

The Pathway Tools Software in 2009: Supplementary Figures

Some of the figures herein are difficult to read at low magnification settings. We recommend that the reader increase the magnification of their PDF viewer to approximately 300% to read figures such as Supplementary Figure 3.

MetaCyc Gene/Protein/RNA Search

▼ Search by gene name or database identifier

Enter a gene name, or a database identifier from this database or from an external database to which this database contain links. Partial names will generate a substring search on gene names only (not on database identifiers).

Examples: "trpA", "trp", "b1236"

▼ Search by protein name, EC number, or database identifier

Enter a protein or RNA name, an EC number, or a database identifier from this database or from an external database to which this database contain links. Partial names will generate a substring search on protein or RNA names only (not on database identifiers).

Examples: "tryptophan synthase", "P0A877", "1.1.2.3"

▶ Search/Filter by sequence length

▶ Search/Filter by replicon and/or gene map position

▶ Search/Filter by product molecular weight

▶ Search/Filter by pI

▼ Search/Filter by small molecule regulator, cofactor, substrate or ligand

Search for all proteins for which the specified small molecule plays one or more of the following roles:

- Enzyme activator
- Enzyme inhibitor
- Enzyme cofactor
- Enzyme or transporter substrate
- Transcription factor ligand

Small molecule:

Enter a compound name and check one or more boxes. Use the autocomplete functionality to select a full compound name, as no substring matching is done on the compound name.

Examples: "L-tryptophan", "pyruvate", "Mn+2"

▶ Search/Filter by evidence code

▶ Search/Filter by cell component

▶ Search/Filter by Gene Ontology term

▶ Search/Filter by MultiFun term

▶ Search/Filter by organism

▶ Search/Filter by publication

Note: Only search criteria that have been marked active will be used in constructing the query. If multiple search criteria are specified, then results must satisfy ALL of them. For more search options, see the [Advanced Search](#) page. For more details on how to use this and other search facilities, see the [Search Help](#) page.

[Report Errors or Provide Feedback](#)

Figure 1: Object-specific query tool for genes, proteins, and RNAs. The user selects which query fields are active by clicking on the triangles to the left. In this example the user is searching for proteins that contain a PQQ (pyrroloquinoline quinone) cofactor.

MetaCyc Reaction: 1.1.1.37

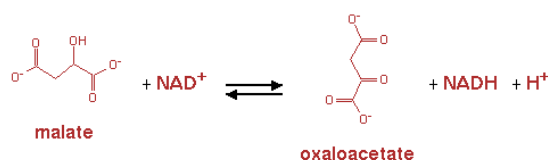
[Cross-Species Comparison](#)

Superclasses: [Reactions-Classified-By-Conversion-Type](#) -> [Simple-Reactions](#) -> [Chemical-Reactions](#) -> [EC-Reactions](#) -> [1--Oxidoreductases](#) -> [1.1--Acting on the CH-OH group of donors](#) -> [1.1.1--With NAD\(+\) or NADP\(+\) as acceptor](#)
[Reactions-Classified-By-Substrate](#) -> [Small-Molecule-Reactions](#)

Enzymes and Genes:

[malate dehydrogenase](#): [mdh](#) (Escherichia coli K-12 substr. MG1655)
[malate dehydrogenase, cytoplasmic](#): [MDH1](#) (Homo sapiens)
[mitochondrial malate dehydrogenase](#): [MDH2](#) (Homo sapiens)
[malate dehydrogenase](#) (Propionibacterium freudenreichii subsp. shermanii)
[malate dehydrogenase](#): [MDH1](#) (Homo sapiens)
[malate dehydrogenase](#): [MDH1](#) (Sus scrofa)
[malate dehydrogenase](#): [mdh](#) (Mycobacterium tuberculosis)
[malate dehydrogenase](#) (Methanococcus maripaludis)
[malate dehydrogenase](#) (Aquifex pyrophilus)
[malate dehydrogenase \(NAD-linked\)](#): [mdh](#) (Methylobacterium extorquens AM1)

In Pathway: [aspartate degradation II](#), [pyruvate fermentation to propionate I](#), [respiration \(anaerobic\)](#), [TCA cycle variation I](#), [reductive TCA cycle I](#), [reductive TCA cycle II](#), [mixed acid fermentation](#), [glyoxylate cycle](#), [TCA cycle](#), [incomplete reductive TCA cycle](#), [formaldehyde assimilation I \(serine pathway\)](#), [TCA cycle variation III \(eukaryotic\)](#), [gluconeogenesis](#), [TCA cycle variation IV](#), [superpathway of glyoxylate cycle](#)



The reaction direction shown, that is, A + B ⇌ C + D versus C + D ⇌ A + B, is in accordance with the Enzyme Commission system.

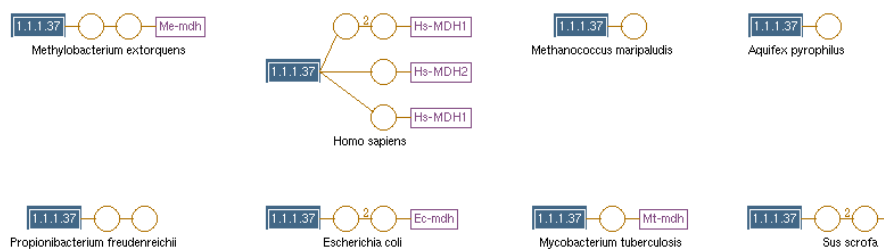
Most BioCyc compounds have been protonated to a reference pH value of 7.3, and some reactions have been computationally balanced for hydrogen by adding free protons. Please see the [BioCyc Guide](#) for more information.

Enzyme Commission Primary Name for this Reaction: Malate dehydrogenase

Enzyme Commission Synonyms for this Reaction: Malic dehydrogenase, malate dehydrogenation

ΔG° (kcal/mol): 7.1 KCAL/MOLE

Gene-Reaction Schematic: [?](#)



Unification Links: [BRENDA:1.1.1.37](#), [ENZYME:1.1.1.37](#), [UniProt:Q24047](#), [UniProt:Q48903](#), [UniProt:Q48904](#), [UniProt:Q48905](#), [UniProt:Q48906](#), [UniProt:Q65363](#), [UniProt:Q65364](#), [UniProt:Q81278](#), [UniProt:Q81279](#), [UniProt:Q81609](#), [UniProt:Q04636](#), [UniProt:P10887](#), [UniProt:P11386](#), [UniProt:P14152](#), [UniProt:P16142](#), [UniProt:P17505](#), [UniProt:P17783](#), [UniProt:P19446](#), [UniProt:P19977](#), [UniProt:P19978](#), [UniProt:P19979](#), [UniProt:P19980](#), [UniProt:P19981](#), [UniProt:P19982](#), [UniProt:P19983](#), [UniProt:P22133](#), [UniProt:P25077](#), [UniProt:P32419](#), [UniProt:P33163](#), [UniProt:P44427](#), [UniProt:P46487](#), [UniProt:P46488](#), [UniProt:P49814](#), [UniProt:P50917](#), [UniProt:P58408](#), [UniProt:P93106](#), [UniProt:Q7M4Y9](#), [UniProt:Q7M4Z0](#), [UniProt:Q8R1P0](#), [UniProt:Q93ZAZ](#), [UniProt:Q9PHY2](#), [UniProt:Q9SN86](#), [UniProt:Q9XTB4](#), [UniProt:Q9ZP05](#), [UniProt:Q9ZP06](#), [UniProt:Q04820](#), [UniProt:Q07841](#), [UniProt:Q42686](#), [UniProt:Q42972](#), [UniProt:Q43743](#), [UniProt:Q43744](#), [UniProt:Q49981](#), [UniProt:Q55383](#), [UniProt:Q59202](#)

Relationship Links: [UniProt:RELATED-TO:P11708](#), [UniProt:RELATED-TO:Q58820](#)

[Report Errors or Provide Feedback](#)

Please cite the following article in publications resulting from the use of MetaCyc: [Caspi et al, Nucleic Acids Research 36:D623-31 2008](#)
Page generated by SRI International [Pathway Tools](#) version 13.0 on Mon Jun 1, 2009, biocyc11.

Figure 2: In addition to the reaction equation, the reaction display page contains many additional information fields, including a list of enzymes in the database that catalyze the reaction, a list of pathways in which the reaction participates, computationally calculated standard free energy, gene-reaction schematics that display relationships between genes, enzymes and reactions, unification links and more.

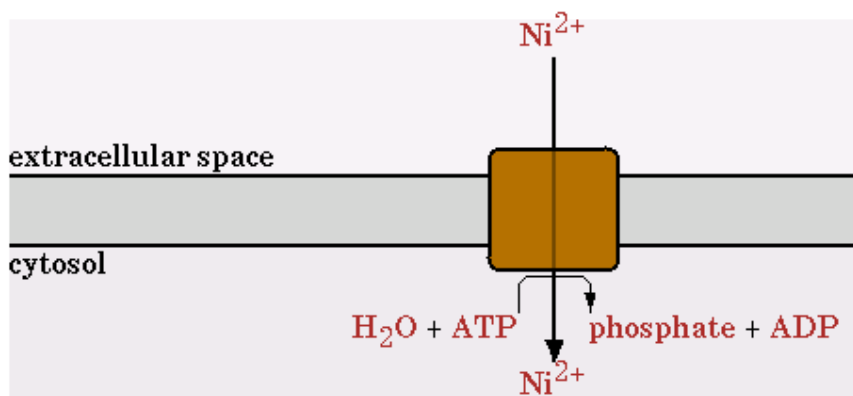
MetaCyc Reaction: 3.6.3.24

Cross-Species Comparison

Superclasses: [Reactions-Classified-By-Conversion-Type](#) -> [Simple-Reactions](#) -> [Chemical-Reactions](#) -> [EC-Reactions](#) -> [3 -- Hydrolyses](#) -> [3.6.3 -- Acting on acid anhydrides; catalyzing transmembrane movement](#)
[Reactions-Classified-By-Conversion-Type](#) -> [Simple-Reactions](#) -> [Transport-Reactions](#)
[Reactions-Classified-By-Substrate](#) -> [Small-Molecule-Reactions](#)

Transporters and Genes:

[nickel ABC transporter](#): [nikE](#), [nikD](#), [nikC](#), [nikB](#), [nikA](#) (Escherichia coli K-12 substr. MG1655)



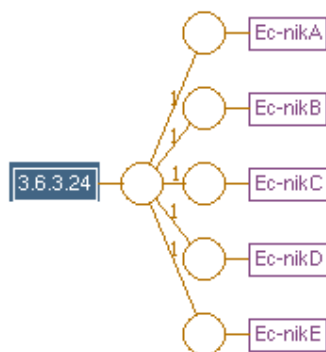
The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the Enzyme Commission

Enzyme Commission Primary Name for this Reaction: Nickel-transporting ATPase

Summary:

ABC-type (ATP-binding cassette-type) ATPase, characterised by the presence of two similar ATP-binding domains. Does not the transport process. A bacterial enzyme that imports Ni²⁺.

Gene-Reaction Schematic:



Unification Links: [BRENDA:3.6.3.24](#), [ENZYME:3.6.3.24](#)

Figure 4: Transport reaction pages include a diagram that depicts the compartments across the membrane and the direction of transport. Like regular reactions, the page includes a list of the genes and proteins associated with the transport reaction, and a gene-reaction schematic.

***Escherichia coli* K-12 substr. MG1655 Polypeptide: MtlR transcriptional repressor**



[Protein Sequence](#)

Synonyms: B3601, MtlR, repressor for mtl

Summary:

The MtlR regulator participates in controlling several genes involved in mannitol utilization. MtlR is auto-regulated through the repression of the promoter upstream of the *mtIADR* operon.

There is no protein family associated with this transcription factor.

Citations: [[Jiang90](#); [Figge94](#); [Sofia94](#)]

Gene: [mtlR](#)

Sequence Length: 195 AAs

Molecular Weight of Polypeptide (from nucleotide sequence): 21.99 kD

pI: 4.6

Component of: [MtlR-mannitol](#)

Unification Links: [EcoliWiki:b3601](#), [RefSeq:NP_418058](#), [UniProt:POAF10](#)

In Reactions:

[MtlR + D-mannitol = MtlR-mannitol](#)

Gene-Reaction Schematic: [?](#)



GO Terms:

Biological Process:	GO:0006350 - transcription [GOA00] GO:0006355 - regulation of transcription, DNA-dependent [GOA00] GO:0016052 - carbohydrate catabolic process
Molecular Function:	GO:0003677 - DNA binding [GOA00] GO:0016564 - transcription repressor activity
Cellular Component:	GO:0005737 - cytoplasm

Multifun Terms: [information transfer -> RNA related -> Transcription related](#)
[location of gene products -> cytoplasm](#)
[metabolism -> carbon utilization -> carbon compounds](#)
[regulation -> type of regulation -> transcriptional level -> repressor](#)

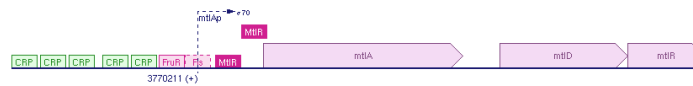
DNA binding site length: 24 base-pairs

Symmetry: Inverted Repeat

Regulated Transcription Units: [?](#)

Notes:

- Key to regulator colors: Green: activator; Magenta: inhibitor; Brown: dual; Gray: unspecified.
- A dashed outline for a transcription factor binding site or a dashed promoter indicates a lack of high quality evidence for the existence or location of that entity.
- Roll the mouse over any element in the diagram for more detailed information.
- Click above or below gene(s) to navigate to detailed transcription unit display.
- Click on a binding site (if any) to navigate to the display for its transcription factor.
- Click on a gene to navigate to the gene display.



Subunit of: [MtlR-mannitol](#)

Synonyms: B3601, MtlR

Subunit composition of [MtlR-mannitol](#) = [[MtlR](#)][[D-mannitol](#)]
[MtlR transcriptional repressor](#) = [MtlR](#)

Relationship Links: [Pfam:IN-FAMILY:PF05068](#)

In Reactions:

[MtlR + D-mannitol = MtlR-mannitol](#)

Multifun Terms: [information transfer -> RNA related -> Transcription related](#)
[location of gene products -> cytoplasm](#)
[metabolism -> carbon utilization -> carbon compounds](#)
[regulation -> type of regulation -> transcriptional level -> repressor](#)

References

[Figge RM, Ramseler TM, Saier MH \(1994\). "The mannitol repressor \(MtlR\) of Escherichia coli." J Bacteriol 194:176\(5\):840-7. PMID: 8300537](#)

[GOA \(2000\). "Gene Ontology annotation based on Swiss-Prot keyword mapping."](#)

[Jiang W, Wu LF, Tomich J, Saier MH, Niehaus WG \(1990\). "Corrected sequence of the mannitol \(mtl\) operon in Escherichia coli." Mol Microbiol 1990:4\(11\):2003-6. PMID: 1964486](#)

[Sofia HJ, Burland V, Daniels DL, Plunkett G, Blattner FR \(1994\). "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes." Nucleic Acids Res 1994:22\(13\):2576-86. PMID: 8041620](#)

Report Errors or Provide Feedback

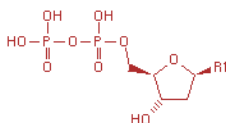
Please cite the following article in publications resulting from the use of EcoCyc: [Nucleic Acids Research 37:D464-70 2009](#)
Page generated by SRI International Pathway Tools version 13.0 on Mon Jun 1, 2009, biocyc08.

Figure 5: Unlike other proteins, the display page for transcription factors (TFs) includes a graphical display of all of the transcription units that are controlled by the TF. The functionality of the TF is indicated by color, and additional information, such as distance from the transcription start site and evidence code is displayed when available by hovering the mouse in top of the TF.

MetaCyc Class: a 2'-deoxyribonucleoside diphosphate

Synonyms: 2'-deoxyribonucleoside diphosphate, deoxynucleoside diphosphate, deoxyribonucleoside diphosphate

Superclasses: [a nucleic acid component](#) -> [a nucleotide](#) -> [a deoxynucleotide](#)
[a nucleic acid component](#) -> [a nucleotide](#) -> [a nucleoside diphosphate](#)



Empirical Formula: C₅H₁₁O₉R₁P₂

Instances:

[2'-deoxyadenosine-5'-diphosphate](#),
[2'-deoxyguanosine-5'-diphosphate](#),
[dCDP](#),
[dTDP](#),
[dUDP](#)

SMILES: C(OP(=O)(O)OP(O)(=O)O)C1(OC([R1])CC(O)1)

In Pathway Reactions as a Product:

[staphyloxanthin biosynthesis](#) :

[4,4'-diaponeurosporenoate + an NDP-glucose = glucosyl-4,4'-diaponeurosporenoate + a nucleoside diphosphate](#)

[phytol salvage pathway](#) :

[phytyl monophosphate + a nucleoside triphosphate = phytyl diphosphate + a nucleoside diphosphate](#)

In Reactions not Assigned to Pathways:

[a 2'-deoxyribonucleoside monophosphate + ATP = a 2'-deoxyribonucleoside diphosphate + ADP](#),
[a ribonucleoside diphosphate + a reduced electron acceptor = a 2'-deoxyribonucleoside diphosphate + an oxidized electron acceptor + H₂O](#),
[a 2'-deoxyribonucleoside diphosphate + an oxidized thioredoxin + H₂O = a ribonucleoside diphosphate + a reduced thioredoxin](#),
[α-D-aldose 1-phosphate + a nucleoside diphosphate = phosphate + NDP-aldose](#),
[RNA_n + phosphate = RNA_{n-1} + a nucleoside diphosphate](#),
[an NDP-glucose + a 1,4-α-D-glucan = a nucleoside diphosphate + a 1,4-α-D-glucan](#),
[tRNA_{\(n+1\)} + phosphate = tRNA_{\(n\)} + a nucleoside diphosphate](#),
[ATP + a nucleoside phosphate = ADP + a nucleoside diphosphate](#),
[a nucleoside triphosphate + adenosine-5'-phosphate = a nucleoside diphosphate + ADP](#),
[D-fructose + an NDP-glucose = a nucleoside diphosphate + sucrose](#),
[a nucleoside triphosphate + H₂O = phosphate + a nucleoside diphosphate](#),
[deoxycytidine + a nucleoside triphosphate = dCMP + a nucleoside diphosphate](#),
[a nucleotide + H₂O = a nucleoside + phosphate](#),
[a nucleotide + a deoxynucleoside = a nucleoside + a 2'-deoxyribonucleoside monophosphate](#),
[a nucleoside diphosphate + H₂O = a nucleotide + phosphate](#),
[ATP + \(deoxynucleotides\)_n + \(deoxynucleotides\)_{\(m\)} = adenosine-5'-phosphate + diphosphate + \(deoxynucleotides\)_{\(n+m\)}](#),
[\(deoxynucleotides\)_n + \(deoxynucleotides\)_{\(m\)} + NAD⁺ = \(deoxynucleotides\)_{\(n+m\)} + nicotinamide mononucleotide + adenosine-5'-phosphate](#)

[Report Errors or Provide Feedback](#)

Please cite the following article in publications resulting from the use of MetaCyc: [Caspi et al, Nucleic Acids Research 36:D623-31 2008](#)
 Page generated by SRI International [Pathway Tools](#) version 13.0 on Mon Jun 1, 2009, biocyc08.

Figure 7: Compound display pages include synonyms, classification, structure, empirical formula, smiles and InChI strings, and lists of all the reactions and pathways present in the database in which the compound participates. Class compounds can include an R residue in their structures, as shown in this figure, and specify the children compound classes and instances that reside within the class. Class compounds do not have an InChI string.

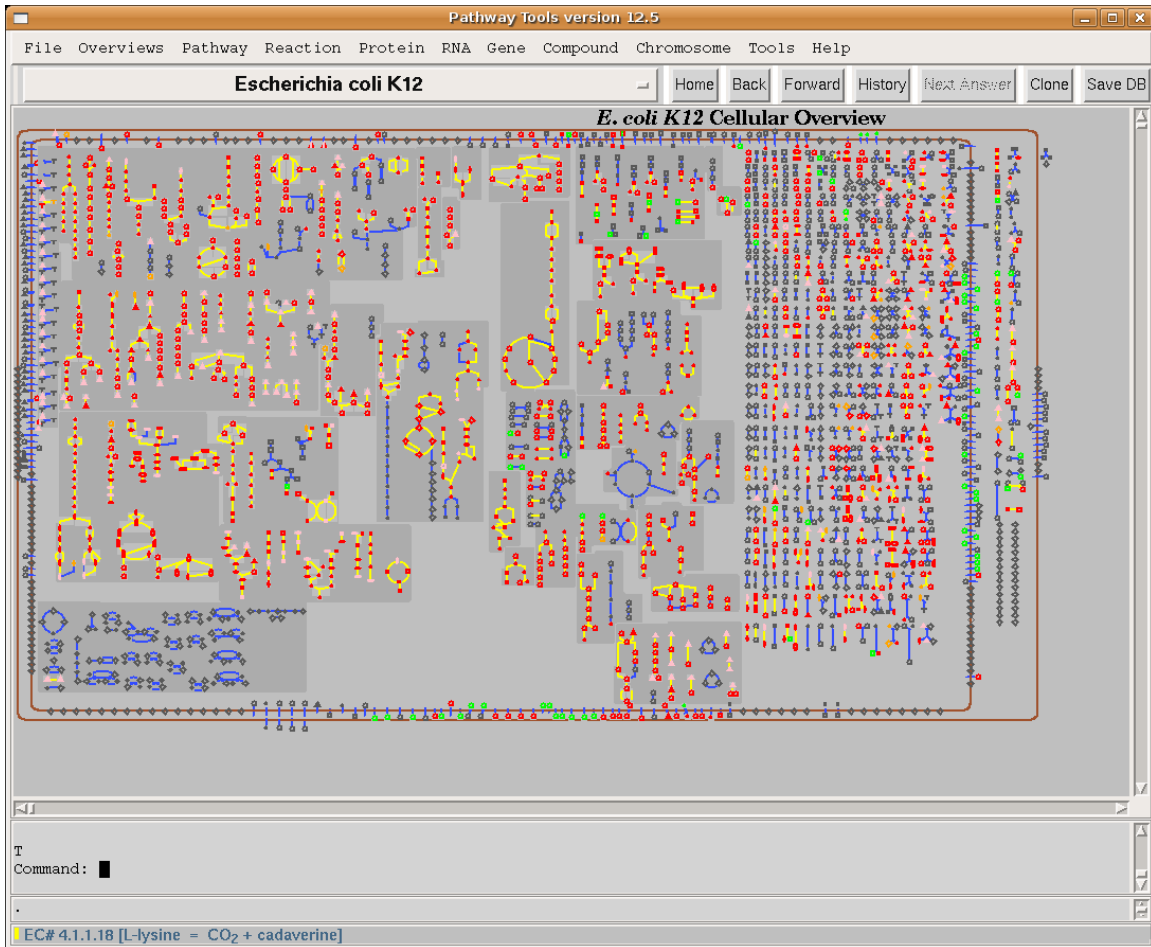


Figure 8: Reachability analysis for EcoCyc. The results are visualized by highlighting reactions and compounds on the cellular overview in different colors. Fired reactions are yellow lines, produced biomass metabolites are pink, other produced metabolites are red. Green metabolites are supplied by the growth medium, and orange indicates auxiliary metabolites.

Escherichia coli K-12 substr. MG1655 Chromosome: dnaA Comparison



[Report Errors or Provide Feedback](#)

Please cite the following article in publications resulting from the use of EcoCyc: [Nucleic Acids Research 37:D464-70 2009](#)
Page generated by SRI International [Pathway Tools](#) version 13.0 on Mon Jun 1, 2009, biocyc08.

Figure 9: Comparative genome browser displaying chromosomal regions around the *dnaA* genes in several organisms.

Comparative Analysis Summary Results

Note: In addition to reflecting differences in biology of different organisms, these statistics will reflect differences in the levels of curation, data availability, and completeness of the PGDBs for these organisms.

Comparative analysis and statistics were computed for the following organism databases:

- *Escherichia coli K-12 substr. MG1655*
- *Francisella tularensis subsp. tularensis FSC198*

Any cell of a table that is a hyperlink can be clicked to see more detail about the contents of the cell (usually an enumeration of all entities represented by the statistic). Clicking on a row or column header will take you to the more detailed view of the entire row or column, and clicking on a table header, where available, will take you to the more detailed view of the entire table. Mouse-over a link in a table (such as a row heading) to see a description of what will be displayed if you click on that link.

Table of Contents

- [Transporters](#)

Transporters

Table 1: Transporters

This table presents statistics on the number of transport proteins present in each organism.

Transporters	E. coli K-12 substr. MG1655	F. tularensis subsp. tularensis FSC198
Uptake transporters	156	66
Efflux transporters	66	6
Transporters assigned to transport reactions	241	75
Genes assigned to transport proteins	399	78
Genes classified in MultiFun as transport genes	683	121

Table 2: Substrate Uptake

This table identifies compounds transported into the cell, and categorizes these compounds further by their metabolic role.

Substrate uptake	E. coli K-12 substr. MG1655	F. tularensis subsp. tularensis FSC198
Compounds transported into the cell	156	29
Compounds transported into the cell that are pathway inputs	114	11
Compounds transported into the cell that are pathway intermediates	0	0
Compounds transported into the cell that are enzyme cofactors	14	0
Compounds that are neither pathway inputs, pathway intermediates nor enzyme cofactors	34	18

Table 3: Substrate Efflux

This table identifies compounds transported out of the cell, and categorizes these compounds further by their metabolic role.

Substrate efflux	E. coli K-12 substr. MG1655	F. tularensis subsp. tularensis FSC198
Compounds transported out of cell	47	4
Compounds transported out of cell that are pathway outputs	21	2
Compounds transported out of cell that are not pathway outputs	26	2
Compounds that are pathway outputs but not transported out of cell	184	193

Table 4: Multiple Transporters and Substrates

This table identifies transporters that transport more than one substrate, and substrates that are transported by more than one transporter.

Multiple transporters and substrates	E. coli K-12 substr. MG1655	F. tularensis subsp. tularensis FSC198
Transporters with multiple substrates	49	12
Substrates with multiple transporters	81	13

Table 5: Transcription

This table identifies transporters that are related through a common operon or chromosomal neighborhood, or through regulation by the same substrate. Clicking on a row of this table will create another table, from which in turn, comparative operon diagrams can be viewed.

Transporter Transcription Unit Organization	E. coli K-12 substr. MG1655	F. tularensis subsp. tularensis FSC198
Transporters in same operon or chromosomal neighborhood as enzyme with same substrate as that transporter. Click on transporter name to view comparative operon diagram.	47	0
Additional transporters in same operon or chromosomal neighborhood as enzyme in same pathway as substrate. Click on transporter name to view comparative operon diagram.	3	1
Transporters in same operon or chromosomal neighborhood as transcription factor that binds transporter substrate. Click on transporter name to view comparative operon diagram.	3	0
Transporters whose transcription is regulated by its substrate. Click on transporter name to view comparative operon diagram.	20	0
The following genes are assigned to the MultiFun gene ontology category 'transporters of unknown substrate' in same operon or chromosomal neighborhood as an enzyme -- may yield clues to transporter substrate	21	9

[Comparative Analysis Start Page](#)

Figure 10: Comparative transporter report for *E. coli* K-12 MG1655 and *Francisella tularensis* FSC198.

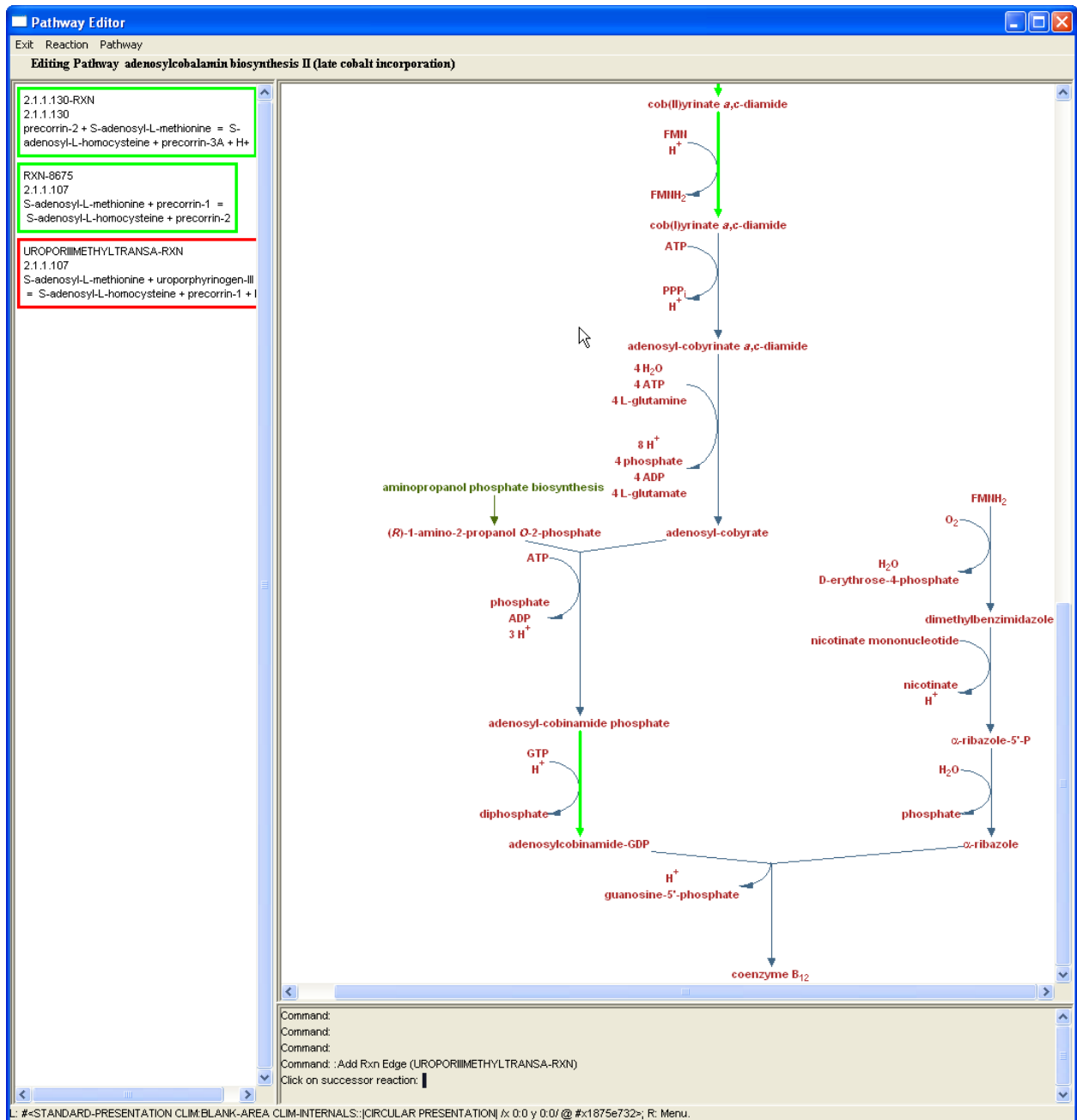


Figure 11: Pathway Tools Pathway Editor.

Edit Protein CPLX-7783

Enzyme: **2-phospho-L-lactate guanylyltransferase**

Class: a protein complex

Evidence for non-enzymatic function of this protein, if any: Evidence Code Citation:

GO Terms

Synonyms:

Citations:

Summary: The [FRAME: G-11181] gene of [FRAME: TAX-2190] has been cloned and expressed in E.coli, and the recombinant protein has been purified, and found to be a homodimer [CITS: [18260642]].

The purified protein was found to catalyze the formation of [FRAME: CPD-7601] from [FRAME: CPD-7599] and [FRAME: GTP] with a Vmax of 3 μmol/min/mg protein. The enzyme was able to utilize other purine nucleotides including dGTP and ITP as cosubstrates in place of GTP but with a lower specific activity. Maximal activity was seen when [FRAME: MG+2] was added to the reaction [CITS: [18260642]]

Molecular Weight (kD, experimental): Citation: pI: Citation:

Locations:

Links to other databases:

Database	ID	Relationship
<input type="text"/>	<input type="text"/>	<input type="text" value="Same Entity"/>
<input type="text"/>	<input type="text"/>	<input type="text" value="Same Entity"/>

Credits:

Date: none yet

Curators:

Organizations:

Current selection(s): Caspi R Current selection(s): SRI International

Update Last-Curated Date ?

Enzyme activity name:

Reaction (shown in EC left-to-right direction): **2-phospho-L-lactate + GTP + H⁺ = lactyl-2-diphospho-5'-guanosine + diphosphate**

Evidence for this activity: EV-EXP-IDA-PURIFIED-PROTEIN-HH Citation: Evidence Code Citation:

Synonyms:

Citations:

Summary:

Reaction Direction: Citation:

Activators/Inhibitors/Cofactors/Alternative substrates:

Activator (allosteric)	<input type="text" value="Mg2+"/>	<input type="checkbox"/> Physiologically relevant?	Citation: <input type="text" value="18260642"/>	Citation: <input type="text"/>
Alt. substrate for GTP	<input type="text" value="dGTP"/>	<input type="checkbox"/> Physiologically relevant?	Citation: <input type="text" value="18260642"/>	Citation: <input type="text"/>
Alt. substrate for GTP	<input type="text" value="ITP"/>	<input type="checkbox"/> Physiologically relevant?	Citation: <input type="text" value="18260642"/>	Citation: <input type="text"/>

Figure 12: Pathway Tools Protein Editor.

Regulatory Interaction Editor

Instances of this class describe regulation of transcription initiation whereby the binding of an RNA-polymerase to a transcription unit promoter is activated or inhibited by the binding of some entity (generally a transcription factor) to some nearby DNA binding site. The regulator in this case is the transcription factor, and the regulated-entity is the transcription unit promoter (although what is really being regulated is the transcription of the transcription unit to produce RNA). If no promoter has been identified for a transcription unit, or no transcription unit for a regulated gene, it is possible to specify the transcription unit or the gene itself as the regulated-entity instead of the promoter, although it is understood that these cases describe incomplete information.

Type of Regulation:

Regulated Promoter, Terminator, Transcription-Unit or Gene:

Binding Site: **Fis DNA binding transcriptional dual regulator activator site in metTp-promoter**

Protein: The protein forms a complex with this small molecule:

Function: The modified form of the protein is the form.

Relative Center Distance from Promoter: Site Length:

Site left position: 696447 Site right position: 696461
 Site sequence: acctaaccAAACAGTCACTTTCGAGcaattttct

Reg. Interaction Citations:

Reg. Interaction Summary:

Site Citations:

Site Summary:

Evidence for Binding Site: Citation: Evidence Code: Citation:

Figure 13: Pathway Tools Regulation Editor.