

Генные сети метаболизма. Представление в базах данных и принципы организации.

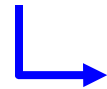
(читала с.н.с. лаб. теоретической генетики, к.б.н.
Игнатьева Е.В.)

НАИБОЛЕЕ ИЗВЕСТНЫЕ БАЗЫ, ВКЛЮЧАЮЩИЕ ДАННЫЕ О МЕТАБОЛИЧЕСКИХ ГЕННЫХ СЕТЯХ:

1) KEGG Kyoto encyclopedia of genes and genomes: integrated suite of databases on genes, proteins, and metabolic pathways

<http://www.genome.ad.jp/kegg>

2) MetaCyc Metabolic Database <http://metacyc.org/>



3) EcoCyc <http://ecocyc.org/>

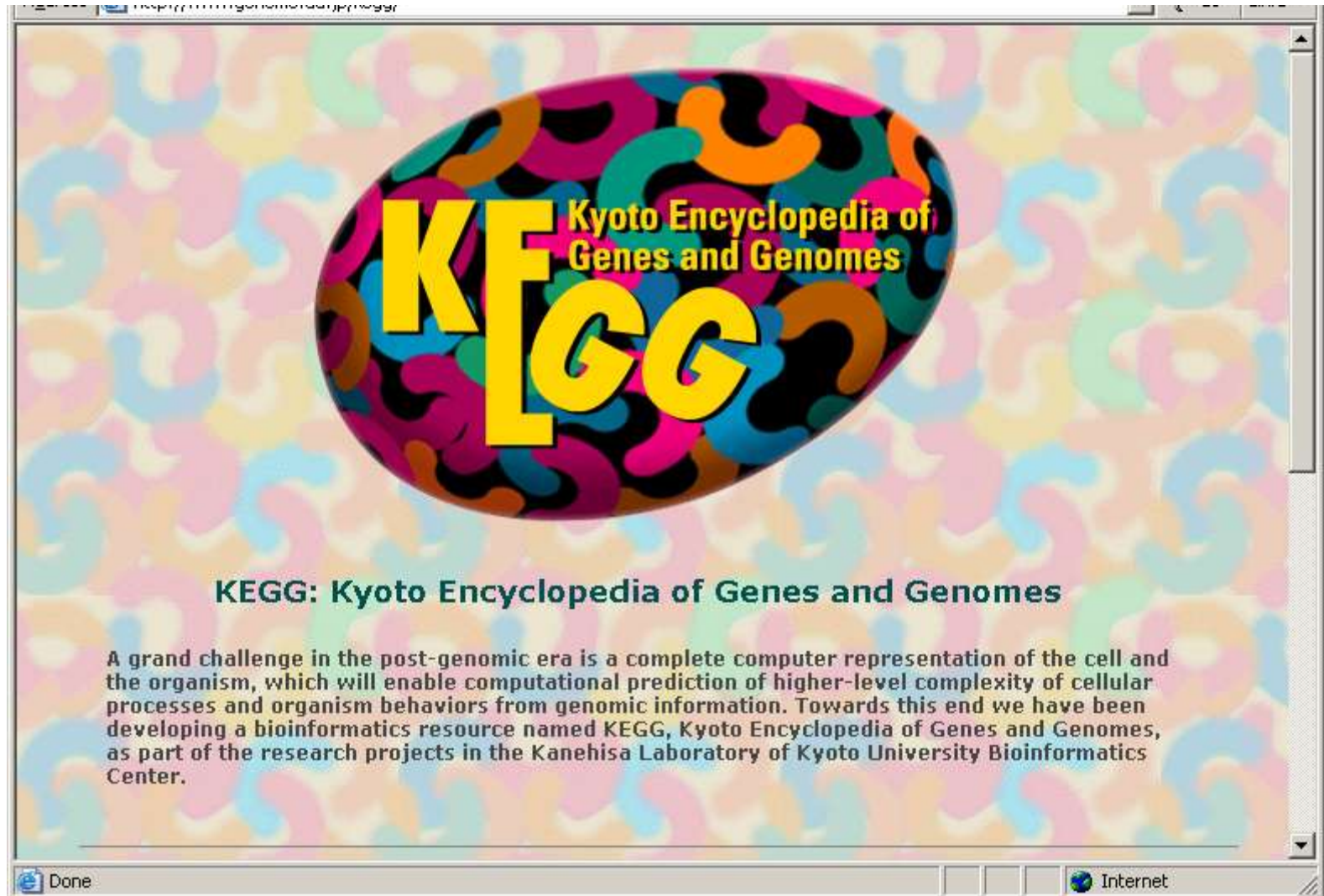
4) TRANSPATH Gene regulatory networks and microarray analysis <http://www.biobase.de/pages/products/transpath.html>

5) GeneNet – ИЦиГ СО РАН , г.Новосибирск

6) WIT What is there? Metabolic reconstruction for completely sequenced microbial genomes <http://wit.mcs.anl.gov/WIT2/> ([в настоящее время не доступна](#))

KEGG: Kyoto Encyclopedia of Genes and Genomes

<http://www.genome.ad.jp/kegg/>



ОСНОВНЫЕ ИНФОРМАЦИОННЫЕ МОДУЛИ БАЗЫ KEGG

Building blocks of life		Wiring diagrams of life	
Genetic materials	Chemical materials	Genetic networks	Chemical networks
KEGG Gene Universe Genes and gene products in complete genomes Genomic contexts Ortholg/paralog relations KO (KEGG Orthology)	KEGG Chemical Universe Chemical compounds Complex carbohydrates Active peptides Chemical reactions RC (Reaction Classification)	KEGG Protein Network Metabolic pathways Regulatory pathways Molecular complexes Network-network relations Network-environment relations Diseases	
Genetic and chemical blueprints of life 🍌 KEGG Table of Contents KEGG Release 29.0, January 2004 (plus daily updates)			
Introduction User manuals References	Standards Data formats API	Links Links to related databases	Distribution Disclaimer FTP access
Feedback form		GenomeNet	
Copyright 1995-2004 Kanehisa Laboratory			



KEGG PATHWAY Database

Current knowledge on molecular interaction networks,
including metabolic pathways, regulatory pathways,
and molecular complexes

[KEGG2](#) [PATHWAY](#) [GENES](#) [LIGAND](#) [EXPRESSION](#) [BRITE](#) [XML](#) [API](#) [DBGET](#)

Go to:

1. Metabolism
2. Genetic Information Processing
3. Environmental Information Processing
4. Cellular Processes
5. Human Diseases

See also: [KO \(KEGG Orthology\)](#)

1. Metabolism

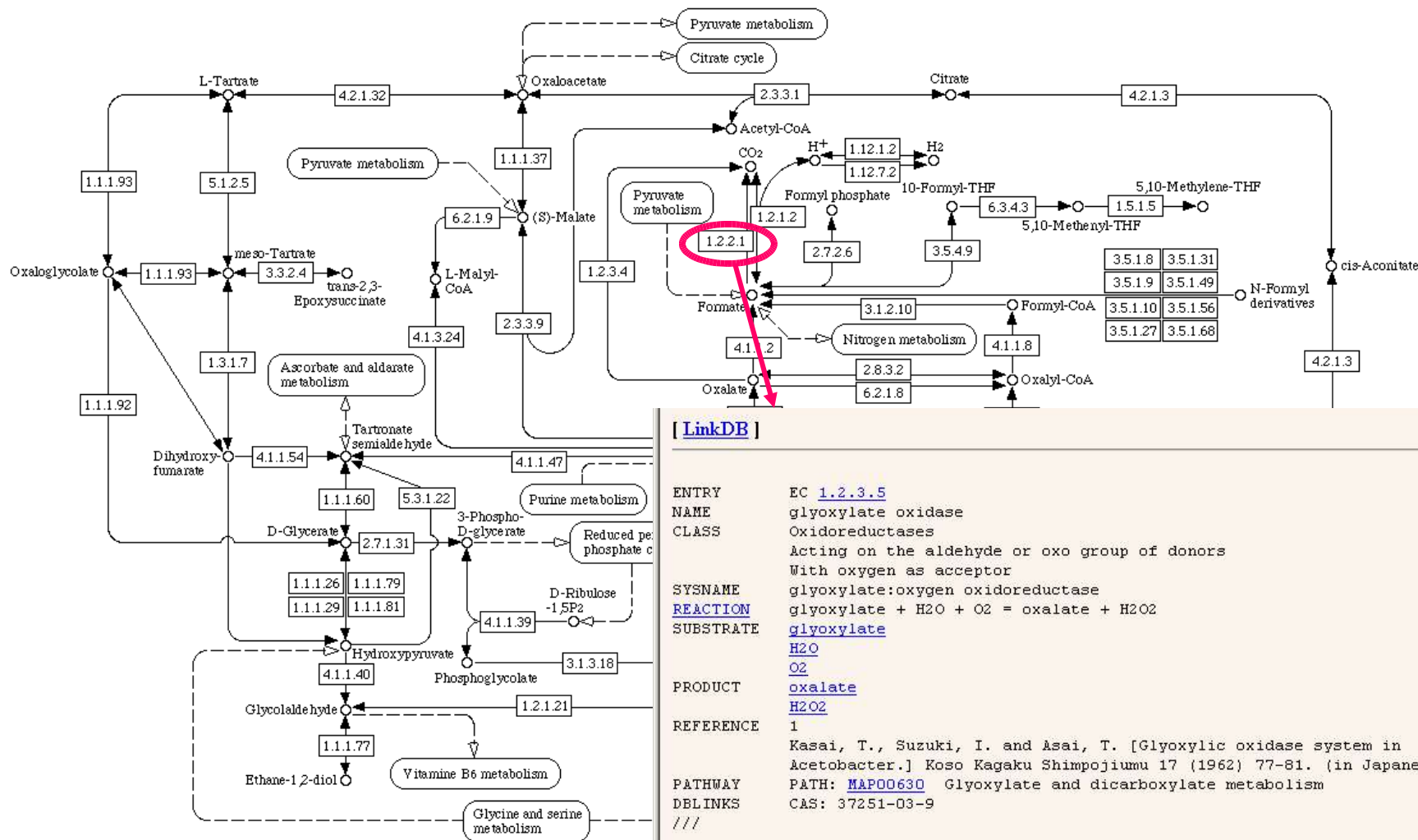
1.1 Carbohydrate Metabolism

Glycolysis / Gluconeogenesis	Ortholog, Oxidoreductases
Citrate cycle (TCA cycle)	Ortholog
Pentose phosphate pathway	Ortholog
Pentose and glucuronate interconversions	Ortholog
Fructose and mannose metabolism	Ortholog, PTS
Galactose metabolism	Ortholog
Ascorbate and aldarate metabolism	Ortholog
Pyruvate metabolism	Ortholog
<u>Glyoxylate and dicarboxylate metabolism</u>	Ortholog
Propanoate metabolism	Ortholog
Butanoate metabolism	Ortholog
C5-Branched dibasic acid metabolism	



Представление данных на тему «Glyoxylate and dicarboxylate metabolism» в базе KEGG

GLYOXYLATE AND DICARBOXYLATE METABOLISM



МОДУЛЬ KEGG Gene Universe: “KEGG Orthology”

572881 генов , 155 организмов

The image shows a screenshot of the KEGG Gene Universe web interface. The left sidebar contains a navigation menu with the following items:

- Building blocks of life**
 - Genetic materials**
 - KEGG Gene Universe** (circled in red)
 - Genes and gene products in complete genomes
 - Genomic contexts
 - Ortholog/paralog relations
 - KO (KEGG Orthology)
 - Chemical materials**
 - KEGG Chemical Universe
 - Chemical compounds
 - Complex carbohydrates
- Wiring diagrams of life**
 - Genetic networks**
 - KEGG Protein Network
 - Metabolic pathways
 - Regulatory pathways
 - Chemical networks**
- Introduction**
 - User manuals
 - References
- Feedback form**
- Copyright 1995-2004 Kanehisa Lab

The main content area is titled "2. Ortholog/paralog clusters" and contains the following search options:

- Search possible orthologs for:**
[] with [best-best] relations & above [100] [Go] [Clear]
- Search possible paralogs for:**
[] above [150] [Go] [Clear]
- Find SSDB ortholog clusters:** (enter keywords)
[] [Go] [Clear]
- Find KO groups:** (enter keywords)
[aceB] [Go] [Clear]

A red arrow points from the "KEGG Gene Universe" link in the sidebar to the "Find KO groups" search box, which contains the text "aceB" (circled in red).

РЕЗУЛЬТАТ ПОИСКА ПО КЛЮЧЕВОМУ СЛОВУ «aceB» В “KEGG Orthology”

DBGET Search Result

Database: KO

KEGG Orthology
Release 29.0+/03-11, Mar 04
Institute for Chemical Research, Kyoto
4,088 entries

Keyword(s): **aceB** (Total 1 hits. / limit=1000)

1. [ko:K01638](#) E2.3.3.9, aceB, gl

[DBGET](#) integrated database retrieval system. [GenomeNet](#)

[[LinkDB](#) | [Clique](#)]

ENTRY	K01638	KO
NAME	E2.3.3.9 , aceB, glcB	
DEFINITION	malate synthase	
CLASS	Metabolism; Carbohydrate Metabolism; Pyruvate metabolism [PATH: ot00620] Metabolism; Carbohydrate Metabolism; Glyoxylate and dicarboxylate metabolism [PATH: ot00630]	
DBLINKS	EC: 2.3.3.9 COG: COG2225 GO: 0004474	
GENES	ATH: At5g03860 (MED24.5) SCE: YIRO31C (DAL7) YNL117W (MLS1) ECO: b2976 (glcB) b4014 (aceB) ECJ: JW2943 (glcB) JW3974 (aceB) ECE: Z5600 (aceB) ECS: ECs4932 ECC: c3705 (glcB) c4971 (aceB) STY: STY4401 (aceB) STT: t4111 (aceB) STM: STM4183 (aceB) YPE: YPO3726 (aceB) YPK: y0015 (aceB) SFL: SF3015 (glcB) SFX: S3216 (glcB) PLU: plu4396 (aceB) XCC: XCC0237 (mls) XAC: XAC0256 (mls) VCH: VCO734 VVU: VV10450 VVY: VV0741 VPA: VPO583 PAE: PA0482 (glcB) PPU: PP0356 (glcB) PST: PSPT00480 (glcB-1) PSPT03559 (glcB-2)	

ВЫХОД НА ОПИСАНИЕ БЕЛКА *glcB*, кодируемого геном *aceB* *E.coli*

[LinkDB Clique]	
ENTRY	K01638
NAME	E2.3.3.9 , <i>aceB</i> , <i>glcB</i>
DEFINITION	malate synthase
CLASS	Metabolism; Carbohydrate Met [PATH: ot00620] Metabolism; Carbohydrate Met metabolism [PATH: ot00630]
DBLINKS	EC: 2.3.3.9 COG: COG2225 GO: 0004474
GENES	ATH: At5g03860 (MED24.5) SCE: YIR031C (DAL7) YML117W (M) ECO: b2976 (<i>glcB</i>) b4014 (<i>aceB</i>) ECJ: JW2943 (<i>glcB</i>) JW3974 (<i>aceB</i>) ECE: Z5600 (<i>aceB</i>) ECS: ECs4932 ECC: c3705 (<i>glcB</i>) c4971 (<i>aceB</i>) STY: STY4401 (<i>aceB</i>) STT: t4111 (<i>aceB</i>) STM: STM4183 (<i>aceB</i>) YPE: YPO3726 (<i>aceB</i>) YPK: y0015 (<i>aceB</i>) SFL: SF3015 (<i>glcB</i>) SFX: S3216 (<i>glcB</i>) PLU: plu4396 (<i>aceB</i>) XCC: XCC0237 (mls) XAC: XAC0256 (mls) VCH: VC0734 VVU: VV10450 VVY: VV0741 VPA: VPO583 PAE: PA0482 (<i>glcB</i>) PPU: PP0356 (<i>glcB</i>) PST: PSPT00480 (<i>glcB</i> -1) PSPT0

[LinkDB](#)
[SSDB](#)
[FASTA-genes](#)
[FASTA-sp](#)
[BLAST-nr](#)
[SOSUI](#)
[PSORT](#)
[MOTIF](#)

ENTRY

b2976

CDS

E.coli

NAME

glcB, glc

DEFINITION

malate synthase G (MSG) [EC:2.3.3.9]

ORTHOLOG

KO: K01638 malate synthase

CLASS

Metabolism; Carbohydrate Metabolism; Pyruvate metabolism
[PATH:eco00620]
Metabolism; Carbohydrate Metabolism; Glyoxylate and dicarboxylate
metabolism [PATH:eco00630]

POSITION

complement(3119650..3121821)

DBLINKS

Wisconsin: b2976
Colibri: glcB
NCBI: 1789348
SPTR: P37330

CODON_USAGE

	T				C				A				G			
T	9	10	11	6	4	2	3	9	6	12	1	0	4	2	0	12
C	3	7	1	41	2	0	4	25	9	8	15	25	19	21	0	4
A	22	21	1	23	5	19	3	6	17	25	30	2	3	14	0	0
G	11	6	3	26	17	18	10	27	30	14	31	14	13	24	2	12

AASEQ

723

MSQTITQSRLRIDANFKRFVDEEVLPGTGLDAAAFWRNFDEIVHDLAPENRQLLAERDRI
QAALDEWHRSNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGDISEITSQAGPQLVVP
AMNARYALNAANARWGSLYDALYGSDIIPQEGAMVSGYDPQRGEQVIAWVRRFLDESPLPL
ENGSYQDVVAFKVVDKQLRIQLKNGKETTLRTPAQFVGVRGDAAPTCILLKMNGLHIEL
QIDANGRIGKDDPAHINDVIVEAAISTILDCEDSVAAVDAEDKILLRYNLLGLMQGTLOE
KMEKNGRQIVRKLNDDRHYTAADGSEISLHGRSLLFIRNVGHLMTIPVIWDSEGNEIPEG
ILDGVMGTGAIALYDLKVQKNSRTGSVYIVKPKMHGPQEVAFANKLFTRIETMLGMAPNTL
KMGIMDEERRTSLNLRSCIAQARNRVAFINTGFLDRTGDEMHSVMEAGPMLRKNQMKSTP
WIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLADMYSQKGDQLRAGANTAWVPSPTA
ATLHALHYHQTNVQSVQANIAQTEFNAAFEPLDDLLTIPVAENANWSAQEIQQELDNNV
QGILGYVVRWVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILTKEQVQASL
ENMAKVVDQONAGDPAYRPMAGNFANSCAFKAAASDLIFLGVKQPNGYTEPLLHAWRLREK
ESH

NTSEQ

2172

atgagtcaaaccataaaccagagccgtttacgcattgacgccaatTTTaaacgttttTgtg

Done

Internet

МОДУЛЬ “KEGG Chemical Universe”

The image displays the KEGG website interface, specifically the 'KEGG Chemical Universe' section. The top navigation bar includes 'Building blocks of life' (Genetic materials, Chemical materials) and 'Wiring diagrams of life' (Genetic networks, Chemical networks). The 'KEGG Chemical Universe' link is highlighted with a red circle. Below it, the 'KEGG LIGAND Database' is featured, described as 'The universe of chemical reactions involving metabolites and other biochemical compounds, as well as xenobiotic compounds'. A red arrow points from the 'KEGG Chemical Universe' link to the 'KEGG LIGAND Database' section.

KEGG LIGAND Database

The universe of chemical reactions involving metabolites and other biochemical compounds, as well as xenobiotic compounds

KEGG2 PATHWAY GENES LIGAND EXPRESSION BRITE XML API DBGET

DBGET Search

- Search COMPOUND (biochemical compounds)
- Search GLYCAN (complex carbohydrates)
- Search REACTION (reactions involving compounds and carbohydrates)
- Search ENZYME (1)
- Search LIGAND (5)

Structure Search

- Search COMPOUND
- Search GLYCAN
- Search REACTION

Hierarchical Classification

- Enzyme classification
- Enzymes in the SC
- Compound classification

Software

Search COMPOUND database using DBGET

Database: COMPOUND

Ligand Chemical Database for Chemical Compound
Release 29.0+ / 03-11, Mar 04
Institute for Chemical Research, Kyoto University
10,784 entries

Input your search keyword(s) into the search box.

example) carboxylate

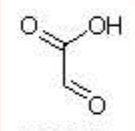
glyoxylate

Submit Reset

☒ bfind mode Max number of hits: 1000

☐ bget mode

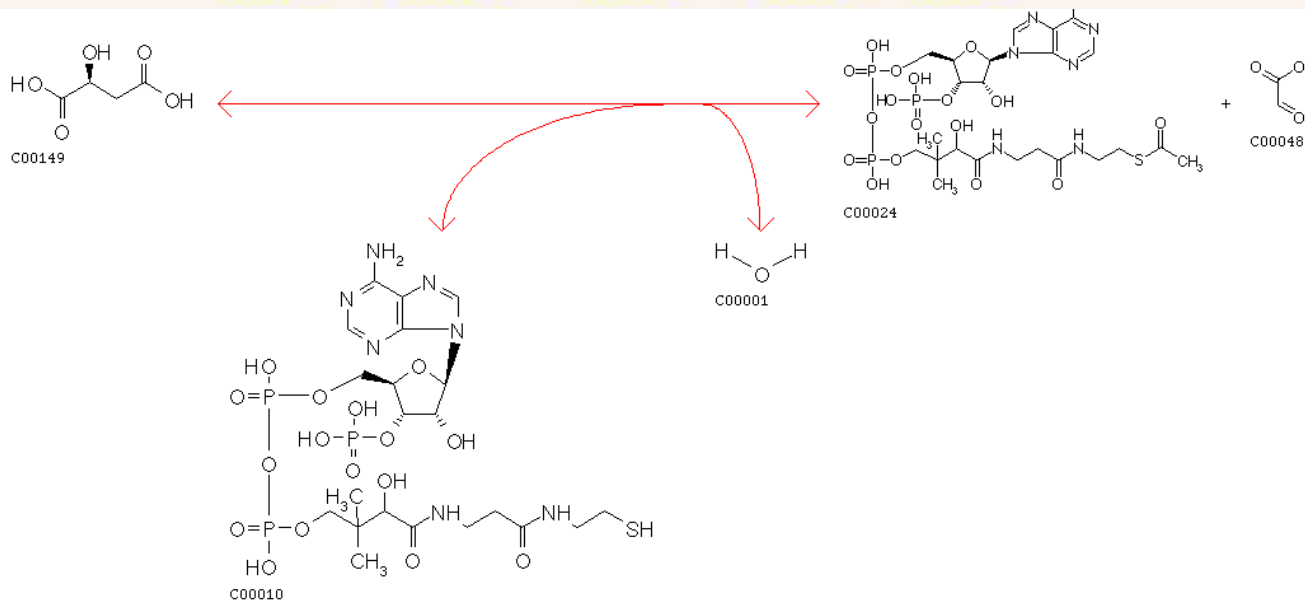
ВХОД “glyoxylate” в “KEGG Chemical Universe”

ENTRY	C00048
NAME	Glyoxylate Glyoxalate Glyoxylic acid
FORMULA	C2H2O3
	 C00048
REACTION	R00013 R00364 R00365 R00366 R00369 R00372 R00373 R00465 R00466 R00468 R00469 R00470 R00471 R00472 R00473 R00474 R00475 R00476 R00477 R00478 R00479 R00588 R00652 R00717 R00776 R00932 R00933 R00934 R01180 R01957 R03040 R03121 R03874 R05418 R05419 R05493 R05862 R05863
PATHWAY	PATH: MA000230 Purine metabolism PATH: MA000260 Glycine, serine and threonine metabolism PATH: MA000330 Arginine and proline metabolism PATH: MA000627 1,4-Dichlorobenzene degradation PATH: MA000630 Glyoxylate and dicarboxylate metabolism PATH: MA000660 C5-Branched dibasic acid metabolism
ENZYME	1.1.1.26 1.1.1.29 1.1.1.79 1.1.3.15 1.1.99.14 1.2.1.17 1.2.3.5 1.4.1.10 1.4.2.1 1.4.3.3 1.4.3.19 2.2.1.5 2.3.3.7 2.3.3.9 2.3.3.11 2.3.3.12 2.6.1.4 2.6.1.35 2.6.1.44 2.6.1.45 2.6.1.60 2.6.1.63 2.6.1.73 3.5.3.19 4.1.1.3 4.1.1.47 4.1.2.14 4.1.3.1 4.1.3.13 4.1.3.14 4.1.3.16 4.1.3.24 4.3.2.3 4.3.2.5
DBLINKS	CAS: 298-12-4 ///

Реакции с
участием
glyoxylate

ПРЕДСТАВЛЕНИЕ ИНФОРМАЦИИ ОБ ОДНОЙ ИЗ РЕАКЦИЙ С УЧАСТИЕМ “glyoxylate” в “KEGG Chemical Universe”

ENTRY [R00472](#)
NAME L-Malate glyoxylate-lyase (CoA-acetylating)
DEFINITION (S)-Malate + CoA <=> Acetyl-CoA + H₂O + Glyoxylate
EQUATION [C00149](#) + [C00010](#) <=> [C00024](#) + [C00001](#) + [C00048](#)

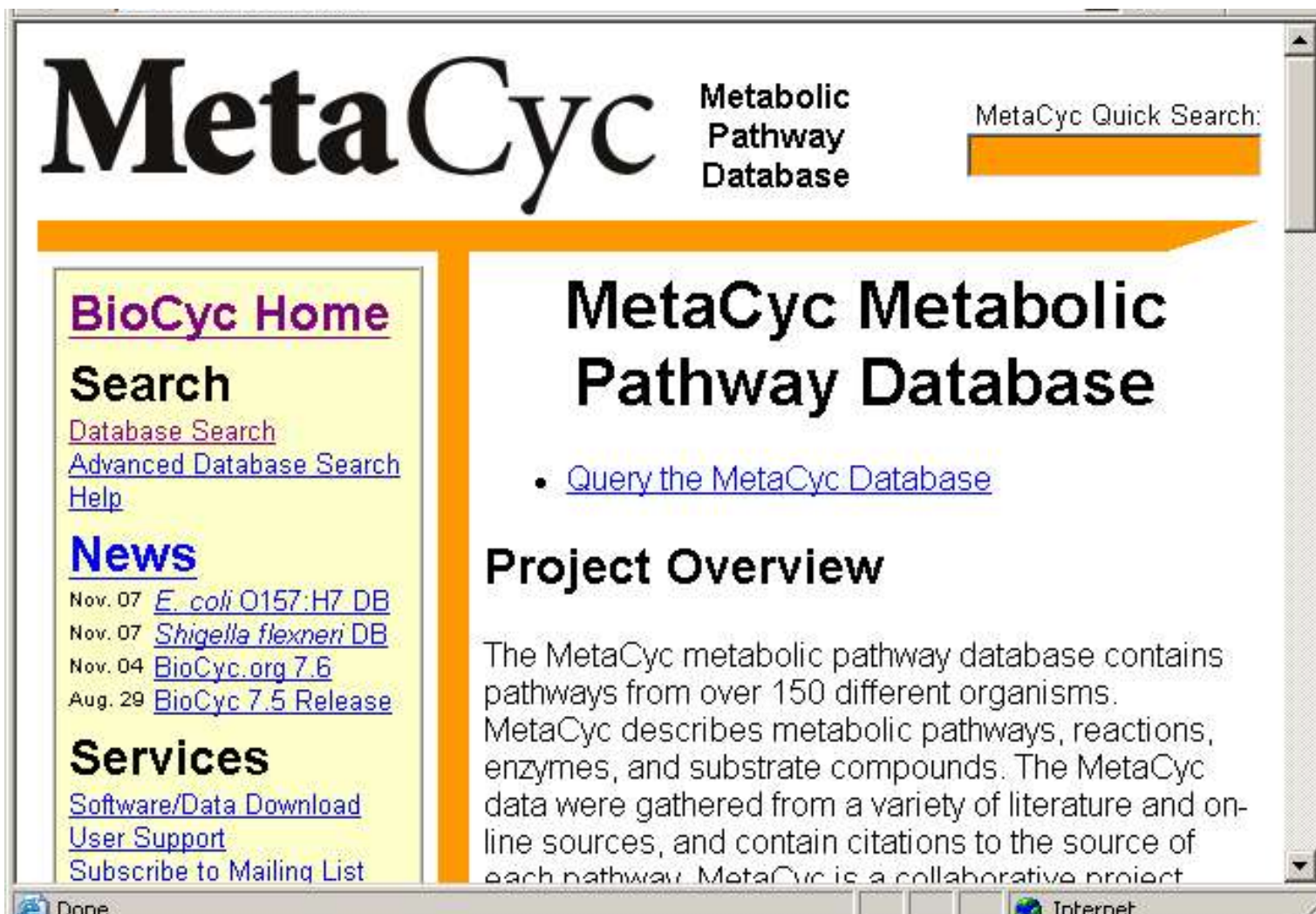


PATHWAY PATH: [R00620](#) Pyruvate metabolism
PATH: [R00630](#) Glyoxylate and dicarboxylate metabolism
ENZYME [2.3.3.9](#)
///

[[KEGG](#) | [DBGET](#) | [GenomeNet](#)]

MetaCyc MetabolicDatabase

<http://metacyc.org/>



The screenshot shows the MetaCyc website interface within a web browser window. The browser's address bar at the bottom displays "Done" and "Internet". The website header features the "MetaCyc" logo in a large, stylized font, followed by the text "Metabolic Pathway Database". To the right of the logo is a search bar labeled "MetaCyc Quick Search:". The main content area is divided into two columns by a vertical orange bar. The left column contains a sidebar with the following sections: "BioCyc Home" (in purple), "Search" (with links for "Database Search", "Advanced Database Search", and "Help"), "News" (with a list of recent updates including "Nov. 07 E. coli O157:H7 DB", "Nov. 07 Shigella flexneri DB", "Nov. 04 BioCyc.org 7.6", and "Aug. 29 BioCyc 7.5 Release"), and "Services" (with links for "Software/Data Download", "User Support", and "Subscribe to Mailing List"). The right column features the title "MetaCyc Metabolic Pathway Database" in large black font, followed by a bullet point linking to "Query the MetaCyc Database". Below this is the "Project Overview" section, which contains a paragraph describing the database: "The MetaCyc metabolic pathway database contains pathways from over 150 different organisms. MetaCyc describes metabolic pathways, reactions, enzymes, and substrate compounds. The MetaCyc data were gathered from a variety of literature and on-line sources, and contain citations to the source of each pathway. MetaCyc is a collaborative project".

MetaCyc Metabolic Pathway Database

MetaCyc Quick Search:

BioCyc Home

Search

[Database Search](#)

[Advanced Database Search](#)

[Help](#)

News

Nov. 07 [E. coli O157:H7 DB](#)

Nov. 07 [Shigella flexneri DB](#)

Nov. 04 [BioCyc.org 7.6](#)

Aug. 29 [BioCyc 7.5 Release](#)

Services

[Software/Data Download](#)

[User Support](#)

[Subscribe to Mailing List](#)

MetaCyc Metabolic Pathway Database

- [Query the MetaCyc Database](#)

Project Overview

The MetaCyc metabolic pathway database contains pathways from over 150 different organisms. MetaCyc describes metabolic pathways, reactions, enzymes, and substrate compounds. The MetaCyc data were gathered from a variety of literature and on-line sources, and contain citations to the source of each pathway. MetaCyc is a collaborative project.

ПРЕДСТАВЛЕННОСТЬ МЕТАБОЛИЧЕСКИХ ПУТЕЙ РАЗЛИЧНЫХ ОРГАНИЗМОВ В БАЗЕ MetaCyc

<i>Escherichia coli</i>	173
<i>Salmonella typhimurium</i>	35
<i>Homo sapiens</i>	31
<i>Sulfolobus solfataricus</i>	20
<i>Bacillus subtilis</i>	18
<i>Soybean</i>	18
<i>Pseudomonas</i>	17
<i>Haemophilus influenzae</i>	15
<i>Mycoplasma capricolum</i>	12

<i>Saccharomyces cerevisiae</i>	8
<i>Pseudomonas putida</i>	7
<i>Mycoplasma pneumoniae</i>	7
<i>Ascomycotina</i>	6
<i>Rhizobiaceae</i>	5
<i>Clostridium</i>	4
<i>Pseudomonas aeruginosa</i>	4
<i>Thauera aromatica</i>	4
<i>Thermotoga maritima</i>	4
<i>Rhodococcus</i>	4
<i>Klebsiella pneumoniae</i>	4
<i>Archaea</i>	3
<i>Pseudomonadaceae</i>	3
<i>Pseudomonas sp</i>	3
<i>Neisseriaceae</i>	3
<i>Klebsiella aerogenes</i>	3
<i>Rattus norvegicus</i>	3
<i>Archaeobacteria</i>	3
<i>Methanosarcina barkeri</i>	3
<i>Sinorhizobium meliloti</i>	3

EcoCyc <http://ecocyc.org/>

EcoCyc Encyclopedia of *Escherichia coli* K12
Genes and Metabolism

EcoCyc Home
Quick Search
 Go
[Database Search](#)
[Advanced Database Search](#)
[BLAST](#)
Browse
[Pathways](#)
[Genes](#)
[Reactions](#)

Project Overview EcoCyc is a scientific database for the bacterium *Escherichia coli* K12 MG1655. The EcoCyc project performs [literature-based curation](#) of the entire genome, and of transcriptional regulation, transporters, and metabolic pathways. [\[more...\]](#)

New Users Take the [guided tour](#) of the EcoCyc web site, or read "The Ecocyc Database" [\[PDF\]](#).

Encyclopedia of *Escherichia coli* K12 Genes and Metabolism

<http://ecocyc.org>

EcoCyc Encyclopedia of *Escherichia coli* K12 Genes and Metabolism

EcoCyc Home

Quick Search

[Database Search](#)
[Advanced Database Search](#)
[BLAST](#)

Browse

[Pathways](#)
[Genes](#)
[Reactions](#)
[Compounds](#)
[Metabolic Chart](#)
[Expression Viewer](#)

About EcoCyc

[Project Overview](#)
[Guided Tour](#)
[Publications](#)
[Update History](#)
[Advisory Board](#)
[Contributors](#)

Services

[Software/Data Download](#)
[User Support](#)
[Subscribe to Mailing List](#)

Project Overview

EcoCyc is a scientific database for the bacterium *Escherichia coli* K12 MG1655. The EcoCyc project performs [literature-based curation](#) of the entire genome, and of transcriptional regulation, transporters, and metabolic pathways. [\[more...\]](#)

New Users

Take the [guided tour](#) of the EcoCyc web site, or read "The Ecocyc Database" [\[PDF\]](#).

New Features

- [E. coli O157:H7](#) and [Shigella flexneri](#) are the newest knowledge bases in the [BioCyc](#) collection.
- We have added information about untranslated RNA species to EcoCyc. A list is available [here](#).
- The full EcoCyc release history is available [here](#).

Update Frequency

The EcoCyc web site is updated quarterly. A new version that you can [install locally](#) on your computer is released semiannually (supported platforms: PC/Windows, PC/Linux, Sun workstation). [[Full EcoCyc release history](#)]

Project Leaders

[Peter D. Karp](#) | [Julio Collado-Vides](#) | John Ingraham | [Ian Paulsen](#) | [Milton Saier](#)

Internet

ЗАПРОС ПО НАЗВАНИЮ ГЕНА

The screenshot displays the EcoCyc website interface. At the top left is the EcoCyc logo, which includes a stylized blue and yellow circular icon. To the right of the logo, the text "Encyclo", "coli K12", and "Metaboli" is visible. Below the logo, there is a navigation bar with links: "Project Overview", "Eco data", and "Eco". On the left side, there is a "Quick Search" box with a text input field containing "aceB" and a "Go" button. Below the search box are links for "Database Search" and "Advanced Database Search". The main content area on the right is titled "Query Results" and contains the text "The query **aceB** matched the following objects:". Under the heading "Proteins", there is a list item: "malate synthase A ([AceB](#))". Under the heading "Genes", there is a list item: "[aceB](#)". The bottom of the browser window shows a taskbar with an "Internet" icon.

EcoCyc Encyclo
coli K12
Metaboli

EcoCyc Home
Quick Search
aceB Go
[Database Search](#)
[Advanced Database Search](#)

Project Overview Eco data Eco

Query Results

The query **aceB** matched the following objects:

Proteins

- malate synthase A ([AceB](#))

Genes

- [aceB](#)

Internet

ИНФОРМАЦИЯ о ГЕНЕ aceB в базе EcoCyc

E. coli K-12 Gene: aceB

Nucleotide Sequence

Nucleotide Sequence Neighborhood

Protein Sequence

ID: EG10023

Synonyms: b4014 , mas

Superclasses: [Genes](#) -> [Physiological-Roles](#) -> [location of gene](#)
[Genes](#) -> [Physiological-Roles](#) -> [metabolism](#) -> [metabolism](#)

Map Position (centisomes): [90.814](#) [click to view in chromosome]

Map Position (nucleotides): 4,213,057 -> 4,214,658

Products: [malate synthase A](#)

Reactions Catalyzed by Enzymes:
[acetyl-CoA + H₂O + glyoxylate = malate](#)

Pathways Involving Enzymes: [glyoxylate cycle](#)

Gene-Reaction Schematic: [?](#)



Chromosome Microsoft Internet Explorer

Specify endpoints of desired sequence in base pairs:

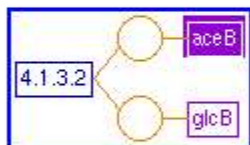
Left End Position: Right End Position:

Reverse Complement? ☐

atgactgaac	aggcaacaac	aacgatgaa	ctggctttca	caaggccgta	tggcgagcag
gagaagcaaa	ttcttactgc	cgaagcggta	gaattttctga	ctgagctggt	gacgcatttt
acgccacaac	gcaataaaact	tctggcagcg	cgcatttcagc	agcagcaaga	tattgataac
ggaacgttgc	ctgattttat	ttcggaaca	gcttccattc	gcgatgctga	ttgaaaaatt
cgcgggattc	ctgcggactt	agaagaccgc	cgcgtagaga	taactggccc	ggtagagcgc
aagatggtga	tcaacgcgct	caacgccaat	gtgaaagtct	ttatggccga	tttcgaagat
tcaactggcac	cagactggaa	caaagtgatc	gaaggccaaa	ttaacctgog	tgatgoggtt
aacggcacca	tcagttacac	caatgaagca	ggcaaaattt	accagctcaa	gccccaatcca
gcggttttga	tttgtcgggt	acgcggtctg	cacttgccgg	aaaaacatgt	cacctggcgt
ggtgaggcaa	tcccggcgag	cctgtttgat	tttgogctct	attttctcca	caactatcag
gcactgttgg	caaaggcgag	tggtccctat	ttctatctgc	cgaaaaccca	gtcctggcag
gaagcggcct	ggtggagcga	agtcttcagc	tatgcagaag	atcgctttaa	ttcgccgcgc
ggcaccatca	aggcgacgtt	gctgattgaa	acgctgcccg	cogtgttcca	gatggatgaa
atccttcacg	cgtcgcgtga	ccatattggt	ggtctgaact	gcggtcgttg	ggattacatc
ttcagctata	tcaaaacgtt	gaaaaactat	cccgatcgcg	tcctgccaga	cagacaggca
gtgacgatgg	ataaaccatt	cctgaatgct	tactcacgcc	tgttgattaa	aacctgccat
aaacgcggtg	cttttgcgat	ggcgccgatg	gcgcgcttta	ttccgagcaa	agatgaagag
cacaataacc	aggtgctcaa	caaagtaaaa	goggataaat	cgctggaagc	caataacggt
cacgatggca	catggatcgc	tcaccagggc	cttgoggaca	cggcaatggc	ggtattcaac
gacattctcg	gctcccgtaa	aaatcagctt	gaagtgatgc	gogaacaaga	cgcgcgattt

ИНФОРМАЦИЯ о ГЕНЕ aceB в базе EcoCyc (продолжение)

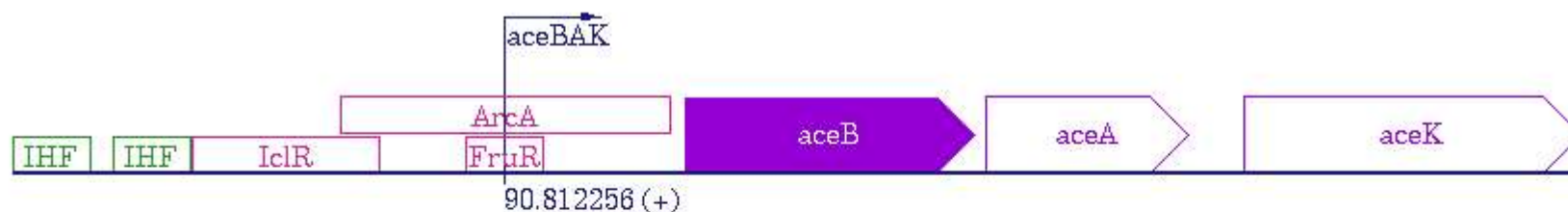
Gene-Reaction Schematic: ?



Unification Links: [CGSC:1051](#), [OUMCF:b4014](#)

History: 10/20/97 Gene b4014 from Blattner lab Genbank (v. M52) entry merged into EcoCyc gene EG10023; confirmed by SwissProt match.

Transcription Unit:



Click above or below gene(s) to display window for full transcription unit; click on binding site (if any) to navigate to transcription factor window; click on gene to navigate to gene window.

[Query Page](#)

[Advanced Query Page](#)

[BioCyc Home](#)

[Report Errors or Provide Feedback](#)

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ИНФОРМАЦИЯ о БЕЛКЕ в базе EcoСус

E. coli K-12 Enzyme: malate synthase A

Protein Sequence

Synonyms: B4014 , Mas , AceB

Superclasses: [Proteins](#) -> [Polypeptides](#)

Species: [Escherichia coli K-12](#)

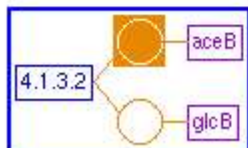
Gene: [aceB](#)

Molecular Weight (kdaltons, from nucleotide sequence): 60.273

Neidhardt Spot Number [[C1](#)]:

Unification Links: [PIR:b4014](#) , [RefSeq:NP_418438](#) , [SWISS-PROT:P08997](#)

Gene-Reaction Schematic: [?](#)



```
> MALATE-SYNTHASE malate synthase A 4213057..4214658 E. coli
MTEQATTTDE LAFTRPYGEQ EKQILTAEAV EFLTELVTDF TPQRNKLLAA RIQQQQDIDN
GTLPDFISET ASIRDADWKI RGIPADLEDR RVEITGPVER KMVINALNAN VKVFMADFED
SLAPDWNKVI DGQINLRDAV NGTISYTNEA GKIYQLKPNP AVLICRVRGL HLPEKHVTWR
GEAIPGSLFD FALYFFHNYQ ALLAKGSGPY FYLPKTQSWQ EAAWWSEVFS YAEDRFNLPR
GTIKATLLIE TLPVAFQMD E ILHALRDHIV GLNCGRWYI FSYIKTLKNY PDRVLPDRQA
VTMDKPFLNA YSRLLIKTCH KRGAFAMGGM AAFIPSKDEE HNNQVLNKVK ADKSLEANNG
HDGTWIAHPG LADTAMAVFN DILGSRKNQL EVMREQDAPI TADQLLAPCD GERTEEGMRA
NIRVAVQYIE AWISGNGCVP IYGLMEDAAT AEISRTSIWQ WIIHQKTLN GKPVTKALFR
QMLGEEMKVI ASELGEERFS QGRFDDAARL MEQITTSDEL IDFLTLPGYR LLA
```

ИНФОРМАЦИЯ о БЕЛКЕ в базе ЕсоСус (продолжение)

Enzymatic reaction of: malate synthase A



The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the direction of the reaction within a pathway.

In Pathways: [glyoxylate cycle](#)

Comment:

Second enzyme of glyoxylate bypass [Maloy82]. Induced by growth on acetate. Malate synthase in *E. coli*. Malate synthase glyoxylate by-pass. It metabolizes glyoxylate. It is coded for by the *glcB* gene, is responsible for the glyoxylate formed during growth on glucose.

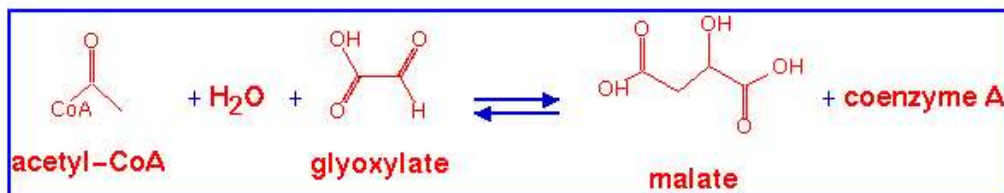
E. coli K-12 Reaction: 4.1.3.2

Superclasses: [Reactions](#) -> [EC-Reactions](#) -> [4 -- LYASES](#) -> [4.1 -- CARBON-CARBON LYASES](#) -> [4.1.3 -- OXO-ACID-LYASES](#)

[malate synthase G](#): [glcB](#)

[malate synthase A](#): [aceB](#)

In Pathway: [glyoxylate degradation](#), [glyoxylate cycle](#)

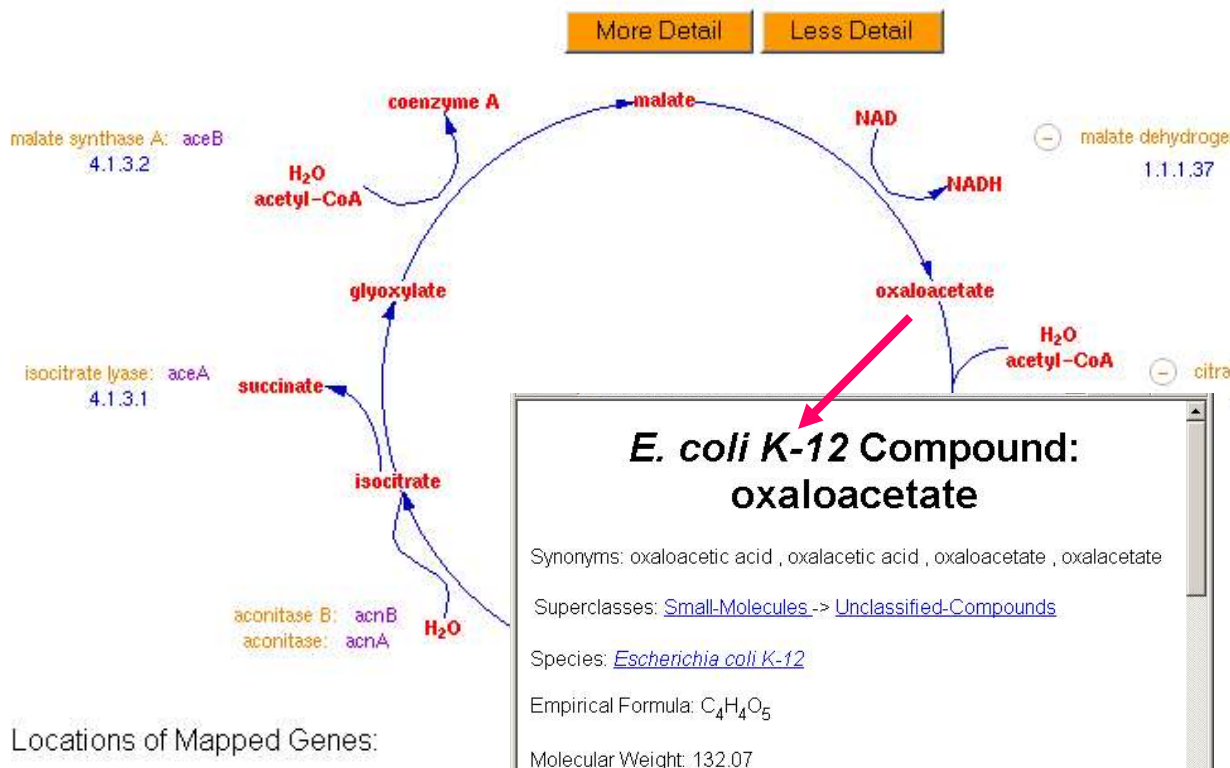


Gene-Reaction Schematic: [?](#)

См. следующий
слайд

ИНФОРМАЦИЯ о МЕТАБОЛИЧЕСКОМ ПУТИ в базе EcoСус (продолжение)

E. coli K-12 Pathway: glyoxylate cycle



E. coli K-12 Compound: oxaloacetate

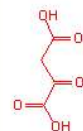
Synonyms: oxaloacetic acid , oxalacetic acid , oxaloacetate , oxalacetate

Superclasses: [Small-Molecules](#) -> [Unclassified-Compounds](#)

Species: [Escherichia coli K-12](#)

Empirical Formula: C₄H₄O₅

Molecular Weight: 132.07

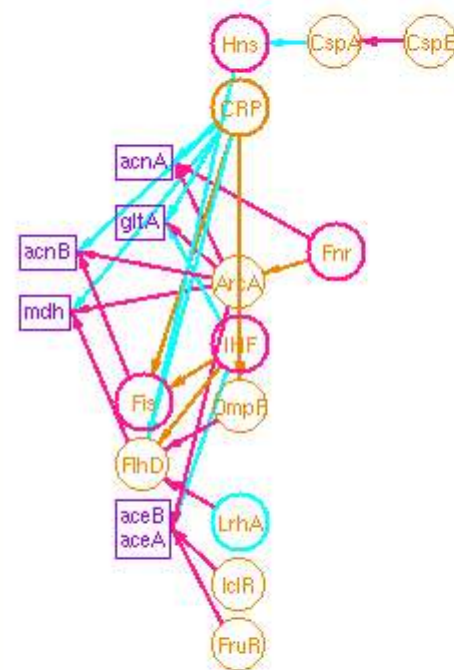


Smiles: C(O)(=O)CC(=O)C(=O)O

Unification Links: CAS:328-42-7

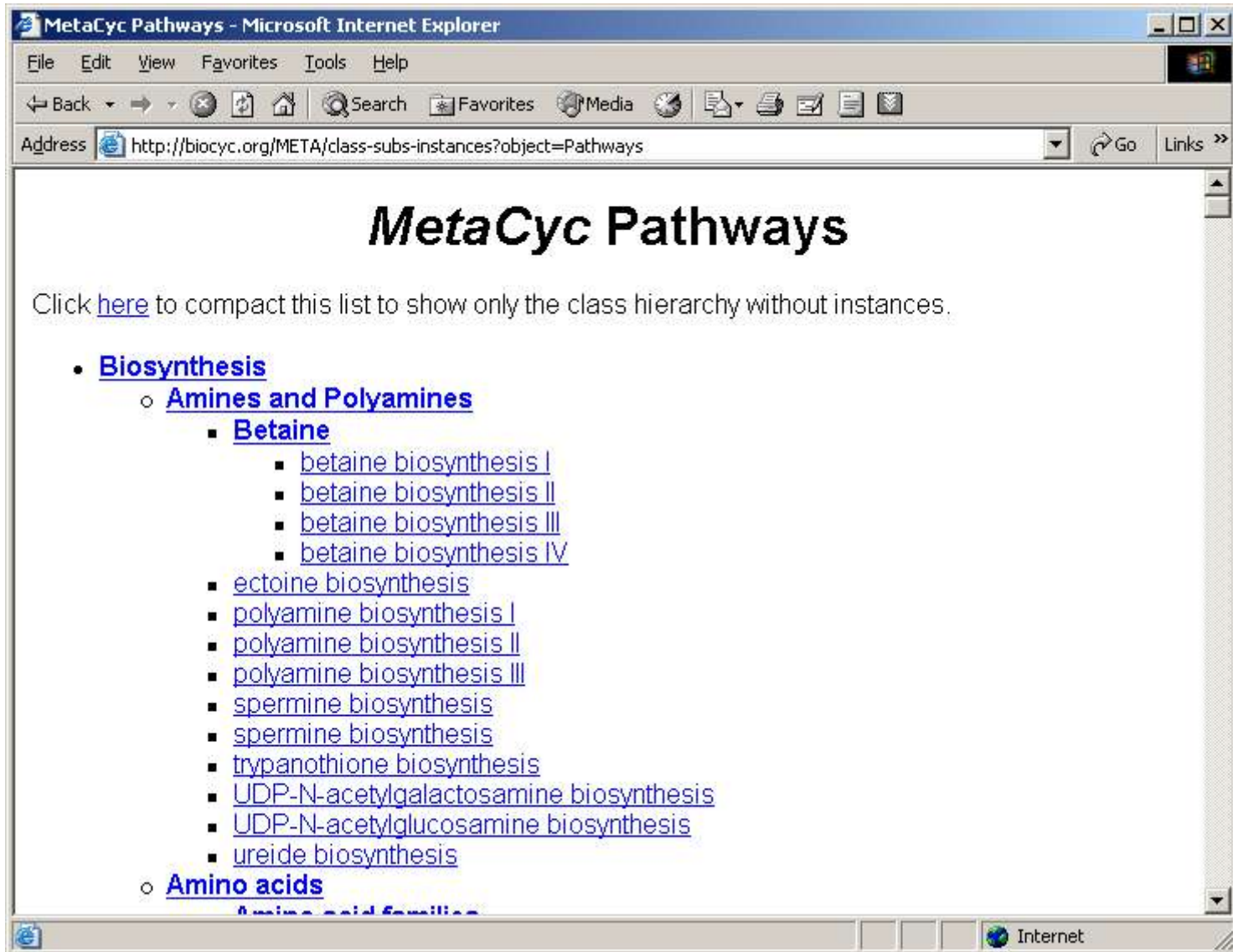
[aspartate biosynthesis and degradation](#) :

Genetic Regulation Schematic: ?



Synonyms: glyoxylate bypass , glyoxbp

Superclasses: [Pathways](#) -> [Generation of pre and energy](#) -> [TCA cycle](#)



TRANSPATH – база по путям сигнальной трансдукции

<http://www.biobase.de/pages/products/transpath.html>

Databases

TRANSFAC®

TRANSCOMP®

PathoDB®

TRANSPATH® Professional

▲ Latest Database Statistics

▲ Guided Tour

▲ Demo-Version TRANSPATH®

TRANSPATH® Professional comprises data a

Browse TRANSPATH pathways.

(TRANSPATH professional 3.4 Release)

Cell cycle control

[p53 network \(p53 phosphorylation\)](#)
[E2F network \(cyclin, Cdk, pRb\)](#),
etc.

Cell adhesion & motility

[Integrins](#)
[Cadherins \(β-catenin\)](#)
FAK
Endocytose
Exocytose, etc.

Degradation

[Ubiquitin-proteasome-mediated degradation \(Ubiquitin ligases, 26S proteasome\)](#), etc.

Immune response

[T cell signaling \(co-receptors\)](#)
[B cell signaling](#)
Cytokines (e.g. [IFN-γ](#), [IL-1](#),
[IL-10](#), [IL-12](#), [TNF](#), [OSM](#))
Chemokines (e.g. [SDF-1](#), [IL-8](#),
RANTES), chemoattractant
peptides (e.g. [fMLP](#))
MSP/ROD receptor
[TLR4-signaling](#)
[TNF-signaling \(NF-κB, AP-1\)](#)
Fc receptor, etc.

Selection of TRANSPATH Topics

G-protein pathways

[Ion channels](#)
Phorbol esters pathway (PLC, PKC)
[Trimeric G-proteins](#), CaM
Chemokine receptor ([CXCR1/2](#))
[Ras-Raf-MAPK-Cascade](#)
[GPIIb/IIIa](#), [NTS1-signaling](#), etc.

Apoptosis

Death receptor transmitted (e.g. [TNF](#), [Fas](#))
Internal stress (mitochondrial control,
[Cyt C](#), [Apaf-1](#), [Bcl-2 family](#), [Caspases](#))
etc.

Growth & Differentiation

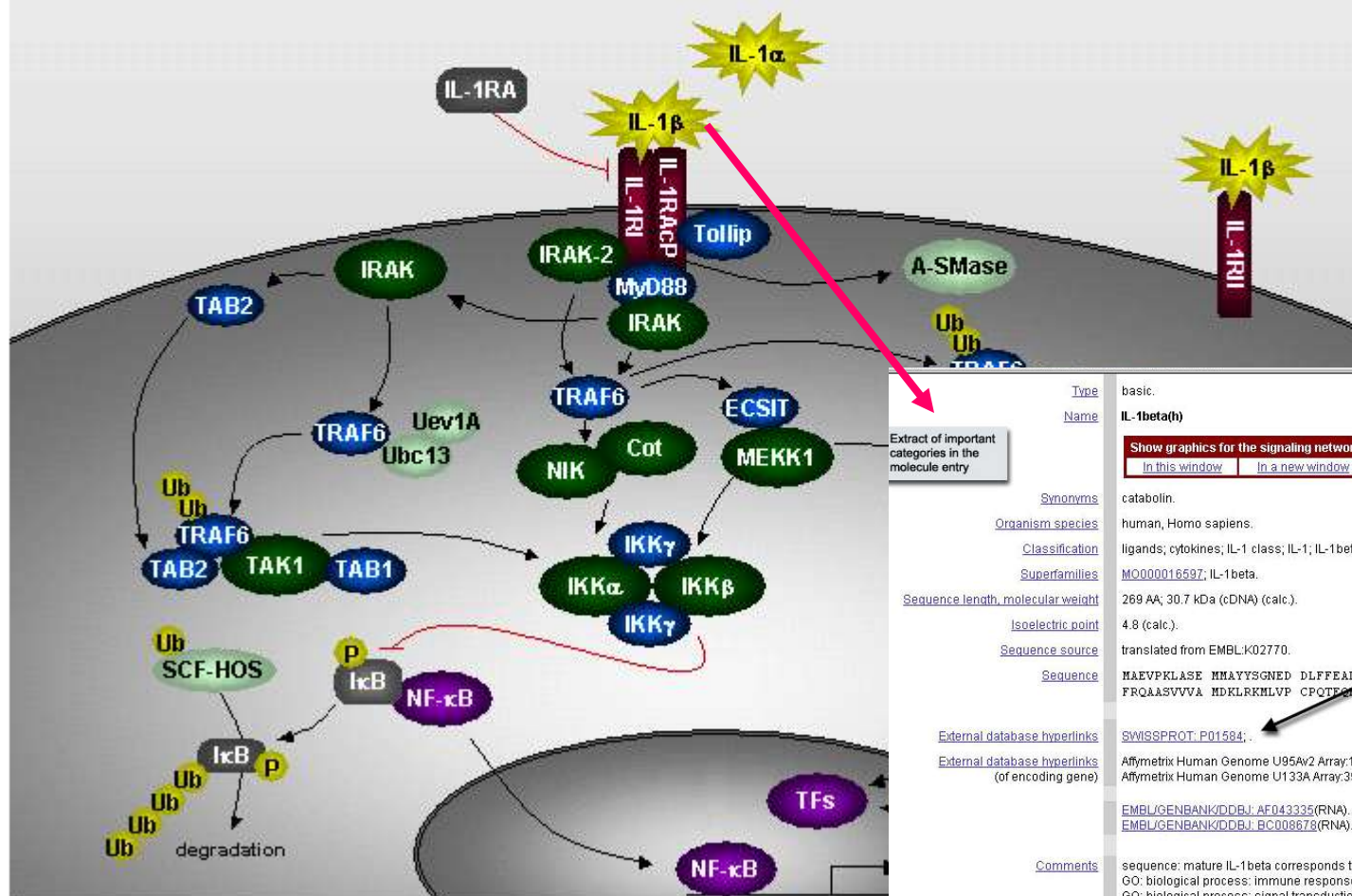
[Wnt / β-catenin pathway](#)
[Ras-Raf-MAPK-Cascade](#)
Growth factors (e.g. [EGF](#), IGF, NGF,
[PDGF](#), [TGFβ](#), [EPO](#), [TPO](#), [VEGF](#))
Hormones ([insulin](#), [prolactin](#), GH)
[Notch](#), [c-Kit](#) etc.

ДЕМОНСТРАЦИОННАЯ ДИАГРАММА В TRANSPATH

IL-1 pathway

Click on the compound of interest to retrieve the corresponding db entry.

(TRANSPATH professional 3.4 Release)



Type	basic.
Name	IL-1beta(h)
Show graphics for the signaling network In this window In a new window	
Synonyms	catabolin.
Organism species	human, Homo sapiens.
Classification	ligands; cytokines; IL-1 class; IL-1; IL-1beta.
Superfamilies	MO000016597; IL-1beta.
Sequence length, molecular weight	269 AA; 30.7 kDa (cDNA) (calc).
Isoelectric point	4.8 (calc).
Sequence source	translated from EMBL:K02770.
Sequence	MAEVPKLASE MHAYYSGNED DLFFEADGGR QMRCSFDQLD LCPLDGGIQL RISDHHYSKG FRQAASVVVA MDKLRKMLVP CPQTEGENDL STFFPFIFEE EPIFFDTWDN EAYVHDAPVR
External database hyperlinks	SWISSPROT: P01584.
External database hyperlinks (of encoding gene)	Affymetrix Human Genome U95Av2 Array:1520_s_at. Affymetrix Human Genome U133A Array:39402_at.
Comments	sequence: mature IL-1beta corresponds to 117-269 AA of its precursor. GO: biological process: immune response; IEA: GO:0008955 [1]. GO: biological process: signal transduction; IEA: GO:0007165 [1]. GO: biological process: cell-cell signaling; IEA: GO:0007267 [1]. GO: biological process: apoptosis; IEA: GO:0006915 [1]. GO: biological process: negative control of cell proliferation; IEA: GO:0008285 [1].

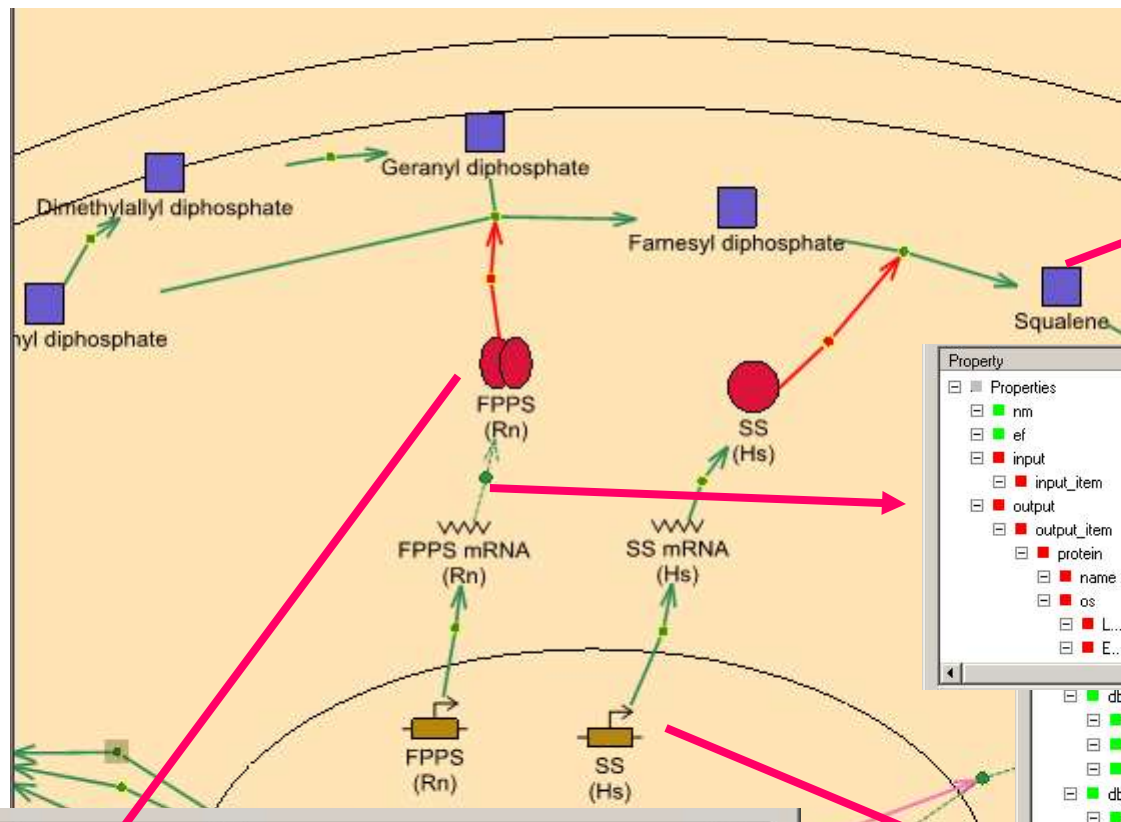
Leads to protein database

Affymetrix probeset-identifiers simplify search for molecules from expression array experiments

Leads to gene/mRNA database

БАЗА GENENET (ИЦиГ СО РАН)

принципы представления данных



Property	Value
Properties	
sn	Squalene
nm	Squalene

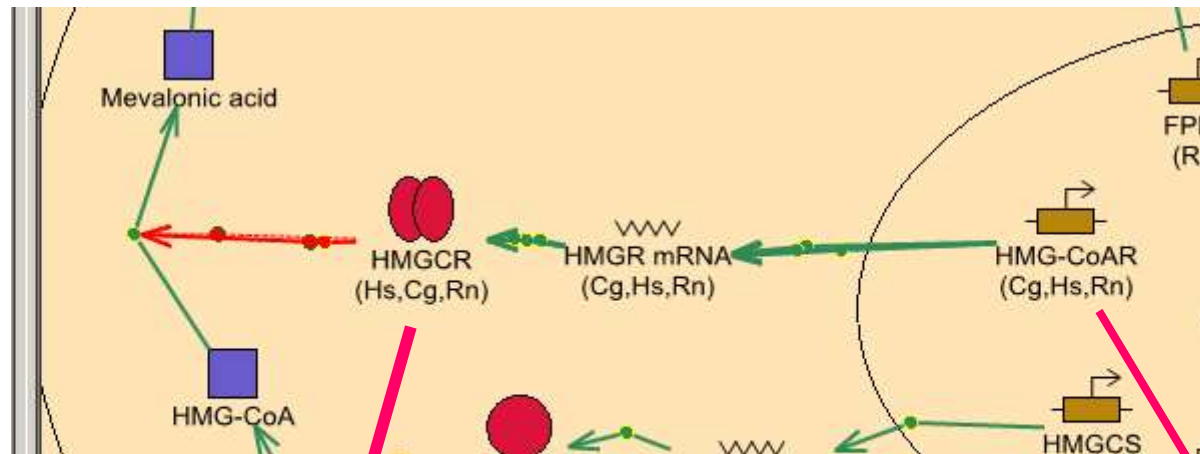
Property	Value
Properties	
nm	reaction
ef	indirect
input	
input_item	
output	
output_item	
protein	
name	farnesyl diphosphate synthase
os	
L...	Rattus norvegicus
E...	rat

Comment
Object properties
short name
full name
Organism Species
Species Latin name
Species English name
DataBase Reference
Database name
accession number of the ...
identifier of the entry in th...
DataBase Reference
Database name
accession number of the ...
identifier of the entry in th...
DataBase Reference
Database name
accession number of the ...
identifier of the entry in th...
Inducer
full name
Cell
short name
description
Organism Species
Species Latin name
Species English name
Cell
short name
description

Property	Value
Properties	
sn	FPPS
nm	farnesyl diphosphate synthase
sy	geranyl-diphosphate: isopentenyl-diphosphate ger...
os	
Latin	Rattus norvegicus
English	rat
dbref	

dbref	
name	EMBL
ac	U18994
id	HS189941
dbref	
name	SWISS-PROT
ac	P37268
id	FDFT_HUMAN
inducer	
name	cholesterol (repression)
cell	
sn	HepG2
de	HepG2 hepatoma cell line
os	
Latin	Homo sapiens
English	human
cell	
sn	liver
de	liver

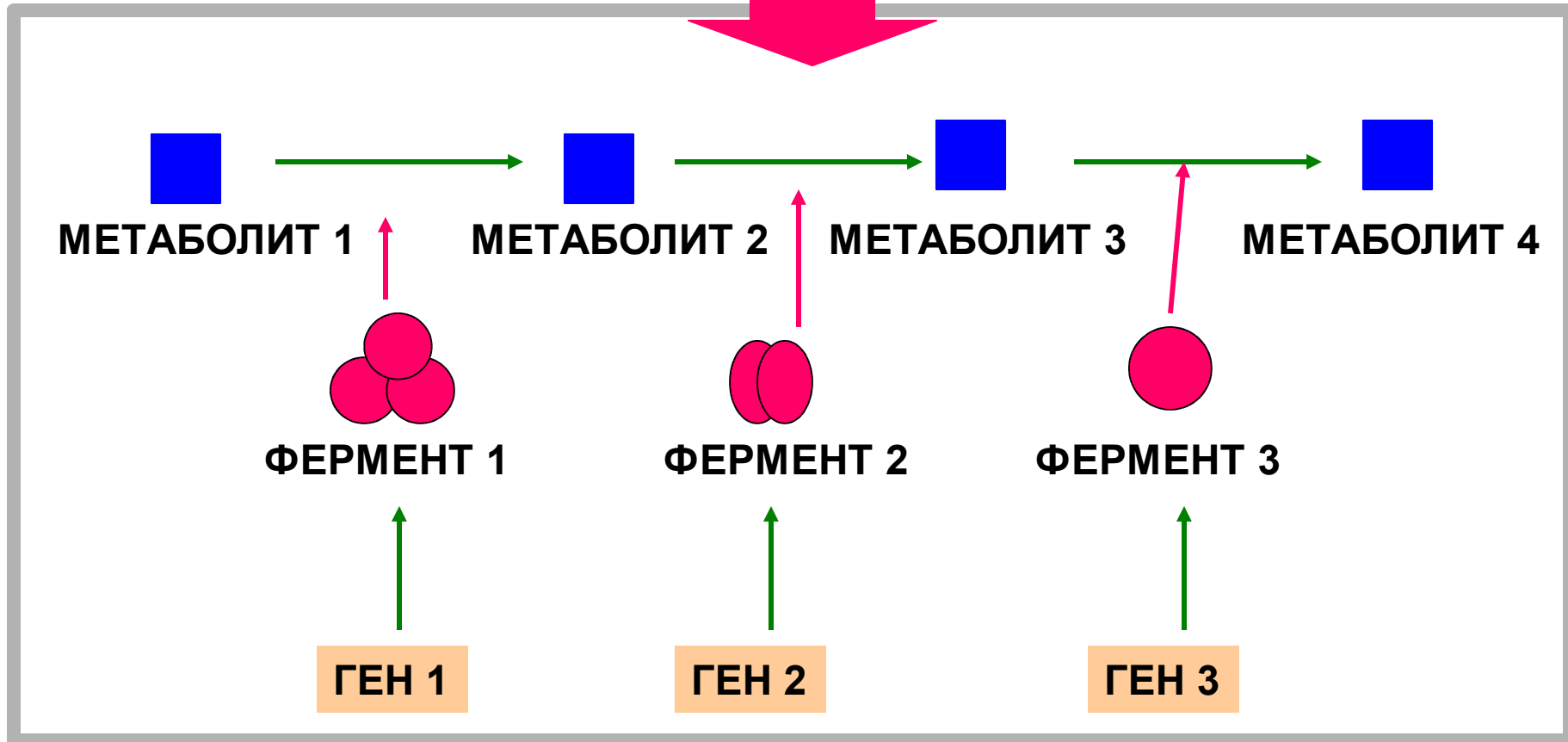
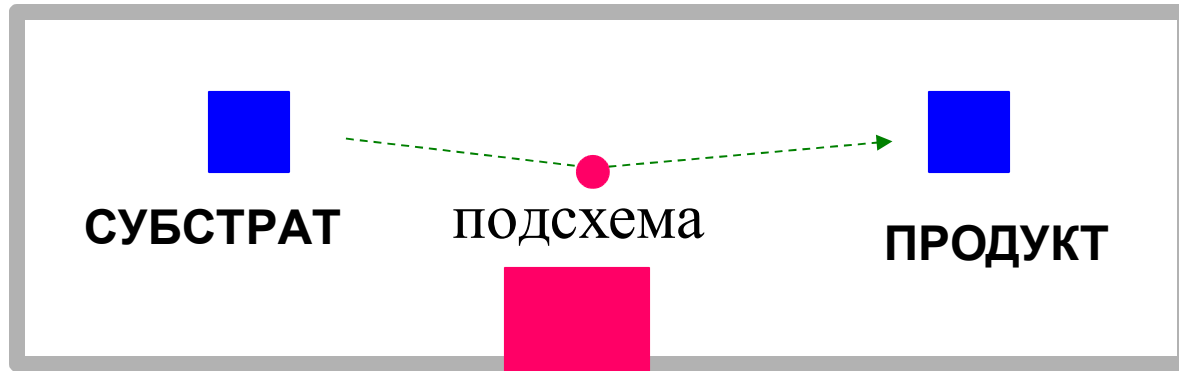
ПРЕДСТАВЛЕНИЕ ДАННЫХ О МЕТАБОЛИЧЕСКИХ ПУТЯХ РАЗНЫХ ВИДОВ В GENENET



Hs : HMGCR : HMG-CoA reductase : 3-hydroxy-3-methylglutaryl-CoA reductase
Cg : HMGCR : HMG-CoA reductase : 3-hydroxy-3-methylglutaryl-CoA reductase
Rn : HMGCR : HMG-CoA reductase : 3-hydroxy-3-methylglutaryl-CoA reductase

Cg : HMG-CoAR : HMG-CoA reductase gene
Hs : HMG-CoAR : HMG-CoA reductase gene
Rn : HMG-CoAR : HMG-CoA reductase gene

ВОЗМОЖНОСТЬ ИСПОЛЬЗОВАНИЯ ПОДСХЕМ В GENENET



<http://www.biocarta.com/genes/allpathways.asp>

BIOCARTA

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Charting Pathways of Life

FEATURES | PATHWAYS | CUSTOM SERVICES | GENES | PRODUCTS | LOGIN

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PATHWAYS > All Pathways

Observe how genes interact in dynamic graphical models. Our online maps depict molecular relationships from areas of active research. In an "open source" approach, this community-fed forum constantly integrates emerging proteomic information from the scientific community. It also catalogs and summarizes important resources providing information for over 120,000 genes from multiple species. Find both classical pathways as well as current suggestions for new pathways.

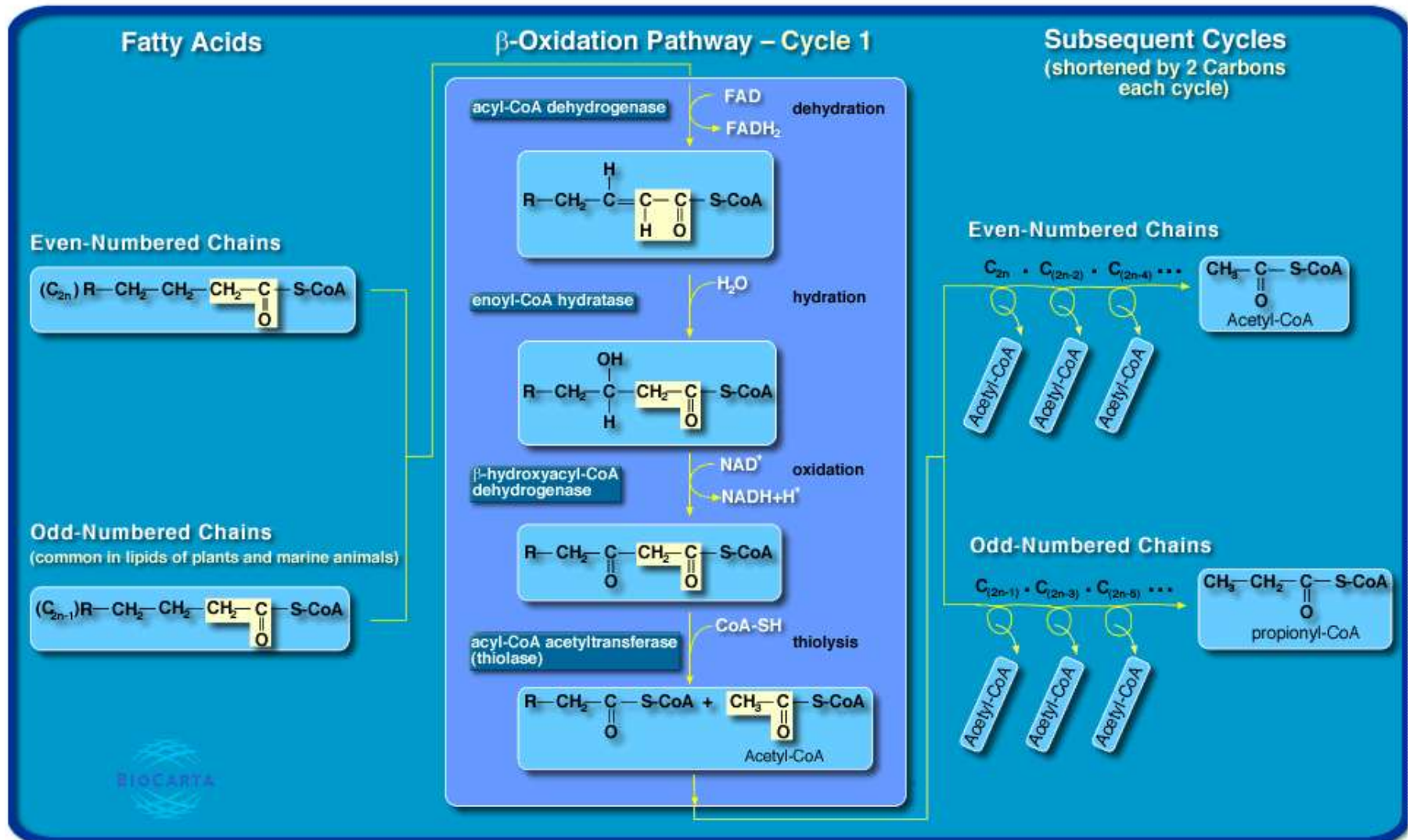
ALL PATHWAYS

A

- ▶ Acetylation and Deacetylation of RelA in The Nucleus [H](#) [M](#)
- ▶ Actions of Nitric Oxide in the Heart [H](#)
- ▶ Activation of cAMP-dependent protein kinase, PKA [H](#) [M](#)
- ▶ Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor [H](#) [M](#)
- ▶ Activation of PKC through G protein coupled receptor [H](#) [M](#)
- ▶ Activation of Src by Protein-tyrosine phosphatase alpha [H](#) [M](#)
- ▶ Acute Myocardial Infarction [H](#)
- ▶ Adhesion and Diapedesis of Granulocytes [H](#)
- ▶ Adhesion and Diapedesis of Lymphocytes [H](#)
- ▶ Adhesion Molecules on Lymphocyte [H](#) [M](#)
- ▶ ADP-Ribosylation Factor [H](#) [M](#)
- ▶ Agrin in Postsynaptic Differentiation [H](#) [M](#)
- ▶ Ahr Signal Transduction Pathway [H](#) [M](#)
- ▶ AKAP95 role in mitosis and chromosome dynamics [H](#) [M](#)
- ▶ AKT Signaling Pathway [H](#) [M](#)
- ▶ ALK in cardiac myocytes [H](#)

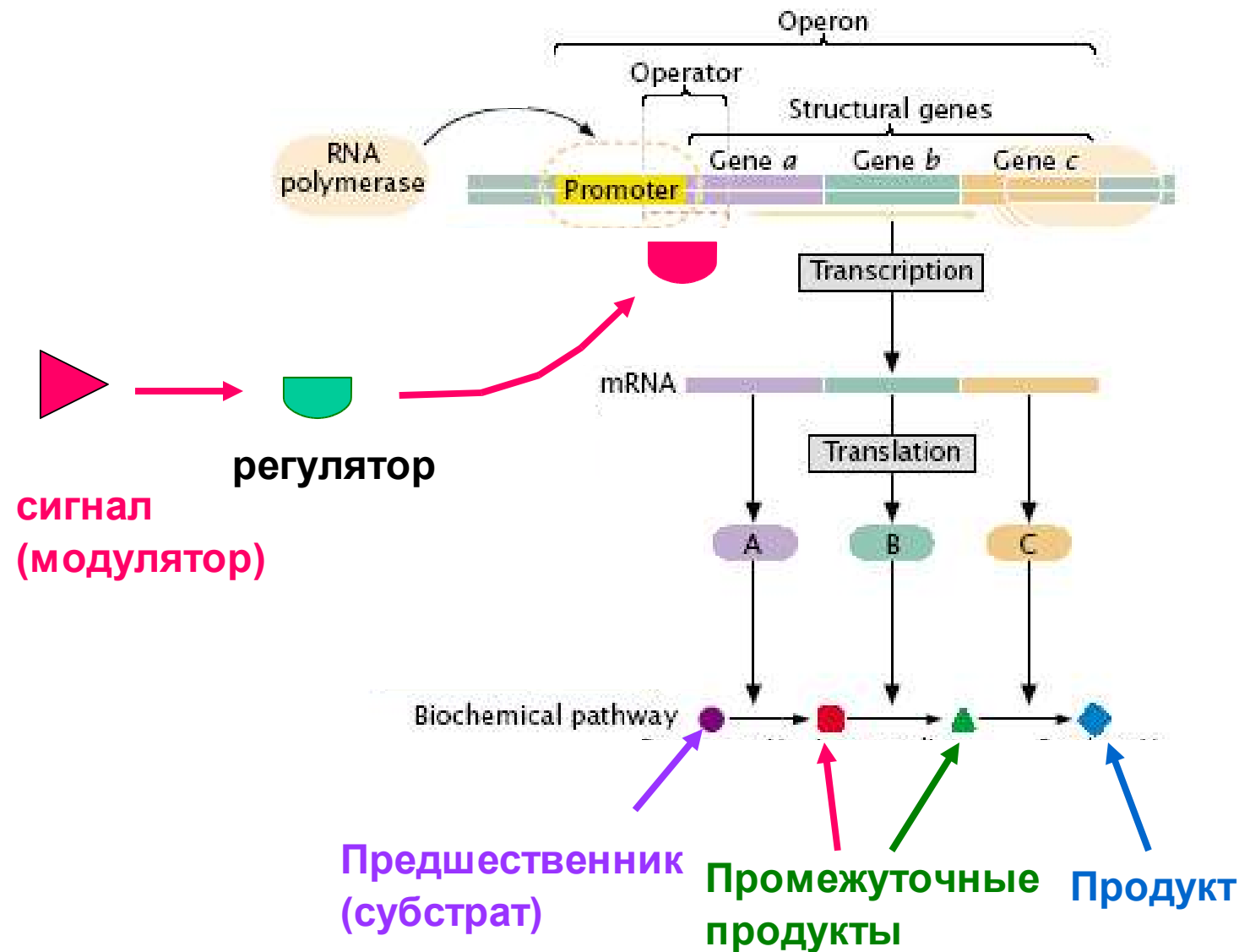
Более 300 диаграмм

ПРЕДСТАВЛЕНИЕ ДАННЫХ О ПУТИ БЕТА-ОКИСЛЕНИЯ ЖИРНЫХ КИСЛОТ В БАЗЕ BIOCARТА



ПРИНЦИПЫ ОРГАНИЗАЦИИ ГЕННЫХ СЕТЕЙ МЕТАБОЛИЗМА .

МОДЕЛЬ РЕГУЛЯЦИИ МЕТАБОЛИЧЕСКОГО ПУТИ (на примере E.coli)



Типы оперонов по уровню экспрессии без регуляторного белка

- 1) Индуцируемые – без регуляторного белка экспрессия очень низкая
- 2) Репрессируемые – без регуляторного белка экспрессия нормальная, белок экспрессию выключает

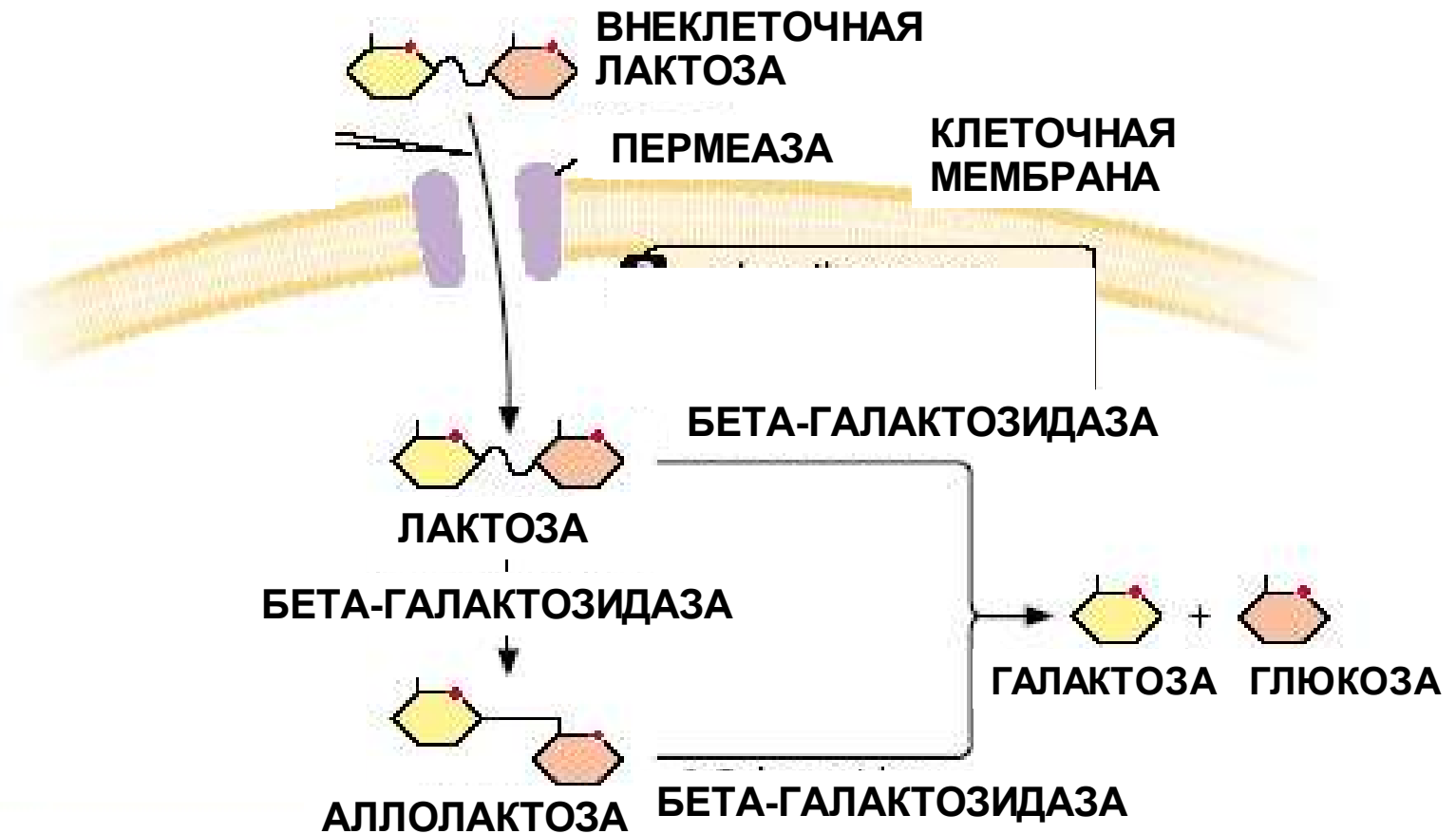
ТИПЫ РЕГУЛЯТОРНЫХ БЕЛКОВ

Регуляторный белок	Эффект регуляторного белка	Влияние модулятора
Активный репрессор	Ингибирует транскрипцию	инактивация
Неактивный репрессор	Ингибирует транскрипцию (после активации)	активация
Неактивный активатор	Стимулирует транскрипцию (после активации)	активация
Активный активатор	Стимулирует транскрипцию	инактивация

Типы регуляции оперонов

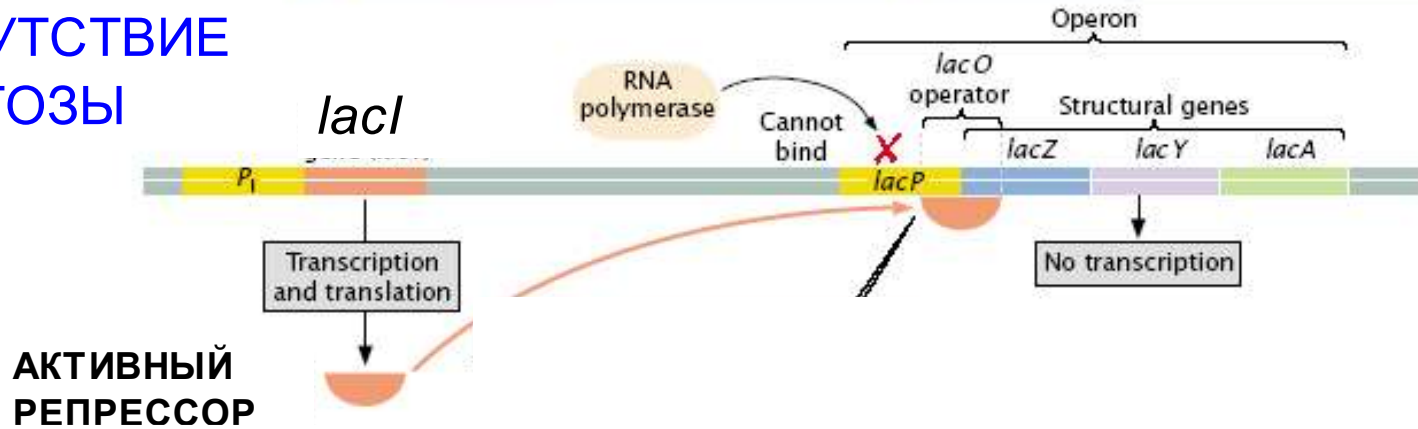
Тип регуляции	Транскрипция в норме	Регуляторный белок	Эффект регуляторного белка	Влияние модулятора
Индукцируемый, вследствие выключения репрессора	~ 0	Активный репрессор	Ингибирует транскрипцию	инактивация
Репрессируемый, вследствие активации репрессора	+	Неактивный репрессор	Ингибирует транскрипцию (после активации)	активация
Индукцируемый, вследствие включения активатора	~ 0	Неактивный активатор	Стимулирует транскрипцию (после активации)	активация
Репрессируемый, вследствие инактивации активатора	+	Активный активатор	Стимулирует транскрипцию	инактивация

ПОСТУПЛЕНИЕ и ДЕГРАДАЦИЯ ЛАКТОЗЫ в КЛЕТКЕ



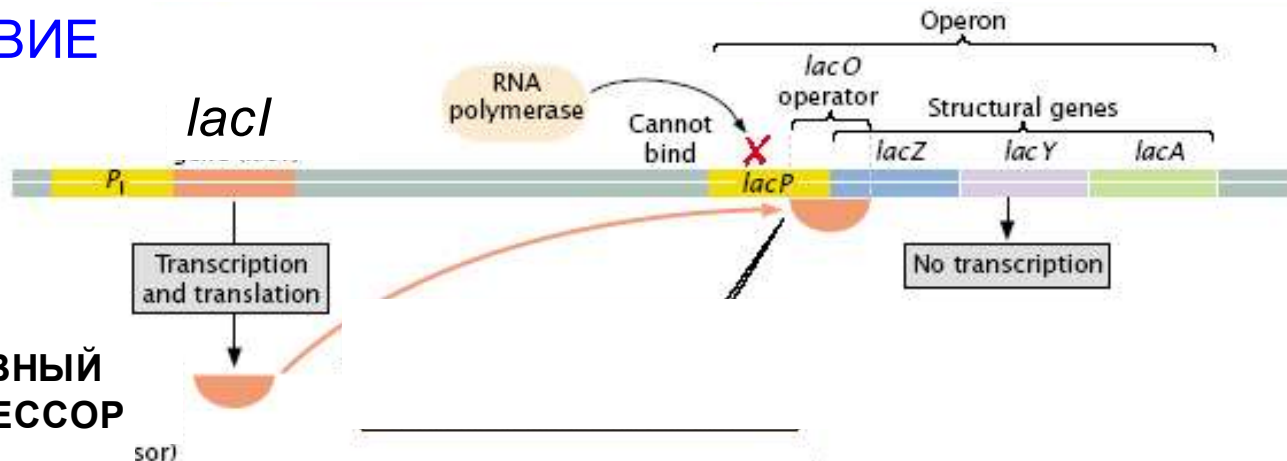
РЕГУЛЯЦИЯ ЭКСПРЕССИИ ГЕНОВ ЛАКТОЗНОГО ОПЕРОНА

ОТСУТСТВИЕ
ЛАКТОЗЫ

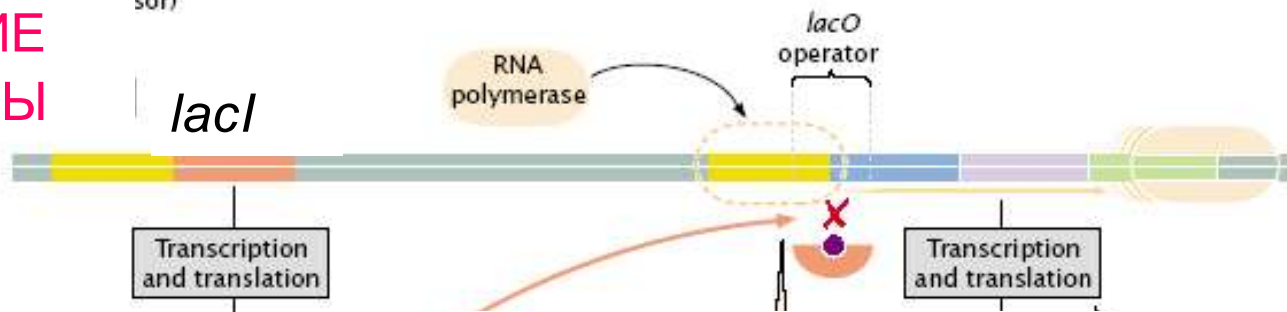


РЕГУЛЯЦИЯ ЭКСПРЕССИИ ГЕНОВ ЛАКТОЗНОГО ОПЕРОНА: индукция лактозой

ОТСУТСТВИЕ
ЛАКТОЗЫ



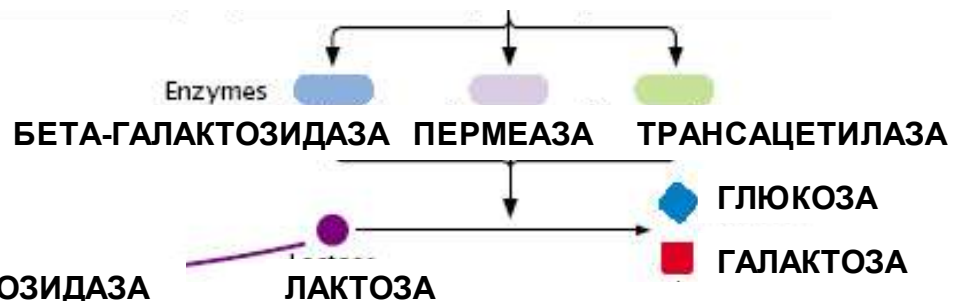
НАЛИЧИЕ
ЛАКТОЗЫ



!!!

НЕАКТИВНЫЙ
РЕПРЕССОР

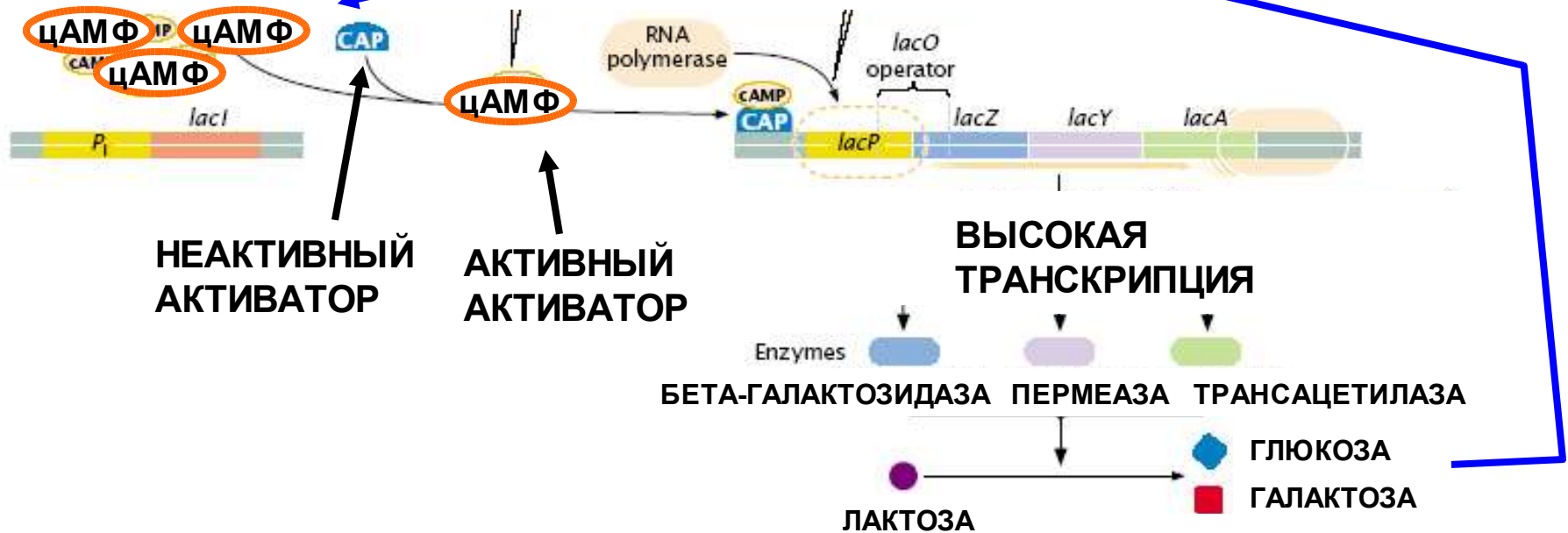
АЛЛОЛАКТОЗА



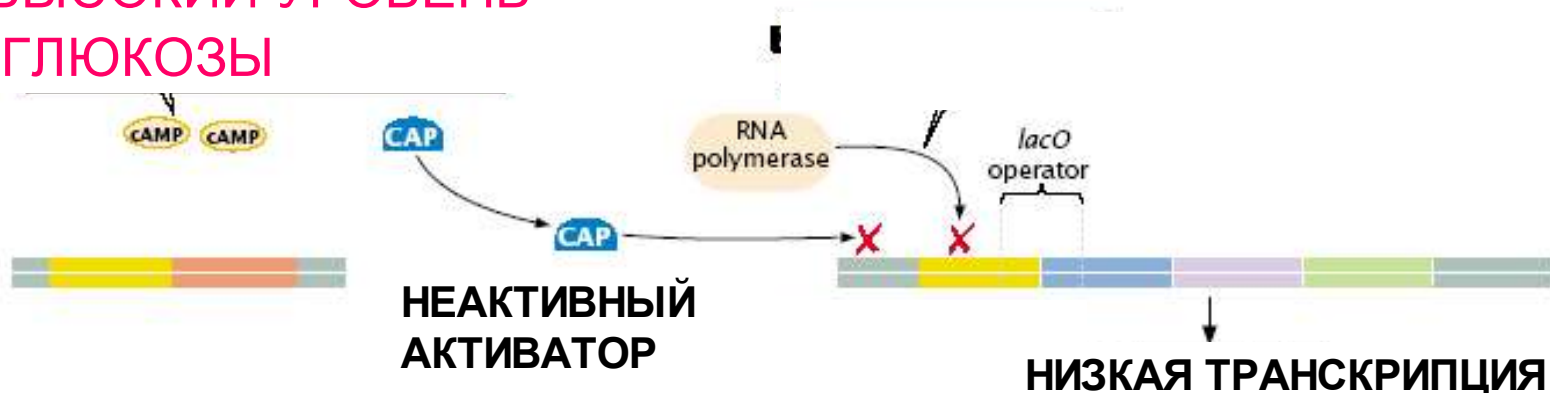
БЕТА-ГАЛАКТОЗИДАЗА

РЕГУЛЯЦИЯ ЭКСПРЕССИИ ГЕНОВ ЛАКТОЗНОГО ОПЕРОНА: индукция при низком уровне глюкозы

НИЗКИЙ УРОВЕНЬ
ГЛЮКОЗЫ

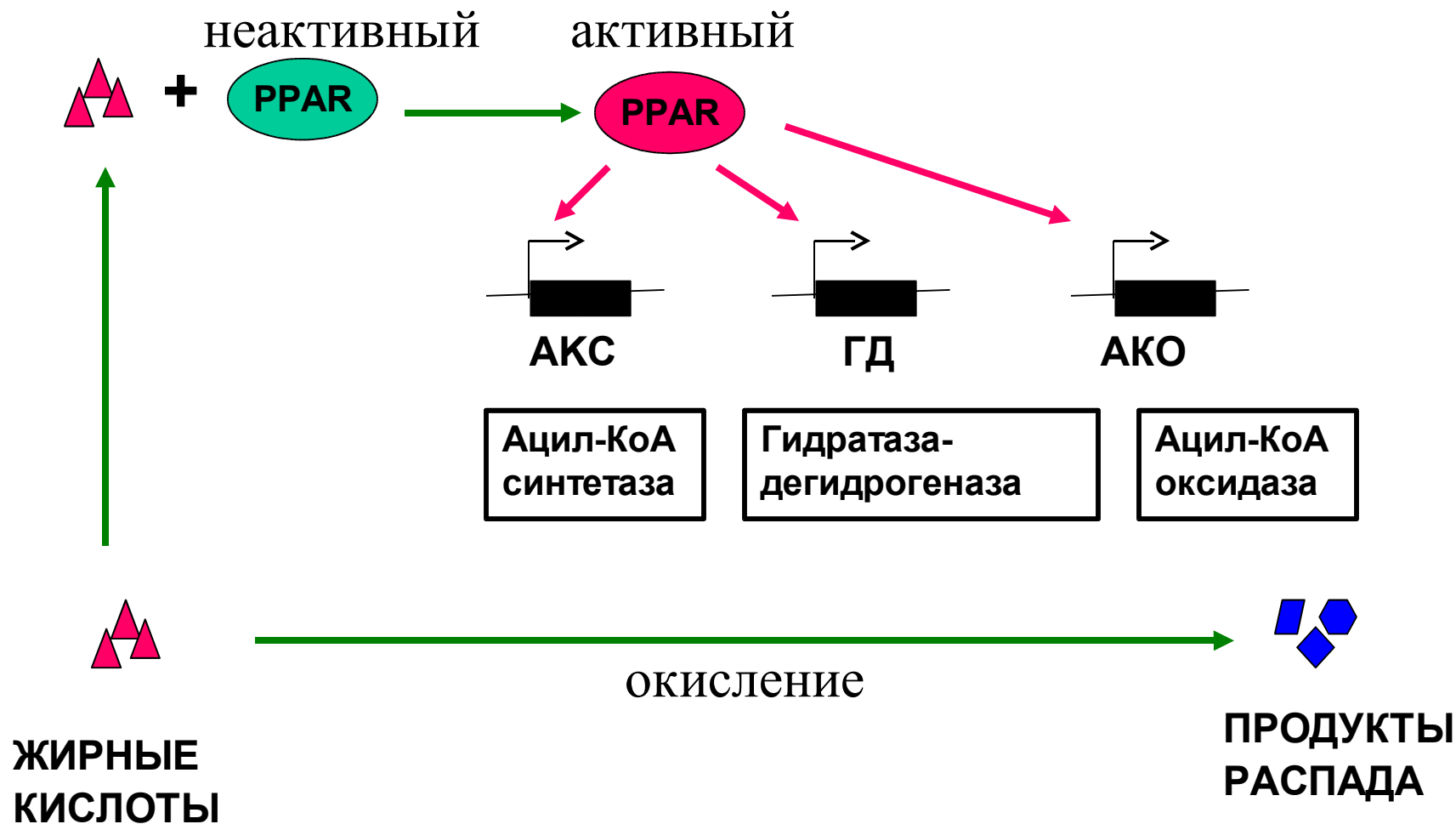


ВЫСОКИЙ УРОВЕНЬ
ГЛЮКОЗЫ



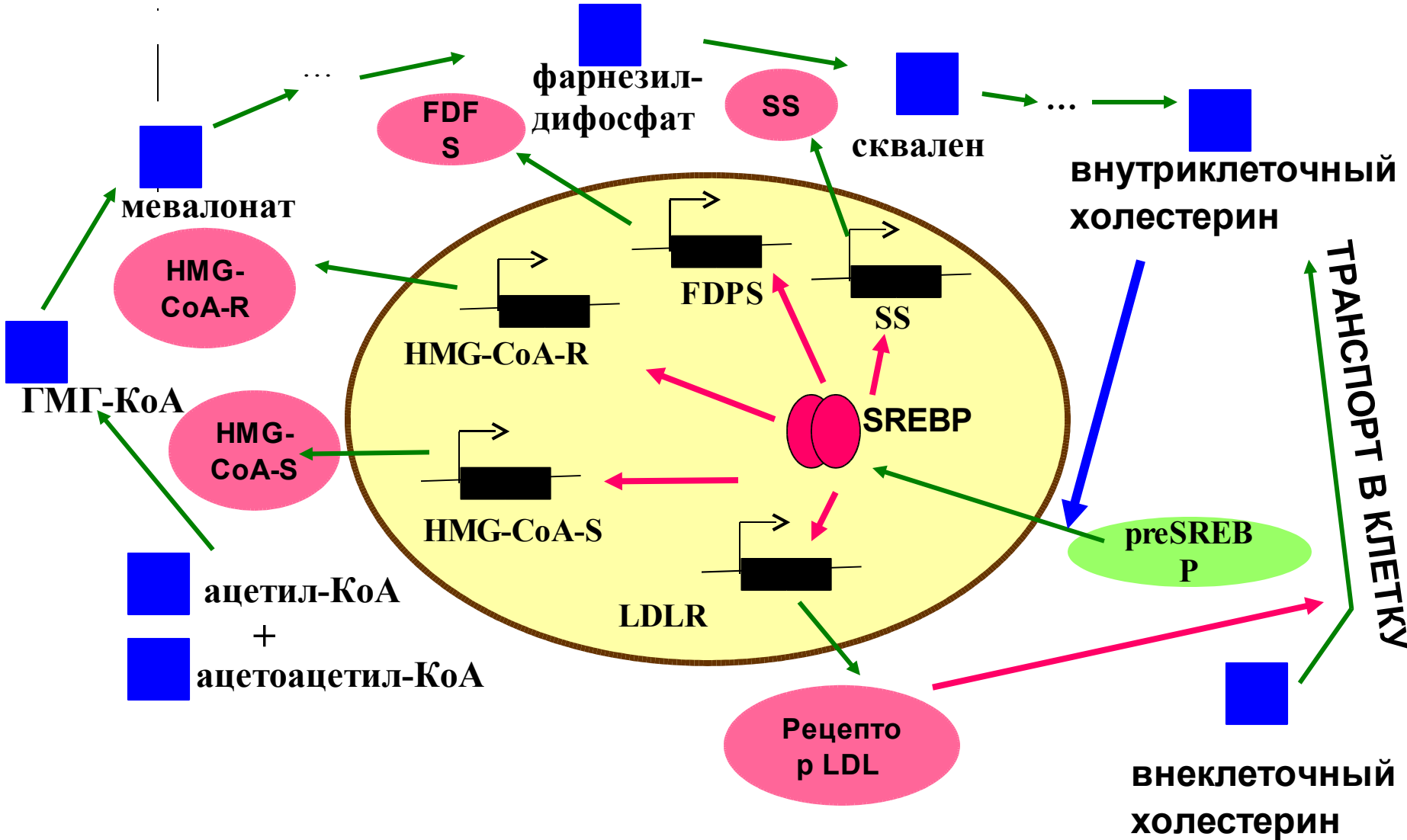
РЕГУЛЯЦИЯ ПРОЦЕССА ОКИСЛЕНИЯ ЖИРНЫХ КИСЛОТ (эукариоты)

- 1) кассетный принцип
- 2) сигнальной молекулой является исходное вещество
- 3) неактивный активатор активируется сигнальной молекулой



РЕГУЛЯЦИЯ УРОВНЯ ХОЛЕСТЕРИНА (эукариоты):

- 1) кассетный принцип
- 2) координированная регуляция биосинтеза и транспорта
- 3) активация неактивного предшественника preSREBP замедляется, если в клетке много холестерина
- 4) сигнальной молекулой является продукт реакции



ПРИМЕРЫ ТРАНСКРИПЦИОННЫХ ФАКТОРОВ, ОБЕСПЕЧИВАЮЩИХ РЕГУЛЯЦИЮ В ОТВЕТ НА МЕТАБОЛИЧЕСКИЙ СИГНАЛ

Название транскрипционного фактора	Семейство	Что является сигналом	Регулируемый метаболический путь
SREBP = Sterol regulatory element binding protein	basic-helix-loop-helix-leucine zipper protein = включает основной домен типа спираль-петля спираль и лейциновую застёжку	холестерин	Биосинтез холестерина (активация)
			биосинтез жирных кислот (активация)
FXR = Farnesoid X-activated receptor = Bile acid receptor	nuclear hormone receptor family = ядерный рецептор	Желчные кислоты (chenodeoxycholic acid, lithocholic acid and deoxycholic acid)	Биосинтез желчных кислот (ингибирование)
PPAR α = Peroxisome proliferator activated receptor α	nuclear hormone receptor family = ядерный рецептор	Жирные кислоты и гипополипидемические вещества	Бета-окисление жирных кислот (активация)
LXR = Liver X receptor alpha = Oxysterols receptor	nuclear hormone receptor family = ядерный рецептор	Оксистеролы: (24-гидроксистерол, 5,6-24 (S).25-ди-эпоксихолестерол, 22 (R)-гидроксихолестерол	Биосинтез холестерина (активация)
RAR = Retinoic acid receptor alpha	nuclear hormone receptor family = ядерный рецептор	Ретиноевая кислота (=морфоген, тератоген)	Широкий круг процессов
RXR	nuclear hormone receptor family= ядерный рецептор	9-цис-ретиноевая кислота	Широкий круг процессов

СПАСИБО ЗА ВНИМАНИЕ !