF EC-1.3.3.3
DB4PS	3,4-Dihydroc [c] : ru5p-D Cofactor and Prosthetic Group Biosyl Cofactor BMA_2145, BMA_0230	RibBec
DBTSr	dethiobiotin [c] : atp + cl Cofactor and Prosthetic Group Biosyl Cofactor BMA_0102	BioDec EC-6.3.3.3
DHFR	dihydrofolate [c] : dhf + h Cofactor and Prosthetic Group Biosyl Cofactor BMA_0387	FolA EC-1.5.1.3
DHFS	dihydrofolate [c] : atp + d Cofactor and Prosthetic Group Biosyl Cofactor BMA_A1717	FolCec EC-6.3.2.12
DHPPDA2	diaminohydrate [c] : 25dhp Cofactor and Prosthetic Group Biosyl Cofactor BMA_2143	RibDec EC-3.5.4.26
DHPS3	dihydropter [c] : 2ahhm Cofactor and Prosthetic Group Biosyl Cofactor BMA_0778	FolP EC-2.5.1.15
DMATT	dimethylall [c] : dmpp + Cofactor and Prosthetic Group Biosyl Cofactor BMA_A0329	IspA EC-2.5.1.1
DMPPS	1-hydroxy-2 [c] : h + h2r Cofactor and Prosthetic Group Biosyl Cofactor BMA_A1962, BMA_2228	LytB
DMQMT	3-Dimethyl [c] : 2omhn Cofactor and Prosthetic Group Biosyl Cofactor BMA_0437	UbiG
DNTPPA	Dihydroneo [c] : ahdt + Cofactor and Prosthetic Group Biosyl Cofactor BMA_0194	NtpA
DXPRI	1-deoxy-D- [c] : dxy15p Cofactor and Prosthetic Group Biosyl Cofactor BMA_1549	Dxr
DXPS	1-deoxy-D- [c] : g3p + h Cofactor and Prosthetic Group Biosyl Cofactor BMA_A0330	Dxs
FCLT	Heme B synth [c] : fe2 + p Cofactor and Prosthetic Group Biosyl Cofactor BMA_2330	HemH EC-4.99.1.1
FMNAT	FMN adenyl [c] : atp + fr Cofactor and Prosthetic Group Biosyl Cofactor BMA_2241	RibFec EC-2.7.7.2
G1SATi	glutamate- [c] : glu1sa Cofactor and Prosthetic Group Biosyl Cofactor BMA_2142, BMA_A1966	HemLec EC-5.4.3.8
GLUCYSL	glutamate- [c] : atp + cl Cofactor and Prosthetic Group Biosyl Cofactor BMA_0117	GshA EC-6.3.2.2
GRTT	geranyltran [c] : grdp + Cofactor and Prosthetic Group Biosyl Cofactor BMA_A0329	IspA EC-2.5.1.10
GTHRD	glutathione [c] : (2) gth Cofactor and Prosthetic Group Biosyl Cofactor BMA_3362	Gor EC-1.8.1.7
GTHS	glutathione [c] : atp + g Cofactor and Prosthetic Group Biosyl Cofactor BMA_3214	GshB EC-6.3.2.3
GTPCI	GTP cyclohy [c] : gtp + h Cofactor and Prosthetic Group Biosyl Cofactor BMA_A0043	FolE EC-3.5.4.16
GTPCII	GTP cyclohy [c] : gtp + (Cofactor and Prosthetic Group Biosyl Cofactor BMA_A1048, BMA_A1349	RibA EC-3.5.4.25
HBZOPT	4-hydroxyb [c] : 4hbz + Cofactor and Prosthetic Group Biosyl Cofactor BMA_2396	UbiA
HEMEOS	Heme O synth [c] : frdp + l Cofactor and Prosthetic Group Biosyl Cofactor BMA_3188	CyoE
HMBS	hydroxyme [c] : h2o + (Cofactor and Prosthetic Group Biosyl Cofactor BMA_0730	HemCec EC-4.3.1.8
HMPK1	hydroxyme [c] : 4ahmn Cofactor and Prosthetic Group Biosyl Cofactor BMA_1577	ThiDec EC-2.7.1.49
HPPK	2-amino-4-l [c] : 2ahhm Cofactor and Prosthetic Group Biosyl Cofactor BMA_2321	FolK EC-2.7.6.3
IPDPS	1-hydroxy-2 [c] : h + h2r Cofactor and Prosthetic Group Biosyl Cofactor BMA_A1962, BMA_2228	LytB
MECDPDH	2C-methyl-l [c] : 2mecdl Cofactor and Prosthetic Group Biosyl Cofactor BMA_1345	GcpE
MECDPS	2-C-methyl- [c] : 2p4c2r Cofactor and Prosthetic Group Biosyl Cofactor BMA_1489	IspF

MEPCT	2-C-methyl- [c] : 2me4p Cofactor and Prosthetic Group Biosy Cofactor BMA_1490	IspD	
MOHMT	3-methyl-2- [c] : 3mob + Cofactor and Prosthetic Group Biosy Cofactor BMA_2323	PanB	EC-2.1.2.11
NADDP	NAD diphos [c] : h2o + r Cofactor and Prosthetic Group Biosy Cofactor BMA_1560	Lig	EC-3.6.1.22
NADK	NAD kinase [c] : atp + n Cofactor and Prosthetic Group Biosy Cofactor BMA_2332	YfjB	EC-2.7.1.23
NADS1	NAD syntha [c] : atp + d Cofactor and Prosthetic Group Biosy Cofactor BMA_A0760	NadEec	EC-6.3.1.5
NAMNPP	nicotinic ac [c] : atp + h Cofactor and Prosthetic Group Biosy Cofactor BMA_0510	PncB	
NMNAT	nicotinamic [c] : atp + h Cofactor and Prosthetic Group Biosy Cofactor BMA_1887	NadD	EC-2.7.7.1
NNAM	nicotinamic [c] : h2o + r Cofactor and Prosthetic Group Biosy Cofactor BMA_1437	PncA	EC-3.5.1.19
NNAT	nicotinate-r [c] : atp + h Cofactor and Prosthetic Group Biosy Cofactor BMA_1887	NadD	EC-2.7.7.18
NNDMBRT	nicotinate-r [c] : dmbzid Cofactor and Prosthetic Group Biosy Cofactor BMA_0688	CobT	EC-2.4.2.21
NNDPR	nicotinate-r [c] : (2) h + Cofactor and Prosthetic Group Biosy Cofactor BMA_2235	NadCec	EC-2.4.2.19
OCTDPS	Octaprenyl [c] : frdp + (Cofactor and Prosthetic Group Biosy Cofactor BMA_2524	IspB	
OHBPAT	O-Phospho- [c] : glu-L + Cofactor and Prosthetic Group Biosy Cofactor BMA_1625, BMA_0433	SerC	EC-2.6.1.52
OHPHM	R04988 [c] : 2ohph Cofactor and Prosthetic Group Biosy Cofactor BMA_0437	UbiG	
OMBZLM	2-Octapren [c] : 2ombzl Cofactor and Prosthetic Group Biosy Cofactor BMA_0186	UbiE	
OMPHHX	2-octapren [c] : 2omph Cofactor and Prosthetic Group Biosy Cofactor BMA_2359	UbiH	
OPHBDC	3-octapren [c] : 3ophb Cofactor and Prosthetic Group Biosy Cofactor BMA_2151, BMA_A0501	UbiD, UbiX	
OPHHX	2-Octapren [c] : 2oph + Cofactor and Prosthetic Group Biosy Cofactor BMA_0189	UbiB	
PANTS	pantothena [c] : ala-B + Cofactor and Prosthetic Group Biosy Cofactor BMA_0701	PanCec	EC-6.3.2.1
PDX5PO	pyridoxine ! [c] : o2 + pc Cofactor and Prosthetic Group Biosy Cofactor BMA_0359	PdxHec	EC-1.4.3.5
PDX5PS	Pyridoxine ! [c] : dxy15p Cofactor and Prosthetic Group Biosy Cofactor BMA_0210+BMA_0546	PdxAJ	
PMPK	phosphome [c] : 4ampn Cofactor and Prosthetic Group Biosy Cofactor BMA_1577	ThiDec	EC-2.7.4.7
PPBNGS	porphobilin [c] : (2) 5ao Cofactor and Prosthetic Group Biosy Cofactor BMA_2601	HemBec	EC-4.2.1.24
PTPATi	pantethein [c] : atp + h Cofactor and Prosthetic Group Biosy Cofactor BMA_3125	CoaD	EC-2.7.7.3
PYAM5PO	pyridoxami [c] : h2o + c Cofactor and Prosthetic Group Biosy Cofactor BMA_0359	PdxHec	EC-1.4.3.5
PYDXK	pyridoxal ki [c] : atp + p Cofactor and Prosthetic Group Biosy Cofactor BMA_0582	PdxYec	EC-2.7.1.35
QULNS	quinolinate [c] : dhap + Cofactor and Prosthetic Group Biosy Cofactor BMA_2236	NadA	
RBFK	riboflavin ki [c] : atp + ri Cofactor and Prosthetic Group Biosy Cofactor BMA_2241	RibFec	EC-2.7.1.26
RBFSa	riboflavin s [c] : 4r5au + Cofactor and Prosthetic Group Biosy Cofactor BMA_2144	RibEec	EC-2.5.1.9
RBFSb	riboflavin s [c] : (2) dml Cofactor and Prosthetic Group Biosy Cofactor BMA_2146	RibH	EC-2.5.1.9
SERAS	(L-seryl)ade [c] : atp + h Cofactor and Prosthetic Group Biosy Cofactor BMA_A1646	EntF	
SHCHD2	sirohydroch [c] : nad + s Cofactor and Prosthetic Group Biosy Cofactor BMA_1157, BMA_0668, BMA_A1089	CysG	
SHCHF	sirohydroch [c] : fe2 + sr Cofactor and Prosthetic Group Biosy Cofactor BMA_1157, BMA_0668, BMA_A1089	CysG	
THZPSN	thiazole ph [c] : atp + c Cofactor and Prosthetic Group Biosy Cofactor BMA_2728, BMA_A0379, BMA_1708	IscS+ThiGH	
TMPKr	thiamine-pl [c] : atp + tl Cofactor and Prosthetic Group Biosy Cofactor BMA_2478	ThiL	EC-2.7.4.16
TMPPP	thiamine-pl [c] : 2mahr Cofactor and Prosthetic Group Biosy Cofactor BMA_2727	ThiE	EC-2.5.1.3

UDCPDPS	Undecapre[c] : frdp + (Cofactor and Prosthetic Group Biosy	Cofactor	BMA_1551	UppS	
UPP3MT	uroporphyr [c] : (2) amCofactor and Prosthetic Group Biosy	Cofactor	BMA_1157, BMA_0668, BMA_A1089	CysG	EC-2.1.1.10
UPPDC1	uroporphyr [c] : (4) h + Cofactor and Prosthetic Group Biosy	Cofactor	BMA_2962	HemE	EC-4.1.1.37
ADSK	adenyl-su [c] : aps + a Cysteine Metabolism	aa	BMA_1639, BMA_A0153, BMA_0637	CysC	EC-2.7.1.25
CYSS	cysteine syr [c] : acser + Cysteine Metabolism	aa	BMA_0418, BMA_1621	CysM, Cys4	EC-4.2.99.8
PAPSR	phosphoad [c] : paps + Cysteine Metabolism	aa	BMA_0665	CysH	
SADT2	sulfate adei [c] : atp + g Cysteine Metabolism	aa	BMA_0667+BMA_1623, BMA_0666+BM	CysD	EC-2.7.7.4
SERAT	serine O-ac [c] : accoa + Cysteine Metabolism	aa	BMA_1662, BMA_A0041, BMA_A0930	CysE	EC-2.3.1.30
SULR	sulfite redu [c] : (3) h2o Cysteine Metabolism	aa	BMA_0663+BMA_A1084, BMA_3052	CysI, NtsR	EC-1.8.1.2
FTHFD	formyltetra [c] : 10fthf - Folate Metabolism	Cofactor	BMA_A0482, BMA_3097	PurUec	EC-3.5.1.10
MTHFC	methenylte [c] : h2o + r Folate Metabolism	Cofactor	BMA_1724	FoID	EC-3.5.4.9
MTHFD	methylenet [c] : mlthf + Folate Metabolism	Cofactor	BMA_1724	FoID	EC-1.5.1.5
MTHFR2	5,10-methy [c] : (2) h + Folate Metabolism	Cofactor	BMA_2840	MetF	
GLNS	glutamine s [c] : atp + g Glutamate Metabolism	aa	BMA_0656, BMA_1743	GlnA, YcjK	EC-6.3.1.2
GLUDy	glutamate c [c] : glu-L + Glutamate Metabolism	aa	BMA_2439	GdhA	EC-1.4.1.4
GLUN	glutaminas [c] : gln-L + Glutamate Metabolism	aa	BMA_A0814	YneH	EC-3.5.1.2
GLUSy	glutamate s [c] : akg + g Glutamate Metabolism	aa	BMA_2735, BMA_2736	GltB+GltBD	EC-1.4.1.13
GHMT2	glycine hyd [c] : ser-L + Glycine and Serine Metabolism	aa	BMA_A0471, BMA_2075	GlyA	EC-2.1.2.1
GLYAT	glycine C-ac [c] : accoa + Glycine and Serine Metabolism	aa	BMA_A0005	KbL	EC-2.3.1.29
PSERT	phosphoser [c] : 3php + Glycine and Serine Metabolism	aa	BMA_1625, BMA_0433	SerC	EC-2.6.1.52
PSP_L	phosphoser [c] : h2o + r Glycine and Serine Metabolism	aa	BMA_1313	SerB	EC-3.1.3.3
SERD_L	L-serine de [c] : ser-L -- Glycine and Serine Metabolism	aa	BMA_2991	SdaAec	EC-4.3.1.17
THRD	L-threonine [c] : nad + t Glycine and Serine Metabolism	aa	BMA_A0006	Tdh	EC-1.1.1.10
ENO	enolase [c] : 2pg <=> Glycolysis/Gluconeogenesis	aa	BMA_1689	Eno	EC-4.2.1.11
FBP	fructose-bis [c] : fdp + h Glycolysis/Gluconeogenesis	aa	BMA_0469	Fbp	EC-3.1.3.11
HEX1	hexokinase [c] : atp + g Glycolysis/Gluconeogenesis	aa	BMA_2132	Glk	EC-2.7.1.2
PFK	phosphofru [c] : atp + f Glycolysis/Gluconeogenesis	aa	BMA_A0117	PfkB	EC-2.7.1.11
PFK_2	Phosphofru [c] : atp + t Glycolysis/Gluconeogenesis	aa	BMA_A0117	PfkB	EC-2.7.1.11
PGI	glucose-6-p [c] : g6p <=> Glycolysis/Gluconeogenesis	aa	BMA_1449	Pgi	EC-5.3.1.9
PGK	phosphogly [c] : 13dpg Glycolysis/Gluconeogenesis	aa	BMA_0295.1	Pgk	EC-2.7.2.3
PPS	phosphoen [c] : atp + h Glycolysis/Gluconeogenesis	aa	BMA_1535	Ppsa	EC-2.7.9.2
PYK	pyruvate kii [c] : adp + f Glycolysis/Gluconeogenesis	aa	BMA_0298	Pyka	EC-2.7.1.40
TPI	triose-phos [c] : dhap < Glycolysis/Gluconeogenesis	aa	BMA_1832	Tpi	EC-5.3.1.1
GLYCK	glycerate ki [c] : atp + g Glyoxylate Metabolism	car	BMA_1468	GlxK	EC-2.7.1.31
GLYCLTDx	Glycolate di [c] : glx + h Glyoxylate Metabolism	car	BMA_0963	YiaE	
GLYCLTDy	Glycolate di [c] : glx + h Glyoxylate Metabolism	car	BMA_0963	YiaE	

HOXPRx	2-hydroxy-3 [c] : glyc-R - Glyoxylate Metabolism	car	BMA_A2000, BMA_A0577	GlxR	EC-1.1.1.60
ATPPRT	ATP phosph [c] : atp + p Histidine Metabolism	aa	BMA_2715	HisG	EC-2.4.2.17
HISTD	histidinol d [c] : h2o + l Histidine Metabolism	aa	BMA_2714	HisD	EC-1.1.1.23
HSTPT	histidinol-p [c] : glu-L + Histidine Metabolism	aa	BMA_2713, BMA_3123	HisC	EC-2.6.1.9
IG3PS	Imidazole-g [c] : gln-L + Histidine Metabolism	aa	BMA_2708+BMA_2710	HisF	
IGPDH	imidazolegl [c] : eig3p + Histidine Metabolism	aa	BMA_2712	HisB	EC-4.2.1.19
PRAMPC	phosphorib [c] : h + h2c Histidine Metabolism	aa	BMA_2707	HisI	EC-3.5.4.19
PRATPP	phosphorib [c] : h2o + r Histidine Metabolism	aa	BMA_2706	PhdP	EC-3.6.1.31
PRMICli	1-(5-phosph [c] : prfp --> Histidine Metabolism	aa	BMA_2709	HisA	EC-5.3.1.16
PRPPS	phosphorib [c] : atp + r Histidine Metabolism	aa	BMA_3120	PrsA	EC-2.7.6.1
ACACT1r	acetyl-CoA [c] : (2) accr Membrane Lipid Metabolism	Lipid	BMA_1436, BMA_0199, BMA_0096, BM/AtoBec, Kth		EC-2.3.1.9
ACCOAC	acetyl-CoA [c] : accoa + Membrane Lipid Metabolism	Lipid	BMA_1654+BMA_2501+BMA_A1718+BN/Acc		EC-6.4.1.2
ACMAT1	Acyl-[acyl-c [c] : acACP Membrane Lipid Metabolism	Lipid	BMA_0534, BMA_A1218	FabB, FabF	EC-2.3.1.41
CLPNS_EC	Cardiolipin [c] : (0.04) r Membrane Lipid Metabolism	Lipid	BMA_1570	ClS	
DASYN_EC	CDP-Diacylg [c] : ctp + h Membrane Lipid Metabolism	Lipid	BMA_1550	CdsA	EC-2.7.7.41
FAO1	Fatty acid o [c] : atp + (7 Membrane Lipid Metabolism	Lipid	BMA_3234, BMA_0370, BMA_A1574, BN/FadB+FadD		
FAO2	Fatty acid o [c] : atp + (8 Membrane Lipid Metabolism	Lipid	BMA_3234, BMA_0370, BMA_A1574, BN/FadB+FadD		
FAO3	Fatty acid o [c] : atp + (9 Membrane Lipid Metabolism	Lipid	BMA_3234, BMA_0370, BMA_A1574, BN/FadB, FadB+FadD		
KAS15	b-ketoacyl s [c] : accoa + Membrane Lipid Metabolism	Lipid	BMA_2880, BMA_0530, BMA_2878	FabHec	
MACPD	Malonyl-AC [c] : h + mal Membrane Lipid Metabolism	Lipid	BMA_A1218	FabB	
MCOATA	Malonyl-Co [c] : ACP + r Membrane Lipid Metabolism	Lipid	BMA_A1458, BMA_3031, BMA_A1209, B	FabD	EC-2.3.1.39
PASYN_EC2	Phosphatid [c] : glyc3p Membrane Lipid Metabolism	Lipid	BMA_0216	PlsC	
PGPP_EC	Phosphatid [c] : h2o + (Membrane Lipid Metabolism	Lipid	BMA_2479	PgpAec	EC-3.1.3.27
PGSA_EC	Phosphatid [c] : (0.02) c Membrane Lipid Metabolism	Lipid	BMA_0553	PgsA	EC-2.7.8.5
AHCYSNS	adenosylho [c] : ahcys + Methionine Metabolism	aa	BMA_0929	Mtn	EC-3.2.2.9
CYSL	cystathionir [c] : cysth-L Methionine Metabolism	aa	BMA_1314	MetC	EC-4.4.1.8
METAT	methionine [c] : atp + h Methionine Metabolism	aa	BMA_3262	MetK	EC-2.5.1.6
GLYOX	hydroxyacy [c] : h2o + l Methylglyoxal Metabolism	car	BMA_0765	GloB	EC-3.1.2.6
LGTHL	lactoylguta [c] : gthrd + Methylglyoxal Metabolism	car	BMA_0213	GloA	EC-4.4.1.5
MGSA	methylglyo [c] : dhap -- Methylglyoxal Metabolism	car	BMA_1881	MgsA	EC-4.2.3.3
ALLTAH	allantoicase [c] : alltt + l Nitrogen	energy	BMA_1505+BMA_2460	AlaC	EC-3.5.3.4
CYNTAH	Cyanate am [c] : cynt + (Nitrogen	energy	BMA_2466	CynS	
DDGALK	2-dehydro- [c] : 2dh3d Nitrogen	energy	BMA_2489	DgoK	EC-2.7.1.58
UGLYCH	Ureidoglycc [c] : (2) h + Nitrogen	energy	BMA_1504	AllA	EC-3.5.3.19
ADA	Adenosine i [c] : adn + l Nucleotide Salvage Pathways	Nucleotic	BMA_0461	Add	EC-3.5.4.4
ADK1	adenylate k [c] : amp + i Nucleotide Salvage Pathways	Nucleotic	BMA_2277	Adk	EC-2.7.4.3

ADK3	guanylate k [c] : amp + i Nucleotide Salvage Pathways	Nucleotide BMA_2277	Adk	EC-2.7.4.8
ADK4	adenylylate [c] : amp + i Nucleotide Salvage Pathways	Nucleotide BMA_2277	Adk	
ADNK1	adenosine l [c] : adn + a Nucleotide Salvage Pathways	Nucleotide BMA_2277	Adk	EC-2.7.1.20
AMPN	AMP nucleic [c] : amp + i Nucleotide Salvage Pathways	Nucleotide BMA_A0309	Amn	EC-3.2.2.4
AP4AH	bis(5'-nucleic [c] : ap4a + i Nucleotide Salvage Pathways	Nucleotide BMA_1991	ApaH	EC-3.6.1.41
AP5AH	Ap5A hydrolase [c] : ap5a + i Nucleotide Salvage Pathways	Nucleotide BMA_1991	ApaH	
CSND	Cytosine deaminase [c] : csn + h Nucleotide Salvage Pathways	Nucleotide BMA_A0603	CodA	EC-3.5.4.1
CYTK1	cytidylate k [c] : atp + ci Nucleotide Salvage Pathways	Nucleotide BMA_0429	Cmk	EC-2.7.4.14
CYTK2	cytidylate k [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_0429	Cmk	EC-2.7.4.14
DADA	Deoxyadenosine [c] : dad-2 + i Nucleotide Salvage Pathways	Nucleotide BMA_0461	Add	
DADK	deoxyadenosine [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_2277	Adk	EC-2.7.4.11
DGK1	deoxyguanylate [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_2096	Gmkec	
DGTPH	dGTPase [c] : dgtp + i Nucleotide Salvage Pathways	Nucleotide BMA_2745	Dgt	EC-3.1.5.1
DTMPK	dTMP kinase [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1425	Tmk	EC-2.7.4.9
DUTDP	dUTP diphosphate [c] : dutp + i Nucleotide Salvage Pathways	Nucleotide BMA_2245	Dutec	EC-3.6.1.23
GK1	guanylate k [c] : atp + g Nucleotide Salvage Pathways	Nucleotide BMA_2096	Gmkec	EC-2.7.4.8
GP4GH	Gp4G hydrolase [c] : gp4g + i Nucleotide Salvage Pathways	Nucleotide BMA_1991	ApaH	
GUAD	guanine deaminase [c] : gua + h Nucleotide Salvage Pathways	Nucleotide BMA_0463	YgfP	EC-3.5.4.3
NDPK1	nucleoside- [c] : atp + g Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK2	nucleoside- [c] : atp + u Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK3	nucleoside- [c] : atp + ci Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK4	nucleoside- [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK5	nucleoside- [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK6	nucleoside- [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK7	nucleoside- [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NDPK8	nucleoside- [c] : atp + d Nucleotide Salvage Pathways	Nucleotide BMA_1348	Ndk	EC-2.7.4.6
NTPTP2	Nucleoside [c] : gtp + h Nucleotide Salvage Pathways	Nucleotide BMA_2745	Dgt	EC-3.1.5.1
RNDR1	ribonucleoside [c] : adp + t Nucleotide Salvage Pathways	Nucleotide BMA_2509+BMA_2510+BMA_A2027	NrdA	EC-1.17.4.1
RNDR2	ribonucleoside [c] : gdp + t Nucleotide Salvage Pathways	Nucleotide BMA_2509+BMA_2510+BMA_A2027	NrdA	EC-1.17.4.1
RNDR3	ribonucleoside [c] : cdp + t Nucleotide Salvage Pathways	Nucleotide BMA_2509+BMA_2510+BMA_A2027	NrdA	EC-1.17.4.1
RNDR4	ribonucleoside [c] : trdrd + i Nucleotide Salvage Pathways	Nucleotide BMA_2509+BMA_2510+BMA_A2027	NrdA	EC-1.17.4.1
RNTR1	ribonucleoside [c] : atp + tr Nucleotide Salvage Pathways	Nucleotide BMA_0629	NrdD	EC-1.17.4.2
RNTR2	ribonucleoside [c] : gtp + tr Nucleotide Salvage Pathways	Nucleotide BMA_0629	NrdD	EC-1.17.4.2
RNTR3	ribonucleoside [c] : ctp + tr Nucleotide Salvage Pathways	Nucleotide BMA_0629	NrdD	EC-1.17.4.2
RNTR4	ribonucleoside [c] : trdrd + i Nucleotide Salvage Pathways	Nucleotide BMA_0629	NrdD	EC-1.17.4.2
TMDPP	thymidine triphosphate [c] : pi + thy Nucleotide Salvage Pathways	Nucleotide BMA_A0114	DeoA	EC-2.4.2.4

TMD5	thymidylate [c] : dump + Nucleotide Salvage Pathways	Nucleotide BMA_0382	ThyA	EC-2.1.1.45
UMP5K	UMP kinase [c] : atp + u Nucleotide Salvage Pathways	Nucleotide BMA_1553	PyrHec	
UPPRT	uracil phospho [c] : prpp + Nucleotide Salvage Pathways	Nucleotide BMA_1995, BMA_1883	Upp, PyrR	EC-2.4.2.9
ATPS4r	ATP synthase adp [c] + (4) Oxidative phosphorylation	energy BMA_2954+BMA_2955+BMA_2956+BM	AtpF0+AtpF	EC-3.6.3.14,
CRNCDH	Carnitine-CoA [c] : crncoa Oxidative phosphorylation	energy BMA_A1216	CaiD	
CYTBD	cytochrome b (2) h [c] + (0) Oxidative phosphorylation	energy BMA_3177+BMA_A1835, BMA_3178+BM	CydA	
CYTBO3	cytochrome b (2.5) h [c] + Oxidative phosphorylation	energy BMA_0600+BMA_3196+BMA_A0194+BM	CyoA	
FDH2	formate dehydrogenase [c] + (3) Oxidative phosphorylation	energy BMA_A1681+BMA_A1682	Fdoec	EC-1.2.2.1,
FDH3	Formate Dehydrogenase [c] + (3) Oxidative phosphorylation	energy BMA_A1681+BMA_A1682	Fdoec	EC-1.2.2.1,
G3PD5	glycerol-3-phosphate [c] : gly3p Oxidative phosphorylation	energy BMA_A0269, BMA_0241	GlpA, GlpD	EC-1.1.99.5
G3PD6	glycerol-3-phosphate [c] : gly3p Oxidative phosphorylation	energy BMA_A0269	GlpA	EC-1.1.99.5
G3PD7	glycerol-3-phosphate [c] : 2dmm Oxidative phosphorylation	energy BMA_A0269	GlpA	EC-1.1.99.5
NADH10	NADH dehydrogenase [c] : h + m Oxidative phosphorylation	energy BMA_A0320	Ndh	EC-1.6.5.3
NADH12	NADH dehydrogenase [c] : h + nac Oxidative phosphorylation	energy BMA_A0320	Ndh	EC-1.6.5.3
NADH6	NADH dehydrogenase (4.5) h [c] + Oxidative phosphorylation	energy BMA_1816+BMA_1817+BMA_1818+BM	Nuo	EC-1.6.5.3,
NADH7	NADH dehydrogenase (3) h [c] + m Oxidative phosphorylation	energy BMA_1816+BMA_1817+BMA_1818+BM	Nuo	EC-1.6.5.3,
NADH8	NADH dehydrogenase 2dmmq8 [c] Oxidative phosphorylation	energy BMA_1816+BMA_1817+BMA_1818+BM	Nuo	EC-1.6.5.3,
NADH9	NADH dehydrogenase [c] : 2dmm Oxidative phosphorylation	energy BMA_A0320	Ndh	EC-1.6.5.3
NO3R1	Nitrate reductase (2) h [c] + n Oxidative phosphorylation	energy BMA_3132, BMA_0663+BMA_A1084, BM	CysI, NarGH	EC-1.7.99.4,
POX	pyruvate oxidase [c] : h2o + p Oxidative phosphorylation	energy BMA_A1650	PoxB	EC-1.2.2.2
THD2	NAD(P) transhydrogenase (2) h [e] + n Oxidative phosphorylation	energy BMA_2367+BMA_2368, BMA_2366+BM	Pnt	EC-1.6.1.1,
THD5	NAD transhydrogenase [c] : nad + r Oxidative phosphorylation	energy BMA_2367+BMA_2368, BMA_2366+BM	Pnt	EC-Undeter
TRDR	thioredoxin [c] : h + nac Oxidative phosphorylation	energy BMA_2123	TrxB	EC-1.8.1.9
EDA	2-dehydro-6-phosphogluconate [c] : 2ddg6p Pentose Phosphate Cycle	car BMA_2445	Eda	EC-4.1.2.14
G6PDHy	glucose 6-phosphate [c] : g6p + n Pentose Phosphate Cycle	car BMA_2130	Zwf	EC-1.1.1.49
PGDH	phosphogluconate [c] : 6pgc + Pentose Phosphate Cycle	car BMA_A0420	Gnd	EC-1.1.1.44
PGDHY	phosphogluconate [c] : 6pgc -- Pentose Phosphate Cycle	car BMA_2446	Edd	EC-4.2.1.12
RPE	ribulose 5-phosphate [c] : ru5p-D Pentose Phosphate Cycle	car BMA_A0535	Rpeec	EC-5.1.3.1
RPI	ribose-5-phosphate [c] : r5p <== Pentose Phosphate Cycle	car BMA_A1815, BMA_1260	RpiB, RpiA	EC-5.3.1.6
TAL	transaldolase [c] : g3p + s Pentose Phosphate Cycle	car BMA_1940	TalB	EC-2.2.1.2
TKT1	transketolase [c] : r5p + x Pentose Phosphate Cycle	car BMA_1629, BMA_2469, BMA_1628	TktA	EC-2.2.1.1
TKT2	transketolase [c] : e4p + x Pentose Phosphate Cycle	car BMA_1629, BMA_2469, BMA_1628	TktA	EC-2.2.1.1
ADSL1r	adenylosuccinate [c] : dcamp Purine and Pyrimidine Biosynthesis	Nucleotide BMA_2442	PurB	EC-4.3.2.2
ADSL2r	adenylosuccinate [c] : 25aics Purine and Pyrimidine Biosynthesis	Nucleotide BMA_2442	PurB	EC-4.3.2.2
ADSS	adenylosuccinate [c] : asp-L + Purine and Pyrimidine Biosynthesis	Nucleotide BMA_1333	PurA	EC-6.3.4.4
AICART	phosphoribosyl [c] : 10fthf Purine and Pyrimidine Biosynthesis	Nucleotide BMA_2356	PurH	EC-2.1.2.3

AIRC2	phosphorib [c] : air + at Purine and Pyrimidine Biosynthesis	NucleotiBMA_0302	PurK	
AIRC3	phosphorib [c] : 5aizc < Purine and Pyrimidine Biosynthesis	NucleotiBMA_0301	PurE	
ASPCT	aspartate c [c] : asp-L + Purine and Pyrimidine Biosynthesis	NucleotiBMA_1994	PyrBec	EC-2.1.3.2
CTPS2	CTP synth [c] : atp + g Purine and Pyrimidine Biosynthesis	NucleotiBMA_1691	PyrG	EC-6.3.4.2
DHORD2	dihydroorot [c] : dhor-S Purine and Pyrimidine Biosynthesis	NucleotiBMA_1253	PyrD	EC-1.3.3.1
DHORD5	dihydroorot [c] : dhor-S Purine and Pyrimidine Biosynthesis	NucleotiBMA_1253	PyrD	EC-1.3.3.1
DHORTS	dihydroorot [c] : dhor-S Purine and Pyrimidine Biosynthesis	NucleotiBMA_1993, BMA_2422	AlIB, PyrC	EC-3.5.2.3
GARFT	phosphorib [c] : 10fthf - Purine and Pyrimidine Biosynthesis	NucleotiBMA_2240	PurN	EC-2.1.2.2
GART	Phosphorib [c] : atp + fc Purine and Pyrimidine Biosynthesis	NucleotiBMA_1922	PurT	EC-Undeter
GLUPRT	glutamine r [c] : gln-L + Purine and Pyrimidine Biosynthesis	NucleotiBMA_A1714	PurF	EC-2.4.2.14
GMPS2	GMP synth [c] : atp + g Purine and Pyrimidine Biosynthesis	NucleotiBMA_2919, BMA_1522	GmpS, Gua	EC-6.3.5.2
IMPC	IMP cyclohy [c] : h2o + i Purine and Pyrimidine Biosynthesis	NucleotiBMA_2356	PurH	EC-3.5.4.10
IMPD	IMP dehydr [c] : h2o + i Purine and Pyrimidine Biosynthesis	NucleotiBMA_A1350, BMA_1524	GuaB, CbsD	EC-1.1.1.20
PRAGS	phosphorib [c] : atp + g Purine and Pyrimidine Biosynthesis	NucleotiBMA_1885	PurDec	EC-6.3.4.13
PRAIS	phosphorib [c] : atp + f Purine and Pyrimidine Biosynthesis	NucleotiBMA_2317	PurM	EC-6.3.3.1
PRFGS	phosphorib [c] : atp + f Purine and Pyrimidine Biosynthesis	NucleotiBMA_1446	PurL	EC-6.3.5.3
CBMK2	Carbamate [c] : atp + c Putative Transporters	TransporBMA_1147	ArcCec	EC-2.7.2.2
ALA_Lt6	L-alanine tr ala-L[e] + h Putative Transporters	TransporBMA_2733	YaaJ	TC-2.A.25
ALLTnt6	allantoin tr: alltn[e] + h Putative Transporters	TransporBMA_1510	AlIP	TC-2.A.39
ARGORnt3	Arginine/or arg-L[e] + o Putative Transporters	TransporBMA_1144	ArcD	TC-2.A.3.2
CHLabc	choline trar atp[c] + chc Putative Transporters	TransporBMA_1139, BMA_1141, BMA_1140, BMA_1141	YehW+YehX+YehY+YehZ	
GALCTRt6	galactarate galctr-D[e] - Putative Transporters	TransporBMA_A0851	GarP	TC-2.A.3.1
GLCRt6	glucarate tr glcr[e] + h Putative Transporters	TransporBMA_A0851	GarP	TC-2.A.3.1
GLYBabc	glycine bet: atp[c] + glyl Putative Transporters	TransporBMA_1139, BMA_1141, BMA_1140, BMA_1141	YehW+YehX+YehY+YehZ	TC-3.A.1.12
GUAt2	guanine tra gua[e] + h Putative Transporters	TransporBMA_1892	YicE	
HCINNMt2	3-hydroxyci 3hcinnm[e] Putative Transporters	TransporBMA_A0632	MhpT	
HPPNt2	3-(3-hydrox 3hpppn[e] - Putative Transporters	TransporBMA_A0632	MhpT	
URAt6	uracil trans h[e] + ura[e Putative Transporters	TransporBMA_3337	YcdG	TC-2.A.40
XANT2	xanthine tr: h[e] + xan Putative Transporters	TransporBMA_1892	YicE	TC-2.A.40
ACS	acetyl-CoA [c] : ac + at Pyruvate metabolism	TransporBMA_0802, BMA_A1794	Acs, AcsA	EC-6.2.1.1
LDH_D	D-lactate d [c] : lac-D + Pyruvate metabolism	TransporBMA_2050	Ldh	EC-1.1.1.28
ASAD	aspartate-s [c] : aspsa + Threonine and Lysine Metabolism	aa BMA_A1725	Asd	EC-1.2.1.11
ASPK	aspartate ki [c] : asp-L + Threonine and Lysine Metabolism	aa BMA_1652	ThrA	EC-2.7.2.4
DAPDC	diaminopir [c] : 26dap- Threonine and Lysine Metabolism	aa BMA_3159, BMA_2756, BMA_A1455	LysA, PddC	EC-4.1.1.20
DAPE	diaminopir [c] : 26dap- Threonine and Lysine Metabolism	aa BMA_3260	DapF	EC-5.1.1.7
DHDPry	dihydrodipi [c] : 23dhdp Threonine and Lysine Metabolism	aa BMA_2456	DapB	EC-1.3.1.26

DHDPs	dihydrodipicolinate [c] : aspsa + Threonine and Lysine Metabolism	aa	BMA_A1420, BMA_1678	DapA, DdpS	EC-4.2.1.52
SDPDS	succinyl-diamide [c] : h2o + s Threonine and Lysine Metabolism	aa	BMA_1568	DapE	EC-3.5.1.18
THDPs	tetrahydrodipicolinate [c] : h2o + s Threonine and Lysine Metabolism	aa	BMA_1566	DapD	EC-2.3.1.11
THRA	threonine alpha [c] : thr-L <= Threonine and Lysine Metabolism	aa	BMA_A1834	LtaA	EC-4.1.2.5
THRS	threonine serine [c] : h2o + r Threonine and Lysine Metabolism	aa	BMA_1384	ThrC	EC-4.2.3.1
ACGApts	N-Acetyl-D- acgam[e] + Transport, Extracellular	Transport	BMA_3211, BMA_3172, BMA_3212	PtsH+PtsI, NagE+PtsH+I	
ACMANApt	N-acetyl-D- acmana[e] + Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI	
ACNAMt2	N-acetyl-D- acnam[e] + Transport, Extracellular	Transport	BMA_1274	NanT	
ADEt2	adenine triphosphate ade[e] + h[e] Transport, Extracellular	Transport	BMA_1892	YicE	
AKGt6	2-oxoglutarate akG[e] + h[e] Transport, Extracellular	Transport	BMA_A0069	KgtPec	TC-2.A.1.6
ALAabc	L-alanine triphosphate ala-L[e] + a Transport, Extracellular	Transport	BMA_2668, BMA_0908, BMA_2934, BMA_2486, BMA_2484, BMA_2485	LivF+LivG+LivH+LivM	
ARBabc	L-arabinose arab-L[e] + Transport, Extracellular	Transport	BMA_0589, BMA_0746, BMA_0745	AraF+AraG+TC-3.A.1.2	
ARGabc	L-arginine triphosphate arg-L[e] + a Transport, Extracellular	Transport	BMA_2136, BMA_2434, BMA_2435, BMA_3228	HisM+HisP+TC-3.A.1.3	
ASpabc	L-aspartate asp-L[e] + a Transport, Extracellular	Transport	BMA_2136, BMA_2434, BMA_2435, BMA_3228	GltI+GltJ+G TC-3.A.1.3	
ASPt2_2	Aspartate triphosphate asp-L[e] + (: Transport, Extracellular	Transport	BMA_3228	DctA	
CHLt6	choline triphosphate chol[e] + h[e] Transport, Extracellular	Transport	BMA_A0971	BetT	TC-2.A.15
CSNt2	cytosine triphosphate csn[e] + h[e] Transport, Extracellular	Transport	BMA_A0601	CodB	
D-LACt2	D-lactate triphosphate h[e] + lac-D Transport, Extracellular	Transport	BMA_A1428	GlcA	
FRUpts	D-fructose 1-fru[e] + pe Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI	
FRUpts2	Fructose triphosphate fru[e] + pe Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI	
FUMt2_2	Fumarate triphosphate fum[e] + (2 : Transport, Extracellular	Transport	BMA_3228	DctA	
GABAt2	4-aminobutyl 4abut[e] + l Transport, Extracellular	Transport	BMA_A0515	GabP	
GALabc	D-galactose atp[c] + gal Transport, Extracellular	Transport	BMA_A1814	MglA	
GALTpts	Galactitol triphosphate galt[e] + pe Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI	
GAMpts	D-glucosamine gam[e] + pe Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI	
GLCNt2	D-gluconate glcn-D[e] + Transport, Extracellular	Transport	BMA_2444	IdnT	
GLCpts	D-glucose triphosphate glc-D[e] + p Transport, Extracellular	Transport	BMA_3211, BMA_3212	PtsH+PtsI, PtsH+PtsI, Pt	
GLNabc	L-glutamine atp[c] + gln Transport, Extracellular	Transport	BMA_A2097, BMA_A2096, BMA_A2098	GlnHec+Glnr TC-3.A.1.3	
GLUabc	L-glutamate atp[c] + glu Transport, Extracellular	Transport	BMA_2136, BMA_2434, BMA_2435, BMA_2742, BMA_2743, BMA_2744, BMA_2486, BMA_2484, BMA_2485	GltI+GltJ+G TC-3.A.1.3	
GLYC3Pabc	sn-Glycerol atp[c] + gly Transport, Extracellular	Transport	BMA_2742, BMA_2743, BMA_2744, BMA_2486, BMA_2484, BMA_2485	UgpA+UgpB+UgpC+Ugp	
GLYCLTt2r	glycolate triphosphate glyclt[e] + h Transport, Extracellular	Transport	BMA_A1428	GlcA	
GLYt6	glycine triphosphate gly[e] + h[e] Transport, Extracellular	Transport	BMA_2733	YaaJ	TC-2.A.3.1
HISabc	L-histidine triphosphate atp[c] + h2c Transport, Extracellular	Transport	BMA_0589, BMA_0747, BMA_0746, BMA_A0666	HisJ+HisM+HisP+HisQ	
HISt6	L-histidine triphosphate h[e] + his-L Transport, Extracellular	Transport	BMA_A0666	AroP	
IDONt2	L-idonate triphosphate h[e] + idon- Transport, Extracellular	Transport	BMA_2444	IdnT	
ILEabc	L-isoleucine atp[c] + h2c Transport, Extracellular	Transport	BMA_2668, BMA_0908, BMA_2934, BMA_2486, BMA_2484, BMA_2485	LivF+LivG+LivH+LivM	

Kabc	potassium t atp[c] + h2c	Transport, Extracellular	Transpor BMA_1874+BMA_1875+BMA_1876	KdpABC	EC-3.6.3.12,
L-LACt2	L-lactate re h[e] + lac-L	Transport, Extracellular	Transpor BMA_A1428	GlcA	
LEUabc	L-leucine tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_2668, BMA_0908, BMA_2934, BMA_3211, BMA_3212	LivF+LivG+LivH+LivK+LivM	
LYSabc	L-lysine tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_0589, BMA_0746, BMA_0745	HisM+HisP+HisQ	
LYSt6	L-lysine tr h[e] + lys-L	Transport, Extracellular	Transpor BMA_A0172	LysP	TC-2.A.3
MALt2_2	Malate tran (2) h[e] + m	Transport, Extracellular	Transpor BMA_3228	DctA	
MALTabc	maltose tra atp[c] + h2c	Transport, Extracellular	Transpor BMA_0337	MalK	TC-3.A.1.1
MALTHXabc	maltohexac atp[c] + h2c	Transport, Extracellular	Transpor BMA_0337	MalK	
MALPTabc	maltopenta atp[c] + h2c	Transport, Extracellular	Transpor BMA_0337	MalK	
MALTpts	maltose tra malt[e] + p	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	
MALTTRabc	Maltotriose atp[c] + h2c	Transport, Extracellular	Transpor BMA_0337	MalK	
MALTTTRabc	maltotetrac atp[c] + h2c	Transport, Extracellular	Transpor BMA_0337	MalK	
MANpts	D-mannose man[e] + p	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	
METabc	L-methionin atp[c] + h2c	Transport, Extracellular	Transpor BMA_3183, BMA_0413, BMA_0414	MetI+MetN+MetQ	
METDabc	D-methionin atp[c] + h2c	Transport, Extracellular	Transpor BMA_3183, BMA_0413, BMA_0414	MetI+MetN+MetQ	
MNLpts	mannitol tr mnl[e] + pe	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	
NAt7	sodium tr h[e] + na1[c]	Transport, Extracellular	Transpor BMA_A1195	ChaA	TC-2.A.36
NH4t	ammonium nh4[e] <=>	Transport, Extracellular	Transpor BMA_3217	AmtB	
NO2t2	nitrite trans h[e] + no2[c]	Transport, Extracellular	Transpor BMA_1730	NarKec	
NO3t7	nitrate tran no2[c] + no	Transport, Extracellular	Transpor BMA_1730	NarKec	
ORNabc	ornithine tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_0589, BMA_0746, BMA_0745	HisM+HisP+HisQ	TC-3.A.1.3
PHEt6	L-phenylala h[e] + phe-L	Transport, Extracellular	Transpor BMA_A0666	AroP	TC-2.A.3.1
Plabc	phosphate t atp[c] + h2c	Transport, Extracellular	Transpor BMA_0781, BMA_0780, BMA_0783, BMA_0784	PstA+PstB+PstC	TC-3.A.1.7
Plt6	phosphate t h[e] + pi[e]	Transport, Extracellular	Transpor BMA_A1572	PitA	TC-2.A.20
PROabc	L-proline tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_A0565, BMA_A0564	ProVec+ProW	
PROt6	L-proline tr h[e] + pro-L	Transport, Extracellular	Transpor BMA_0760	ProPec	TC-2.A.3.1
PTRCabc	putrescine t atp[c] + h2c	Transport, Extracellular	Transpor BMA_1298, BMA_1300, BMA_1779, BMA_1780	YdcT, PotA, PotB	TC-3.A.1.11
RIBabc	D-ribose tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_0915, BMA_1198, BMA_1196, BMA_1197	Yjff, RbsB+RbsC	TC-3.A.1.2
SBTpts	D-sorbitol t pep[c] + sbi	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	
SPMDabc	spermidine atp[c] + h2c	Transport, Extracellular	Transpor BMA_A1821, BMA_A0431, BMA_A1130, BMA_A1131	YdcT, PotA, PotB	TC-3.A.1.11
SUCct2_2	succinate tr (2) h[e] + s	Transport, Extracellular	Transpor BMA_3228	DctA	
SUCpts	sucrose tra pep[c] + su	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	
SULabc	sulfate tran atp[c] + h2c	Transport, Extracellular	Transpor BMA_1208, BMA_1209, BMA_1207, BMA_1206	CysA +CysU	TC-3.A.1.6
TAURabc	taurine tr atp[c] + h2c	Transport, Extracellular	Transpor BMA_A1580, BMA_A1582, BMA_2679, BMA_2680	TauA+TauB+TauC	TC-3.A.1.17
THRabc	L-threonine atp[c] + h2c	Transport, Extracellular	Transpor BMA_2668, BMA_0908, BMA_2934, BMA_2935	LivF+LivG+LivH+LivM	
TREpts	trehalose tr pep[c] + tre	Transport, Extracellular	Transpor BMA_3211, BMA_3212	PtsH+PtsI	

TRPt6	L-tryptophan h[e] + trp-L Transport, Extracellular	Transport BMA_A0666	AroP	TC-2.A.3.1
TSULabc	thiosulfate atp[c] + h2c Transport, Extracellular	Transport BMA_1208, BMA_1209, BMA_1207, BMA_1206	CysA + CysU	TC-3.A.1.6
TYRt6	L-tyrosine t h[e] + tyr-L Transport, Extracellular	Transport BMA_A0666	AroP	TC-2.A.3.1
VALabc	L-valine tra atp[c] + h2c Transport, Extracellular	Transport BMA_2668, BMA_0908, BMA_2934, BMA_2935	LivF+LivG+LivH+LivM	
ANPRT	anthranilate [c] : anth + Tyrosine, Tryptophan, and Phenylalanine	BMA_A0531	TrpDec	EC-2.4.2.18
CHORM	chorismate [c] : chor --> Tyrosine, Tryptophan, and Phenylalanine	BMA_0432	PheA	EC-5.4.99.5
CHORS	chorismate [c] : 3psme Tyrosine, Tryptophan, and Phenylalanine	BMA_0946	AroC	EC-4.2.3.5
DAHPS	3-deoxy-D-ribose [c] : e4p + h Tyrosine, Tryptophan, and Phenylalanine	BMA_2339, BMA_A0987	AroGec	EC-4.1.2.15
DHQS	3-dehydroquinate [c] : 2dda7c Tyrosine, Tryptophan, and Phenylalanine	BMA_2746	AroB	EC-4.2.3.4
IGPS	indole-3-glyoxylate [c] : 2cpr5p Tyrosine, Tryptophan, and Phenylalanine	BMA_A0530	TrpCec	EC-4.1.1.48
PPNDH	prephenate [c] : h + ppf Tyrosine, Tryptophan, and Phenylalanine	BMA_0432	PheA	EC-4.2.1.51
PRAli	phosphoribosyl [c] : pran --> Tyrosine, Tryptophan, and Phenylalanine	BMA_A0530	TrpCec	EC-5.3.1.24
PSCVT	3-phosphoserine [c] : pep + s Tyrosine, Tryptophan, and Phenylalanine	BMA_0430, BMA_0235	AroA	EC-2.5.1.19
SHK3D	shikimate diphosphate [c] : 3dhs k Tyrosine, Tryptophan, and Phenylalanine	BMA_2494	AroEec	EC-1.1.1.25
SHKK	shikimate kinase [c] : atp + sl Tyrosine, Tryptophan, and Phenylalanine	BMA_2747	AroK	EC-2.7.1.71
TRPS1	tryptophan [c] : 3ig3p + Tyrosine, Tryptophan, and Phenylalanine	BMA_A1719, BMA_A1721	TrpA+TrpB	EC-4.2.1.20
TRPS2	tryptophan [c] : indole + Tyrosine, Tryptophan, and Phenylalanine	BMA_A1719, BMA_A1721	TrpA+TrpB	EC-4.2.1.20
TRPS3	tryptophan [c] : 3ig3p - Tyrosine, Tryptophan, and Phenylalanine	BMA_A1719, BMA_A1721	TrpA+TrpB	EC-4.2.1.20
TYRTA	tyrosine transferase [c] : ak g + t Tyrosine, Tryptophan, and Phenylalanine	BMA_A0879, BMA_A0667	TyrB	EC-2.6.1.5
BADH	betaine-aldehyde [c] : betald Unassigned	Unassign BMA_A0915	BetB	EC-1.2.1.8
BETALDHy	betaine-aldehyde [c] : betald Unassigned	Unassign BMA_A0915	BetB	EC-1.2.1.8
CAT	catalase [c] : (2) h2o Unassigned	Unassign BMA_A1223, BMA_2391	KatE, KatG	EC-1.11.1.6
HCO3E	carbonate reductase [c] : co2 + h Unassigned	Unassign BMA_2465, BMA_1839, BMA_0095	YadF, CynT	EC-4.2.1.1
SELNPS	Selenophosphate [c] : atp + h Unassigned	Unassign BMA_A1473	SelD	EC-2.7.9.3
SOD	superoxide dismutase [c] : (2) h + Unassigned	Unassign BMA_2271	SodB	EC-1.15.1.1
ACHBS	2-aceto-2-hydroxybutyrate [c] : 2obut - Valine, leucine, and isoleucine meta aa	BMA_1847, BMA_1848+BMA_2989+BMA_2990	IlvB+IlvH	
ACLS	acetolactate [c] : h + (2) Valine, leucine, and isoleucine meta aa	BMA_1847, BMA_1848+BMA_2989+BMA_2990	IlvB+IlvH	
AHAI	acetohydroxyase [c] : alac-S + Valine, leucine, and isoleucine meta aa	BMA_1846	IlvCec	EC-1.1.1.86
DHAD1	dihydroxyacetone [c] : 23dhm Valine, leucine, and isoleucine meta aa	BMA_0677	IlvD	EC-4.2.1.9
DHAD2	Dihydroxyacetone [c] : 23dhm Valine, leucine, and isoleucine meta aa	BMA_0677	IlvD	
ILETA	isoleucine transferase [c] : ak g + il Valine, leucine, and isoleucine meta aa	BMA_0293	IlvE	EC-2.6.1.42
IPMD	3-isopropylmalate [c] : 3c2hm Valine, leucine, and isoleucine meta aa	BMA_A1726	LeuB	EC-1.1.1.85
IPPMla	3-isopropylmalate [c] : 3c2hm Valine, leucine, and isoleucine meta aa	BMA_A1727+BMA_A1729	LeuC	EC-4.2.1.33
IPPMlb	2-isopropylmalate [c] : 2ippm Valine, leucine, and isoleucine meta aa	BMA_A1727+BMA_A1729	LeuC	
IPPS	2-isopropylmalate [c] : 3mob + Valine, leucine, and isoleucine meta aa	BMA_3135	LeuA	EC-4.1.3.12
KARA2i	ketol-acid reductase [c] : 2ahbut Valine, leucine, and isoleucine meta aa	BMA_1846	IlvCec	EC-1.1.1.86

LEUTAI	leucine trans [c] : 4mop + Valine, leucine, and isoleucine meta aa		BMA_A0879, BMA_A0667, BMA_0293	TyrB, IlvE	EC-2.6.1.42
OMCDC	2-Oxo-4-me [c] : 3c4mo Valine, leucine, and isoleucine meta aa		BMA_A1726	LeuB	
THRD_L	L-threonine [c] : thr-L -- Valine, leucine, and isoleucine meta aa		BMA_0181, BMA_2154, BMA_1494	IlvA, TdyC, TdcB	
VALTA	valine trans [c] : akgl + v Valine, leucine, and isoleucine meta aa		BMA_0293	IlvE	EC-2.6.1.42
23CN2P1	2',3'-cyclic-1 [c] : 23camp + h2o <==> 3amp + h	Nucleotide	BMA_0067	CnpD	EC-3.1.4.16
23CN2P2	2',3'-cyclic-1 [c] : 23cump + h2o <==> 3ump + h	Nucleotide	BMA_0067	CnpD	EC-3.1.4.16
23CN2P3	2',3'-cyclic-1 [c] : 23ccmp + h2o <==> 3cmp + h	Nucleotide	BMA_0067	CnpD	EC-3.1.4.16
2INSD	2-Inosose d [c] : 2ins --> dkdi + h2o	car	BMA_0911	IolE	
4H2OGA	4-hydroxy-2 [c] : 4h2oxg <==> glx + pyr	car	BMA_2445	Eda	EC-4.1.3.16
5CMHISC	5-carboxym [c] : 5cmhm <==> 5cohe	aa	BMA_A1136	ChdI	EC-5.3.3.10
ACCOAL	acetate-CoA [c] : atp + coa + ppa --> adp + pi + ppcoa	car	BMA_A0367	AcaS	EC-6.2.1.13
ACGK	acetylglut [c] : acglu + atp --> acg5p + adp	aa	BMA_3249	ArgB	EC-2.7.2.8
ACGS	N-acetylglu [c] : accoa + glu-L --> acglu + coa + h	aa	BMA_2539, BMA_1751	ArgA, GnaC	EC-2.3.1.1
ACKr	acetate kinase [c] : ac + atp <==> actp + adp	car	BMA_A0120	AckA	EC-2.7.2.1
ACOAD2	acyl-CoA de [c] : h + hx2coa + nadh <==> hxcoa + nad	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOAD3	acyl-CoA de [c] : nad + occoa <==> h + nadh + oc2coa	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOAD4	acyl-CoA de [c] : dcco + nad <==> dc2coa + h + nadh	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOAD5	acyl-CoA de [c] : ddcoa + nad <==> h + nadh + trans-dd2coa	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOAD6	acyl-CoA de [c] : nad + tdcoa <==> h + nadh + td2coa	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOAD7	acyl-CoA de [c] : nad + pmtcoa <==> h + hdd2coa + nadh	car	BMA_0042+BMA_1755+BMA_1806+BM/AcoD		EC-1.3.99.3
ACOTA	acetylornit [c] : acorn + akgl <==> acg5sa + glu-L	aa	BMA_1967, BMA_0591	AstC	EC-2.6.1.11
ACP1e	acid phosph [e] : fmn + h2o --> pi + ribflv	car	BMA_0886, BMA_1357	AcpA, SurE	EC-3.1.3.2
ACPP	Acyl phosph [c] : acmp + h2o --> Rtotal + (3) h + pi	car	BMA_A1957	AcpH	EC-3.6.1.7
ADCL	4-aminoben [c] : 4adcho --> 4abz + h + pyr	cofactor	BMA_2324	ChoM	
ADPRDP	ADP-ribose [c] : adprib + h2o --> amp + (2) h + r5p	Nucleotide	BMA_1814	MprP	EC-3.6.1.13
AHCl	adenosylho [c] : ahcys + h2o --> adn + hcys-L	aa	BMA_2842	AdhM	EC-3.3.1.1
AHSERL	O-acetylho [c] : achms + ch4s --> ac + h + met-L	aa	BMA_A1890	OacA	EC-4.2.99.11
AKGD	2-oxoglutar [c] : akgl + coa + nad --> co2 + nadh + succoa	car	BMA_1052	SucAec	
AKGDb	oxoglutarat [c] : coa + sdhlm <==> dhlm + succoa	aa	BMA_1051	SucBec	EC-2.3.1.61
ALARi	alanine rac [c] : ala-L --> ala-D	aa	BMA_1575	DadX	EC-5.1.1.1
ALATA_L	L-alanine tr [c] : akgl + ala-L <==> glu-L + pyr	aa	BMA_0057	DaaT	EC-2.6.1.2
ALCD2x	alcohol de [c] : etoh + nad <==> acald + h + nadh	car	BMA_0324, BMA_A0163, BMA_A0132	AdhA, GerC	EC-1.1.1.1
ALDD20x	aldehyde de [c] : h2o + imzacd + nad --> (2) h + imzac + nadh	car	BMA_A1451, BMA_0735, BMA_2986, BM	AdhD, PuuC	EC-1.2.1.3
AMID	amidase [c] : 4gudbd + h2o --> 4gubut + nh4	aa	BMA_A1320, BMA_1864, BMA_A2061	AmiD	EC-3.5.1.4
AMID2	amidase [c] : h2o + pheacm --> nh4 + pheac	aa	BMA_A1320, BMA_1864, BMA_A2061	AmiD	EC-3.5.1.4
AMID3	amidase [c] : h2o + id3aca --> ind3ac + nh4	aa	BMA_A1320, BMA_1864, BMA_A2061	AmiD	EC-3.5.1.4

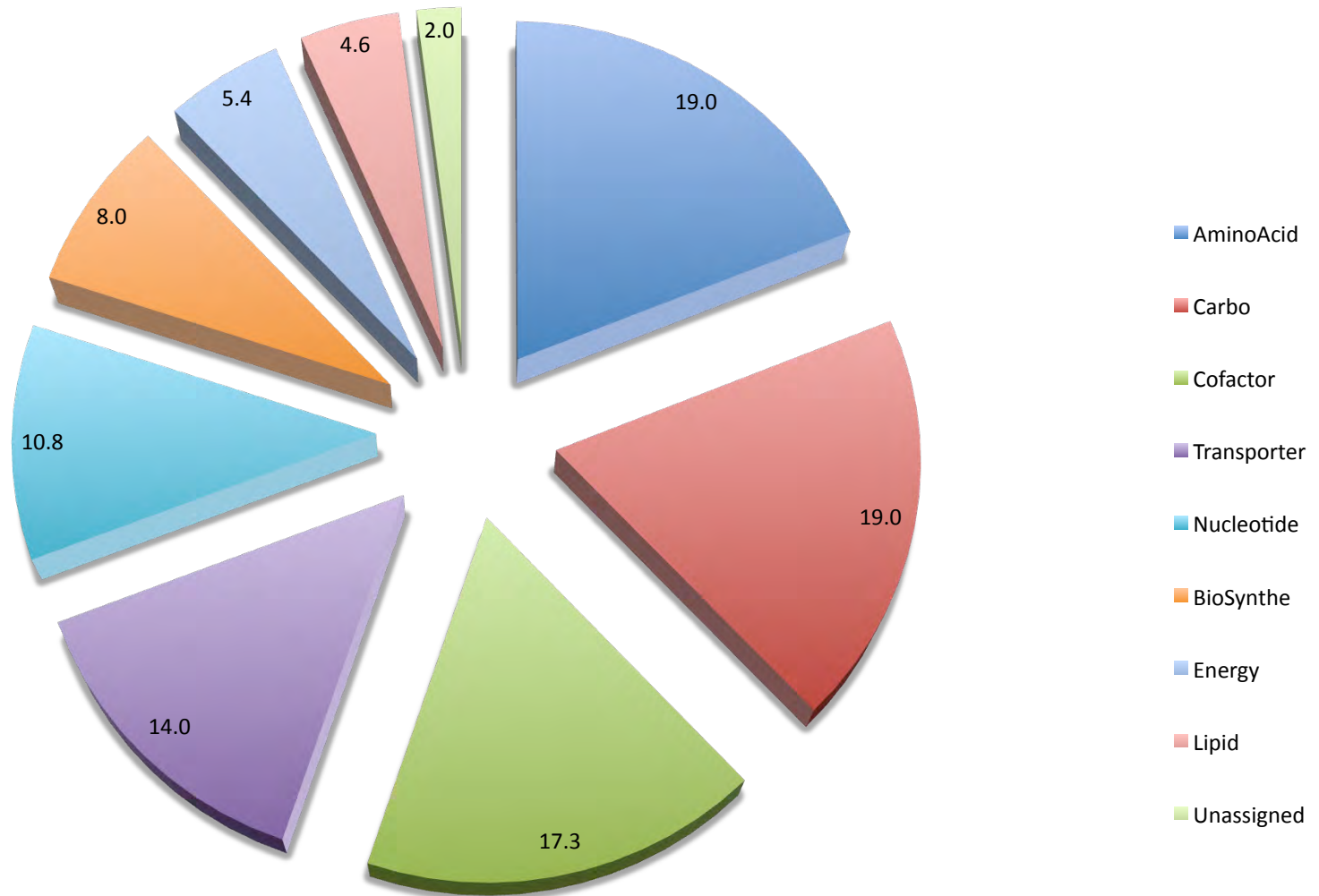
ANS1	anthranilate [c] : chor + gln-L --> anth + glu-L + h + pyr	aa	BMA_A0532, BMA_A0533	TrpEec	EC-4.1.3.27
APT	beta-alanine [c] : ala-L + msa <==> ala-B + pyr	car	BMA_2175+BMA_A1380	OamP	EC-2.6.1.18
ARGDr	arginine de [c] : arg-L + h2o <==> citr-L + nh4	aa	BMA_1145	ArcA	
ATPM	ATP mainte [c] : atp + h2o --> adp + h + pi	Nucleotic	BMA_2099	MutT	EC-3.6.1.15
CDPDSP	CDPdiacylg [c] : cdpdag + ser-L --> cmp + h + ps	Lipid	BMA_1844	PssA	EC-2.7.8.8
CELLSYN	Cellulose sy [c] : udpg --> cell + h + udp	car	BMA_A1585	YfdH	EC-2.4.1.12
CHOLD2	choline deh [c] : chol + fad --> betald + fadh2	aa	BMA_2933+BMA_A0914	BetA	EC-1.1.99.1
CHRPL	chorismate [c] : chor --> 4hbz + pyr	cofactor	BMA_1946	ChrL	
COL	Carbon-oxy [c] : cdpdddg [deleted 06/01/2007 08:38:28 PM	Lipid	BMA_1544	FabZ	
CYSTS	cystathionir [c] : hcys-L + ser-L --> cysth-L + h2o	Energy	BMA_0418, BMA_1621	Cys4, CysM	EC-4.2.1.22
CYTD	cytidine de [c] : cytd + h + h2o --> nh4 + uri	Nucleotic	BMA_A0115	Cdd	EC-3.5.4.5
D5KGK	2-Deoxy-5-l [c] : atp + d5kg --> adp + d5kgp + h	car	BMA_0913	IoIC	EC-2.7.1.92
DARD	D-arabinito [c] : abt-D + nad <==> h + nadh + xylu-D	car	BMA_0344	Mntd	EC-1.1.1.11
DCYSL	D-cysteine [c] : cys-D + h2o --> h + h2s + nh4 + pyr	aa	BMA_2137	YedO	
DDGLK	2-dehydro- [c] : 2ddglcn + atp --> 2ddg6p + adp + h	car	BMA_0961	KdgK	EC-2.7.1.45
DGC3D	2-deoxy-D- [c] : 2dglcn + nad --> 3ddgc + h + nadh	car	BMA_1115+BMA_A1811	OsyD	EC-1.1.1.12
DGCN	gluconolact [c] : g15lac + h2o --> glcn-D + h	car	BMA_A0036	GlcT	EC-3.1.1.17
DGNSK	deoxyguanc [c] : atp + dgsn --> adp + dgmp + h	Nucleotic	BMA_2322	DncK	EC-2.7.1.11
DHPDO	3,4-dihydro [c] : 34dhpha + o2 --> 5cmhmsa + h	aa	BMA_A1137	DphD	
DMOCT	3-deoxy-ma [c] : ctp + kdo --> ckdo + ppi	Biosynth	BMA_2275	KdsBec	EC-2.7.7.38
DPCOAK	dephospho [c] : atp + dpcoa --> adp + coa + h	cofactor	BMA_2534	CoaE	EC-2.7.1.24
DPR	2-dehydrop [c] : 2dhp + h + nadph --> nadp + pant-R	cofactor	BMA_0348+BMA_1471+BMA_2264	DdpR	EC-1.1.1.16
DRI	dihydrolipo [c] : accoa + dhlam --> coa + h + sadls	car	BMA_1720	AceFec	EC-2.3.1.12
ECOAH1	3-hydroxyar [c] : 3hbycoa <==> b2coa + h2o	car	BMA_0076+BMA_0200+BMA_1803+BM	HcoH+PaaF	EC-4.2.1.17
ECTB	diaminobut [c] : 24dab + akg <==> aspsa + glu-L	aa	BMA_3149+BMA_A1647	EctB	EC-2.6.1.76
ENRD	enoyl-[acyl- [c] : ddcaACP + nad --> 2ddACP + h + nadh	Lipid	BMA_1608, BMA_A1403	FabI	EC-1.3.1.9
EP PP	exopolypho [c] : h2o + polypi --> (2) h + pi	Nucleotic	BMA_0789	Ppx	EC-3.6.1.11
FBA	fructose-bis [c] : fdp <==> dhap + g3p	car	BMA_0299	CbbA	EC-4.1.2.13
FDH	formate del [c] : for + nad --> co2 + nadh	car	BMA_0451, BMA_0448+BMA_1681, BM	Fdh1+FdhB	EC-1.2.1.2
FGD	N-formylglu [c] : Nforglu + h2o --> for + glu-L	car	BMA_0652	HutG	EC-3.5.1.68
FNOR	ferredoxin-l [c] : fdxr-4:2 + h + nadp <==> fdxo-4:2 + nadph	Lipid	BMA_A0206, BMA_A1326	PyrO, FerD	EC-1.18.1.2
FORM	formimidoy [c] : forglu + h2o --> Nforglu + nh4	aa	BMA_0650	FogD	EC-3.5.3.13
FRUK	fructokinas [c] : atp + fru --> adp + f6p + h	car	BMA_3386, BMA_0331	CbhK+YdhR	EC-2.7.1.4
FUMACA	fumarylac [c] : 4fumacac + h2o --> acac + fum + h	aa	BMA_2055	FmaE	EC-3.7.1.2
GALO	galactose o [c] : gal + o2 --> dgalhxald + h2o2	car	BMA_0847	GalO	EC-1.1.3.9
GAPD	glyceraldeh [c] : g3p + nad + pi <==> 13dpdg + h + nadh	car	BMA_2468	GapA	EC-1.2.1.12

GCCa	glycine-clea [c] : gly + h + lpro --> alpro + co2	aa	BMA_2993	GcvP	EC-1.4.4.2
GCCb	glycine clea [c] : alpro + thf --> dhlpro + mlthf + nh4	aa	BMA_2994.1	GcvT	EC-2.1.2.10
GCCc	glycine-clea [c] : dhlpro + nad --> h + lpro + nadh	car	BMA_1719, BMA_1050, BMA_A2010	LpdA	EC-1.8.1.4
GDH	glutaryl-CoA [c] : glutcoa + nad --> b2coa + co2 + nadh	Lipid	BMA_2064	GcdH	EC-1.3.99.7
GLTDs	S-(hydroxyr [c] : nad + shgut <==> fglut-S + h + nadh	car	BMA_0324	GerD	
GLUDxi	glutamate c [c] : glu-L + h2o + nad --> akg + h + nadh + nh4	Energy	BMA_2439	GdhA	EC-1.4.1.2
GLUSx	glutamate s [c] : akg + gln-L + h + nadh --> (2) glu-L + nad	Energy	BMA_2735, BMA_2736	GltB+GltBD	EC-1.4.1.14
GLUTRR	glutamyl-tR [c] : glutrna + h + nadph --> glu1sa + nadp + trna	cofactor	BMA_A0505	HemA	
GLUTRS	Glutamyl-tF [c] : atp + glu-L + trnaglu --> amp + glutrna + ppi	cofactor	BMA_1600	GltX	EC-6.1.1.17
GTPDPK	GTP diphos [c] : atp + gtp --> amp + gdptp + h	Nucleotide	BMA_1098	RelA	EC-2.7.6.5
HACD1	3-hydroxyar [c] : aacoa + h + nadh <==> 3hbcoa + nad	Lipid	BMA_1438, BMA_0198	YusL, YusL,	EC-1.1.1.35
HACD2	3-hydroxyar [c] : 3ohcoa + h + nadh <==> 3hhcoa + nad	Lipid	BMA_1438, BMA_0198	YusL, FoxA	EC-1.1.1.35
HACD3	3-hydroxyar [c] : 3oocoa + h + nadh <==> 3hocoa + nad	Lipid	BMA_1438, BMA_0198	FoxA, YusL	EC-1.1.1.35
HACD4	3-hydroxyar [c] : 3odcoa + h + nadh <==> 3hdcoa + nad	Lipid	BMA_1438, BMA_0198	FoxA, YusL	EC-1.1.1.35
HACD5	3-hydroxyar [c] : 3oddcOA + h + nadh <==> 3hddcoa + nad	Lipid	BMA_1438, BMA_0198	YusL, FoxA	EC-1.1.1.35
HACD6	3-hydroxyar [c] : 3otdcOA + h + nadh <==> 3htdcOA + nad	Lipid	BMA_1438, BMA_0198	FoxA, YusL	EC-1.1.1.35
HACD7	3-hydroxyar [c] : 3ohdcOA + h + nadh <==> 3hhdcoa + nad	Lipid	BMA_1438, BMA_0198	YusL, FoxA	EC-1.1.1.35
HACD8	3-hydroxyar [c] : 3hmbcoa + nad <==> 2maacoa + h + nadh	Lipid	BMA_1438, BMA_0198	FoxA, YusL	EC-1.1.1.35
HACOADr	3-hydroxyar [c] : 3hmp + nad --> h + mmalsa + nadh	Lipid	BMA_1438, BMA_0198	YusL, FoxA	EC-1.1.1.35
HBUR1	(3R)-3-Hydr [c] : actACP + h + nadph --> 3hbACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10
HDDR5	(3R)-3-Hydr [c] : 3oxddACP + h + nadph --> 3hddACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10
HDER4	(3R)-3-Hydr [c] : 3oxdeACP + h + nadph --> 3hdeACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10
HGENDO	homogentis [c] : hgents + o2 --> 4mlacac + h	aa	BMA_2056	HmgA	EC-1.13.11.1
HHDR7	(3R)-3-Hydr [c] : 3oxhdACP + h + nadph --> 3hpaACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10
HHYR2	(3R)-3-Hydr [c] : 3oxhACP + h + nadph --> 3hhACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10
HIBD	3-hydroxyis [c] : 3hmp + nad --> 2mop + h + nadh	aa	BMA_A2000, BMA_A0577	GlxR	EC-1.1.1.31
HISD1i	histidase [c] : his-L --> nh4 + urcan	Unassign	BMA_0645	HutH	EC-4.3.1.3
HMGCOAS	Hydroxyme [c] : coa + h + hmgcoa <==> aacoa + accoa + h2o	aa	BMA_A1212	PkeB	EC-4.1.3.5
HOCR3	(3R)-3-Hydr [c] : 3oxocACP + h + nadph --> 3hocACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B FabGec, Ors		EC-1.1.1.10
HODR8	(3R)-3-Hydr [c] : 3oxocdacp + h + nadph --> 3hocdacp + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B FabGec, Ors		EC-1.1.1.10
HPPDO1	4-hydroxyp [c] : 34hpp + o2 --> co2 + hgents	aa	BMA_A0848, BMA_2582	ApeD	EC-1.13.11.1
HPYRI	hydroxypyr [c] : hpyr <==> 2h3opp	car	BMA_A0573	Hyi	EC-5.3.1.22
HSAT	Acetyl-CoA: [c] : accoa + hom-L <==> achms + coa	aa	BMA_3246	HseA	EC-2.3.1.31
HSDy	homoserine [c] : hom-L + nadp <==> aspsa + h + nadph	aa	BMA_1385	MetL	EC-1.1.1.3
HSK	homoserine [c] : atp + hom-L --> adp + h + phom	aa	BMA_A0307	ThrB	EC-2.7.1.39
HTDR6	(3R)-3-Hydr [c] : 3oxtdACP + h + nadph --> 3htdACP + nadp	Lipid	BMA_1882+BMA_A0644+BMA_A1104, B OrsD, FabG		EC-1.1.1.10

HXPRT	hypoxanthi [c] : hxn + prpp <==> imp + ppi	Nucleoti BMA_2515	Hpt	EC-2.4.2.8
HYDE	4-hydroxyp [c] : 4hpro-LT <==> 4hpro_CS	aa BMA_A1419	HdpE	EC-5.1.1.8
ILETRS	Isoleucyl-tR [c] : atp + ile-L + trnaile --> amp + iletrna + ppi	Unassign BMA_2242+BMA_A0963	IleS	EC-6.1.1.5
INS2D	inositol 2-d [c] : inost + nad --> 2ins + h + nadh	car BMA_0918	MinD	EC-1.1.1.18
ISCD	isovaleryl-C [c] : ivcoa + o2 --> 3mb2coa + h2o2	aa BMA_A0802	IvD	EC-1.3.99.1
IZPN	imidazoloni [c] : 4izp + h2o --> forglu	aa BMA_0649	HutI	EC-3.5.2.7
L-LACD2	L-Lactate de [c] : lac-L + ubq8 --> pyr + ubq8h2	aa BMA_A0283, BMA_A0374, BMA_A1565,	LldD	EC-1.1.2.3
L-LACD3	L-Lactate de [c] : lac-L + mqn8 --> mql8 + pyr	aa BMA_A0283, BMA_A0374, BMA_A1565,	LldD	EC-1.1.2.3
LDH_D2	D-lactate de [c] : lac-D + ubq8 --> pyr + ubq8h2	car BMA_2415+BMA_A0959, BMA_2412+B	GlcDF	EC-1.1.2.4
LEUTRS	Leucyl-tRN [c] : atp + leu-L + trnaleu --> amp + leutrna + ppi	Unassign BMA_2453	LeuT	EC-6.1.1.4
MALS	malate synt [c] : accoa + glx + h2o --> coa + h + mal-L	car BMA_1590	AceB	EC-4.1.3.2
MAN6PI	mannose-6 [c] : man6p <==> f6p	car BMA_0029, BMA_2310	ManC	EC-5.3.1.8
MCST	3-mercapto [c] : cyan + mercppyr <==> h + pyr + tcynt	car BMA_A0325	GlpE1	EC-2.8.1.2
MDH	malate deh [c] : mal-L + nad <==> h + nadh + oaa	car BMA_A1751	Mdh	EC-1.1.1.37
MECH	methylglut [c] : hmgcoa --> 3mgcoa + h2o	aa BMA_A0804	EcoH	EC-4.2.1.18
MEGL	methionine [c] : h2o + met-L --> 2obut + ch4s + nh4	aa BMA_A1317	MetB	EC-4.4.1.11
MLACI	maleylacet [c] : 4mlacac --> 4fumacac	aa BMA_3128	MaiA	EC-5.2.1.2
MMSAD1	methylmalc [c] : 2mop + coa + nad --> co2 + nadh + ppcoa	car BMA_2931+BMA_A1379	MmsA	EC-1.2.1.27
MMSAD2	methylmalc [c] : coa + nad + ppal --> h + nadh + ppcoa	car BMA_2931+BMA_A1379	MmsA	EC-1.2.1.27
MMSAD3	methylmalc [c] : coa + msa + nad --> accoa + co2 + nadh	car BMA_2931+BMA_A1379	MmsA	EC-1.2.1.27
MMSDHir	methylmalc [c] : coa + mmalsa + nad --> co2 + nadh + ppcoa	car BMA_2931+BMA_A1379	MmsA	EC-1.2.1.27
MTART	tartrate de [c] : nad + tart-M --> h + nadh + oxglyc	car BMA_A0011	TtuC	EC-1.1.1.93
MTCC	methylcrotr [c] : 3mb2coa + atp + hco3 --> 3mgcoa + adp + h	aa BMA_A0805, BMA_A0803	AcoA+CarT	EC-6.4.1.4
MTHPTGHM	5-methyltel [c] : 5mthglu + hcys-L --> met-L + thglu	aa BMA_0467	MetE	EC-2.1.1.14
NCP	N-carbamoy [c] : cbmps + h + h2o --> co2 + nh3 + ptrc	aa BMA_0125	CnH	EC-3.5.1.53
NTP3	nucleoside- [c] : gtp + h2o --> gdp + h + pi	Nucleoti BMA_2099	MutT	EC-3.6.1.15
NTP4	nucleoside- [c] : dgtp + h2o --> dgdp + h + pi	Nucleoti BMA_2099	MutT	EC-3.6.1.15
NTRIR2x	Nitrite Red [c] : (5) h + (3) nadh + no2 --> (2) h2o + (3) nad +	Energy BMA_A1085+BMA_A1086, BMA_3130+B	NirBD	
OCOAT1r	3-oxoacid C [c] : acac + succoa <==> aacoa + succ	transpor BMA_A0047, BMA_1108, BMA_A0046, B	OosT+OosT	EC-2.8.3.5
OMPDC	orotidine-5 [c] : h + orot5p --> co2 + ump	Nucleoti BMA_2481	PyrF	EC-4.1.1.23
ORCD	ornithine c [c] : orn-L --> nh4 + pro-L	aa BMA_A1290	OrnC	EC-4.3.1.12
ORNTAC	ornithine tr [c] : acorn + glu-L <==> acglu + orn-L	aa BMA_2539	GnaC	EC-2.3.1.35
ORPT	orotate phc [c] : orot5p + ppi <==> orot + prpp	Nucleoti BMA_2587	PyrE	EC-2.4.2.10
OXADC	oxalate dec [c] : h + oxa --> co2 + for	car BMA_A1259	CpF	EC-4.1.1.2
OXCT	3-oxoadipa [c] : 3oxadp + succoa <==> oxadpcoa + succ	transpor BMA_A0047, BMA_1108, BMA_A0046, B	OosT+OosT	EC-2.8.3.6
PDH	pyruvate de [c] : coa + nad + pyr --> accoa + co2 + nadh	car BMA_1721, BMA_A1737	AceEec	EC-1.2.4.1

PGCD	phosphogly [c] : 3pg + nad --> 3php + h + nadh	energy	BMA_0137	SerA	EC-1.1.1.95
PGL	6-phosphog [c] : 6pgl + h2o --> 6pgc + h	car	BMA_2131	Pgl	EC-3.1.1.31
PGM	phosphogly [c] : 3pg <==> 2pg	car	BMA_3208, BMA_1804, BMA_2350	GpmB, Gpn	EC-5.4.2.1
PGMT	phosphoglu [c] : g1p <==> g6p	car	BMA_2191	CpsG	EC-5.4.2.2
PhnN	ribose 1,5-l [e] : atp + r15bp --> adp + prpp	car	BMA_2397	PhnN	
PHOC	phospholip [c] : 12dagpc + h2o --> 12dgr + cholp + h	car	BMA_0886, BMA_1268+BMA_A0611+BM	PhoE, PhoC	EC-3.1.4.3
PNTK	pantothena [c] : atp + pnto-R --> 4ppan + adp + h	cofactor	BMA_0070	CoaA	EC-2.7.1.33
PPCDC	phosphopa [c] : 4ppcys + h --> co2 + pan4p	cofactor	BMA_2244	CoaBC	EC-4.1.1.36
PPCKG	phosphoen [c] : gtp + oaa --> co2 + gdp + pep	car	BMA_3042	Pck	EC-4.1.1.32
PPGPP	PpGpp pho [c] : gdpdp + h2o <==> gdp + ppi	Nucleoti	BMA_2094	GpyP	EC-3.1.7.2
PPNCL2	phosphopa [c] : 4ppan + ctp + cys-L --> 4ppcys + cmp + h + p	cofactor	BMA_2244	CoaBC	EC-6.3.2.5
PRASCS	phosphorib [c] : 5aizc + asp-L + atp <==> 25aics + adp + h + p	Nucleoti	BMA_0300	PhsC	EC-6.3.2.6
PTAr	phosphotra [c] : accoa + pi <==> actp + coa	car	BMA_A0121	PacT	EC-2.3.1.8
RBK	ribokinase [c] : atp + rib-D --> adp + h + r5p	Nucleoti	BMA_2506	DeoK	EC-2.7.1.15
SARCO	sarcosine o [c] : h2o + o2 + sarcs --> fald + gly + h2o2	aa	BMA_A0892	SolA	EC-1.5.3.1
SDPTA	succinyldia [c] : akgl + sl26da <==> glu-L + sl2a6o	aa	BMA_1565, BMA_1967, BMA_0591	SdaT, AstC	EC-2.6.1.17
SERD_D	D-serine de [c] : ser-D --> nh4 + pyr	aa	BMA_0176	DsdA	EC-4.3.1.18
SLCYSS	O-acetyl-L- [c] : acser + tsul --> ac + slcys	aa	BMA_0418, BMA_1621	CysM, Cys4	
THMDPe	thiamin dip [e] : (2) h2o + thmpp --> h + (2) pi + thm	Nucleoti	BMA_1357	SurE	EC-3.1.3.2
TSULST	thiosulfate [c] : cyan + tsul --> h + so3 + tcynt	aa	BMA_A0325	GlpE1	EC-2.8.1.1
URCN	urocanase [c] : h2o + urcan --> 4izp	aa	BMA_0647	HutU	EC-4.2.1.49
UREA2	urease [c] : (2) h + h2o + urea --> co2 + (2) nh4	Nucleoti	BMA_2183, BMA_2184, BMA_2182	UreA+UreB	EC-3.5.1.5
UREASE	urea carbox [c] : atp + hco3 + urea <==> adp + allphn + h + pi	aa	BMA_A1883	UrcB	EC-6.3.4.6
UREI	beta-ureidc [c] : cala + h + h2o --> ala-B + co2 + nh3	Nucleoti	BMA_A1099	AlIC	EC-3.5.1.6
VALTRS	Valyl-tRNA : [c] : atp + trnaval + val-L --> amp + ppi + valtrna	Unassign	BMA_0927	ValS	EC-6.1.1.9
XANDa	xanthine de [c] : h2o + hxan + nad --> h + nadh + xan	Nucleoti	BMA_2042, BMA_2041	XanDc, Xan	EC-1.1.1.20
XANdb	xanthine de [c] : h2o + nad + xan --> h + nadh + urate	Nucleoti	BMA_2042, BMA_2041	XanD, XanD	EC-1.1.1.20
XYLTD_D	xylitol dehy [c] : nad + xylt --> h + nadh + xylu-D	car	BMA_A1076	OziN	EC-1.1.1.9

Burkholderia pseudomallei: gene-protein reactions



Abbreviation	Name	Equation	Gene	Protein
CBMK2	Carbamate kinase	$[c] : \text{atp} + \text{co2} + \text{nh4} \rightarrow \text{adp} + \text{cbp} + (2) \text{h}$	BPSL1745	ArcCec
ALA_Lt6	L-alanine transport in/out via pr	$\text{ala-L}[e] + \text{h}[e] \rightleftharpoons \text{ala-L}[c] + \text{h}[c]$	BPSL3157	YaaJ
ALLTnt6	allantoin transport in/out via pr	$\text{alltn}[e] + \text{h}[e] \rightleftharpoons \text{alltn}[c] + \text{h}[c]$	BPSL2120	AIIP
ARGORnt3	Arginine/ornithine antiporter	$\text{arg-L}[e] + \text{orn-L}[c] \rightleftharpoons \text{arg-L}[c] + \text{orn-L}[e]$	BPSL1742	ArcD
CHLabc	choline transport via ABC system	$\text{atp}[c] + \text{chol}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{chol}[c] + \text{h}[c] + \text{pi}[c]$	BPSL1739, BPSL1	YehW+YehX+YehY+YehZ
GALCTRt6	galactarate transport in/out via	$\text{galctr-D}[e] + \text{h}[e] \rightleftharpoons \text{galctr-D}[c] + \text{h}[c]$	BPSS0342	GarP
GLCRt6	glucarate transport in/out via pr	$\text{glcr}[e] + \text{h}[e] \rightleftharpoons \text{glcr}[c] + \text{h}[c]$	BPSS0342	GarP
GLYBabc	glycine betaine transport via AB	$\text{atp}[c] + \text{glyb}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{glyb}[c] + \text{h}[c] + \text{pi}[c]$	BPSL1739, BPSL1	YehW+YehX+YehY+YehZ
GUAT2	guanine transport in via proton	$\text{gua}[e] + \text{h}[e] \rightarrow \text{gua}[c] + \text{h}[c]$	BPSL1136	YicE
HCINNmt2	3-hydroxycinnamic acid transpo	$3\text{hcinm}[e] + \text{h}[e] \rightleftharpoons 3\text{hcinm}[c] + \text{h}[c]$	BPSS0782	MhpT
HPPPNt2	3-(3-hydroxyphenyl)propionate	$3\text{hpppn}[e] + \text{h}[e] \rightleftharpoons 3\text{hpppn}[c] + \text{h}[c]$	BPSS0782	MhpT
URAT6	uracil transport in/out via proto	$\text{h}[e] + \text{ura}[e] \rightleftharpoons \text{h}[c] + \text{ura}[c]$	BPSL0282	YcdG
XANT2	xanthine transport in via proton	$\text{h}[e] + \text{xan}[e] \rightarrow \text{h}[c] + \text{xan}[c]$	BPSL1136	YicE
ACGApts	N-Acetyl-D-glucosamine transp	$\text{acgam}[e] + \text{pep}[c] \rightarrow \text{acgam6p}[c] + \text{pyr}[c]$	BPSL0499, BPSL0	PtsH+PtsI, NagE+PtsH+Pt
ACMANApts	N-acetyl-D-mannosamine trans	$\text{acmana}[e] + \text{pep}[c] \rightarrow \text{acmanap}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI
ACNAMt2	N-acetylneuraminate proton syr	$\text{acnam}[e] + \text{h}[e] \rightarrow \text{acnam}[c] + \text{h}[c]$	BPSL1881	NanT
ADEt2	adenine transport via proton syr	$\text{ade}[e] + \text{h}[e] \rightleftharpoons \text{ade}[c] + \text{h}[c]$	BPSL1136	YicE
AKGt6	2-oxoglutarate transport in/out	$\text{akg}[e] + \text{h}[e] \rightleftharpoons \text{akg}[c] + \text{h}[c]$	BPSL1825	KgtPec
ALAabc	L-alanine transport via ABC syst	$\text{ala-L}[e] + \text{atp}[c] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{ala-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSL3417, BPSL0	LivF+LivG+LivH+LivJ+LivI
ARBabc	L-arabinose transport via ABC s	$\text{arab-L}[e] + \text{atp}[c] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{arab-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSS0774, BPSL2	AraF+AraG+AraH
ARGabc	L-arginine transport via ABC sys	$\text{arg-L}[e] + \text{atp}[c] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{arg-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSL1030, BPSL1	HisM+HisP+HisQ
ASPabc	L-aspartate transport via ABC s	$\text{asp-L}[e] + \text{atp}[c] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{asp-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSL2922, BPSL2	GltI+GltJ+GltK+GltL
ASPt2_2	Aspartate transport via proton s	$\text{asp-L}[e] + (2) \text{h}[e] \rightarrow \text{asp-L}[c] + (2) \text{h}[c]$	BPSL0425	DctA
CHLt6	choline transport in/out via prot	$\text{chol}[e] + \text{h}[e] \rightleftharpoons \text{chol}[c] + \text{h}[c]$	BPSS1310	BetT
CSNt2	cytosine transport in via proton	$\text{csn}[e] + \text{h}[e] \rightarrow \text{csn}[c] + \text{h}[c]$	BPSS0759	CodB
D-LACT2	D-lactate transport via proton s	$\text{h}[e] + \text{lac-D}[e] \rightleftharpoons \text{h}[c] + \text{lac-D}[c]$	BPSS0324	GlcA
FRUpts	D-fructose transport via PEP:Pyr	$\text{fru}[e] + \text{pep}[c] \rightarrow \text{f1p}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI
FRUpts2	Fructose transport via PEP:Pyr	$\text{fru}[e] + \text{pep}[c] \rightarrow \text{f6p}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI
FUMt2_2	Fumarate transport via proton s	$\text{fum}[e] + (2) \text{h}[e] \rightarrow \text{fum}[c] + (2) \text{h}[c]$	BPSL0425	DctA
GABAt2	4-aminobutyrate transport in vi	$4\text{abut}[e] + \text{h}[e] \rightarrow 4\text{abut}[c] + \text{h}[c]$	BPSL3065	GabP
GALTpts	Galactitol transport via PEP:Pyr	$\text{galt}[e] + \text{pep}[c] \rightarrow \text{galt1p}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI
GAMpts	D-glucosamine transport via PE	$\text{gam}[e] + \text{pep}[c] \rightarrow \text{gam6p}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI
GLCNt2	D-gluconate transport via proto	$\text{glcn-D}[e] + \text{h}[e] \rightleftharpoons \text{glcn-D}[c] + \text{h}[c]$	BPSL2930	IdnT
GLCpts	D-glucose transport via PEP:Pyr	$\text{glc-D}[e] + \text{pep}[c] \rightarrow \text{g6p}[c] + \text{pyr}[c]$	BPSL0440, BPSL0	PtsH+PtsI, PtsH+PtsI, PtsI
GLNabc	L-glutamine transport via ABC s	$\text{atp}[c] + \text{gln-L}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{gln-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSS2337, BPSS2	GlnHec+GlnPec+GlnQec
GLUabc	L-glutamate transport via ABC s	$\text{atp}[c] + \text{glu-L}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{glu-L}[c] + \text{h}[c] + \text{pi}[c]$	BPSL2922, BPSL2	GltI+GltJ+GltK+GltL
GLYC3Pabc	sn-Glycerol 3-phosphate transp	$\text{atp}[c] + \text{glyc3p}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{glyc3p}[c] + \text{h}[c] + \text{pi}[c]$	BPSL3166, BPSL3	UgpA+UgpB+UgpC+UgpE
GLYCLTt2r	glycolate transport via proton s	$\text{glyclt}[e] + \text{h}[e] \rightleftharpoons \text{glyclt}[c] + \text{h}[c]$	BPSS0324	GlcA
GLYt6	glycine transport in/out via prot	$\text{gly}[e] + \text{h}[e] \rightleftharpoons \text{gly}[c] + \text{h}[c]$	BPSL3157	YaaJ
HISabc	L-histidine transport via ABC sy	$\text{atp}[c] + \text{his-L}[e] + \text{h2o}[c] \rightarrow \text{adp}[c] + \text{h}[c] + \text{his-L}[c] + \text{pi}[c]$	BPSL1033, BPSL1	HisJ+HisM+HisP+HisQ
HISt6	L-histidine transport in via prot	$\text{h}[e] + \text{his-L}[e] \rightleftharpoons \text{h}[c] + \text{his-L}[c]$	BPSS0807	AroP
IDONt2	L-idonate transport via proton s	$\text{h}[e] + \text{idon-L}[e] \rightleftharpoons \text{h}[c] + \text{idon-L}[c]$	BPSL2930	IdnT

ILEabc	L-isoleucine transport via ABC syst atp[c] + h2o[c] + ile-L[e] --> adp[c] + h[c] + ile-L[c] + pi[c]	BPSL3417, BPSL0 LivF+LivG+LivH+LivJ+LivI
Kabc	potassium transport via ABC syst atp[c] + h2o[c] + k[e] --> adp[c] + h[c] + k[c] + pi[c]	BPSL1171+BPSL1 KdpABC
L-LACt2	L-lactate reversible transport via h[e] + lac-L[e] <==> h[c] + lac-L[c]	BPSS0324 GlcA
LEUabc	L-leucine transport via ABC syst atp[c] + h2o[c] + leu-L[e] --> adp[c] + h[c] + leu-L[c] + pi[c]	BPSL3417, BPSL0 LivF+LivG+LivH+LivJ+LivI
LYSabc	L-lysine transport via ABC syst atp[c] + h2o[c] + lys-L[e] --> adp[c] + h[c] + lys-L[c] + pi[c]	BPSL1030, BPSL1 HisM+HisP+HisQ
LYSt6	L-lysine transport in/out via pro h[e] + lys-L[e] <==> h[c] + lys-L[c]	BPSS1913 LysP
MALt2_2	Malate transport via proton sym (2) h[e] + mal-L[e] --> (2) h[c] + mal-L[c]	BPSL0425 DctA
MALTabc	maltose transport via ABC syst atp[c] + h2o[c] + malt[e] --> adp[c] + h[c] + malt[c] + pi[c]	BPSL0833 MalK
MALTHXabc	maltohexaose transport via ABC atp[c] + h2o[c] + malthx[e] --> adp[c] + h[c] + malthx[c] + pi[c]	BPSL0833 MalK
MALTPTabc	maltopentaose transport via ABC atp[c] + h2o[c] + maltpt[e] --> adp[c] + h[c] + maltpt[c] + pi[c]	BPSL0833 MalK
MALTpts	maltose transport via PEP:Pyr P malt[e] + pep[c] --> malt6p[c] + pyr[c]	BPSL0440, BPSL0 PtsH+PtsI
MALTTRabc	Maltotriose transport via ABC syst atp[c] + h2o[c] + malttr[e] --> adp[c] + h[c] + malttr[c] + pi[c]	BPSL0833 MalK
MALTTTRabc	maltotetraose transport via ABC atp[c] + h2o[c] + maltttr[e] --> adp[c] + h[c] + maltttr[c] + pi[c]	BPSL0833 MalK
MANpts	D-mannose transport via PEP:Pyr P man[e] + pep[c] --> man6p[c] + pyr[c]	BPSL0440, BPSL0 PtsH+PtsI
METabc	L-methionine transport via ABC atp[c] + h2o[c] + met-L[e] --> adp[c] + h[c] + met-L[c] + pi[c]	BPSL2502, BPSL2 MetI+MetN+MetQ
METDabc	D-methionine transport via ABC atp[c] + h2o[c] + met-D[e] --> adp[c] + h[c] + met-D[c] + pi[c]	BPSL2502, BPSL2 MetI+MetN+MetQ
MNLpts	mannitol transport via PEP:Pyr P mnl[e] + pep[c] --> mnl1p[c] + pyr[c]	BPSL0440, BPSL0 PtsH+PtsI
NAt7	sodium transport in/out via pro h[e] + na1[c] <==> h[c] + na1[e]	BPSS1016 ChaA
NH4t	ammonium transport via diffusi nh4[e] <==> nh4[c]	BPSL0435 AmtB
NO2t2	nitrite transport in via proton sy h[e] + no2[e] <==> h[c] + no2[c]	BPSL2308 NarKec
NO3t7	nitrate transport in via nitrite ar no2[c] + no3[e] --> no2[e] + no3[c]	BPSL2308 NarKec
ORNabc	ornithine transport via ABC syst atp[c] + h2o[c] + orn-L[e] --> adp[c] + h[c] + orn-L[c] + pi[c]	BPSL1030, BPSL1 HisM+HisP+HisQ
PHET6	L-phenylalanine transport in/out h[e] + phe-L[e] <==> h[c] + phe-L[c]	BPSL0900, BPSS2 PheP, AroP
Plabc	phosphate transport via ABC syst atp[c] + h2o[c] + pi[e] --> adp[c] + h[c] + (2) pi[c]	BPSL1362, BPSL1 PstA+PstB+PstC+PstD
Plt6	phosphate transport in/out via h[e] + pi[e] <==> h[c] + pi[c]	BPSS1566 PitA
PROabc	L-proline transport via ABC syst atp[c] + h2o[c] + pro-L[e] --> adp[c] + h[c] + pi[c] + pro-L[c]	BPSS1425, BPSS1 ProVec+ProW
PROt6	L-proline transport in/out via pro h[e] + pro-L[e] <==> h[c] + pro-L[c]	BPSL1339 ProPec
PTRCabc	putrescine transport via ABC syst atp[c] + h2o[c] + ptrc[e] --> adp[c] + h[c] + pi[c] + ptrc[c]	BPSS0075, BPSL1 YdcT, PotF+PotG+PotH+PotI
RIBabc	D-ribose transport via ABC syst atp[c] + h2o[c] + rib-D[e] --> adp[c] + h[c] + pi[c] + rib-D[c]	BPSS0257, BPSS0 RbsA+RbsC, Yjff+YtfQ
SBTpts	D-sorbitol transport via PEP:Pyr pep[c] + sbt-D[e] --> pyr[c] + sbt6p[c]	BPSL0440, BPSL0 PtsH+PtsI
SPMDabc	spermidine transport via ABC syst atp[c] + h2o[c] + spmd[e] --> adp[c] + h[c] + pi[c] + spmd[c]	BPSS0075, BPSL1 PotA+PotB+PotC, YdcT
SUCct2_2	succinate transport via proton s (2) h[e] + succ[e] --> (2) h[c] + succ[c]	BPSL0425 DctA
SUCpts	sucrose transport via PEP:Pyr P pep[c] + suc[r] --> pyr[c] + suc6p[c]	BPSL0440, BPSL0 PtsH+PtsI
SULabc	sulfate transport via ABC system atp[c] + h2o[c] + so4[e] --> adp[c] + h[c] + pi[c] + so4[c]	BPSL1836, BPSL1 CysA +CysU+CysW+Sbp,
TAURabc	taurine transport via ABC system atp[c] + h2o[c] + taur[e] --> adp[c] + h[c] + pi[c] + taur[c]	BPSS1574, BPSS1 TauA+TauB+TauC
THRabc	L-threonine transport via ABC syst atp[c] + h2o[c] + thr-L[e] --> adp[c] + h[c] + pi[c] + thr-L[c]	BPSL3417, BPSL0 LivF+LivG+LivH+LivJ+LivI
TREpts	trehalose transport via PEP:Pyr pep[c] + tre[e] --> pyr[c] + tre6p[c]	BPSL0440, BPSL0 PtsH+PtsI
TRPt6	L-tryptophan transport in/out vi h[e] + trp-L[e] <==> h[c] + trp-L[c]	BPSS0807 AroP
TSULabc	thiosulfate transport via ABC syst atp[c] + h2o[c] + tsul[e] --> adp[c] + h[c] + pi[c] + tsul[c]	BPSL1836, BPSL1 CysA +CysU+CysW, CysA
TYRt6	L-tyrosine transport in/out via p h[e] + tyr-L[e] <==> h[c] + tyr-L[c]	BPSL0900, BPSS2 PheP, AroP
VALabc	L-valine transport via ABC syst atp[c] + h2o[c] + val-L[e] --> adp[c] + h[c] + pi[c] + val-L[c]	BPSL3417, BPSL0 LivF+LivG+LivH+LivJ+LivI
ASNN	L-asparaginase [c] : asn-L + h2o --> asp-L + nh4	BPSS2060, BPSL1 YbiK, AnsB
ASNS1	asparagine synthase (glutamine [c] : asp-L + atp + gln-L + h2o --> amp + asn-L + glu-L + h + ppi	BPSS0677, BPSS0 AsnB

DAAD	D-Amino acid dehydrogenase	[c] : ala-D + fad + h2o --> fadh2 + nh4 + pyr	BPSS0154, BPSS0 DadA
ABTA	4-aminobutyrate transaminase	[c] : 4abut + akglu --> glu-L + sucsal	BPSL0476, BPSS1 GabT, GoaG
ACGS	N-acetylglutamate synthase	[c] : accoa + glu-L --> acglu + coa + h	BPSL2325, BPSL0 ArgA
ACODA	acetylornithine deacetylase	[c] : acorn + h2o --> ac + orn-L	BPSL2101 ArgE
AGMT	agmatinase	[c] : agm + h2o --> ptrc + urea	BPSS1587, BPSS0 SpeB
AGPR	N-acetyl-g-glutamyl-phosphate	[c] : acg5sa + nadp + pi <==> acg5p + h + nadph	BPSL3246 ArgC
ARGDC	arginine decarboxylase	[c] : arg-L + h --> agm + co2	BPSL1003 AdiA
ARGSL	argininosuccinate lyase	[c] : argsuc <==> arg-L + fum	BPSL1006, BPSL1 ArgH
ARGSS	argininosuccinate synthase	[c] : asp-L + atp + citr-L --> amp + argsuc + h + ppi	BPSL0298, BPSL1 ArgG
AST	Arginine succinyltransferase	[c] : arg-L + succoa --> coa + h + sucarg	BPSL2389, BPSL2 AstA
CBPS	carbamoyl-phosphate synthase	[c] : (2) atp + gln-L + h2o + hco3 --> (2) adp + cbp + glu-L + (2) h + pi	BPSL1349+BPSL1 Car
G5SD	glutamate-5-semialdehyde dehydrogenase	[c] : glu5p + h + nadph --> glu5sa + nadp + pi	BPSL2935 ProA
GLU5K	glutamate 5-kinase	[c] : atp + glu-L --> adp + glu5p	BPSL3002 ProB
MTAN	methylthioadenosine nucleosidase	[c] : 5mta + h2o --> 5mtr + ade	BPSL1978 Mtn
NACODA	N-acetylornithine deacetylase	[c] : acg5sa + h2o --> ac + glu5sa	BPSL2101 ArgE
OCBT	ornithine carbamoyltransferase	[c] : cbp + orn-L <==> citr-L + h + pi	BPSL1744, BPSL0 ArgI
ORNTA	ornithine transaminase	[c] : akglu + orn-L --> glu-L + glu5sa	BPSS2333, BPSS0 YgjG
P5CD	1-pyrroline-5-carboxylate dehydrogenase	[c] : 1pyr5c + (2) h2o + nad --> glu-L + h + nadh	BPSL3389 PutAec
P5CR	pyrroline-5-carboxylate reductase	[c] : 1pyr5c + (2) h + nadph --> nadp + pro-L	BPSL2847 ProC
PRO1z	proline oxidase	[c] : fad + pro-L --> 1pyr5c + fadh2 + h	BPSL3389 PutAec
SADH	Succinylarginine dihydrolase	[c] : (2) h + (2) h2o + sucarg --> co2 + (2) nh4 + sucorn	BPSS0468, BPSL2 AstC
SGDS	Succinylglutamate desuccinylase	[c] : h2o + sucglu --> glu-L + succ	BPSL2385 AstE
SGSAD	Succinylglutamic semialdehyde dehydrogenase	[c] : h2o + nad + sucgsa --> (2) h + nadh + sucglu	BPSL2387 AstD
SOTA	Succinylornithine transaminase	[c] : akglu + sucorn --> glu-L + sucgsa	BPSL2386 AstB
SPMDAT1	Spermidine acetyltransferase	[c] : accoa + spmd --> N1aspmd + coa + h	BPSL0096 SpeG
SPMDAT2	Spermidine acetyltransferase (N1)	[c] : accoa + spmd --> N8aspmd + coa + h	BPSL0096 SpeG
SPMS	spermidine synthase	[c] : ametam + ptrc --> 5mta + h + spmd	BPSL2954 SpeE
SSALy	succinate-semialdehyde dehydrogenase	[c] : h2o + nadp + sucsal --> (2) h + nadph + succ	BPSS0280 GabD
ADSK	adenylyl-sulfate kinase	[c] : aps + atp --> adp + h + paps	BPSS1926, BPSL2 CysC
CYSS	cysteine synthase	[c] : acser + h2s --> ac + cys-L	BPSL2507 CysM
PAPSR	phosphoadenylyl-sulfate reductase	[c] : paps + trdrd --> (2) h + pap + so3 + trdox	BPSL0958 CysH
SADT2	sulfate adenylyltransferase	[c] : atp + gtp + h2o + so4 --> aps + gdp + pi + ppi	BPSL0959+BPSL0 CysD
SERAT	serine O-acetyltransferase	[c] : accoa + ser-L <==> acser + coa	BPSS1344, BPSL2 CysE
SULR	sulfite reductase (NADPH2)	[c] : (3) h2o + h2s + (3) nadp <==> (4) h + (3) nadph + so3	BPSL0956+BPSS1 CysI
GLNS	glutamine synthetase	[c] : atp + glu-L + nh4 --> adp + gln-L + h + pi	BPSL2318, BPSS0 YcjK, GlnA
GLUDC	glutamate decarboxylase	[c] : glu-L + h --> 4abut + co2	BPSS2025, BPSS2 GadB
GLUDy	glutamate dehydrogenase (NADH)	[c] : glu-L + h2o + nadp <==> akglu + h + nadph + nh4	BPSL2925 GdhA
GLUN	glutaminase	[c] : gln-L + h2o --> glu-L + nh4	BPSS0628, BPSS2 YneH, AnsB, PabBec
GLUSy	glutamate synthase (NADPH)	[c] : akglu + gln-L + h + nadph --> (2) glu-L + nadp	BPSL3158+BPSL3 GltB
GHMT2	glycine hydroxymethyltransferase	[c] : ser-L + thf --> gly + h2o + mlthf	BPSL2758, BPSS0 GlyA
GLYAT	glycine C-acetyltransferase	[c] : accoa + gly <==> 2aobut + coa	BPSL2787, BPSS0 Kbl
PGCD	phosphoglycerate dehydrogenase	[c] : 3pg + nad --> 3php + h + nadh	BPSL1250, BPSL0 SerA
PSERT	phosphoserine transaminase	[c] : 3php + glu-L --> akglu + pser-L	BPSL2219, BPSL2 SerC

PSP_L	phosphoserine phosphatase (L-serine)	[c] : h2o + pser-L --> pi + ser-L	BPSL1543	SerB
SERD_L	L-serine deaminase	[c] : ser-L --> nh4 + pyr	BPSS1370, BPSL3	SdaB
THRD	L-threonine dehydrogenase (w/	[c] : nad + thr-L --> 2aobut + h + nadh	BPSS0006	Tdh
ATPPRT	ATP phosphoribosyltransferase	[c] : atp + prpp --> ppi + prbatp	BPSL3140	HisG
HISTD	histidinol dehydrogenase	[c] : h2o + histd + (2) nad --> (3) h + his-L + (2) nadh	BPSL3139	HisD
HISTP	histidinol-phosphatase	[c] : h2o + hisp --> histd + pi	BPSL3137	HisB
HSTPT	histidinol-phosphate transaminase	[c] : glu-L + imacp --> akp + h + hisp	BPSL0518, BPSL3	HisC
IG3PS	Imidazole-glycerol-3-phosphate	[c] : gln-L + prlp --> aicar + eig3p + glu-L + (2) h	BPSL3133+BPSL3	HisF
IGPDH	imidazoleglycerol-phosphate dehydratase	[c] : eig3p + h --> h2o + imacp	BPSL3137	HisB
PRAMPC	phosphoribosyl-AMP cyclohydrolase	[c] : h + h2o + prbamp --> prfp	BPSL3132	HisI
PRATPP	phosphoribosyl-ATP pyrophosphatase	[c] : h2o + prbatp --> h + ppi + prbamp	BPSL3132	HisI
PRMICli	1-(5-phosphoribosyl)-5-phosphoribosyl-5-phosphate	[c] : prfp --> prlp	BPSL3134	HisA
PRPPS	phosphoribosylpyrophosphate synthetase	[c] : atp + r5p <==> amp + h + prpp	BPSL0521	PrsA
AHCYSNS	adenosylhomocysteine nucleosyltransferase	[c] : ahcys + h2o --> ade + rhcys	BPSL1978	Mtn
CYSTL	cystathionine b-lyase	[c] : cysth-L + h2o --> hcys-L + nh4 + pyr	BPSL1542	MetC
METAT	methionine adenosyltransferase	[c] : atp + h2o + met-L --> amet + pi + ppi	BPSL0212	MetK
METS	methionine synthase	[c] : 5mthf + hcys-L --> h + met-L + thf	BPSL0386, BPSL0	MethH, MetE
SHSL1	O-succinylhomoserine lyase (L-homoserine)	[c] : cys-L + suchms --> cysth-L + h + succ	BPSS0913, BPSL0	MetB
ASAD	aspartate-semialdehyde dehydrogenase	[c] : aspsa + nadp + pi <==> 4pasf + h + nadph	BPSS1704	Asd
ASPK	aspartate kinase	[c] : asp-L + atp <==> 4pasf + adp	BPSL2239	ThrA
DAPDC	diaminopimelate decarboxylase	[c] : 26dap-M + h --> co2 + lys-L	BPSS0303, BPSL3	LysA
DAPE	diaminopimelate epimerase	[c] : 26dap-LL <==> 26dap-M	BPSL0210	DapF
DHDPRy	dihydrodipicolinate reductase (NADPH-dependent)	[c] : 23dhdp + h + nadph --> nadp + thdp	BPSL2941	DapB
DHDPS	dihydrodipicolinate synthase	[c] : aspsa + pyr --> 23dhdp + h + (2) h2o	BPSL2258, BPSL0	DapA
HSDy	homoserine dehydrogenase (NADPH-dependent)	[c] : hom-L + nadp <==> aspsa + h + nadph	BPSL2239	ThrA
SDPDS	succinyl-diaminopimelate desuccinylase	[c] : h2o + sl26da --> 26dap-LL + succ	BPSL2171	DapE
THDPS	tetrahydrodipicolinate succinylase	[c] : h2o + succoa + thdp --> coa + sl2a6o	BPSL2169	DapD
THRA	threonine aldolase	[c] : thr-L <==> acald + gly	BPSS0236, BPSL1	GlyA, LtaA
THRS	threonine synthase	[c] : h2o + phom --> pi + thr-L	BPSL1478	ThrC
ANPRT	anthranilate phosphoribosyltransferase	[c] : anth + prpp --> ppi + pran	BPSL3052	TrpDec
ANS1	anthranilate synthase	[c] : chor + gln-L --> anth + glu-L + h + pyr	BPSL3050, BPSL3	TrpDec+TrpEec
CHORM	chorismate mutase	[c] : chor --> pphn	BPSL2518	PheA
CHORS	chorismate synthase	[c] : 3psme --> chor + pi	BPSL1962	AroC
DAHPS	3-deoxy-D-arabino-heptulosonate synthase	[c] : e4p + h2o + pep --> 2dda7p + pi	BPSL2839, BPSS1	AroGec
DHQS	3-dehydroquinate synthase	[c] : 2dda7p --> 3dhq + pi	BPSL3168	AroB
IGPS	indole-3-glycerol-phosphate synthase	[c] : 2cpr5p + h --> 3ig3p + co2 + h2o	BPSL3053	TrpCec
PHETA1	phenylalanine transaminase	[c] : akp + phe-L <==> glu-L + phpyr	BPSS1810, BPSS0	IlvE, TyrB
PPNDH	prephenate dehydratase	[c] : h + pphn --> co2 + h2o + phpyr	BPSL2518	PheA
PRAli	phosphoribosylanthranilate isomerase	[c] : pran --> 2cpr5p	BPSL3053	TrpCec
PSCVT	3-phosphoshikimate 1-carboxyvinyltransferase	[c] : pep + skm5p <==> 3psme + pi	BPSL2517, BPSL0	AroA
SHK3D	shikimate dehydrogenase	[c] : 3dhsk + h + nadph <==> nadp + skm	BPSL2976	AroEec
SHKK	shikimate kinase	[c] : atp + skm --> adp + h + skm5p	BPSL3169	AroK
TRPS1	tryptophan synthase (indoleglycerol phosphate-dependent)	[c] : 3ig3p + ser-L --> g3p + h2o + trp-L	BPSS1697+BPSS1	TrpA

TRPS2	tryptophan synthase (indole)	[c] : indole + ser-L --> h2o + trp-L	BPSS1697+BPSS1TrpA
TRPS3	tryptophan synthase (indoleglyc	[c] : 3ig3p --> g3p + indole	BPSS1697+BPSS1TrpA
TYRTA	tyrosine transaminase	[c] : akgl + tyr-L <==> 34hpp + glu-L	BPSS0808, BPSS0TyrB
ACHBS	2-aceto-2-hydroxybutanoate sy	[c] : 2obut + h + pyr --> 2ahbut + co2	BPSSL1196+BPSSL1IlvH
ACLS	acetolactate synthase (Also cat	[c] : h + (2) pyr --> alac-S + co2	BPSSL1196+BPSSL1IlvH
AHAI	acetohydroxy acid isomeroreduc	[c] : alac-S + h + nadph --> 23dhmb + nadp	BPSSL1198, BPSS0IlvCec
DHAD1	dihydroxy-acid dehydratase (2,3	[c] : 23dhmb --> 3mob + h2o	BPSSL0969 IlvD
DHAD2	Dihydroxy-acid dehydratase (2,3	[c] : 23dhmp --> 3mop + h2o	BPSSL0969 IlvD
ILETA	isoleucine transaminase	[c] : akgl + ile-L <==> 3mop + glu-L	BPSS1810 IlvE
IPMD	3-isopropylmalate dehydrogena	[c] : 3c2hmp + nad --> 3c4mop + h + nadh	BPSS1705 LeuB
IPPM1a	3-isopropylmalate dehydratase	[c] : 3c2hmp <==> 2ippm + h2o	BPSS1706+BPSS1LeuC
IPPM1b	2-isopropylmalate hydratase	[c] : 2ippm + h2o <==> 3c3hmp	BPSS1706+BPSS1LeuC
IPPS	2-isopropylmalate synthase	[c] : 3mob + accoa + h2o --> 3c3hmp + coa + h	BPSSL1201 LeuA
KARA2i	ketol-acid reductoisomerase (2-	[c] : 2ahbut + h + nadph --> 23dhmp + nadp	BPSSL1198, BPSS0IlvCec
LEUTAi	leucine transaminase (irreversib	[c] : 4mop + glu-L --> akgl + leu-L	BPSS1810, BPSS0TyrB, IlvE
OMCDC	2-Oxo-4-methyl-3-carboxypent	[c] : 3c4mop + h --> 4mop + co2	BPSS1705 LeuB
THRD_L	L-threonine deaminase	[c] : thr-L --> 2obut + nh4	BPSS1279, BPSSL0IlvA, SdaB, TdcB
VALTA	valine transaminase	[c] : akgl + val-L <==> 3mob + glu-L	BPSS1810 IlvE
ALARI	alanine racemase (irreversible)	[c] : ala-L --> ala-D	BPSS0711, BPSSL2179 DadX
GLUTRR	glutamyl-tRNA reductase	[c] : glutrna + h + nadph --> glu1sa + nadp + trnaglu	BPSSL3072 HemA
GLUTRS	Glutamyl-tRNA synthetase	[c] : atp + glu-L + trnaglu --> amp + glutrna + ppi	BPSSL2197 GltX
NCP	N-carbamoylputrescine amidase	[c] : cbmps + h + h2o --> co2 + nh3 + ptrc	BPSSL0110 CanH
SERD_D	D-serine deaminase	[c] : ser-D --> nh4 + pyr	BPSS2116 DsdA
THDPO	thiol peroxidase	[c] : h2o2 + trdrd --> (2) h2o + trdox	BPSSL2865 KatG
AGMHE	ADP-D-glycero-D-manno-heptos	[c] : adpheap-D,D --> adpheap-L,D	BPSSL2509 RfaD
ALAALA	D-alanine-D-alanine ligase (revers	[c] : (2) ala-D + atp <==> adp + alaala + h + pi	BPSSL3023 DdIB
DAGK_EC	Diacylglycerol kinase	[c] : (0.02) 12dgr_EC + atp --> adp + h + (0.02) pa_EC	BPSSL1189 DgkA
EDTXS1	Endotoxin Synthesis (lauroyl tra	[c] : ddcaACP + kdo2lipid4 --> ACP + kdo2lipid4L	BPSSL0211 LpxL
ETHAAL	ethanolamine ammonia-lyase	[c] : etha --> acald + nh4	BPSSL3371+BPSSL3EutBC
G1PACT	glucosamine-1-phosphate N-ac	[c] : accoa + gam1p --> acgam1p + coa + h	BPSSL0313 GlmUec
G1PTMT	glucose-1-phosphate thymidyl	[c] : dttp + g1p + h --> dtdpglc + ppi	BPSSL2685 RfbA
GALUi	UTP-glucose-1-phosphate uridyl	[c] : g1p + h + utp --> ppi + udpg	BPSSL1981, BPSSL2GalUec
GDPMD	GDPmannose 4,6-dehydratase	[c] : gdpman --> gdpddm + h2o	BPSS1688, BPSSL2Gmd
GF6PTA	glutamine-fructose-6-phosphate	[c] : f6p + gln-L --> gam6p + glu-L	BPSSL1312, BPSS2GlmS
GLUR	glutamate racemase	[c] : glu-D <==> glu-L	BPSS0370 Muri
GMHEPAT	D-glycero-D-manno-hepose 1-p	[c] : atp + gmh1p + h --> adpheap-D,D + ppi	BPSSL0395, BPSSL2RfaEec
GMHEPK	D-glycero-D-manno-heptose 7- γ	[c] : atp + gmh7p --> adp + gmh17bp + h	BPSSL0395, BPSSL2RfaEec
GMHEPPA	D-glycero-D-manno-heptose 1, γ	[c] : gmh17bp + h2o --> gmh1p + pi	BPSSL0666, BPSS2GmhB
GPDDA1	Glycerophosphodiester phospho	[c] : g3pc + h2o --> chol + glyc3p + h	BPSSL2712 GlpQ
GPDDA2	Glycerophosphodiester phospho	[c] : g3pe + h2o --> etha + glyc3p + h	BPSSL2712 GlpQ
GPDDA3	Glycerophosphodiester phospho	[c] : g3ps + h2o --> glyc3p + h + ser-L	BPSSL2712 GlpQ
GPDDA4	Glycerophosphodiester phospho	[c] : g3pg + h2o --> glyc + glyc3p + h	BPSSL2712 GlpQ
GPDDA5	Glycerophosphodiester phospho	[c] : g3pi + h2o --> glyc3p + h + inost	BPSSL2712 GlpQ

KDOPS	2-dehydro-3-deoxy-phosphooc	[c] : ara5p + h2o + pep --> kdo8p + pi	BPSL2772, BPSL2	KdsA
LPADSS	Lipid A disaccharide synthase	[c] : lipidX + u23ga --> h + lipidAds + udp	BPSL2146	LpxB
LPSSYN_EC	Lipopolysaccharide synthesis (E	[c] : (3) adphep-L,D + (2) cdpea + (3) ckdo + lipa + (2) udpg --> (3) adp	BPSL2665, BPSL2	RfaC+RfaF
MAN1PT2	mannose-1-phosphate guanylyl	[c] : gdp + h + man1p --> gdpman + pi	BPSL2810, BPSL0	ManC
MI1PP	myo-inositol 1-phosphatase	[c] : h2o + mi1p-D --> inost + pi	BPSL2250	SuhB
MOAT	3-deoxy-D-manno-octulosonic a	[c] : ckdo + lipidA --> cmp + h + kdolipid4	BPSL2663	KdtA
MOAT2	3-deoxy-D-manno-octulosonic a	[c] : ckdo + kdolipid4 --> cmp + h + kdo2lipid4	BPSL2663	KdtA
PAPPT3	phospho-N-acetylmuramoyl-per	[c] : udcpp + ugmda --> uagmda + ump	BPSL3028	MraY
PGAMT	phosphoglucosamine mutase	[c] : gam1p <==> gam6p	BPSL1358	MrsA
S7PI	sedoheptulose 7-phosphate isor	[c] : s7p <==> gmh7p	BPSL2795	GmhA
TDPDRE	dTDP-4-dehydrorhamnose 3,5-ε	[c] : dtdpddg <==> dtdpddm	BPSL2684	RfbC
TDPDRR	dTDP-4-dehydrorhamnose reduc	[c] : dtdprm + nadp <==> dtdpddm + h + nadph	BPSL2683	RfbD
TDPGDH	dTDPglucose 4,6-dehydratase	[c] : dtdpglc --> dtdpddg + h2o	BPSL2686, BPSL2	RfbB
TDSK	Tetraacyldisaccharide 4'kinase	[c] : atp + lipidAds --> adp + h + lipidA	BPSL0878	LpxK
U23GAAT	UDP-3-O-(3-hydroxymyristoyl)g	[c] : 3htdACP + u3hga --> ACP + h + u23ga	BPSL2149	LpxD
UAAGDS	UDP-N-acetylmuramoyl-L-alanyl	[c] : 26dap-M + atp + uamag --> adp + h + pi + ugmd	BPSL3030	MurEec
UAG2E	UDP-N-acetylglucosamine 2-epi	[c] : uacgam <==> uacmam	BPSS2016	WecB
UAGAAT	UDP-N-acetylglucosamine acyltr	[c] : 3htdACP + uacgam <==> ACP + u3aga	BPSL2147	LpxA
UAGCVT	UDP-N-acetylglucosamine 1-car	[c] : pep + uacgam --> pi + uaccg	BPSL3141, BPSS0	MurA
UAGDP	UDP-N-acetylglucosamine diph	[c] : acgam1p + h + utp --> ppi + uacgam	BPSL0313	GlmUec
UAGPT3	UDP-N-acetylglucosamine-N-ac	[c] : uacgam + uagmda --> h + uaagmda + udp	BPSL3025	MurGec
UAMAGS	UDP-N-acetylmuramoyl-L-alanyl	[c] : atp + glu-D + uama --> adp + h + pi + uamag	BPSL3027	MurD
UAMAS	UDP-N-acetylmuramoyl-L-alanin	[c] : ala-L + atp + uamr --> adp + h + pi + uama	BPSL3024	MurC
UAPGR	UDP-N-acetylenolpyruvoylgluco	[c] : h + nadph + uaccg --> nadp + uamr	BPSL0868	MurB
UDPGD	UDPglucose 6-dehydrogenase	[c] : h2o + (2) nad + udpg <==> (3) h + (2) nadh + udpglcur	BPSS1833, BPSL2	Ugd
UGMDDS	UDP-N-acetylmuramoyl-L-alanyl	[c] : alaala + atp + ugmd --> adp + h + pi + ugmda	BPSL3029	MurFec
UHGADA	UDP-3-0-acyl N-acetylglucosam	[c] : h2o + u3aga --> ac + u3hga	BPSL3018, BPSL2	LpxC
DMOCT	3-deoxy-manno-octulosonate cytidyl	[c] : ctp + kdo --> ckdo + ppi	BPSL0876	KdsBec
2DGLCNRx	2-dehydro-D-gluconate reducta	[c] : 2dhglcn + h + nadh --> glcn-D + nad	BPSL1577	YiaE
2DGLCNRy	2-dehydro-D-gluconate reducta	[c] : 2dhglcn + h + nadph --> glcn-D + nadp	BPSL1577	YiaE
2DGULRx	2-dehydro-L-gulonate reductase	[c] : 2dhguln + h + nadh --> idon-L + nad	BPSL1577	YiaE
2DGULRy	2-dehydro-L-gulonate reductase	[c] : 2dhguln + h + nadph --> idon-L + nadp	BPSL1577	YiaE
3HCINNMH	3-hydroxycinnamate hydroxylas	[c] : 3hcinnm + h + nadh + o2 --> dhcinnm + h2o + nad	BPSL2532, BPSL2	MhpA
3HPPPNH	3-(3-hydroxy-phenyl)propionate	[c] : 3hpppn + h + nadh + o2 --> dhpppn + h2o + nad	BPSL2532, BPSL2	MhpA
ACACCT	acetyl-CoA:acetoacetyl-CoA trar	[c] : acac + accoa --> acoa + ac	BPSL1955+BPSS0	AtoADec
ACALDi	acetaldehyde dehydrogenase (a	[c] : acald + coa + nad --> accoa + h + nadh	BPSS1808	MhpF
AGDC	N-acetylglucosamine-6-phospha	[c] : acgam6p + h2o --> ac + gam6p	BPSL0496	NagA
ALCD19	alcohol dehydrogenase (glycero	[c] : glyald + h + nadh <==> glyc + nad	BPSL0820	AdhC
ALDD25x	aldehyde dehydrogenase (Phen)	[c] : h2o + nad + pacald --> (2) h + nadh + pheac	BPSS0868, BPSL0	FeaB
ALDD2x	aldehyde dehydrogenase (aceta	[c] : acald + h2o + nad --> ac + (2) h + nadh	BPSS0473	AldH
ALTRH	altronate hydrolase	[c] : altrn --> 2ddglcn + h2o	BPSS0790	UxaA
AMALT1	Amylomaltase (maltotriose)	[c] : malt + malttr --> glc-D + maltttr	BPSL2079	MalQ
AMALT2	Amylomaltase (maltotetraose)	[c] : malt + maltttr --> glc-D + maltpt	BPSL2079	MalQ

AMALT3	Amylomaltase (maltopentaose) [c] : malt + maltpt --> glc-D + malthx	BPSL2079	MalQ
AMALT4	Amylomaltase (maltohexaose) [c] : malt + malthx --> glc-D + malthp	BPSL2079	MalQ
BUTCT	Acetyl-CoA:butyrate-CoA transfr [c] : accoa + but --> ac + btcoa	BPSL1955+BPSS0	AtoADec
CINND0	Cinnamate dioxygenase [c] : cinnm + h + nadh + o2 --> cenchddd + nad	BPSS0906+BPSS1	HcaCDEF
DDGLK	2-dehydro-3-deoxygluconokinase [c] : 2ddglcn + atp --> 2ddg6p + adp + h	BPSL1539	KdgK
DDPGALA	2-dehydro-3-deoxy-6-phosphog [c] : 2dh3dgal6p <==> g3p + pyr	BPSL2970, BPSL0	DgoA
DHAPT	Dihydroxyacetone phosphotrans [c] : dha + pep --> dhap + pyr	BPSL1613, BPSS0	DhaK+DhaL+PtsH+PtsI
DKGLCNR2x	2,5-diketo-D-gluconate reducta [c] : 25dkglcn + h + nadh --> 5dglcn + nad	BPSL1577	YiaE
DKGLCNR2y	2,5-diketo-D-gluconate reducta [c] : 25dkglcn + h + nadph --> 5dglcn + nadp	BPSL1577	YiaE
DRPA	deoxyribose-phosphate aldolase [c] : 2dr5p --> acald + g3p	BPSS1962	DeoC
FAO4	fatty acid oxidation (Butanoyl-C [c] : btcoa + fad + h2o + nad --> aacoa + fadh2 + h + nadh	BPSL1424, BPSL0	FadB
FCLPA	L-fucose 1-phosphate aldolase [c] : fc1p <==> dhap + lald-L	BPSS1417, BPSL0	FucA, Ygbl
G3PD2	glycerol-3-phosphate dehydroge [c] : glyc3p + nadp <==> dhap + h + nadph	BPSL0447	GpsA
GALCTND	galactonate dehydratase [c] : galctn-D --> 2dh3dgal + h2o	BPSL2970, BPSL0	DgoA
GALU	UTP-glucose-1-phosphate uridyl [c] : g1p + h + utp <==> ppi + udpg	BPSL1981, BPSL2	GalUec
GLCRAL	5-dehydro-4-deoxyglucarate ald [c] : 5d4dglcr --> 2h3opp + pyr	BPSL0180	GarL
GLYCTO2	Glycolate oxidase [c] : glyclt + ubq8 --> glx + ubq8h2	BPSL2843+BPSS2	GlcDF
GLYCTO3	Glycolate oxidase [c] : glyclt + mqn8 --> glx + mql8	BPSL2843+BPSS2	GlcDF
GLYCTO4	Glycolate oxidase [c] : 2dmmq8 + glyclt --> 2dmmql8 + glx	BPSL2843+BPSS2	GlcDF
GLYK	glycerol kinase [c] : atp + glyc --> adp + glyc3p + h	BPSL0687	GlpK
GNK	gluconokinase [c] : atp + glcn-D --> 6pgc + adp + h	BPSL2929	GntK
HOXVA	4-hydroxy-2-oxovalerate aldola [c] : 4h2oxv --> acald + pyr	BPSS1807	MhpE
HPYRI	hydroxypyruvate isomerase [c] : hpyr <==> 2h3opp	BPSL1451	Hyi
HPYRRx	hydroxypyruvate reductase [c] : h + hpyr + nadh --> glyc-R + nad	BPSL0334, BPSL1	YcdW, YiaE
HPYRRy	hydroxypyruvate reductase [c] : h + hpyr + nadph --> glyc-R + nadp	BPSL0334, BPSL1	YiaE, YcdW
LACZ	lactase [c] : h2o + lcts --> gal + glc-D	BPSS1657	BglX
LCAD	lactaldehyde dehydrogenase [c] : h2o + lald-L + nad <==> (2) h + lac-L + nadh	BPSS0473, BPSL3	AdhC, AldH, AldB
MANAO	Mannonate oxidoreductase [c] : mana + nad <==> fruor + h + nadh	BPSS1476	UxB
MCITD	2-methylcitrate dehydratase [c] : 2mcit --> 2mcacn + h2o	BPSS1725	PrpD
MCITS	2-methylcitrate synthase [c] : h2o + oaa + ppcoa --> 2mcit + coa + h	BPSS0207	PrpC
MICITH	2-methylisocitrate hydratase [c] : 2mcacn + h2o --> micit	BPSS0208, BPSS1	AcnA
MICITL	methylisocitrate lyase [c] : micit <==> pyr + succ	BPSS0509, BPSS0	PrpB
OP4ENH	2-oxopent-4-enoate hydratase [c] : 2h24pd + h + h2o --> 4h2oxv	BPSS0697	MhpD
PACCOAL	phenylacetate-CoA ligase [c] : atp + coa + pheac --> amp + phaccoa + ppi	BPSL3045	PaaK
PFK_2	Phosphofructokinase [c] : atp + tag6p-D --> adp + h + tagdp-D	BPSL0320, BPSS1	PfkB, AgaZ
PGLYCP	phosphoglycolate phosphatase [c] : 2pglyc + h2o --> glyclt + pi	BPSL3049	Gph
PMANM	phosphomannomutase [c] : man1p <==> man6p	BPSL2666	CpsG
PPAK	Propionate kinase [c] : adp + ppap <==> atp + ppa	BPSS1956	TdcD
PPCSCT	Propanoyl-CoA: succinate CoA-t [c] : ppcoa + succ --> ppa + succoa	BPSS0514	YgfH
PPPND0	Phenylpropanoate Dioxygenase [c] : h + nadh + o2 + pppn --> cechddd + nad	BPSS0906+BPSS1	HcaCDEF
RBK	ribokinase [c] : atp + rib-D --> adp + h + r5p	BPSL1830	RbsK
TAUDO	taurine dioxygenase [c] : akg + o2 + taur --> amacald + co2 + h + so3 + succ	BPSS1575	TauD
TGBPA	Tagatose-bisphosphate aldolase [c] : tagdp-D <==> dhap + g3p	BPSL0798, BPSL0	AgaZ, GatZ

TRE6PH	trehalose-6-phosphate hydrolase	[c] : h2o + tre6p --> g6p + glc-D	BPSL2075	TreC
TRE6PP	trehalose-phosphatase	[c] : h2o + tre6p --> pi + tre	BPSL2411	OtsB
TRE6PS	alpha,alpha-trehalose-phosphatase	[c] : g6p + udpg --> h + tre6p + udp	BPSL2410, BPSL1	OtsA
TREHe	alpha,alpha-trehalase	[e] : h2o + tre --> (2) glc-D	BPSS0671	TreA
UDPG4E	UDPglucose 4-epimerase	[c] : udpg <==> udpgal	BPSL2670	GalE
XYLK	xylulokinase	[c] : atp + xylu-D --> adp + h + xu5p-D	BPSL0839	XylB
ICL	Isocitrate lyase	[c] : icit --> glx + succ	BPSL2188	AceA
MALS	malate synthase	[c] : accoa + glx + h2o --> coa + h + mal-L	BPSL2192	AceB
ME2	malic enzyme (NADP)	[c] : mal-L + nadp --> co2 + nadph + pyr	BPSL3242, BPSL2	Mae
PPA	inorganic diphosphatase	[c] : h2o + ppi --> h + (2) pi	BPSL1021	Ppa
PPC	phosphoenolpyruvate carboxylase	[c] : co2 + h2o + pep --> h + oaa + pi	BPSL1013	Ppc
ACONT	aconitase	[c] : cit <==> icit	BPSS0208, BPSS1	AcnA
AKGD	2-oxoglutarate dehydrogenase	[c] : akc + coa + nad --> co2 + nadh + succoa	BPSL1908, BPSS2	LpdA+SucAec+SucBec
CITL	Citrate lyase	[c] : cit --> ac + oaa	BPSS2159	CitDEF
CS	citrate synthase	[c] : accoa + h2o + oaa --> cit + coa + h	BPSS1715	GltA
FUM	fumarase	[c] : fum + h2o <==> mal-L	BPSL2469, BPSS0	FumCec, FumA
ICDHy	isocitrate dehydrogenase (NADP)	[c] : icit + nadp <==> akc + co2 + nadph	BPSL0896	Icd
SUCD1i	succinate dehydrogenase	[c] : fad + succ --> fadh2 + fum	BPSS1718+BPSS1	Sdh
SUCOAS	succinyl-CoA synthetase (ADP-forming)	[c] : atp + coa + succ <==> adp + pi + succoa	BPSL0779+BPSL0	SucC
ENO	enolase	[c] : 2pg <==> h2o + pep	BPSL2270	Eno
FBP	fructose-bisphosphatase	[c] : fdp + h2o --> f6p + pi	BPSL2547	Fbp
HEX1	hexokinase (D-glucose:ATP)	[c] : atp + glc-D --> adp + g6p + h	BPSL2614	Glc
PDH	pyruvate dehydrogenase	[c] : coa + nad + pyr --> accoa + co2 + nadh	BPSL2301, BPSS1	AceEec+AceFec+LpdA
PFK	phosphofructokinase	[c] : atp + f6p --> adp + fdp + h	BPSL0320, BPSS1	PfkB
PGI	glucose-6-phosphate isomerase	[c] : g6p <==> f6p	BPSL1413	Pgi
PGK	phosphoglycerate kinase	[c] : 13dpg + adp <==> 3pg + atp	BPSL2902, BPSL0	GpmB, GpmA, Pgk
PPS	phosphoenolpyruvate synthase	[c] : atp + h2o + pyr --> amp + (2) h + pep + pi	BPSL2140	Ppsa
PYK	pyruvate kinase	[c] : adp + h + pep --> atp + pyr	BPSL0797, BPSS0	Pyka
TPI	triose-phosphate isomerase	[c] : dhap <==> g3p	BPSL1209	Tpi
GLXCBL	glyoxalate carboligase	[c] : (2) glx + h --> 2h3opp + co2	BPSL1452	Gcl
GLYCK	glycerate kinase	[c] : atp + glyc-R --> 3pg + adp + h	BPSL1401, BPSS0	GlxK, GarK
GLYCLTDx	Glycolate dehydrogenase (NAD)	[c] : glx + h + nadh --> glyclt + nad	BPSL0334, BPSL1	YcdW, YiaE
GLYCLTDy	Glycolate dehydrogenase (NADP)	[c] : glx + h + nadph --> glyclt + nadp	BPSL0334, BPSL1	YcdW, YiaE
HOXPRx	2-hydroxy-3-oxopropionate reductase	[c] : glyc-R + nad <==> 2h3opp + h + nadh	BPSS2264, BPSL1	GlxR
GLYOX	hydroxyacylglutathione hydrolase	[c] : h2o + lgt-S --> gthrd + h + lac-D	BPSL1344	GloB
LGTHL	lactoylglutathione lyase	[c] : gthrd + mthgxl --> lgt-S	BPSL0663	GloA
MGSA	methylglyoxal synthase	[c] : dhap --> mthgxl + pi	BPSL1168	MgsA
EDA	2-dehydro-3-deoxy-phosphogluconate dehydratase	[c] : 2ddg6p --> g3p + pyr	BPSL2931	Eda
G6PDHy	glucose 6-phosphate dehydrogenase	[c] : g6p + nadp <==> 6pgl + h + nadph	BPSL2612	Zwf
PGDH	phosphogluconate dehydrogenase	[c] : 6pgc + nadp --> co2 + nadph + ru5p-D	BPSS1749	Gnd
PGDHY	phosphogluconate dehydratase	[c] : 6pgc --> 2ddg6p + h2o	BPSL2932	Edd
RPE	ribulose 5-phosphate 3-epimerase	[c] : ru5p-D <==> xu5p-D	BPSL3048	Rpeec
RPI	ribose-5-phosphate isomerase	[c] : r5p <==> ru5p-D	BPSL1871, BPSS0	RpiB, RpiA

TAL	transaldolase	[c] : g3p + s7p <==> e4p + f6p	BPSL1095	TalB
TKT1	transketolase	[c] : r5p + xu5p-D <==> g3p + s7p	BPSL2953	TktA
TKT2	transketolase	[c] : e4p + xu5p-D <==> f6p + g3p	BPSL2953	TktA
ACKr	acetate kinase	[c] : ac + atp <==> actp + adp	BPSS1956, BPSL1	TdcD, PurT
ACS	acetyl-CoA synthetase	[c] : ac + atp + coa --> accoa + amp + ppi	BPSS0618, BPSL1	Acs
FHL	Formate-hydrogen lyase	[c] : for + h --> co2 + h2	BPSS1142+BPSS1	FdhF+HycB
LDH_D	D-lactate dehydrogenase	[c] : lac-D + nad <==> h + nadh + pyr	BPSL2734	Ldh
FRUK	fructokinase	[c] : atp + fru --> adp + f6p + h	BPSS0320, BPSS1957, I	PfkB, ScrK
HMGL	hydroxymethylglutaryl-CoA lyase	[c] : hmgcoa --> acac + accoa	BPSL0333	HdmC
L-LACD2	L-Lactate dehydrogenase (ubiquinone)	[c] : lac-L + ubq8 --> pyr + ubq8h2	BPSS1800, BPSS2125, I	LidD
L-LACD3	L-Lactate dehydrogenase (menaquinone)	[c] : lac-L + mqn8 --> mql8 + pyr	BPSS1800, BPSS2125, I	LidD
ACBIPGT	Adenosyl cobainamide GTP tran	[c] : adcobap + gtp + h --> adgcoba + ppi	BPSL0986	CobU
ACPS1	acyl-carrier protein synthase	[c] : apoACP + coa --> ACP + h + pap	BPSL2425	AcpS
ADCOBAK	Adenosyl cobinamide kinase	[c] : adcoba + atp --> adcobap + adp + h	BPSL0986	CobU
ADCS	4-amino-4-deoxychorismate syr	[c] : chor + gln-L --> 4adcho + glu-L	BPSS13051, BPSL2	PabA+PabBec
ALATA_D2	D-alanine transaminase	[c] : ala-D + pydx5p --> pyam5p + pyr	BPSS2758, BPSS0	GlyA
ALATA_L2 [d	alanine transaminase	[c] : ala-L + pydx5p --> pyam5p + pyr	BPSS2758, BPSS0	GlyA
AMAOT	adenosylmethionine-8-amino-7-	[c] : 8aonn + amet <==> amob + dann	BPSL2650, BPSS0	BioAec
AMMQT8_2	S-adenosylmethionine:2-demethy	[c] : 2dmmq8 + amet --> ahcys + h + mqn8	BPSL2194	MenG
AMPMS	4-amino-2-methyl-5-phosphom	[c] : air + h2o --> 4ampm + (2) for + (4) h	BPSL1290	ThiC
AOXS	8-amino-7-oxononanoate synth	[c] : ala-L + h + pmcoa <==> 8aonn + co2 + coa	BPSL0366	BioF
APRAUR	5-amino-6-(5-phosphoribosylar	[c] : 5apru + h + nadph --> 5aprbu + nadp	BPSS1125, BPSL2	RibDec
ASP1DC	aspartate 1-decarboxylase	[c] : asp-L + h --> ala-B + co2	BPSL0990	PanD
ASPO3	L-aspartate oxidase	[c] : asp-L + ubq8 --> h + iasp + ubq8h2	BPSL0914	NadB
ASPO4	L-aspartate oxidase	[c] : asp-L + mqn8 --> h + iasp + mql8	BPSL0914	NadB
ASPO5	L-aspartate oxidase	[c] : asp-L + fum --> h + iasp + succ	BPSL0914	NadB
ASPO6	L-aspartate oxidase	[c] : asp-L + o2 --> h + h2o2 + iasp	BPSL0914	NadB
BTS2	biotin synthase (ala-L produc	[c] : cys-L + dtbt <==> ala-L + btn + (2) h	BPSL0364	BioBec
CBIAT	Cobinamide adenyltransferase	[c] : atp + cbi + h2o <==> adcobap + pi + ppi	BPSL1772	BtuR
CBL1abc	Cob(1)alamin transport via ABC	atp[c] + cbl1[e] + h2o[c] --> adp[c] + cbl1[c] + h[c] + pi[c]	BPSS0976, BPSL0	BtuB+BtuC+BtuF
CBLAT	cob(I)alamin adenosyltransferase	[c] : atp + cbl1 + h2o <==> cobamcoa + pi + ppi	BPSL1772	BtuR
CDPMEK	4-(cytidine 5'-diphospho)-2-C- π	[c] : 4c2me + atp --> 2p4c2me + adp + h	BPSL0523	IspE
CPPPGO	coproporphyrinogen oxidase	[c] : cpppg3 + (2) h + o2 --> (2) co2 + (2) h2o + pppg9	BPSS1163	HemF
DB4PS	3,4-Dihydroxy-2-butanone-4-ph	[c] : ru5p-D --> db4p + for + h	BPSS2626, BPSL0	RibBec
DBTSr	dethiobiotin synthase	[c] : atp + co2 + dann <==> adp + dtbt + (3) h + pi	BPSL0365	BioDec
DHBSr	2,3-dihydroxybenzoate adenyla	[c] : 23dhb + atp + h <==> 23dhba + ppi	BPSS0584	EntE
DHFR	dihydrofolate reductase	[c] : dhf + h + nadph <==> nadp + thf	BPSL2476	FolA
DHFS	dihydrofolate synthase	[c] : atp + dhpt + glu-L --> adp + dhf + h + pi	BPSS1695	FolCec
DHPPDA2	diaminohydroxyphosphoribosyla	[c] : 25dhpp + h + h2o --> 5apru + nh4	BPSS1125, BPSL2	RibDec
DHPS3	dihydropteroate synthase	[c] : 2ahhmd + 4abz --> dhpt + ppi	BPSL1357	FolP
DMATT	dimethylallyltranstransferase	[c] : dmpp + ipdp --> grdp + ppi	BPSS1763	IspA
DMPPS	1-hydroxy-2-methyl-2-(E)-butel	[c] : h + h2mb4p + nadh --> dmpp + h2o + nad	BPSL0919, BPSS2	LytB
DMQMT	3-Dimethylubiquinonol 3-methy	[c] : 2omhmb1 + amet --> ahcys + h + ubq8h2	BPSL2523	UbiG

DNTPPA	Dihydroneopterin triphosphate [c] : ahdt + h2o --> dhmp + h + ppi	BPSL0645	NtpA
DPR	2-dehydropanthoate 2-reductase [c] : 2dhp + h + nadph --> nadp + pant-R	BPSL1198, BPSS0	IlvCec
DXPRI	1-deoxy-D-xylulose-5-phosphate [c] : dxyl5p + h + nadph <==> 2me4p + nadp	BPSL2153	Dxr
DXPS	1-deoxy-D-xylulose 5-phosphate [c] : g3p + h + pyr --> co2 + dxyl5p	BPSS1762	Dxs
DXYLK	1-Deoxy-D-xylulose kinase [c] : atp + dxyl --> adp + dxyl5p + h	BPSL0839	XylB
E4PD	Erythrose 4-phosphate dehydrogenase [c] : e4p + h2o + nad <==> 4per + (2) h + nadh	BPSL2952	Epd
FCLT	Heme B synthesis reaction [c] : fe2 + ppp9 --> h + pheme	BPSL2831	HemH
FMNAT	FMN adenylyltransferase [c] : atp + fmn + h --> fad + ppi	BPSL0907	RibFec
G1SATi	glutamate-1-semialdehyde aminotransferase [c] : glu1sa --> 5aop	BPSL2623, BPSS2	HemLec
GLUCYSL	glutamate-cysteine ligase [c] : atp + cys-L + glu-L --> adp + glucys + h + pi	BPSL0102	GshA
GRTT	geranyltranstransferase [c] : grdp + ipdp --> frdp + ppi	BPSS1763	IspA
GTHRD	glutathione-disulfide reductase [c] : (2) gthrd + nadp <==> gthox + h + nadph	BPSL0297	Gor
GTHS	glutathione synthase [c] : atp + glucys + gly --> adp + gthrd + h + pi	BPSL0437	GshB
GTPCI	GTP cyclohydrolase I [c] : gtp + h2o --> ahdt + for + h	BPSS0040	FolE
GTPCII	GTP cyclohydrolase II [c] : gtp + (3) h2o --> 25dhpp + for + (2) h + ppi	BPSS0883, BPSS1	RibA
HBZOPT	4-hydroxybenzoate octaprenyltransferase [c] : 4hbz + octdp --> 3ophb + ppi	BPSL2861	UbiA
HEMEOS	Heme O synthase [c] : frdp + h2o + pheme --> h + hemeO + ppi	BPSL0462	CyoE
HETZK	hydroxyethylthiazole kinase [c] : 4mhetz + atp --> 4mpetz + adp + h	BPSS1135	ThiMec
HMBS	hydroxymethylbilane synthase [c] : h2o + (4) ppbng --> hmbil + (4) nh4	BPSL1015	HemCec
HMPK1	hydroxymethylpyrimidine kinase [c] : 4ahmmp + atp --> 4ampm + adp + h	BPSL2181, BPSS1	ThiDec
HPPK	2-amino-4-hydroxy-6-hydroxyphenylpyruvate decarboxylase [c] : 2ahhmp + atp --> 2ahhmd + amp + h	BPSL2822	FolK
ICHORSi	Isochorismate Synthase [c] : chor --> ichor	BPSS0581	EntC
IPDPS	1-hydroxy-2-methyl-2-(E)-butyryl-CoA dehydrogenase [c] : h + h2mb4p + nadh --> h2o + ipdp + nad	BPSL0919, BPSS2	LytB
MECDPDH	2C-methyl-D-erythritol 2,4-cyclohydrolase [c] : 2mecdp + nadh --> h2mb4p + h2o + nad	BPSL1513	GcpE
MECDPS	2-C-methyl-D-erythritol 2,4-cyclohydrolase [c] : 2p4c2me --> 2mecdp + cmp	BPSL2098	IspF
MEPCT	2-C-methyl-D-erythritol 4-phosphatase [c] : 2me4p + ctp + h --> 4c2me + ppi	BPSL2099	IspD
MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransferase [c] : 3mob + h2o + mlthf --> 2dhp + thf	BPSL2824	PanB
NADDP	NAD diphosphatase [c] : h2o + nad --> amp + (2) h + nmh	BPSL2164	Lig
NADK	NAD kinase [c] : atp + nad --> adp + h + nadp	BPSL2833	YfjB
NADS1	NAD synthase (nh4) [c] : atp + dnad + nh4 --> amp + h + nad + ppi	BPSS1482	NadEec
NAMNPP	nicotinic acid mononucleotide pyrophosphoryltransferase [c] : atp + h2o + nac + prpp --> adp + nicrnt + pi + ppi	BPSL2462	PncB
NMNAT	nicotinamide-nucleotide adenylyltransferase [c] : atp + h + nmh --> nad + ppi	BPSL1162	NadD
NNAM	nicotinamidase [c] : h2o + ncam --> nac + nh4	BPSL1425	PncA
NNAT	nicotinate-nucleotide adenylyltransferase [c] : atp + h + nicrnt --> dnad + ppi	BPSL1162	NadD
NNDMBRT	nicotinate-nucleotide-dimethylbenzoyltransferase [c] : dmbzid + nicrnt --> 5prdmzb + h + nac	BPSL0979	CobT
NNDPR	nicotinate-nucleotide diphosphoryltransferase [c] : (2) h + prpp + quln --> co2 + nicrnt + ppi	BPSL0913	NadCec
OCTDPS	Octaprenyl pyrophosphate synthetase [c] : frdp + (5) ipdp --> octdp + (5) ppi	BPSL3006	IspB
OHBPAT	O-Phospho-4-hydroxy-L-threonine phosphatase [c] : glu-L + ohpb <==> akp + phthr	BPSL2219, BPSL2	SerC
OHPHM	R04988 [c] : 2ohph + amet --> 2omph + ahcys + h	BPSL2523	UbiG
OMBZLM	2-Octaprenyl-6-methoxy-benzoyl-CoA synthetase [c] : 2ombzl + amet --> 2ommbzl + ahcys + h	BPSL0637	UbiE
OMPHHX	2-octaprenyl-6-methoxyphenol methyltransferase [c] : 2omph + (0.5) o2 --> 2ombzl	BPSL2893	UbiH
OPHBDC	3-octaprenyl-4-hydroxybenzoate decarboxylase [c] : 3ophb + h --> 2oph + co2	BPSL2631, BPSL3	UbiX, UbiD
OPHHX	2-Octaprenylphenol hydroxylase [c] : 2oph + (0.5) o2 --> 2ohph	BPSL0640	UbiB

PANTS	pantothenate synthase	[c] : ala-B + atp + pant-R --> amp + h + pnto-R + ppi	BPSL0991	PanCec
PDX5PO	pyridoxine 5'-phosphate oxidase	[c] : o2 + pdx5p <==> h + h2o2 + pydx5p	BPSL0854	PdxHec
PDX5PS	Pyridoxine 5'-phosphate synthase	[c] : dxy15p + nad + phthr --> co2 + h + (2) h2o + nadh + pdx5p + pi	BPSL0660+BPSL2	PdxAJ
PMPK	phosphomethylpyrimidine kinase	[c] : 4ampm + atp --> 2mahmp + adp	BPSL2181, BPSS1	ThiDec
PPBNGS	porphobilinogen synthase	[c] : (2) 5aop --> h + (2) h2o + ppbng	BPSL3183	HemBec
PTPATi	pantetheine-phosphate adenylate	[c] : atp + h + pan4p --> dpcoa + ppi	BPSL0516	CoaD
PYAM5PO	pyridoxamine-phosphate oxidase	[c] : h2o + o2 + pyam5p --> h2o2 + nh4 + pydx5p	BPSL0854	PdxHec
PYDXK	pyridoxal kinase (Pyridoxal)	[c] : atp + pydx --> adp + (2) h + pydx5p	BPSL2402	PdxYec
QULNS	quinolinate synthase	[c] : dhap + iasp --> (2) h2o + pi + quln	BPSL0912	NadA
RBFK	riboflavin kinase	[c] : atp + ribflv --> adp + fmh + h	BPSL0907	RibFec
RBFSa	riboflavin synthase	[c] : 4r5au + db4p --> dmlz + (2) h2o + pi	BPSL2625	RibEec
RBFsb	riboflavin synthase	[c] : (2) dmlz --> 4r5au + ribflv	BPSL2627	RibH
SERAS	(L-seryl)adenylate synthase	[c] : atp + h + ser-L <==> ppi + seramp	BPSS1634	EntF
SHCHD2	sirohydrochlorin dehydrogenase	[c] : nad + shcl --> (2) h + nadh + srch	BPSL1755, BPSS1	CysG
SHCHF	sirohydrochlorin ferrochetalase	[c] : fe2 + srch --> (2) h + sheme	BPSL1755, BPSS1	CysG
THZPSN	thiazole phosphate synthesis	[c] : atp + cys-L + dxy15p + tyr-L --> 4hba + 4mpetz + ala-L + amp + co	BPSL3152, BPSL2	IscS+ThiGH
TMKPr	thiamine-phosphate kinase	[c] : atp + thmmp <==> adp + thmmp	BPSL2960	ThiL
TMPPP	thiamine-phosphate diphosphor	[c] : 2mahmp + 4mpetz + h --> ppi + thmmp	BPSL3151	ThiE
UDCPDPS	Undecaprenyl diphosphate synth	[c] : frdp + (8) ipdp --> (8) ppi + udcpgp	BPSL2155	UppS
UPP3MT	uroporphyrinogen methyltransfer	[c] : (2) amet + uppg3 --> (2) ahcys + h + shcl	BPSL1755, BPSS1	CysG
UPPDC1	uroporphyrinogen decarboxylase	[c] : (4) h + uppg3 --> (4) co2 + cpppg3	BPSL3391	HemE
FTHFD	formyltetrahydrofolate deformyl	[c] : 10fthf + h2o --> for + h + thf	BPSS0558, BPSL0	PurUec
GLYCL	Glycine Cleavage System	[c] : gly + nad + thf --> co2 + mlthf + nadh + nh4	BPSL3361, BPSL3	GcvH+GcvP+GcvT+LpdA
MTHFC	methenyltetrahydrofolate cyclot	[c] : h2o + methf <==> 10fthf + h	BPSL2304	FoID
MTHFD	methylenetetrahydrofolate dehy	[c] : mlthf + nadp <==> methf + nadph	BPSL2304	FoID
MTHFR2	5,10-methylenetetrahydrofolate	[c] : (2) h + mlthf + nadh --> 5mthf + nad	BPSL3288	MetF
ALLTAH	allantoicase	[c] : alltt + h2o --> urdglyc + urea	BPSL1682, BPSS1	AlIC
ALLTN	allantoinase	[c] : alltn + h2o --> alltt + h	BPSL2689	AlIB
CYNTAH	Cyanate aminohydrolase	[c] : cynt + (3) h + hco3 --> (2) co2 + nh4	BPSL2950	CynS
DDGALK	2-dehydro-3-deoxygalactonokin	[c] : 2dh3dgal + atp --> 2dh3dgal6p + adp + h	BPSL2971	DgoK
UGLYCH	Ureidoglycolate hydrolase	[c] : (2) h + h2o + urdglyc --> co2 + glx + (2) nh4	BPSL2944, BPSL2	AlIA
HSAT	Acetyl-CoA:L-homoserine O-acetyltransf	[c] : accoa + hom-L <==> achms + coa	BPSL0197	HseA
NMO	nitronate monooxygenase	[c] : (2) O + ethn + fmhRD --> acald + fmh + h2o + no2	BPSL3285, BPSL2363, I	NtdO+OxdR
NTRIR2x	Nitrite Reductase	[c] : (5) h + (3) nadh + no2 --> (2) h2o + (3) nad + nh4	BPSS1242+BPSS1243, I	NirBD
PPIK	polyphosphate kinase	[c] : atp + ppi --> adp + pppi	BPSL1366	Ppk
ATPS4r	ATP synthase (four protons for c	adp[c] + (4) h[e] + pi[c] <==> atp[c] + (3) h[c] + h2o[c]	BPSL3395+BPSL3	AtpF0+AtpF1
CRNCDH	Carnityl-CoA dehydratase	[c] : crncoa <==> ctbcoa + h2o	BPSS1000	CaiD
CYTBD	cytochrome oxidase bd (ubiquin	(2) h[c] + (0.5) o2[c] + ubq8h2[c] --> (2) h[e] + h2o[c] + ubq8[c]	BPSL0501+BPSL0	CydA
CYTBO3	cytochrome oxidase bo3 (ubiqui	(2.5) h[c] + (0.5) o2[c] + ubq8h2[c] --> (2.5) h[e] + h2o[c] + ubq8[c]	BPSL2379+BPSL2	CyoA
FDH2	formate dehydrogenase (quinon for	[c] + (3) h[c] + ubq8[c] --> co2[c] + (2) h[e] + ubq8h2[c]	BPSS1665+BPSS1	FdhF, Fdoec
FDH3	Formate Dehydrogenase (mena for	[c] + (3) h[c] + mqn8[c] --> co2[c] + (2) h[e] + mql8[c]	BPSS1665+BPSS1	Fdoec
G3PD5	glycerol-3-phosphate dehydrogen	[c] : glyc3p + ubq8 --> dhap + ubq8h2	BPSS1838, BPSL0	GlpA, GlpD
G3PD6	glycerol-3-phosphate dehydrogen	[c] : glyc3p + mqn8 --> dhap + mql8	BPSS1838	GlpA

G3PD7	glycerol-3-phosphate dehydrogenase	[c] : 2dmmq8 + glyc3p --> 2dmmql8 + dhap	BPSS1838	GlpA
HYD1	hydrogenase (ubiquinone-8)	2 h[c] + h2[c] + ubq8[c] --> (2) h[e] + ubq8h2[c]	BPSS1142+BPSS1	HycB
NADH10	NADH dehydrogenase (menaquinone)	[c] : h + mqn8 + nadh --> mql8 + nad	BPSS1769	Ndh
NADH12	NADH dehydrogenase (ubiquinol)	[c] : h + nadh + ubq8 --> nad + ubq8h2	BPSS1769	Ndh
NADH6	NADH dehydrogenase (ubiquinol)	(4.5) h[c] + nadh[c] + ubq8[c] --> (3.5) h[e] + nad[c] + ubq8h2[c]	BPSL1211+BPSL1	Nuo
NADH7	NADH dehydrogenase (menaquinone)	(3) h[c] + mqn8[c] + nadh[c] --> (2) h[e] + mql8[c] + nad[c]	BPSL1211+BPSL1	Nuo
NADH8	NADH dehydrogenase (demethylnad)	2dmmq8[c] + (3.8) h[c] + nadh[c] --> 2dmmql8[c] + (2.8) h[e] + nad[c]	BPSL1211+BPSL1	Nuo
NADH9	NADH dehydrogenase (demethylnad)	[c] : 2dmmq8 + h + nadh --> 2dmmql8 + nad	BPSS1769	Ndh
NO3R1	Nitrate reductase (Ubiquinol-8)	(2) h[c] + no3[c] + ubq8h2[c] --> (2) h[e] + h2o[c] + no2[c] + ubq8[c]	BPSL2309+BPSL2	NarGHIJ
NO3R2	Nitrate reductase (Menaquinol-8)	(2) h[c] + mql8[c] + no3[c] --> (2) h[e] + h2o[c] + mqn8[c] + no2[c]	BPSL2309+BPSL2	NarGHIJ
POX	pyruvate oxidase	[c] : h2o + pyr + ubq8 --> ac + co2 + ubq8h2	BPSS1636	PoxB
SUCD4	succinate dehydrogenase	[c] : fadh2 + ubq8 <==> fad + ubq8h2	BPSS1718+BPSS1	Sdh
THD2	NAD(P) transhydrogenase	(2) h[e] + nadh[c] + nadp[c] --> (2) h[c] + nad[c] + nadph[c]	BPSL2885+BPSL2	Pnt
THD5	NAD transhydrogenase	[c] : nad + nadph --> nadh + nadp	BPSL2885+BPSL2	Pnt
TRDR	thioredoxin reductase (NADPH)	[c] : h + nadph + trdoh --> nadp + trdrd	BPSL2605	TrxB
ACACT1r	acetyl-CoA C-acetyltransferase	[c] : (2) accoa <==> aacoa + coa	BPSL1540	AtoBec
ACCOAC	acetyl-CoA carboxylase	[c] : accoa + atp + hco3 --> adp + h + malcoa + pi	BPSL2241+BPSL2	Acc
ACMAT1	Acyl-[acyl-carrier-protein]:malonyl-CoA transferase	[c] : acACP + h + malACP --> ACP + actACP + co2	BPSL2438, BPSS0	FabF, FabB
ACOATA	Acetyl-CoA ACP transacylase	[c] : ACP + accoa <==> acACP + coa	BPSL2442, BPSS0	FabHec
C120SN	Fatty acid biosynthesis (n-C12:0)	[c] : actACP + (14) h + (4) malACP + (10) nadph --> (4) ACP + (4) co2 + BPSL2440, BPSL2	FabF+FabGec+FabI+FabZ,	
C140SN	Fatty acid biosynthesis (n-C14:0)	[c] : actACP + (17) h + (5) malACP + (12) nadph --> (5) ACP + (5) co2 + BPSL2440, BPSL2	FabF+FabGec+FabI+FabZ,	
C141SN	Fatty acid biosynthesis (n-C14:1)	[c] : actACP + (16) h + (5) malACP + (11) nadph --> (5) ACP + (5) co2 + BPSL2440, BPSL2	FabB+FabGec+FabI+FabZ,	
C160SN	Fatty acid biosynthesis (n-C16:0)	[c] : actACP + (20) h + (6) malACP + (14) nadph --> (6) ACP + (6) co2 + BPSL2440, BPSL2	FabF+FabGec+FabI, FabB,	
C161SN	Fatty acid biosynthesis (n-C16:1)	[c] : actACP + (19) h + (6) malACP + (13) nadph --> (6) ACP + (6) co2 + BPSL2440, BPSL2	FabB+FabGec+FabI+FabZ,	
C181SN	Fatty acid biosynthesis (n-C18:1)	[c] : actACP + (22) h + (7) malACP + (15) nadph --> (7) ACP + (7) co2 + BPSL2440, BPSL2	FabB+FabF+FabGec+FabI,	
CLPNS_EC	Cardiolipin Synthase (E.coli)	[c] : (0.04) pg_EC <==> (0.02) clpn_EC + glyc	BPSL2174	Clis
DASYN_EC	CDP-Diacylglycerol synthetase	[c] : ctp + h + (0.02) pa_EC <==> (0.02) cdpdag_EC + ppi	BPSL2154	CdsA
FAO1	Fatty acid oxidation (tetradecanoate)	[c] : atp + (7) coa + (6) fad + (6) h2o + (6) nad + ttdca --> (7) accoa + (6) nad + BPSL1424, BPSL0	FadA+FadB+FadD	
FAO2	Fatty acid oxidation (n-C16:0)	[c] : atp + (8) coa + (7) fad + (7) h2o + hdca + (7) nad --> (8) accoa + (7) nad + BPSL1424, BPSL0	FadA+FadB+FadD	
FAO3	Fatty acid oxidation (octadecanoate)	[c] : atp + (9) coa + (8) fad + (8) h2o + (8) nad + ocdca --> (9) accoa + (8) nad + BPSL1424, BPSL0	FadA+FadB+FadD, FadB	
KAS15	b-ketoacyl synthase	[c] : accoa + h + malACP --> actACP + co2 + coa	BPSL2442, BPSS0	FabHec
KAS16	3-hydroxy-myristoyl-ACP synthase	[c] : ddcaACP + (2) h + malACP + nadph --> 3htdACP + ACP + co2 + nad	BPSL2440, BPSL2	FabF+FabGec, FabB+FabG
MACPD	Malonyl-ACP decarboxylase	[c] : h + malACP --> acACP + co2	BPSS0998	FabB
MCOATA	Malonyl-CoA-ACP transacylase	[c] : ACP + malcoa <==> coa + malACP	BPSS1004, BPSS0	FabD
PASYN_EC2	Phosphatidic acid synthase (E.coli)	[c] : glyc3p + (0.14) hdeACP + (0.04) myrsACP + octeACP + (0.72) palmACP --> BPSL0665	PlsC	
PGPP_EC	Phosphatidylglycerol phosphate	[c] : h2o + (0.02) pgp_EC --> (0.02) pg_EC + pi	BPSL2961	PgpAec
PGSA_EC	Phosphatidylglycerol synthase	[c] : (0.02) cdpdag_EC + glyc3p <==> cmp + h + (0.02) pgp_EC	BPSL2419	PgsA
HACD1	3-hydroxyacyl-CoA dehydrogenase (acetyl-CoA)	[c] : aacoa + h + nadh <==> 3hbycoa + nad	BPSL1424, BPSL0419, I	FadB+FatOa+HCoaD
HACD2	3-hydroxyacyl-CoA dehydrogenase (3-oxoacyl-CoA)	[c] : 3ohcoa + h + nadh <==> 3hhcoa + nad	BPSL1424, BPSL0419, I	FadB+FatOa+HCoaD
HACD3	3-hydroxyacyl-CoA dehydrogenase (3-oxoacyl-CoA)	[c] : 3oocoa + h + nadh <==> 3hocoa + nad	BPSL1424, BPSL0419, I	FadB+FatOa+HCoaD
HACD4	3-hydroxyacyl-CoA dehydrogenase (3-oxoacyl-CoA)	[c] : 3odcoa + h + nadh <==> 3hdcoa + nad	BPSL1424, BPSL0419, I	FadB+FatOa+HCoaD
HACD5	3-hydroxyacyl-CoA dehydrogenase (3-oxoacyl-CoA)	[c] : 3oddcoa + h + nadh <==> 3hddcoa + nad	BPSL1424, BPSL0419, I	FadB+FatOa+HCoaD
ADA	Adenosine deaminase	[c] : adn + h + h2o --> ins + nh4	BPSL2539	Add

ADK1	adenylate kinase	[c] : amp + atp <==> (2) adp	BPSL0875	Adk
ADK3	guanylate kinase (aMP:gTP)	[c] : amp + gtp <==> adp + gdp	BPSL0875	Adk
ADK4	adentylate kinase (ITP)	[c] : amp + itp <==> adp + idp	BPSL0875	Adk
ADNK1	adenosine kinase	[c] : adn + atp --> adp + amp + h	BPSL0875	Adk
ADPT	adenine phosphoribosyltransferase	[c] : ade + prpp --> amp + ppi	BPSL0540	Apt
AMPN	AMP nucleosidase	[c] : amp + h2o --> ade + r5p	BPSS1777	Amn
AP4AH	bis(5'-nucleosyl)-tetraphosphate	[c] : ap4a + h2o --> (2) adp + (2) h	BPSL2687	ApaH
AP5AH	Ap5A hydrolase	[c] : ap5a + h2o --> adp + atp + (2) h	BPSL2687	ApaH
CSND	Cytosine deaminase	[c] : csn + h + h2o --> nh4 + ura	BPSS0761	CodA
CYTK1	cytidylate kinase (CMP)	[c] : atp + cmp <==> adp + cdp	BPSL2516	Cmk
CYTK2	cytidylate kinase (dCMP)	[c] : atp + dcmp <==> adp + dcdp	BPSL2516	Cmk
DADA	Deoxyadenosine deaminase	[c] : dad-2 + h + h2o --> din + nh4	BPSL2539	Add
DADK	deoxyadenylate kinase	[c] : atp + damp <==> adp + dadp	BPSL0875	Adk
DGK1	deoxyguanylate kinase (dGMP:ATP)	[c] : atp + dgmp <==> adp + dgdp	BPSL2563	Gmkec
DGTPH	dGTPase	[c] : dgtp + h2o --> dgsn + pppi	BPSL3167	Dgt
DTMPK	dTMP kinase	[c] : atp + dtmp <==> adp + dtdp	BPSL1436	Tmk
DURIPP	purine-nucleoside phosphatase	[c] : duri + pi <==> 2dr1p + ura	BPSS1960	DeoA
DUTPDP	dUTP diphosphatase	[c] : dutp + h2o --> dump + h + ppi	BPSL0903	Dutec
GK1	guanylate kinase (GMP:ATP)	[c] : atp + gmp <==> adp + gdp	BPSL2563	Gmkec
GP4GH	Gp4G hydrolase	[c] : gp4g + h2o --> (2) gdp + (2) h	BPSL2687	ApaH
GUAD	guanine deaminase	[c] : gua + h + h2o --> nh4 + xan	BPSL2112, BPSL2	YgfP
NDPK1	nucleoside-diphosphate kinase (GTP)	[c] : atp + gdp <==> adp + gtp	BPSL1510	Ndk
NDPK2	nucleoside-diphosphate kinase (UTP)	[c] : atp + udp <==> adp + utp	BPSL1510	Ndk
NDPK3	nucleoside-diphosphate kinase (CTP)	[c] : atp + cdp <==> adp + ctp	BPSL1510	Ndk
NDPK4	nucleoside-diphosphate kinase (dGTP)	[c] : atp + dtgp <==> adp + dtdp	BPSL1510	Ndk
NDPK5	nucleoside-diphosphate kinase (dGTP)	[c] : atp + dgdp <==> adp + dgtp	BPSL1510	Ndk
NDPK6	nucleoside-diphosphate kinase (dUTP)	[c] : atp + dudp <==> adp + dutp	BPSL1510	Ndk
NDPK7	nucleoside-diphosphate kinase (dCTP)	[c] : atp + dcdp <==> adp + dctp	BPSL1510	Ndk
NDPK8	nucleoside-diphosphate kinase (dATP)	[c] : atp + dadp <==> adp + datp	BPSL1510	Ndk
NTPTP2	Nucleoside triphosphate tripolyphosphatase	[c] : gtp + h2o --> gsn + pppi	BPSL3167	Dgt
RNDR1	ribonucleoside-diphosphate reductase	[c] : adp + trdrd --> dadp + h2o + trdox	BPSL2991+BPSL2	NrdA
RNDR2	ribonucleoside-diphosphate reductase	[c] : gdp + trdrd --> dgdp + h2o + trdox	BPSL2991+BPSL2	NrdA
RNDR3	ribonucleoside-diphosphate reductase	[c] : cdp + trdrd --> dcdp + h2o + trdox	BPSL2991+BPSL2	NrdE, NrdA
RNDR4	ribonucleoside-diphosphate reductase	[c] : trdrd + udp --> dudp + h2o + trdox	BPSL2991+BPSL2	NrdA
RNTR1	ribonucleoside-triphosphate reductase	[c] : atp + trdrd --> datp + h2o + trdox	BPSL2356	NrdD
RNTR2	ribonucleoside-triphosphate reductase	[c] : gtp + trdrd --> dgtp + h2o + trdox	BPSL2356	NrdD
RNTR3	ribonucleoside-triphosphate reductase	[c] : ctp + trdrd --> dctp + h2o + trdox	BPSL2356	NrdD
RNTR4	ribonucleoside-triphosphate reductase	[c] : trdrd + utp --> dutp + h2o + trdox	BPSL2356	NrdD
TMDPP	thymidine phosphorylase	[c] : pi + thymd <==> 2dr1p + thym	BPSS1960	DeoA
TMDS	thymidylate synthase	[c] : dump + mlthf --> dhf + dtmp	BPSL2473	ThyA
UMPK	UMP kinase	[c] : atp + ump <==> adp + udp	BPSL2516, BPSL2	PyrHec, Cmk
UPPRT	uracil phosphoribosyltransferase	[c] : prpp + ura --> ppi + ump	BPSL1166	Upp
URIDK3	uridylate kinase (dUMP)	[c] : atp + dump <==> adp + dudp	BPSL2157	PyrHec

ADSL1r	adenylsuccinate lyase	[c] : dcamp <==> amp + fum	BPSL2928	PurB
ADSL2r	adenylosuccinate lyase	[c] : 25aics <==> aicar + fum	BPSL2928	PurB
ADSS	adenylosuccinate synthetase	[c] : asp-L + gtp + imp --> dcamp + gdp + (2) h + pi	BPSL1524	PurA
AICART	phosphoribosylaminoimidazole c	[c] : 10fthf + aicar <==> fprica + thf	BPSL2896	PurH
AIRC2	phosphoribosylaminoimidazole c	[c] : air + atp + hco3 --> 5caiz + adp + h + pi	BPSL0801	PurK
AIRC3	phosphoribosylaminoimidazole c	[c] : 5aizc <==> 5caiz	BPSL0800	PurE
ASPCT	aspartate carbamoyltransferase	[c] : asp-L + cbp --> cbasp + h + pi	BPSL2690, BPSS1	PyrBec
CTPS2	CTP synthase (glutamine)	[c] : atp + gln-L + h2o + utp --> adp + ctp + glu-L + (2) h + pi	BPSL2272	PyrG
DHORD2	dihydroorotic acid dehydrogenas	[c] : dhor-S + ubq8 --> orot + ubq8h2	BPSL1866	PyrD
DHORD5	dihydroorotic acid (menaquinon	[c] : dhor-S + mqn8 --> mql8 + orot	BPSL1866	PyrD
DHORTS	dihydroorotase	[c] : dhor-S + h2o <==> cbasp + h	BPSL2914	PyrC
GARFT	phosphoribosylglycinamide form	[c] : 10fthf + gar <==> fgam + h + thf	BPSL0908	PurN
GART	Phosphoribosylglycinamide form	[c] : atp + for + gar --> adp + fgam + h + pi	BPSL1111	PurT
GLUPRT	glutamine phosphoribosyldiphos	[c] : gln-L + h2o + prpp --> glu-L + ppi + pram	BPSS1692	PurF
GMPS2	GMP synthase (glutamine-hydro	[c] : atp + gln-L + h2o + xmp --> amp + glu-L + gmp + (2) h + ppi	BPSL2127	GuaA
IMPC	IMP cyclohydrolase	[c] : h2o + imp <==> fprica	BPSL2896	PurH
IMPD	IMP dehydrogenase	[c] : h2o + imp + nad --> h + nadh + xmp	BPSL2129	GuaB
PRAGS	phosphoribosylglycinamide synt	[c] : atp + gly + pram --> adp + gar + h + pi	BPSL1164	PurDec
PRAIS	phosphoribosylaminoimidazole s	[c] : atp + fpram --> adp + air + h + pi	BPSL2818	PurM
PRFGS	phosphoribosylformylglycinamid	[c] : atp + fgam + gln-L + h2o --> adp + fpram + glu-L + (2) h + pi	BPSL1416	PurL
BADH	betaine-aldehyde dehydrogenas	[c] : betald + h2o + nad --> glyb + (2) h + nadh	BPSS1354	BetB
BETALDH	betaine-aldehyde dehydrogenas	[c] : betald + h2o + nadp --> glyb + (2) h + nadph	BPSS1354	BetB
CAT	catalase	[c] : (2) h2o2 --> (2) h2o + o2	BPSL2865, BPSS2	CatG, KatG, KatE
HCO3E	carbonate dehydratase (HCO3 e	[c] : co2 + h2o <==> h + hco3	BPSL1203, BPSL0	YadF, CynT
SELNPS	Selenophosphate synthase	[c] : atp + h2o + seln --> amp + pi + selnp	BPSS0287	SelD
SOD	superoxide dismutase	[c] : (2) h + (2) o2- --> h2o2 + o2	BPSL0880	SodB
ACOAD2	acyl-CoA dehydrogenase (hexar	[c] : h + hx2coa + nadh <==> hxcoa + nad	BPSL0061+BPSL0	FadE
ACOAD3	acyl-CoA dehydrogenase (octan	[c] : nad + occoa <==> h + nadh + oc2coa	BPSL0061+BPSL0	FadE
ACOAD4	acyl-CoA dehydrogenase (decan	[c] : dccoa + nad <==> dc2coa + h + nadh	BPSL0061+BPSL0	FadE
ACOAD5	acyl-CoA dehydrogenase (dodec	[c] : ddcoa + nad <==> h + nadh + trans-dd2coa	BPSL0061+BPSL0	FadE
ACOAD6	acyl-CoA dehydrogenase (tetrac	[c] : nad + tdcoa <==> h + nadh + td2coa	BPSL0061+BPSL0	FadE
ACOAD7	acyl-CoA dehydrogenase (hexac	[c] : nad + pmtcoa <==> h + hdd2coa + nadh	BPSL0061+BPSL0	FadE
4HTHRS	4-Hydroxy-L-threonine synthase	[c] : h2o + phthr --> 4hthr + pi	BPSL1478	ThrC

Synthetic lethals in Burkholderia mallei under in-vivo (intra-macrophage) conditions

Iteration 1

BMA1493 Arginine_and_Proline_Metabolism ArgE "acetylornithine deacetylase"

BMA2539 ArgJ "glutamate N-acetyltransferase/amino-acid acetyltransferase"

Iteration 2

BMAA0603 Nucleotide_Salvage_Pathways CodA "Cytosine deaminase"

BMA0429 Nucleotide_Salvage_Pathways Cmk "cytidylate kinase"

Iteration 3

BMA1145 ArcA "arginine deiminase"

(BMA0718_or_BMA1620) Arginine_and_Proline_Metabolism ArgH "argininosuccinate lyase" "argininosuccinate lyase domain protein"

Iteration 4

BMA2277 Nucleotide_Salvage_Pathways Adk "adenylate kinase"

BMA2515 Ffh "hypoxanthine-guanine phosphoribosyltransferase, putative"

Iteration 5

(BMA1751_or_BMA2539) ArgA "amino-acid N-acetyltransferase" ArgJ "glutamate N-acetyltransferase/amino-acid

BMA2539 ArgJ "glutamate N-acetyltransferase/amino-acid

Iteration 6

BMAA0307 ThrB "homoserine kinase"

BMAA1834 Threonine_and_Lysine LtaA "threonine aldolase"

Iteration 7

BMA1145 ArcA "arginine deiminase"

BMA3363 Arginine_and_Proline_Metabolism ArgG "argininosuccinate synthase"

Iteration 8

BMA2277 Nucleotide_Salvage_Pathways Adk "adenylate kinase"

BMA3120 Histidine_Metabolism PrsA "ribose-phosphate pyrophosphokinase"

Iteration 9

BMAA0420 Pentose_Phosphate_Cycle Gnd "phosphogluconate dehydrogenase"

BMAA0535 Pentose_Phosphate_Cycle Rpe "ribulose-5-phosphate 3-epimerase"

Iteration 10

BMA0057 DaaT "D-amino acid aminotransferase"

BMA0700 Cofactor_and_Prosthetic_Group Biosynthesis PanD "aspartate 1-decarboxylase"

Iteration 11

BMA1384 Cofactor_and_Prosthetic_Group_Biosynthesis ThrC "threonine synthase"

BMAA1834 Threonine_and_Lysine_Metabolism LtaA "threonine aldolase"

Iteration 12

BMA2240 Purine_and_Pyrimidine PurN "phosphoribosylglycinamide formyltransferase"

BMA1724 Folate_Metabolism Fcld "methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase"

Iteration 13

BMA0486 Citrate_Cycle_TCA Icd "isocitrate dehydrogenase, NADP-dependent"

BMA0647 HutU "urocanate hydratase"

Iteration 14

BMA1922 Purine_and_Pyrimidine_Biosynthesis PurT "phosphoribosylglycinamide formyltransferase 2"

BMA1724 Folate_Metabolism Fcld "methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase"

Iteration 15

BMA0652 HutG "N-formylglutamate amidohydrolase"

BMA0486 Citrate_Cycle_TCA Icd "isocitrate dehydrogenase, NADP-dependent"

Iteration 16

BMA2240 Purine_and_Pyrimidine_Biosynthesis PurN "phosphoribosylglycinamide formyltransferase"

BMA1922 Purine_and_Pyrimidine_Biosynthesis PurT "phosphoribosylglycinamide formyltransferase 2"

Iteration 17

BMA0486 Citrate_Cycle_TCA Icd "isocitrate dehydrogenase, NADP-dependent"

BMA0649 HutI "imidazolonepropionase"

Iteration 18

BMA0650 HutF "formiminoglutamate deiminase"

BMA0486 Citrate_Cycle_TCA Icd "isocitrate dehydrogenase, NADP-dependent"

Iteration 19

BMA3262 Methionine_Metabolism MetK "S-adenosylmethionine synthetase"

BMA2470 Arginine_and_Proline_Metabolism Tkt "spermidine synthase, putative"

Iteration 20

BMA0645 HutH "histidine ammonia-lyase"

BMA0486 Citrate_Cycle_TCA Icd "isocitrate dehydrogenase, NADP-dependent"

Iteration 21

BMA2515 Ffh "hypoxanthine-guanine phosphoribosyltransferase,

BMA3120 Histidine_Metabolism PrsA "ribose-phosphate pyrophosphokinase"

Iteration 22

BMA0736 Anaplerotic_reactions Ppa "inorganic pyrophosphatase"

BMA3120 Histidine_Metabolism PrsA "ribose-phosphate pyrophosphokinase"

Iteration 23

BMA2515 Ffh "hypoxanthine-guanine phosphoribosyltransferase,

BMA0736 Anaplerotic_reactions Ppa "inorganic pyrophosphatase"

Iteration 24

(BMA0534_or_BMAA1218) Membrane_Lipid_Metabolism FabF "3-oxoacyl-(acyl-carrier-protein) synthase II"

(BMA2880_or_BMA0530_or_BMA2878) Membrane_Lipid_Metabolism "3-oxoacyl-(acyl-carrier-protein) synthase III, FabH "3-oxoacyl-(acyl-carrier-protein) synthase III" "3-oxoacyl-(acyl-carrier-protein) synthase III,

Iteration 25

BMAA1890 OacA "O-acetylhomoserine/O-acetylserine sulfhydrylase"

(BMA2154_or_BMA0181_or_BMA1494) Valine_Leucine_and_Isoleucine_Metabolism TdyC "serine/threonine dehydratase family protein" IlvA "threonine ammonia-lyase, biosynthetic" TdcB "threonine dehydratase catabolic"

Iteration 26

(BMA1524_or_BMAA1350) Purine_and_Pyrimidine_Biosynthesis GuaB "inosine-5'-monophosphate dehydrogenase"

(BMA2042_or_BMA2041) XanD "xanthine dehydrogenase, N-terminal subunit" "xanthine dehydrogenase, C-terminal subunit"

Iteration 27

BMA0057 DaaT "D-amino acid aminotransferase"

(BMA2175_and_BMAA1380) OamP "omega-amino acid--pyruvate aminotransferase"

Iteration 28

(BMAA1744_or_BMA2258) Citrate_Cycle_TCA GltA "citrate synthase" "citrate synthase family protein"

BMA0647 HutU "urocanate hydratase"

Iteration 29

BMA1147 Putative ArcC "carbamate kinase"

(BMA0770_and_BMA0772) Arginine_and_Proline_Metabolism CarA "carbamoyl-phosphate synthase, small subunit" CarB "carbamoyl-phosphate synthase, large subunit"

Iteration 30

BMA1384 Cofactor_and_Prosthetic_Group_Biosynthesis ThrC "threonine synthase"

(BMAA0471_or_BMA2075) Glycine_and_Serine_Metabolism GlyA-1 "serine hydroxymethyltransferase"

Iteration 31

(BMAA0471_or_BMA2075) Glycine_and_Serine_Metabolism GlyA-1 "serine hydroxymethyltransferase"

BMAA0307 ThrB "homoserine kinase"

Iteration 32

BMA0057 DaaT "D-amino acid aminotransferase"

(BMA2931_and_BMAA1379) MmsA-1 "methylmalonate-semialdehyde dehydrogenase"

Iteration 33

(BMAA1744_or_BMA2258) Citric_Acid_Cycle_TCA GltA "citrate synthase" "citrate synthase family protein"

BMA0652 HutG "N-formylglutamate amidohydrolase"

Iteration 34

BMAA1290 OrnC "ornithine cyclodeaminase/mu-crystallin family protein"

BMA2410 Arginine_and_Proline_Metabolism ProC "pyrroline-5-carboxylate reductase"

Iteration 35

(BMAA1744_or_BMA2258) Citric_Acid_Cycle_TCA GltA "citrate synthase" "citrate synthase family protein"

BMA0650 HutF "formiminoglutamate deiminase"

Iteration 36

(BMAA1744_or_BMA2258) Citric_Acid_Cycle_TCA GltA "citrate synthase" "citrate synthase family protein"

BMA0645 HutH "histidine ammonia-lyase"

Iteration 37

(BMAA1744_or_BMA2258) Citric_Acid_Cycle_TCA GltA "citrate synthase" "citrate synthase family protein"

BMA0649 HutI "imidazolonepropionase"

Iteration 38

BMAA1317 MetB "trans-sulfuration enzyme family protein"

(BMA2154_or_BMA0181_or_BMA1494) Valine_Leucine_and_Isoleucine_Metabolism "serine/threonine dehydratase family protein" IlvA "threonine ammonia-lyase, biosynthetic"
TdcB "threonine dehydratase catabolic"

Iteration 39

BMA3246 HseA "homoserine O-acetyltransferase"

(BMA2154_or_BMA0181_or_BMA1494) Valine_Leucine_and_Isoleucine_Metabolism "serine/threonine dehydratase family protein" IlvA "threonine ammonia-lyase, biosynthetic"
TdcB "threonine dehydratase catabolic"

Iteration 40

(BMA0422_or_BMA0072) Cell_Envelope_Biosynthesis RfaE "ADP-heptose synthase" "cytidyltransferase-related domain protein"

BMA2470 Arginine_and_Proline_Metabolism Tkt "spermidine synthase, putative"

Iteration 41

(BMA0422_or_BMA0072) Cell_Envelope_Biosynthesis RfaE "ADP-heptose synthase" "cytidyltransferase-related domain protein"

BMA3262 Methionine_Metabolism MetK "S-adenosylmethionine synthetase"

Iteration 42

((BMA2951_and_BMA2953)_and_((BMA2954_and_BMA2956_and_BMA2958_and_BMAA0123_and_BMAA0130)_or_(BMA2954_and_BMA2955_and_BMA2956_and_BMA2958_and_BMAA0123)_or_(BMA2954_and_BMA2956_and_BMA2957_and_BMA2958_and_BMAA0130)_or_(BMA2954_and_BMA2955_and_BMA2956_and_BMA2957_and_BMA2958))))
AtpB-1 "ATP synthase F0, A subunit" AtpF "ATP synthase F0, B subunit" AtpH "ATP synthase F1, delta subunit" AtpG "ATP synthase F1, gamma subunit" AtpC-1 "ATP synthase F1, epsilon subunit" AtpH "ATP synthase F1, delta subunit" AtpA-1 "ATP synthase F1, alpha subunit" AtpG "ATP synthase F1, gamma subunit" AtpC-1 "ATP synthase F1, epsilon subunit" AtpH "ATP synthase F1, delta subunit" AtpG "ATP synthase F1, gamma subunit" AtpD-1 "ATP synthase F1, beta subunit" AtpC-1 "ATP synthase F1, epsilon subunit" AtpH "ATP synthase F1, delta subunit" AtpA-1 "ATP synthase F1, alpha subunit" AtpG "ATP synthase F1, gamma subunit" AtpD-1 "ATP synthase F1, beta subunit" AtpC-1 "ATP synthase F1, epsilon subunit"

BMA2468 Gap "glyceraldehyde-3-phosphate dehydrogenase, type