

JAVA project

KEEG Browser

Project objectives

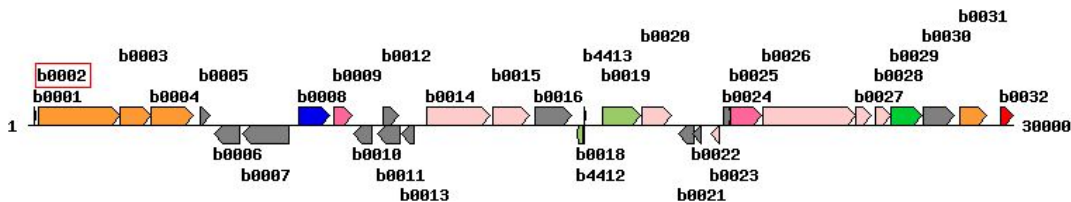
Do OOP.

Programming in Java.

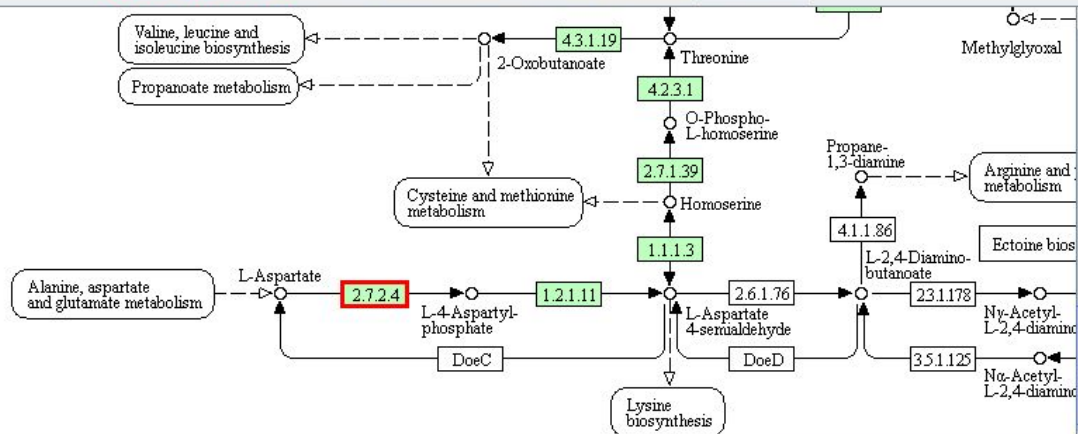
Use a API.

Establish a graphical user interface, to easily switch from a metabolic pathway to the genome and vice versa.

from 1bp to 150000bp



Search



Gene information

ENTRY	b0002	CDS	T00007
NAME	thrA		
DEFINITION	(RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 1		
ORTHOLOGY	K12524 bifunctional aspartokinase / homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.3]		
ORGANISM	eco Escherichia coli K-12 MG1655		
PATHWAY	eco00260 Glycine, serine and threonine metabolism		
	eco00261 Monobactam biosynthesis		

Involved in reaction(s)

R00480 @ eco00260

R01773 @ eco00260

R01775 @ eco00260

R01773 @ eco00270

R01775 @ eco00270

R00480 @ eco00270

R00480 @ eco00300

R01773 @ eco00300

R01775 @ eco00300

Image

ENTRY	R00480	Reaction
NAME	ATP:L-aspartate 4-phosphotransferase	
DEFINITION	ATP + L-Aspartate \rightleftharpoons ADP + 4-Phospho-L-aspartate	
EQUATION	C00002 + C00049 \rightleftharpoons C00008 + C03082	
RCLASS	RC00002 C00002_C00008 RC00043 C00049_C03082	
ENZYME	2.7.2.4	
PATHWAY	rn00260 Glycine, serine and threonine metabolism	

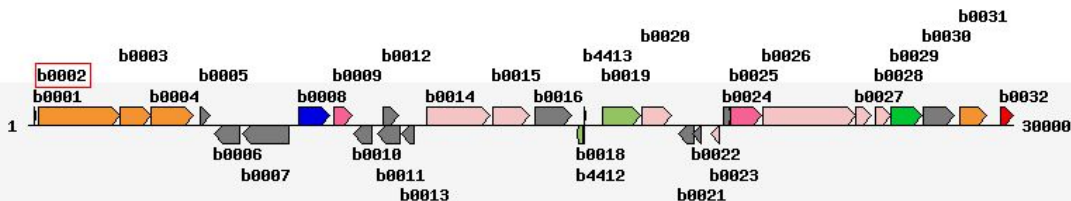
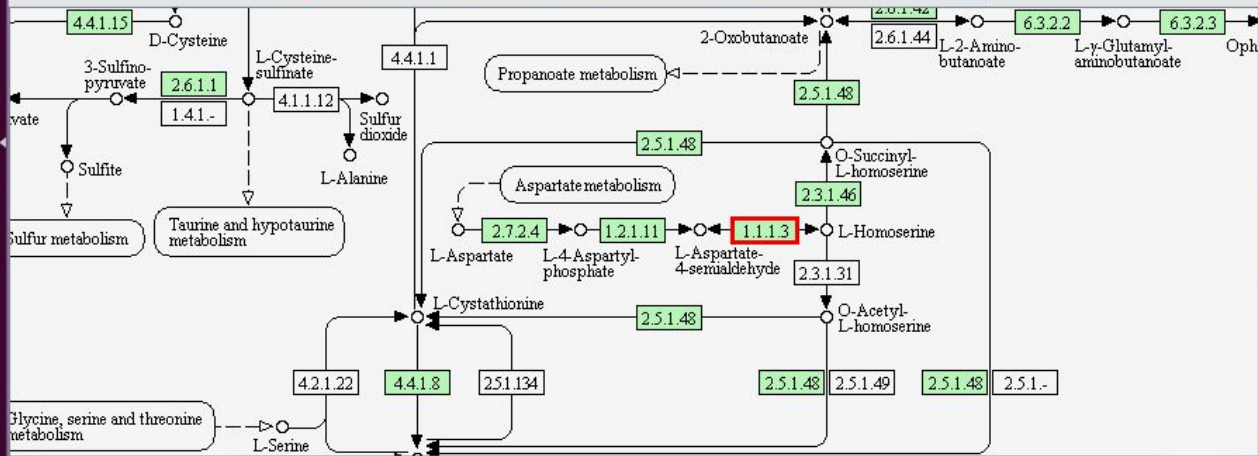
Involves gene(s)

b0002
b3940
b4024

Genome Browser Species Gene ID Search

KEGG Genome map - Escherichia coli K-12 MG1655

from 1bp to 150000bp

Pathway Browser Species Map ID Search

Gene information

ENTRY	b0002	CDS	T00007
NAME	thrA		
DEFINITION	(RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 1		
ORTHOLOGY	K12524 bifunctional aspartokinase / homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.3]		
ORGANISM	eco Escherichia coli K-12 MG1655		
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	eco00261 Monobactam biosynthesis		

Involved in reaction(s)

R00480 @ eco00260
R01773 @ eco00260
R01775 @ eco00260
R01773 @ eco00270
R01775 @ eco00270
R00480 @ eco00270
R00480 @ eco00300
R01773 @ eco00300
R01775 @ eco00300

Reaction information Image

ENTRY	R01773	Reaction
NAME	L-Homoserine:NAD ⁺ oxidoreductase	
DEFINITION	L-Homoserine + NAD ⁺ <=> L-Aspartate 4-semialdehyde + NADH + H ⁺	
EQUATION	C00263 + C00003 <=> C00441 + C00004 + C00080	
COMMENT	NADP ⁺ (see R01775)	
RCLASS	RC00001 C00003_C00004 RC00087 C00263_C00441	
ENZYME	1.1.1.3	

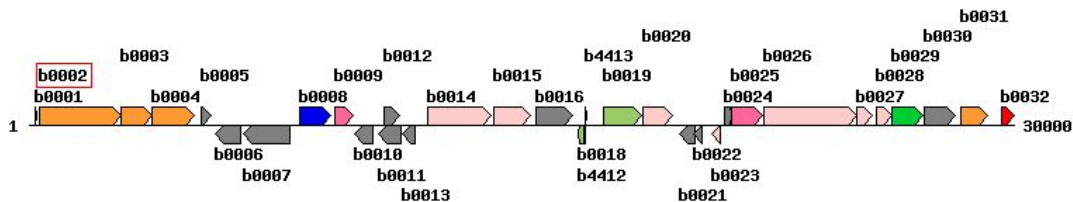
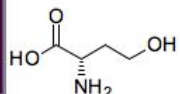
Involves gene(s)

b0002
b3940

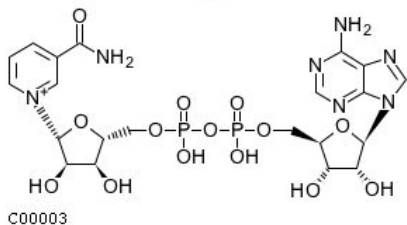
Genome Browser Species Gene ID Search

KEGG Genome map - Escherichia coli K-12 MG1655

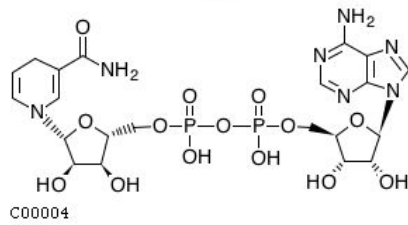
from 1bp to 150000bp

Pathway Browser Species Map ID Search

C00263



C00003



C00004



C00080



C00441

Gene information

ENTRY	b0002	CDS	T00007
NAME	thrA		
DEFINITION	(RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 1		
ORTHOLOGY	K12524 bifunctional aspartokinase / homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.3]		
ORGANISM	eco Escherichia coli K-12 MG1655		
PATHWAY	eco00260 Glycine, serine and threonine metabolism		
	eco00261 Monobactam biosynthesis		

Involved in reaction(s)

R00480 @ eco00260
R01773 @ eco00260
R01775 @ eco00260
R01773 @ eco00270
R01775 @ eco00270
R00480 @ eco00270
R00480 @ eco00300
R01773 @ eco00300
R01775 @ eco00300

Reaction information

Image

ENTRY	R01773	Reaction
NAME	L-Homoserine:NAD+ oxidoreductase	
DEFINITION	L-Homoserine + NAD+ <=> L-Aspartate 4-semialdehyde + NADH + H+	
EQUATION	C00263 + C00003 <=> C00441 + C00004 + C00080	
COMMENT	NADP+ (see R01775)	
RCLASS	RC00001 C00003_C00004 RC00087 C00263_C00441	
ENZYME	1.1.1.3	

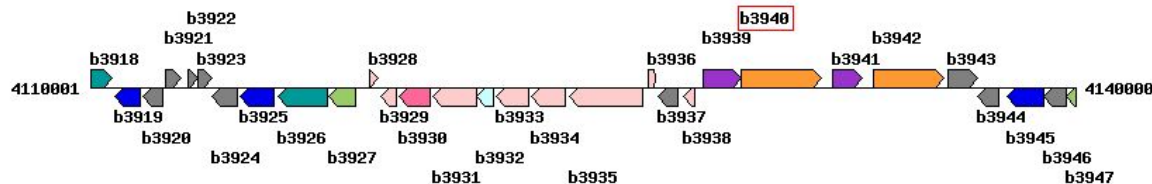
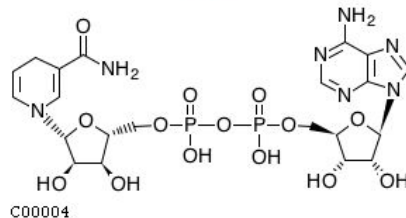
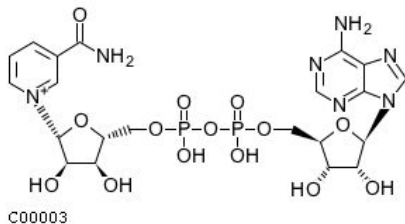
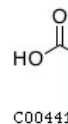
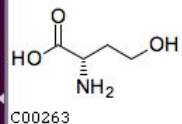
Involves gene(s)

b0002
b3940

Genome Browser Species Gene ID Search

KEGG Genome map - Escherichia coli K-12 MG1655

from 4110001bp to 4260000bp

Pathway Browser Species Map ID Search

Gene information

ENTRY	b3940	CDS	T00007
NAME	metL		
DEFINITION	(RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 2		
ORTHOLOGY	K12525 bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]		
ORGANISM	eco Escherichia coli K-12 MG1655		
PATHWAY	eco00260 Glycine, serine and threonine metabolism		
	eco00261 Monobactam biosynthesis		

Involved in reaction(s)

R00480 @ eco00260
R01773 @ eco00260
R01775 @ eco00260
R01773 @ eco00270
R01775 @ eco00270
R00480 @ eco00270
R00480 @ eco00300
R01773 @ eco00300
R01775 @ eco00300

Reaction information

Image

ENTRY	R01773	Reaction
NAME	L-Homoserine:NAD ⁺ oxidoreductase	
DEFINITION	L-Homoserine + NAD ⁺ <=> L-Aspartate + 4-semialdehyde + NADH + H ⁺	
EQUATION	C00263 + C00003 <=> C00441 + C00004 + C00080	
COMMENT	NAD ⁺ (see R01775)	
RCLASS	RC00001 C00003 C00004 RC00087 C00263_C00441	
ENZYME	1.1.1.3	

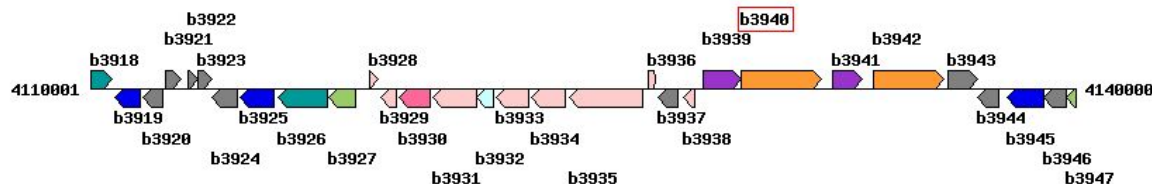
Involves gene(s)

b0002
b3940

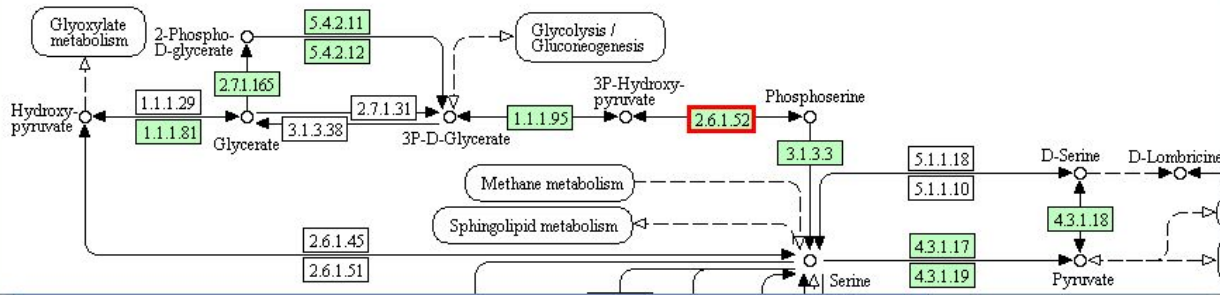
Genome Browser Species Gene ID Search

KEGG Genome map - Escherichia coli K-12 MG1655

from 4110001bp to 4260000bp

Pathway Browser Species Map ID Search

GLYCINE, SERINE AND THREONINE METABOLISM



Gene information

ENTRY b3940 CDS T00007
NAME metL
DEFINITION (RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 2
ORTHOLOGY K12525 bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]
ORGANISM eco Escherichia coli K-12 MG1655
PATHWAY eco00260 Glycine, serine and threonine metabolism
eco00261 Monobactam biosynthesis

Involved in reaction(s)

R00480 @ eco00260
R01773 @ eco00260
R01775 @ eco00260
R01773 @ eco00270
R01775 @ eco00270
R00480 @ eco00270
R00480 @ eco00300
R01773 @ eco00300
R01775 @ eco00300

Reaction information

Image

ENTRY R04173 Reaction
NAME 3-Phosphoserine:2-oxoglutarate aminotransferase
DEFINITION O-Phospho-L-serine + 2-Oxoglutarate <=> 3-Phosphonooxypyruvate + L-Glutamate
EQUATION C01005 + C00026 <=> C03232 + C00025
RCLASS RC00006 C00025_C00026 C01005_C03232
ENZYME 2.6.1.52
PATHWAY rn00260 Glycine, serine and threonine metabolism

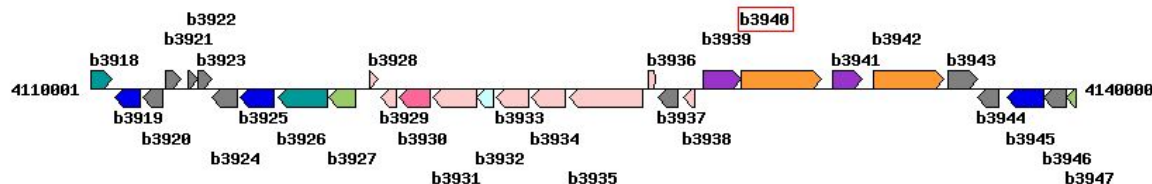
Involves gene(s)

b0907

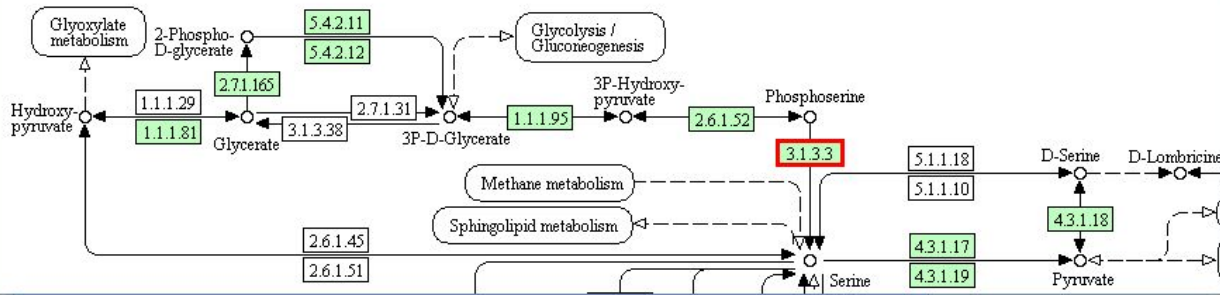
Genome Browser Species Gene ID Search

KEGG Genome map - Escherichia coli K-12 MG1655

from 4110001bp to 4260000bp

Pathway Browser Species Map ID Search

GLYCINE, SERINE AND THREONINE METABOLISM



Gene information

ENTRY	b3940	CDS	T00007
NAME	metL		
DEFINITION	(RefSeq) Bifunctional aspartokinase/homoserine dehydrogenase 2		
ORTHOLOGY	K12525 bifunctional aspartokinase / homoserine dehydrogenase 2 [EC:2.7.2.4 1.1.1.3]		
ORGANISM	eco Escherichia coli K-12 MG1655		
PATHWAY	eco00260 Glycine, serine and threonine metabolism		
	eco00261 Monobactam biosynthesis		

Involved in reaction(s)

R00480 @ eco00260
R01773 @ eco00260
R01775 @ eco00260
R01773 @ eco00270
R01775 @ eco00270
R00480 @ eco00270
R00480 @ eco00300
R01773 @ eco00300
R01775 @ eco00300

Reaction information

Image

ENTRY	R00582	Reaction
NAME	0-phospho-L-serine phosphohydrolase	
DEFINITION	0-Phospho-L-serine + H2O <=> L-Serine + Orthophosphate	
EQUATION	C01005 + C00001 <=> C00065 + C00009	
COMMENT	see R02853 (D-form)	
RCLASS	RC00017 C00065_C01005	
ENZYME	3.1.3.3	
PATHWAY	rn00260 Glycine, serine and threonine metabolism	

Involves gene(s)

b4388

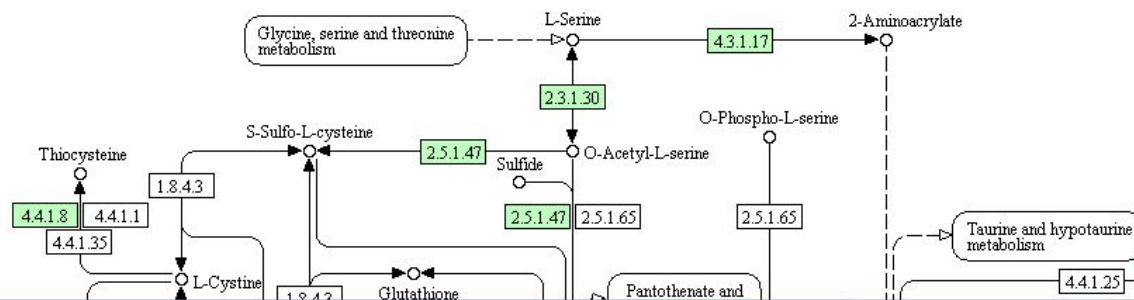
Genome Browser Species Gene ID Search

Sorry

No suc entry in GENES DB.(b00,b00)

Pathway Browser Species Map ID Search

CYSTEINE AND METHIONINE METABOLISM



Gene information

ERROR: incorrect gene entry

Involved in reaction(s)

Reaction information

Image

ENTRY R01775 Reaction
NAME L-homoserine:NADP+ oxidoreductase
DEFINITION L-Homoserine + NADP+ <=> L-Aspartate
4-semialdehyde + NADPH + H+
EQUATION C00263 + C00006 <=> C00441 + C00005 + C00080
COMMENT NAD+ (see R01773)
RCLASS RC00001 C00005_C00006
RC00087 C00263_C00441
ENZYME 1.1.1.3

Involves gene(s)

b0002
b3940