

Моделирование метаболических путей

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Метабо́лизм (от греч. μεταβολή — «превращение, изменение»), — набор химических реакций, которые протекают в живом организме и способствуют поддержанию жизни.

Метаболический путь — совокупность метаболических реакций

Метаболиты — субстраты и продукты, участвующие в реакциях

Цели и задачи метаболического моделирования

Научные задачи:

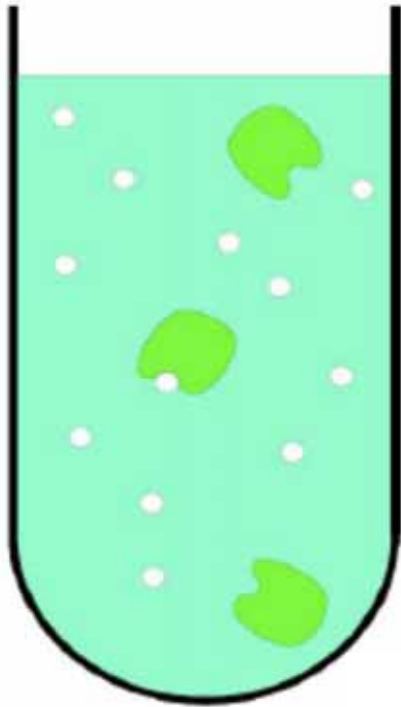
- систематизация накопленных экспериментальных данных
- исследование механизмов клеточной регуляции в сложных биохимических системах
- объяснение экспериментально установленных фактов и предсказание новых ещё не выявленных внутриклеточных явлений

Биоинженерные задачи:

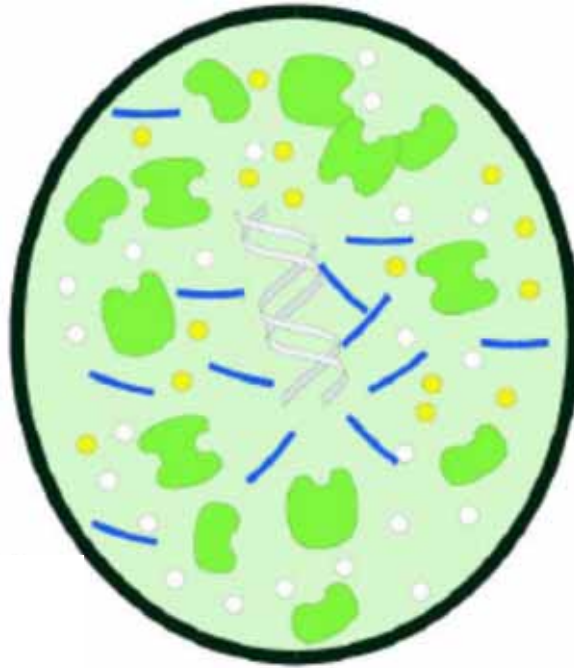
- разработка новых лекарств
- оптимизация получения необходимых веществ из бактериальных клеток и других организмов
- разработка новых штаммов с наперед заданными свойствами
- оптимизация уже существующих промышленных штаммов

Уровни исследования метаболических реакций

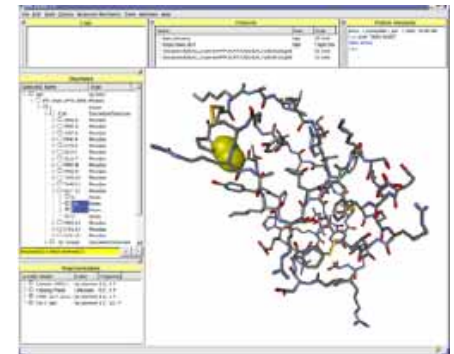
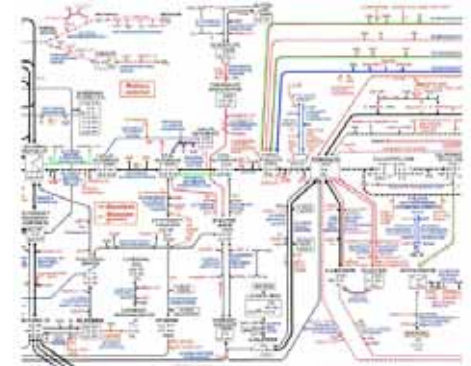
In vitro



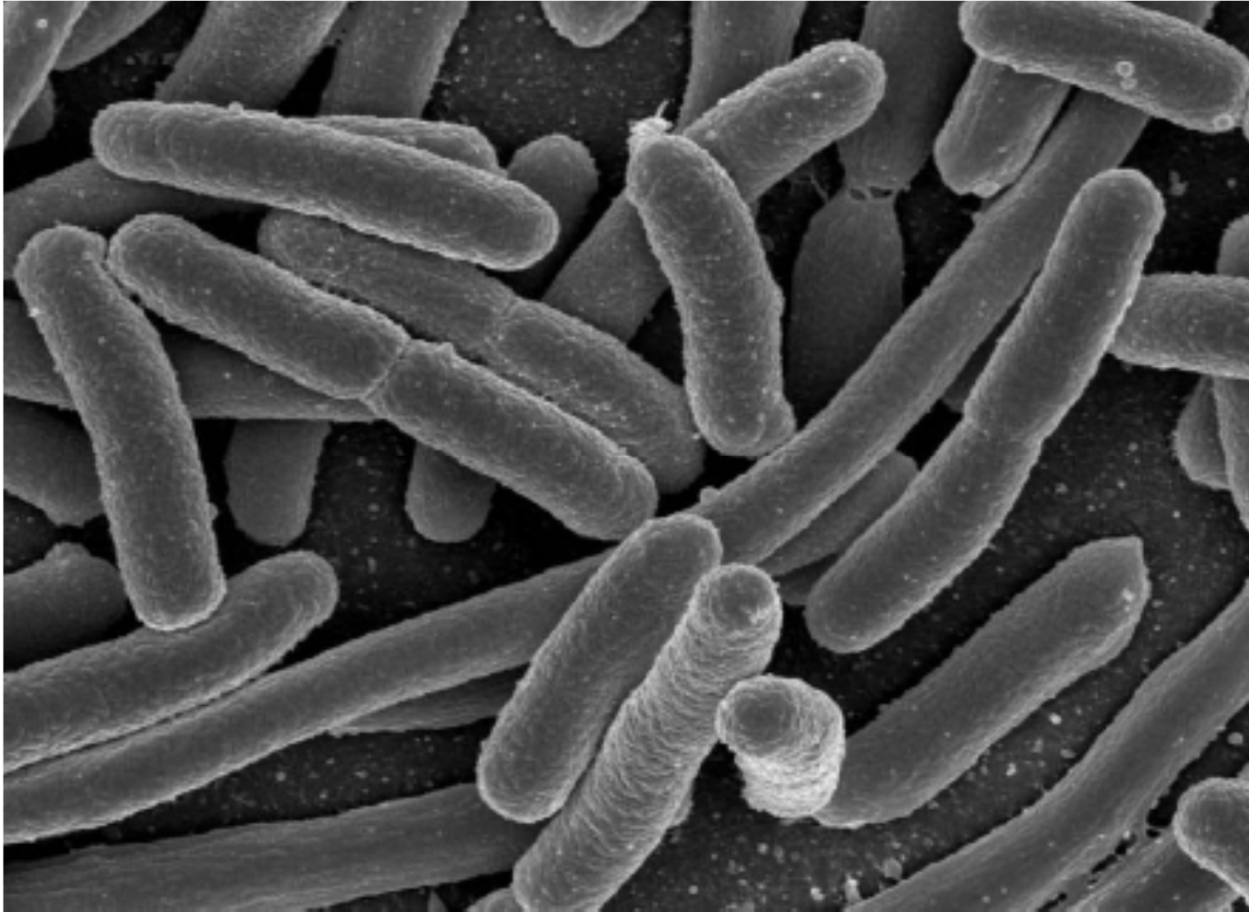
In vivo



In silico



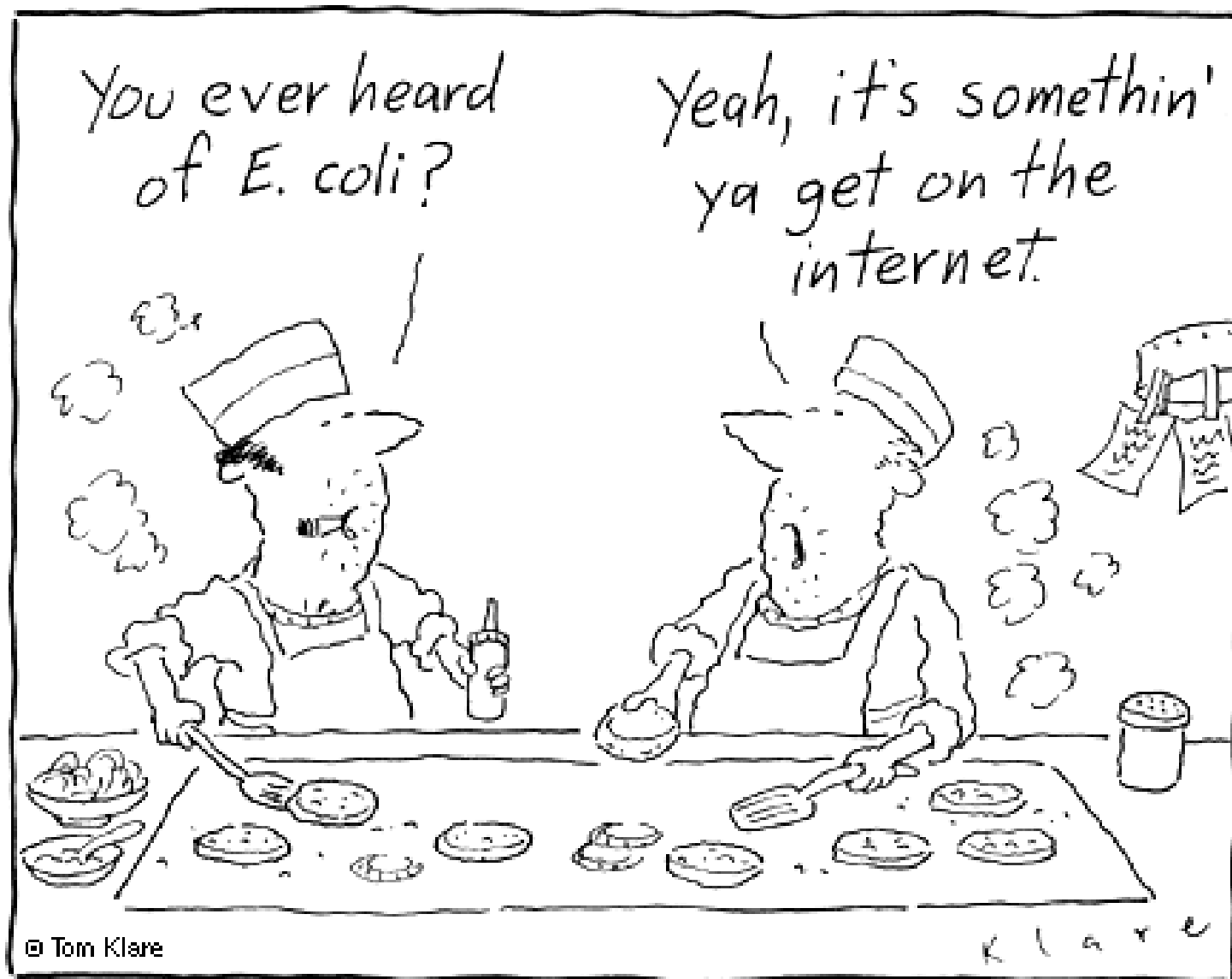
Моделирование метаболических путей *Escherichia coli*



http://www3.niaid.nih.gov/NR/rdonlyres/49477C30-0513-47BE-88FC-17974CB1F952/0/e_coli.jpg

Escherichia coli – удобный объект для моделирования клеточного метаболизма

Электронная клетка: миф или реальность?



Теоретические подходы и концепции метаболического моделирования

Классический системный подход

1. выделить элементарные единицы системы
2. охарактеризовать все значимые взаимодействия между единицами
3. организовать единицы как иерархию взаимодействующих модулей
4. описать состояние каждой единицы и каждого взаимодействия количественно

Данные для верификации метаболической модели

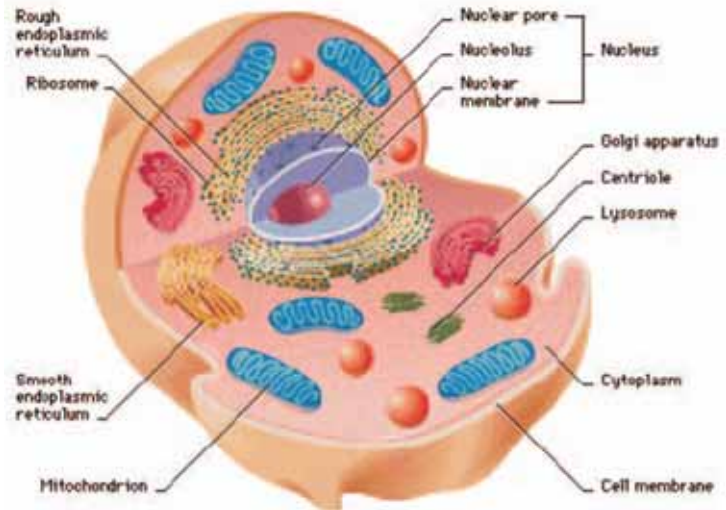
1. Многие (но не все) внутриклеточные концентрации метаболитов могут быть измерены.
2. Активности ферментов могут быть определены из клеточных экстрактов.
3. В стационарном состоянии большинство метаболических потоков может быть определено с помощью изотопа ^{13}C .
4. Кинетические константы многих реакций измерены и собраны в базы данных.

Количественные знания ограничены

1. Существует большая разница между дискретными данными, получаемыми в экспериментах и непрерывными физиологическими процессами.
2. Технические ограничения (несовершенство приборов).
3. Данные о некоторых клеточных процессах отсутствуют.
4. Данные собираются для разных штаммов, разных организмов, в разных экспериментальных условиях.

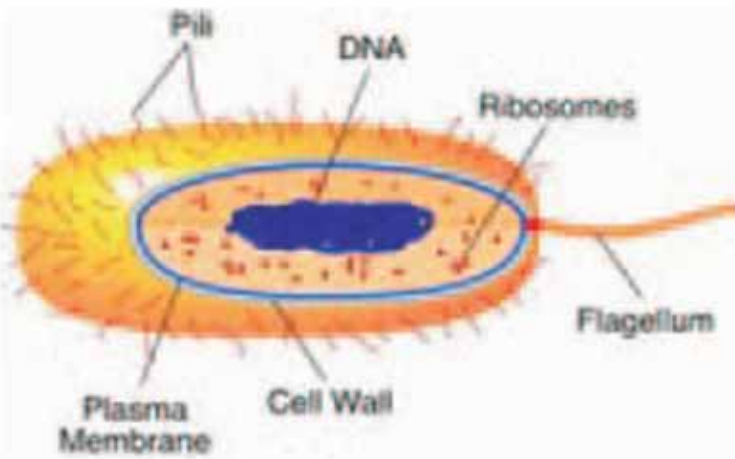
Разные уровни сложности организации клеток

Клетка эукариот



Клеточные процессы локализованы в разных компартментах

Клетка прокариот

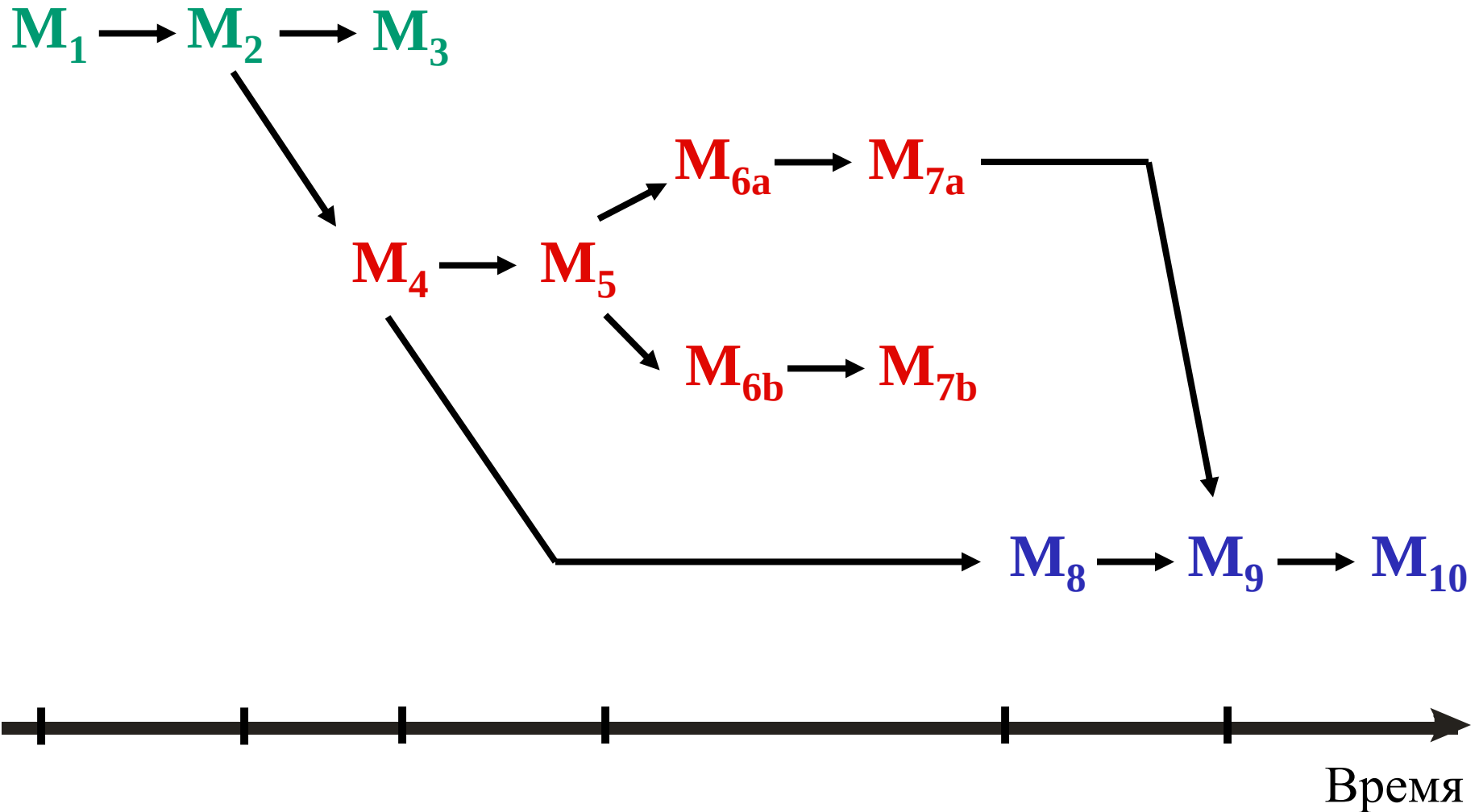


Все процессы протекают в одном компартменте

Как строятся метаболические модели

1. Метаболическая реакция добавляется, убирается или заменяется на другую.
2. Механизм реакции усложняется, упрощается, заменяется другим.
3. Неизвестные кинетические параметры оцениваются с помощью фитирования.

Эволюция модели



Типы метаболических моделей

кинетические модели – системы ОДУ

- (~10-50 уравнений, ~100-500 параметров)
- описание отдельных метаболических путей
- решение модели – динамическое поведение метаболитов во времени

стехиометрические модели – системы линейных алгебраических уравнений

- (~100-1000 уравнений)
- описание метаболизма целой клетки
- решение модели – стационарное распределение метаболических потоков

“The simplest living cell is so complex that supercomputer models may never simulate its behavior perfectly.
But even imperfect models could shake the foundations of biology.”

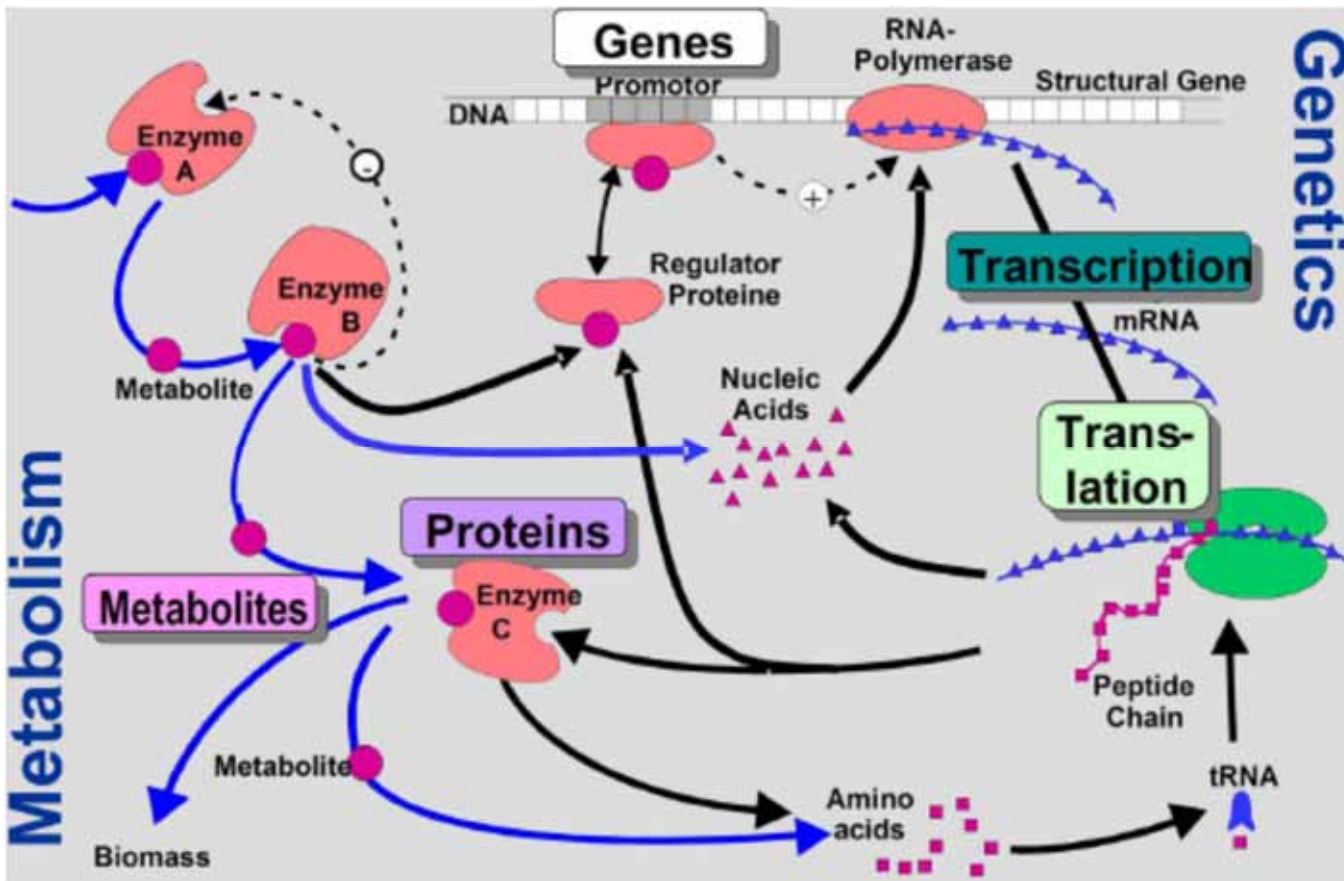
W.Wayt Gibbs. Scientific American, 2001

«Простейшая клетка настолько сложна, что даже моделирование на суперкомпьютерах никогда не воспроизведет ее поведение в совершенстве. Но даже несовершенные модели могут потрясти основы биологии.»

Кинетические модели

- построение схемы метаболического пути
- вывод уравнений скорости (по типу Михаэлиса-Ментен) для каждой реакции и объединение в систему дифференциальных уравнений (ОДУ)
- подбор параметров по экспериментальным данным

Escherichia coli



720 метаболических
процессов
436 метаболитов
540 ферментов

Описание метаболизма включает:
мембранные транспортные процессы,
центральные катаболические пути,
биосинтетические пути (продукция всех компонент биомассы),
использование альтернативных источников углерода

Figure from Ermir Qeli
Information Visualization Techniques for Metabolic Engineering
Dissertation zur Erlangung des akademischen Grades Doktor der
Naturwissenschaften (Dr. rer. nat)

Метаболические пути *Escherichia coli*

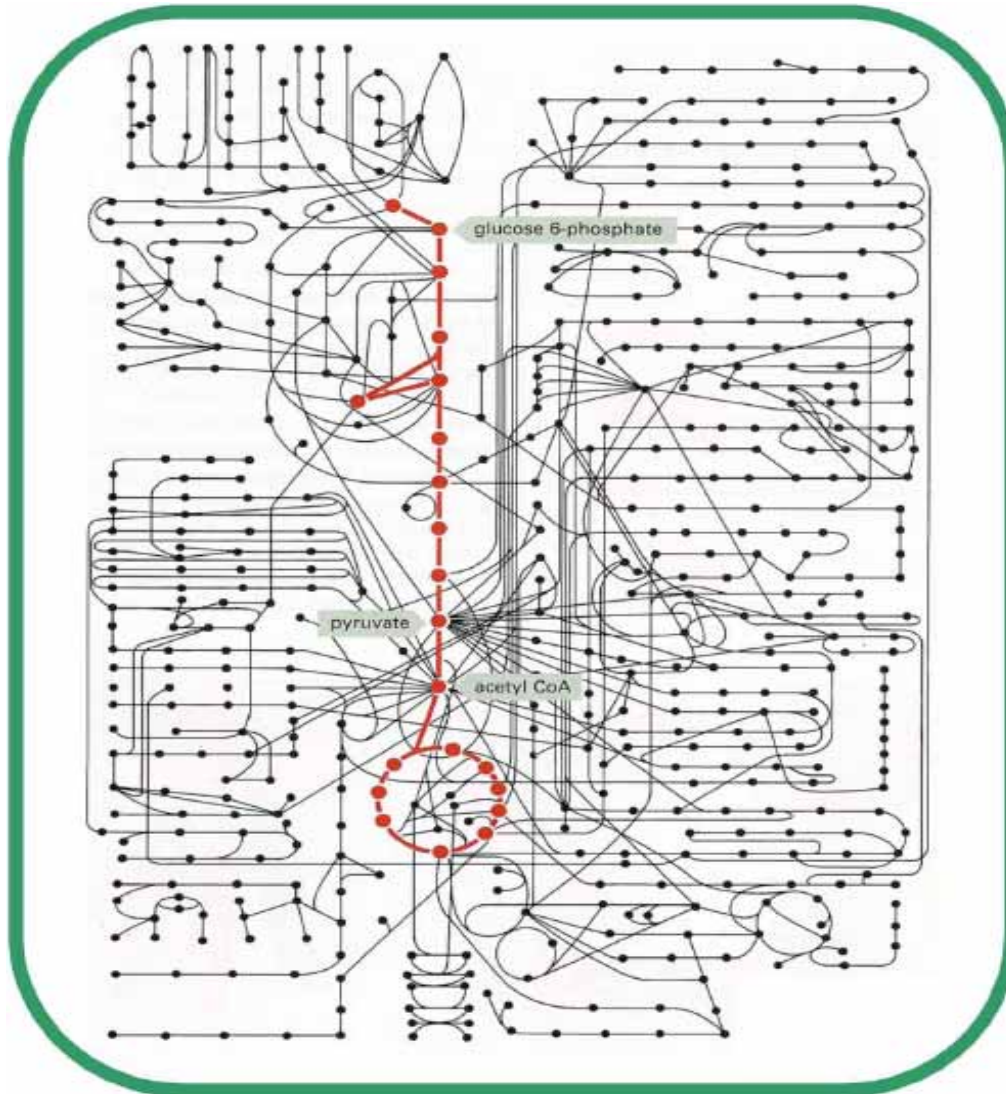
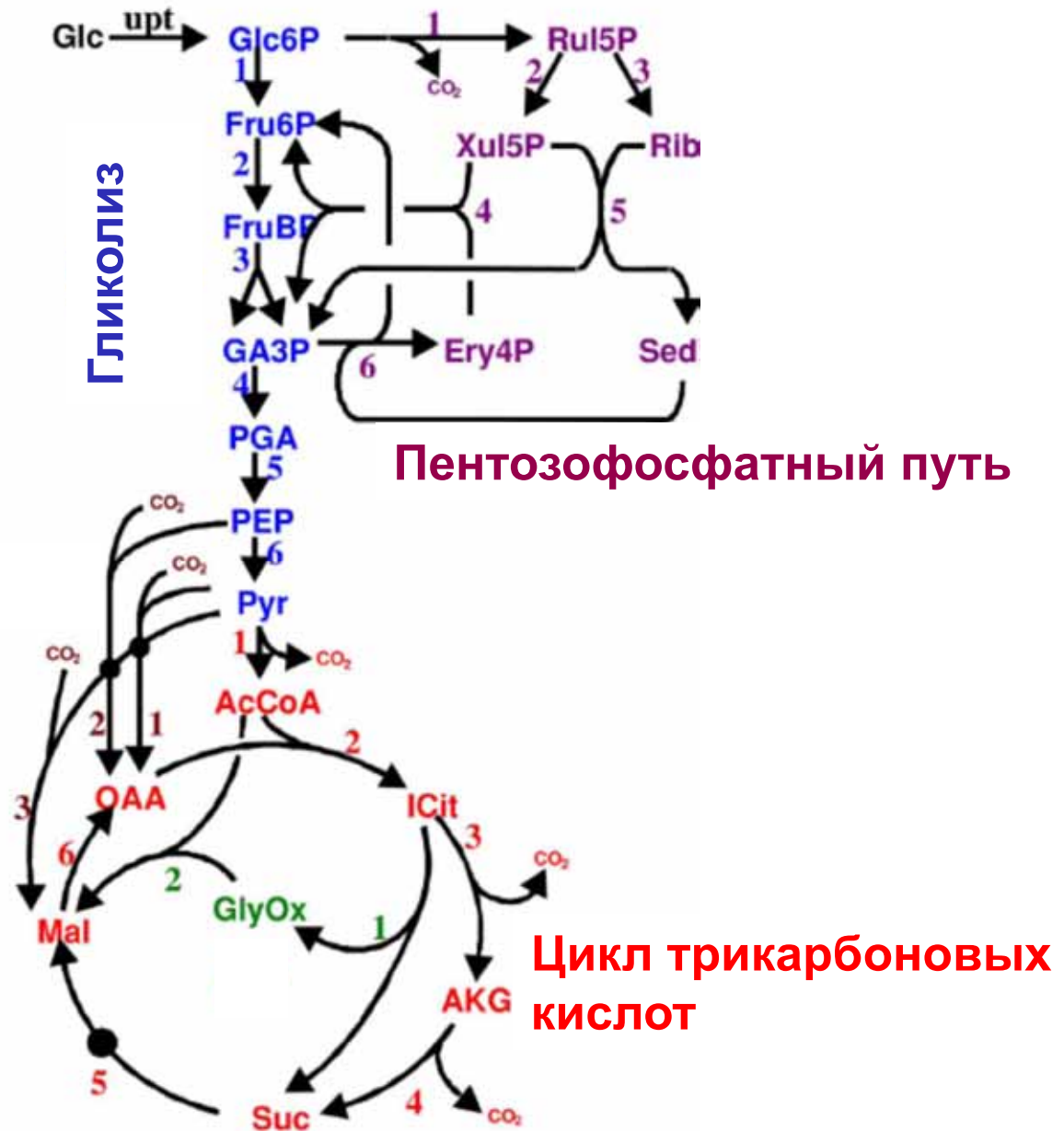


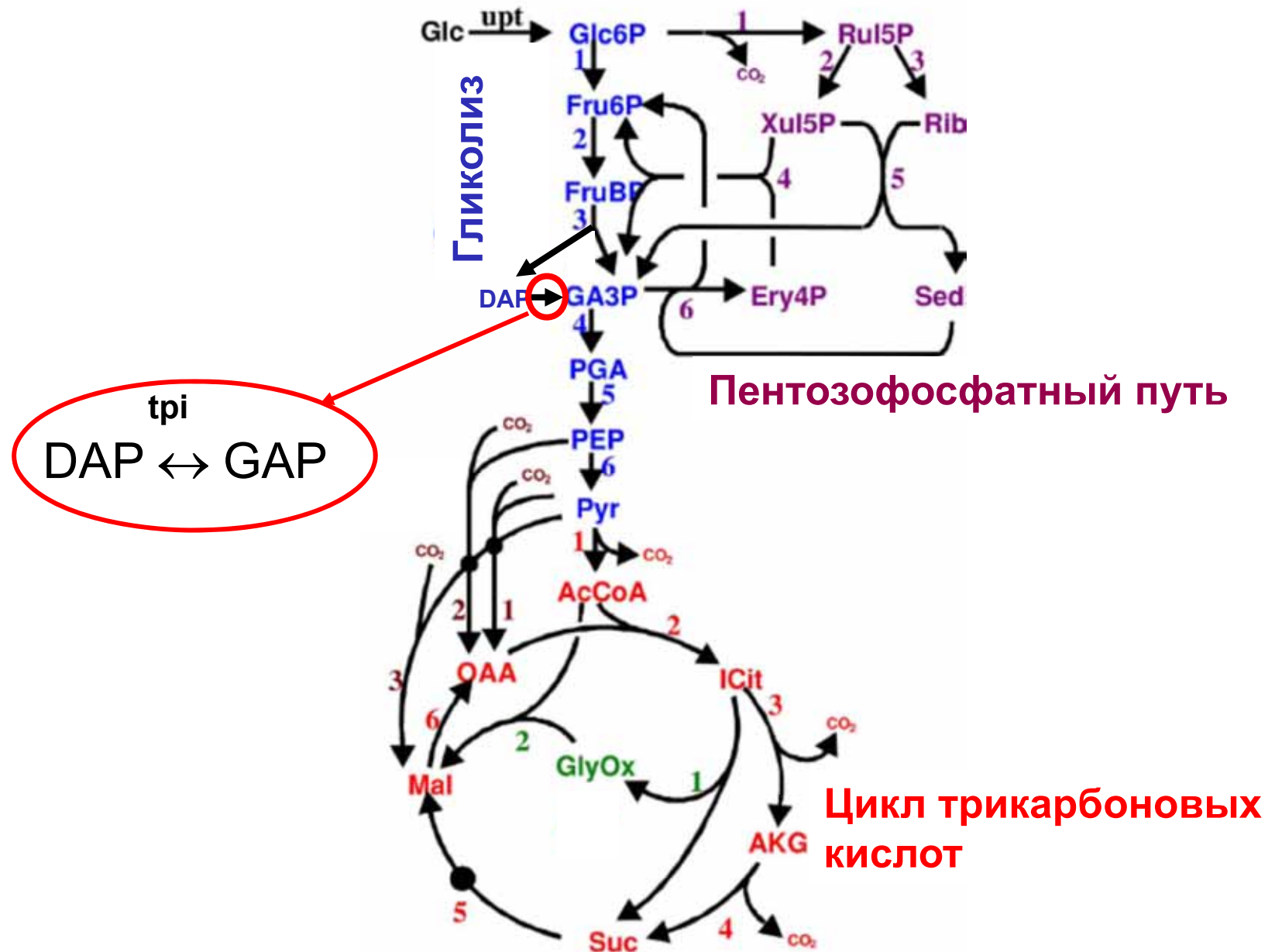
Figure from Ermir Qeli
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Красным цветом выделены центральные метаболические пути

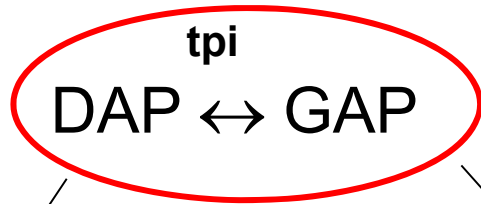
Центральные метаболические пути



Центральные метаболические пути

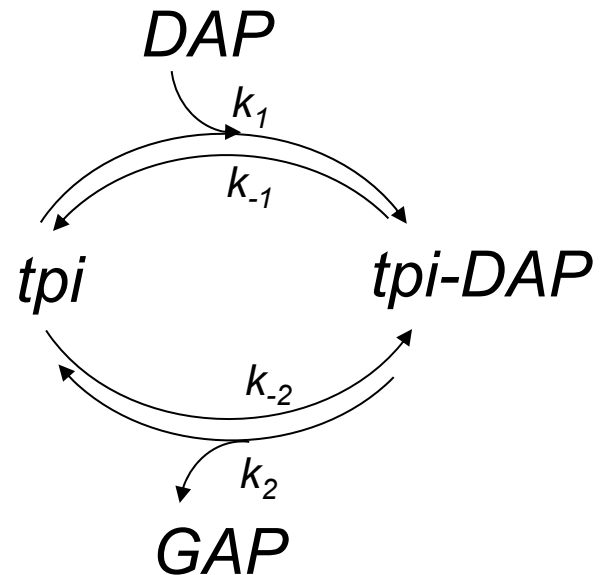
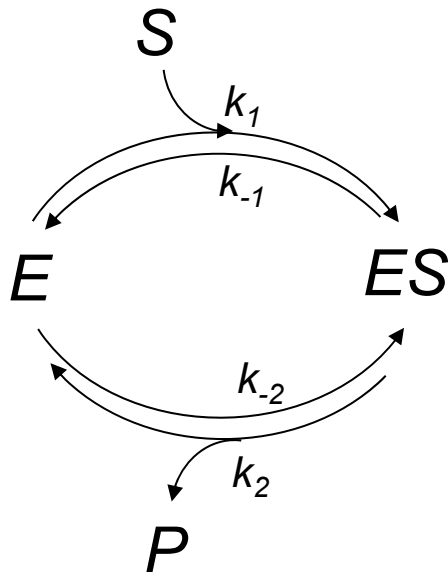


Вывод уравнения скорости



Кинетическая схема взаимодействия субстрата и продукта с ферментом

Каталитический цикл фермента



Вывод уравнения скорости

Кинетическая схема взаимодействия субстрата и продукта с ферментом:



Соответствующая система дифференциальных уравнений:

$$\left. \begin{aligned} \frac{dS}{dt} &= -k_1 \cdot S \cdot E + k_{-1} \cdot ES \\ \frac{dP}{dt} &= k_2 \cdot ES - k_{-2} \cdot E \cdot P \end{aligned} \right\} \text{медленные переменные}$$

$$\left. \begin{aligned} \frac{dE}{dt} &= -k_1 \cdot S \cdot E + k_{-1} \cdot ES + k_2 \cdot ES - k_{-2} \cdot E \cdot P \\ \frac{dES}{dt} &= k_1 \cdot S \cdot E - k_{-1} \cdot ES - k_2 \cdot ES + k_{-2} \cdot E \cdot P \end{aligned} \right\} \text{быстрые переменные}$$

Уравнение скорости:

$$\frac{dP}{dt} = -\frac{dS}{dt} = V = E_0 \frac{k_2 \frac{S}{K_m^S} - k_{-2} \frac{P}{K_m^P}}{1 + \frac{S}{K_m^S} + \frac{P}{K_m^P}}$$

Описание ферментативной реакции

кинетическая схема
(каталитический цикл фермента)



система диф. уравнений



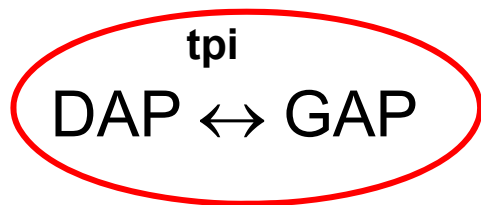
иерархия времен
использование теоремы Тихонова
редукция системы

уравнение скорости



оценка параметров

Уравнения скорости для триозофосфат изомеразы (tpi)



$$V = E_0 \frac{k_2 \frac{C_{DAP}}{K_m^{DAP}} - k_{-2} \frac{C_{GAP}}{K_m^{GAP}}}{1 + \frac{C_{DAP}}{K_m^{DAP}} + \frac{C_{GAP}}{K_m^{GAP}}}$$

Определение констант:

эксперимент



литература
базы данных

$$K_m^{DAP} = 2.3 \text{ mM}$$

$$K_m^{GAP} = 1.5 \text{ mM}$$

$$k_2 = 45000 \text{ 1/min,}$$

$$k_{-2} = 520000 \text{ 1/min}$$

константы Михаэлиса для
субстрата и продукта

каталитические константы для
прямой и обратной реакций
(число оборотов фермента)

экспериментально
измеряемые константы

Вывод системы уравнений

В общем случае

Уравнения, описывающие изменения во времени каждого метаболита:

$$\frac{dC_j}{dt} = \sum V_{ij} - \mu C_j$$

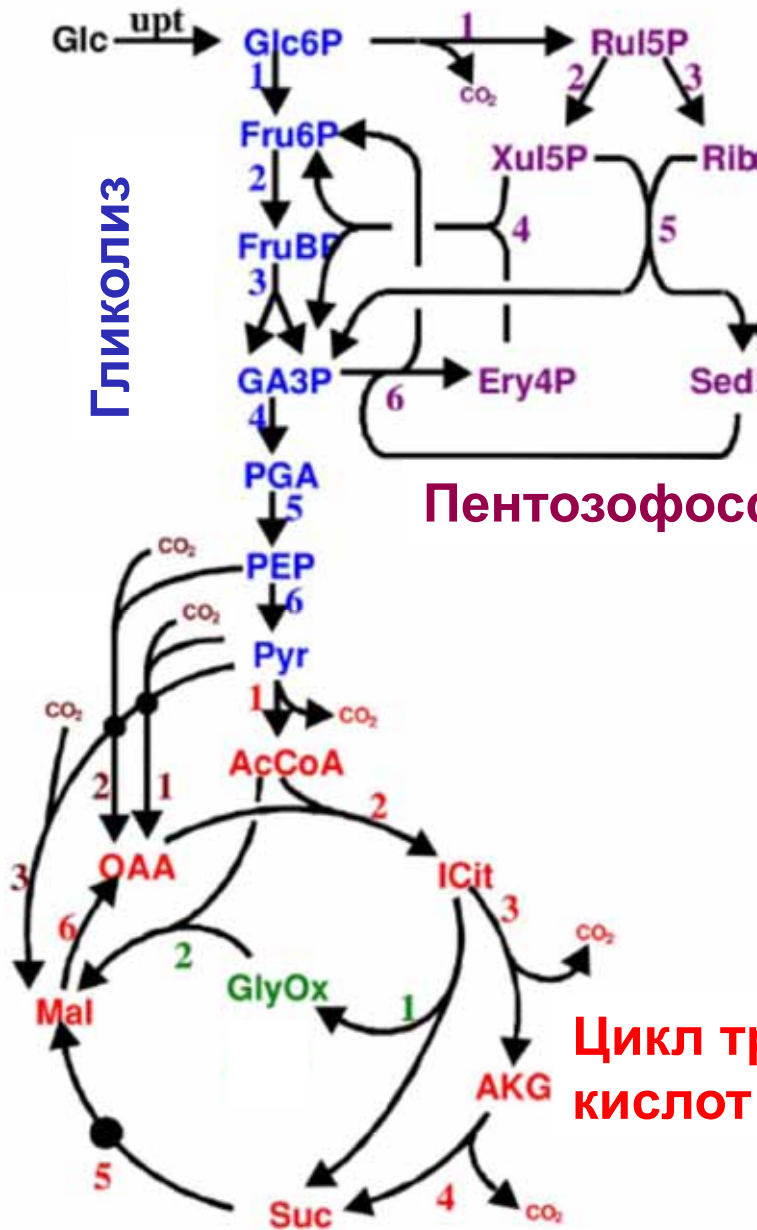
C_j – концентрация j -го метаболита

V_{ij} – скорость образования или распада j -го метаболита в i -той реакции

μC_j – уменьшение концентрации за счет клеточного роста

Моделирование центрального метаболизма *E.coli*

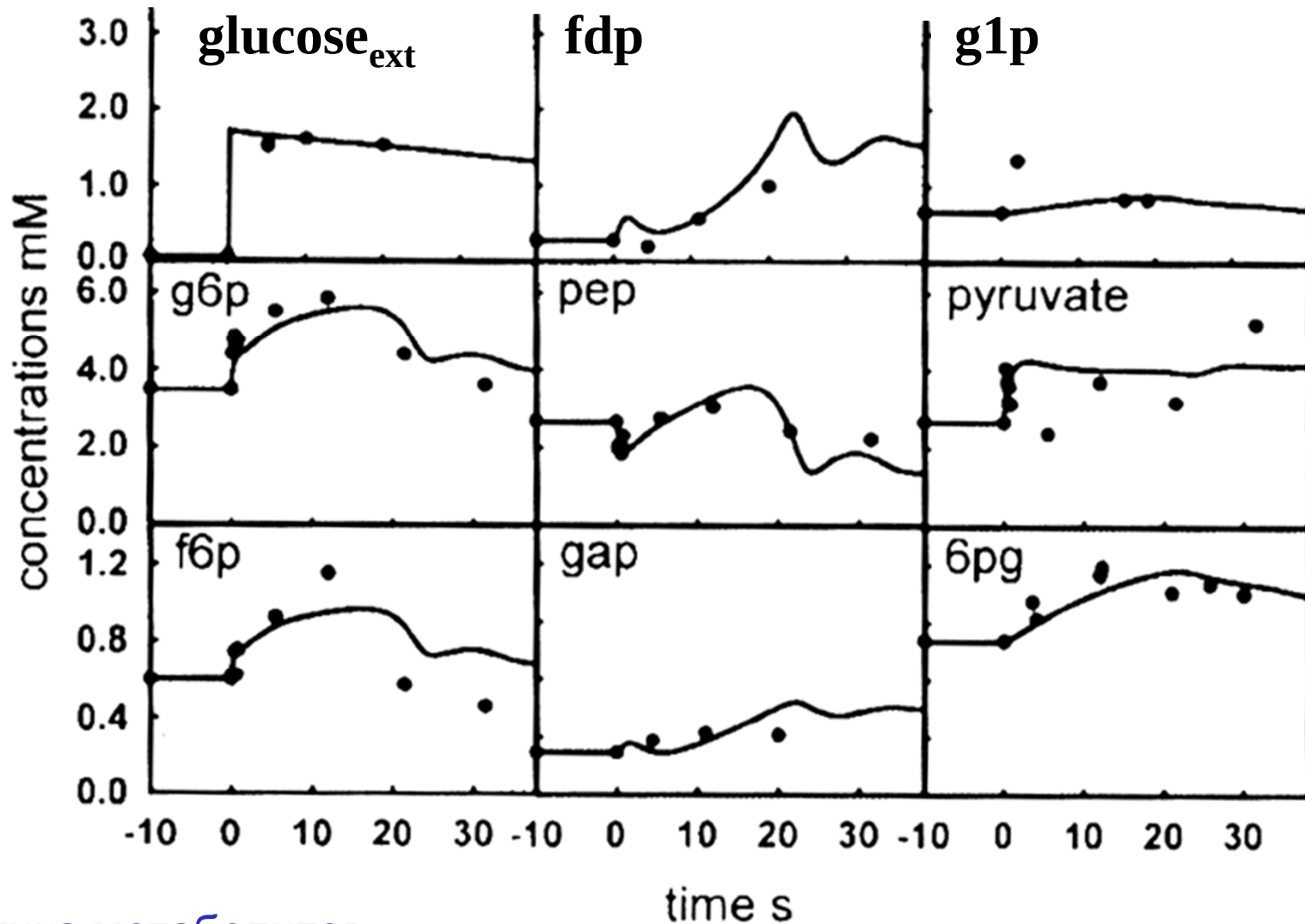
Manfred Rizzi et al,
Institute of Biochemical Engineering,
University of Stuttgart, Germany



1. Вывод уравнения скорости для каждого фермента.
2. Объединение в систему уравнений для всего пути.
3. Оценка параметров.

Цикл трикарбоновых кислот

Результаты фитирования модели



Кинетика метаболитов.

Точки – экспериментальные данные

Линии – результаты численного счета

Manfred Rizzi et al,
Institute of Biochemical Engineering,
University of Stuttgart, Germany

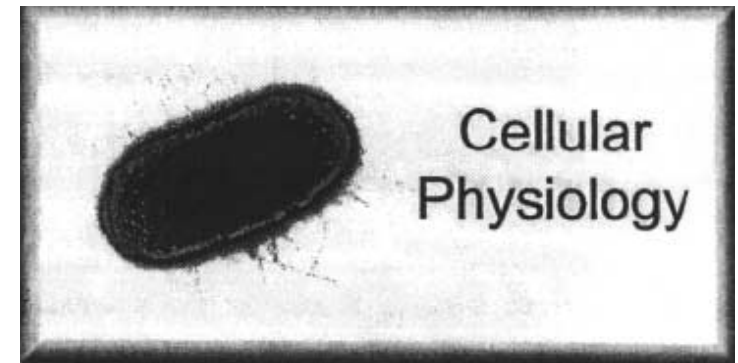
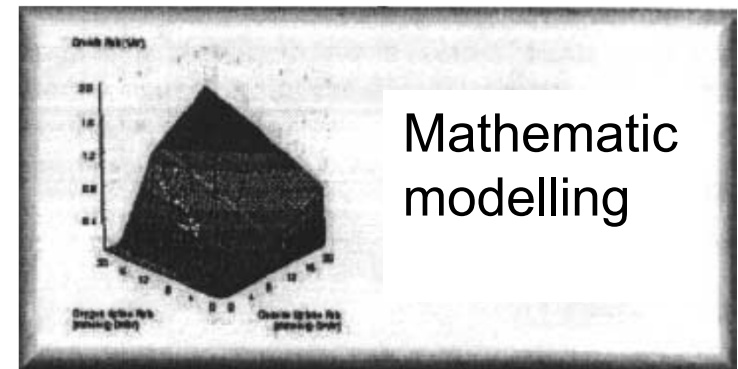
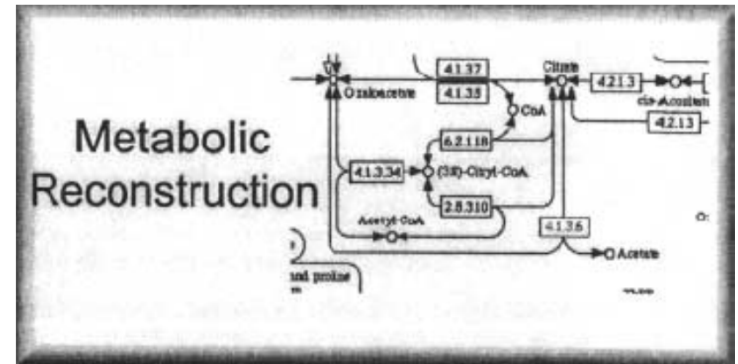
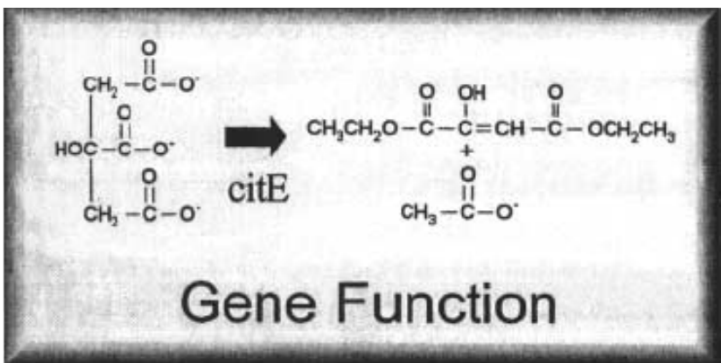
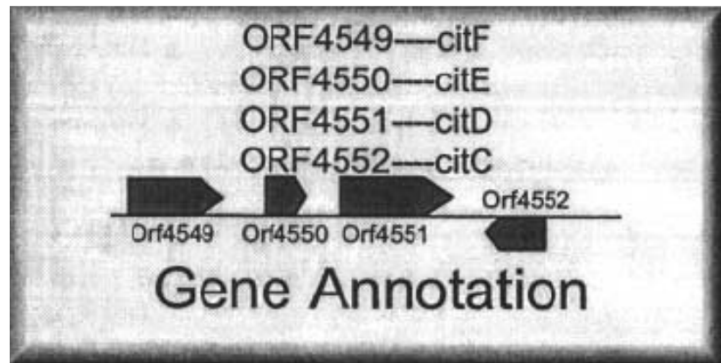
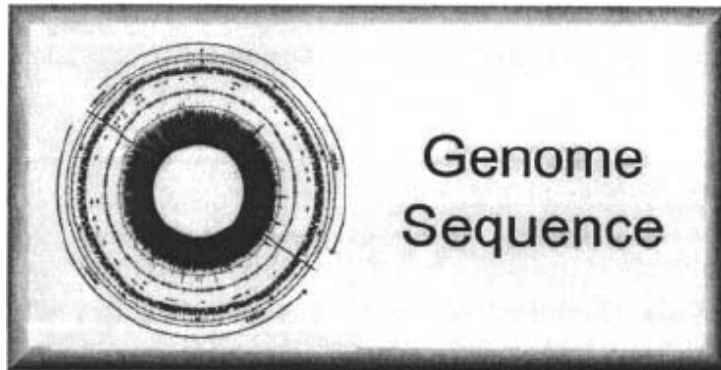
Результаты моделирования

- Описана экспериментально наблюдаемая динамика (в том числе и колебательный процесс).
- Показано, что поглощение глюкозы в основном контролируется двумя системами: транспортной (PTS) и ее ингибиторами.

Использование баз данных для построения метаболических моделей

От генома до фенотипа

J. Edwards, M. Covert and B. Palsson
Environmental Microbiology (2002) 4(3), 133–140



Построение метаболических моделей

Основные шаги:

- Определили последовательность генов (эксперимент)
- Выделили интересующий ген (эксперимент)
- Определили аминокислотную последовательность (базы данных)
- Определили белок (базы данных)
- Определили метаболическую реакцию (базы данных)
- Внесли в схему метаболических путей (моделирование)
- Получили картину метаболических путей (моделирование)

Базы данных по базам данным

Русскоязычный ресурс

Молекулярно-биологические базы данных

<http://www.jcbi.ru/baza/index.shtml>

Англоязычный ресурс

NCBI Центр биотехнологической информации

<http://www.ncbi.nlm.nih.gov/>

Молекулярно-биологические базы данных

ОБЪЕДИНЕННЫЙ ЦЕНТР ВЫЧИСЛИТЕЛЬНОЙ БИОЛОГИИ И БИОИНФОРМАТИКИ



► Карта сайта

[| Заглавная](#) | [| Научный Совет](#) | [| Кластер](#) | [| Проекты](#) | [| Базы данных](#) | [| Ссылки](#) | [| Объявления](#) | [| Контакты](#) |

Молекулярно-биологические базы данных

[По алфавиту](#) | [ДНК](#) | [РНК](#) | [Белки](#) | [Метаболические пути](#) | [Библиография](#) | [Прочие](#)

Поиск по названию:

Поиск по слову:

В настоящее время существуют сотни Web-сайтов, которые доступны для обзора и поиска данных по молекулярной биологии и другим смежным дисциплинам. Каждая из них имеет свой формат хранения данных, различную степень избыточности, взаимосвязи с родственными или аналогичными базами данных. Каждая база данных имеет также свои средства доступа к информации - различные поисковые программы, программные средства визуализации, пополнения базы. Крупнейшие хранилища первичных структур ДНК и аминокислотных последовательностей (такие, как EMBL, GenBank, DDBJ, SWISS-PROT, PIR и др.) пополняются аннотированными последовательностями непосредственно исследователями, расшифровавшими их, с помощью автоматизированной системы пополнения баз данных по сети Интернет. Конечно, впоследствии эти данные проверяются персоналом администраций баз данных и существенно пополняются. Вторым основным источником информации во всех базах является специальная научная литература. Многие базы данных, работающие над коллекционированием однородной информации, координируют свои усилия, осуществляя международное разделение труда, это можно проиллюстрировать примером сотрудничества трех всемирных коллекций последовательностей нуклеотидов EMBL (Европа), GenBank (США), DDBJ (Япония).

Наряду с общими базами данных в последнее время появилось много специализированных информационных ресурсов. Многие из них хранят данные, полученные с помощью компьютерных методов, результаты теоретических предсказаний. Большую роль в биоинформатике играют хранилища последовательностей ДНК и κДНК, специализированные базы данных по отдельным регуляторным мотивам нуклеотидных последовательностей, базы данных по экспрессии генов, библиотеки геномов, карт, последовательностей РНК, белков, белковых мотивов, по продукции белков. Есть базы данных по протеомике, структурам белков, мутациям, метаболическим путям и регуляции, по трансгенным организмам, анатомии, биохимии, а также по научной литературе, по существующему в этих областях исследований программному обеспечению. Есть даже база данных по базам данных, она имеет адрес <http://www.infobiogen.fr/services/dbcat>. Это текстовый файл с аннотациями более чем на 500 биологических баз данных. Он содержит краткое описание назначения базы, авторов, ссылки и адреса. Для того, чтобы обеспечить ориентирование в этом обширном информационном пространстве, журнал Nucleic Acids Research в течение ряда последних лет первый номер года посвящает описаниям баз данных, сделанным их авторами.

Список аннотированных ссылок на молекулярно-биологические базы данных, представленный на нашем сайте, обновляется постоянно и отражает положение вещей на сегодняшний день.

Молекулярно-биологические базы данных

По алфавиту | ДНК | РНК | **Белки** | Метаболические пути | Библиография | Прочие

1D-структуры | 2D-структуры | 3D-структуры | Семейства | Домены | Мотивы | >>

[AARSDb](#) - AminoAcyl-tRNA Synthetases DataBase
[ASTRAL](#) - The ASTRAL Compendium for Sequence and Structure Analysis
[BioImage](#) - Biological Images for scientific research
[BioMagResBank \(BMRB\)](#) - repository for data from NMR on proteins, peptides, and nucleic acids
[Blocks](#) - most highly conserved regions of proteins
[BRENDA](#) - enzyme database
[CE](#) - Databases and Tools for 3-D Protein Structure Comparison and Alignment
[ClusTr](#) - a database of clusters of SWISS-PROT+TrEMBL proteins
[COG](#) - the database of Clusters of Orthologous Groups of proteins
[DaliDO](#) - Dali Domain Dictionary
[DIP](#) - Database of Interacting Proteins
[DOMO](#) - protein domain database
[DSSP](#) - Dictionary of Secondary Structure of Proteins
[ENZYME](#) - ENZYME nomenclature database
[FSSP](#) - Fold classification based on Structure-Structure alignment of Proteins
[GEO](#) - Gene Expression Omnibus
[GTOP](#) - Genomes TO Protein structures and functions
[Histones](#) - Histone sequence database
[HSSP](#) - Homology-derived Secondary Structure of Proteins
[HUGE](#) - Human Unidentified Gene-Encoded large protein database
[InParanoid](#) - Eukaryotic Ortholog Groups Database
[iProClass](#) - an integrated, comprehensive and annotated Protein Classification database
[ISSD](#) - Integrated Sequence-Structure Database
[Kabat](#) - Kabat database of sequences of proteins of immunological interest
[Klotz](#) - biochemical compounds declarative database
[LGIC](#) - Ligand Gated Ion Channel subunit database
[LIGAND](#) - LIGAND chemical database for enzyme reactions
[MEROPS](#) - Peptidase database
[MetaFam](#) - a comprehensive protein family resource
[MMDB](#) - Molecular Modelling DataBase
[MSD](#) - Macromolecular Structure Database
[OWL](#) - Composite Protein Sequence Database
[PALI](#) - a database of Phylogeny and ALignment of homologous protein structures
[PDB](#) - Brookhaven Protein DataBank
[PFAM](#) - Protein families database of alignments and HMMs
[PIR](#) - Protein Information Resource
[PIR-ALN](#) - database of Protein sequence ALigNments
[PMD](#) - Protein Mutant Database
[Predictome](#) - a database of putative functional links between proteins
[PRINTS](#) - database of protein family fingerPRINTS
[ProDom](#) - Protein Domain families database
[PROSITE](#) - PROtein SITEs and patterns dictionary
[ProtRepeatsDB](#)
[Rebase](#) - Restriction Enzyme DataBase
[SBASE](#) - protein domain library
[SCOP](#) - Structural Classification Of Proteins
[SWISS-2DPAGE](#)
[SWISS-PROT](#) - the protein sequence data bank
[The Homeodomain Resource](#)
[TIGRFAMs](#) - a protein family resource for the functional identification of proteins
[trEMBL](#) - EMBL protein-coding DNA sequence features translated into peptide sequences
[UniProt](#) - the Universal Protein knowledgebase

Молекулярно-биологические базы данных

ОБЪЕДИНЕННЫЙ ЦЕНТР ВЫЧИСЛИТЕЛЬНОЙ БИОЛОГИИ И БИОИНФОРМАТИКИ



Карта сайта

Заглавная | Научный Совет | Кластер | Проекты | Базы данных | Ссылки | Объявления | Контакты

Молекулярно-биологические базы данных

По алфавиту	ДНК	РНК	Белки	Метаболические пути	Библиография	Прочие
-------------	-----	-----	-------	---------------------	--------------	--------

ENZYME - ENZYME nomenclature database

Bairoch A. (1994) *Nucl. Acids Res.* 22, 3020-3027
 Bairoch A. (1999) *Nucl. Acids Res.* 27, 310-311
 Bairoch A. (2000) *Nucl. Acids Res.* 2000, Vol. 28, 304-305.

ENZYME - хранилище информации, касающейся номенклатуры ферментов. В первую очередь она основана на рекомендациях номенклатурного комитета IUBMB (Nomenclature Committee of the International Union of Biochemistry and Molecular Biology) и описывает все типы энзимов, которым присвоен номер EC (Enzyme Commission). Поиск в базе реализован по ЕС-номеру, классам ферментов, по химическим компонентам, по описанию (рекомендованному или альтернативному имени), по кофакторам, по названиям болезней, связанных с ферментом. Версия 25.0, датированная июлем 1999 года и исправленная на 18.10.99 насчитывает 3705 единиц хранения. Автор базы - Dr. Amos Bairoch в Swiss Institute of Bioinformatics.

Адрес:
<http://www.expasy.ch/enzyme/>

Молекулярно-биологические базы данных

ОБЪЕДИНЕННЫЙ ЦЕНТР ВЫЧИСЛИТЕЛЬНОЙ БИОЛОГИИ И БИОИНФОРМАТИКИ



| [Заглавная](#) | [Научный Совет](#) | [Кластер](#) | [Проекты](#) | [Базы данных](#) | [Ссылки](#) | [Объявления](#) | [Контакты](#) |

Молекулярно-биологические базы данных

[По алфавиту](#) | [ДНК](#) | [РНК](#) | [Белки](#) | [Метаболические пути](#) | [Библиография](#) | [Прочие](#)

[BioCyc](#) - BioCyc Database collection
[BRITE](#) - Biomolecular Reaction Pathways fo Information Transfer and Expression database
[EcoCyc](#) - Encyclopedia of E.coli Genes and Metabolism
[EMP](#) - the Enzymes and Metabolic Pathways database
[KEGG](#) - Kyoto Encyclopedia of Genes and Genomes
[MetaCyc](#) - Database of metabolic pathways and enzymes
[MPW](#) - Metabolic PathWays database
[SoiBase](#) - Soybean metabolism dataBase
[SPAD](#) - Signaling PAthway Database
[UM-BBD](#) - University of Minnesota Biocatalysis/Biodegradation Database

Copyright 2001-2011 © Институт математических проблем биологии РАН

Можно использовать для построения метаболических моделей

NCBI Центр биотехнологической информации

<http://www.ncbi.nlm.nih.gov/>

англоязычный ресурс

The screenshot displays the NCBI (National Center for Biotechnology Information) homepage. At the top, there is a navigation bar with "NCBI", "Resources", and "How To" links. Below this, the NCBI logo and name are prominently displayed. A search bar is located in the upper right, with a dropdown menu currently open, showing a list of databases including "PubMed", "All Databases", "Protein", "Nucleotide", "GSS", "EST", "Structure", "Genome", "BioSample", "BioSystems", "Books", "CancerChromosomes", "Conserved Domains", "dbGaP", "dbVar", "Epigenomics", "Gene", "Genome Project", "GENSAT", and "GEO Datasets". The "PubMed" option in the dropdown is highlighted with a red circle. To the right of the search bar are "Search" and "Clear" buttons. On the left side, a vertical navigation menu lists various categories such as "NCBI Home", "Site Map (A-Z)", "All Resources", "Chemicals & Bioassays", "Data & Software", "DNA & RNA", "Domains & Structures", "Genes & Expression", "Genetics & Medicine", "Genomes & Maps", "Homology", "Literature", "Proteins", "Sequence Analysis", "Taxonomy", "Training & Tutorials", and "Variation". The main content area features a large banner with the text "NCBI" and "National Center for Biotechnology Information advances science and biomedical and genomic information." Below this, there are links for "Organization", "Research", and "RSS Feeds". To the right, a "Popular Resources" section lists various tools and databases, with "PubMed" highlighted by a red circle. Below this, an "NCBI News" section provides updates on new news issues and the retirement of certain archives. At the bottom, an "Education Resources" section offers help documents, teaching materials, and news outlets, accompanied by a small image of a person using a computer. A pagination bar at the very bottom shows the current page as 2 out of 5.

NCBI Resources How To

NCBI
National Center for
Biotechnology Information

Search PubMed
All Databases
PubMed
Protein
Nucleotide
GSS
EST
Structure
Genome
BioSample
BioSystems
Books
CancerChromosomes
Conserved Domains
dbGaP
dbVar
Epigenomics
Gene
Genome Project
GENSAT
GEO Datasets

Search Clear

NCBI Home
Site Map (A-Z)
All Resources
Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation

NCBI
National Center for Biotechnology Information advances science and
biomedical and genomic information.
Organization | Research | RSS Feeds

Popular Resources

- BLAST
- Bookshelf
- Gene
- Genome
- Nucleotide
- OMIM
- Protein
- PubChem
- PubMed
- PubMed Central
- SNP

NCBI News

New NCBI News Issue
28 Mar 2011
Information about the new
PubMed Mobile and Bookshelf

Retirement of Peptidome, SRA &
Trace Archive
16 Feb 2011
Due to budget constraints, NCBI

Education Resources

Central point of access for help
documents, teaching materials, news
outlets, and other educational resources.

1 2 3 4 5

База данных по публикациям в биологии и медицине

<http://www.ncbi.nlm.nih.gov/pubmed/>

 NCBI [Resources](#) ☒ [How To](#) ☒

 PubMed.gov
U.S. National Library of Medicine
National Institutes of Health

Search: [Limits](#) [Advanced search](#) [Help](#)

My NCBI [Sign In](#)



PubMed

PubMed comprises more than 20 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

Using PubMed

[PubMed Quick Start Guide](#)

[Full Text Articles](#)

[PubMed FAQs](#)

[PubMed Tutorials](#)

[New and Noteworthy](#) 

PubMed Tools

[PubMed Mobile](#)

[Single Citation Matcher](#)

[Batch Citation Matcher](#)

[Clinical Queries](#)

[Topic-Specific Queries](#)

More Resources

[MeSH Database](#)

[Journals in NCBI Databases](#)

[Clinical Trials](#)

[E-Utilities](#)

[LinkOut](#)

База данных по публикациям в биологии и медицине

NCBI Resources ▾ How To ▾

PubMed.gov
U.S. National Library of Medicine
National Institutes of Health

Search: PubMed ▾

[RSS](#) [Save search](#) [Limits](#) [Advanced search](#) [Help](#)

metabolic pathway **Search** **Clear**

[Display Settings:](#) ☒ Summary, 20 per page, Sorted by Recently Added

[Send to:](#) ☐

Results: 1 to 20 of 81030

<< First < Prev Page **1** of 4052 Next > Last >>

☐ [Investigating the plant response to cadmium exposure by proteomic and metabolomic approaches.](#)

1. Villiers F, Ducruix C, Hugouvieux V, Jarno N, Ezan E, Garin J, Junot C, Bourguignon J.
Proteomics. 2011 Mar 8. doi: 10.1002/pmic.201000645. [Epub ahead of print]
PMID: 21462346 [PubMed - as supplied by publisher]
[Related citations](#)

☐ [Targeting phosphatidylinositol 3-kinase signaling with novel phosphatidylinositol 3,4,5-triphosphate antagonists.](#)

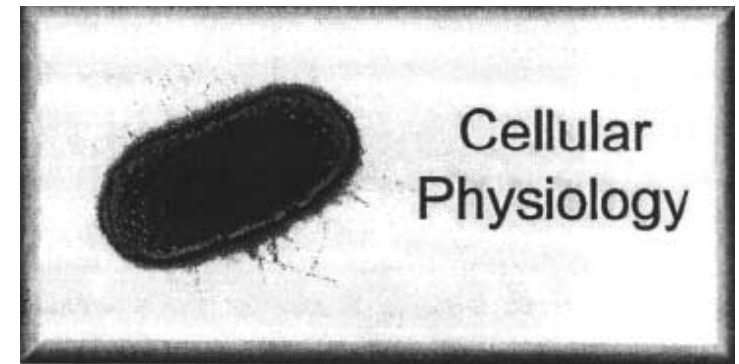
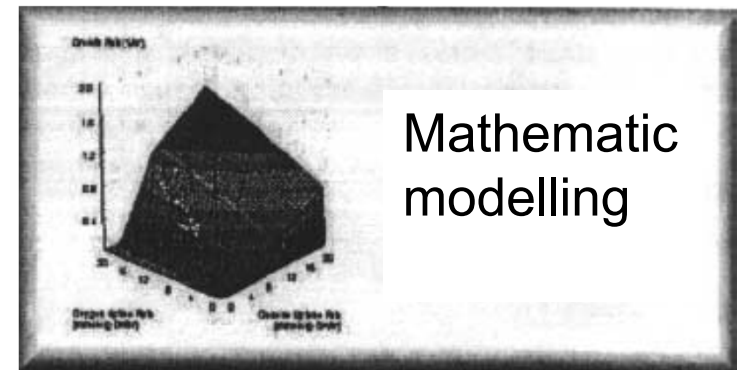
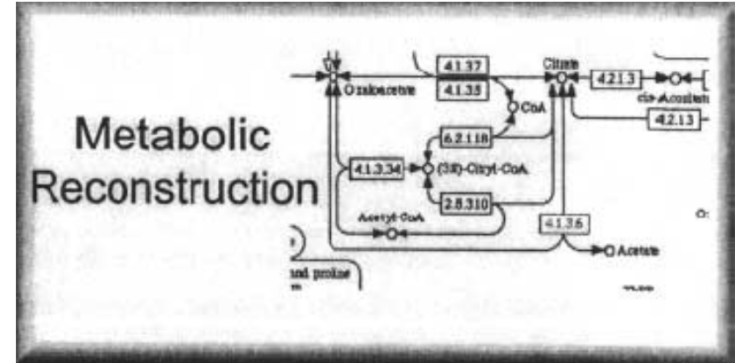
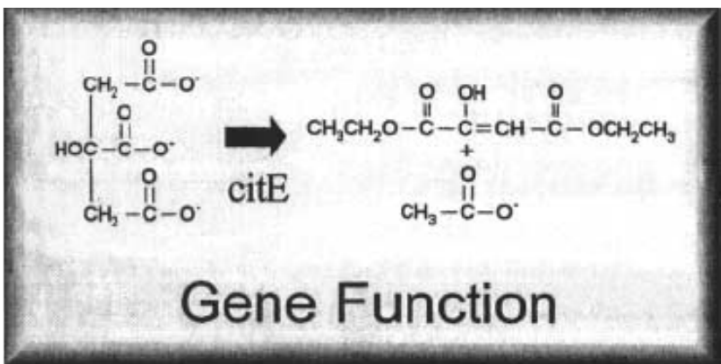
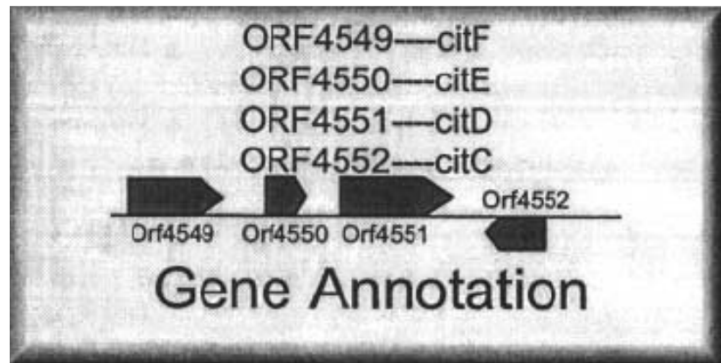
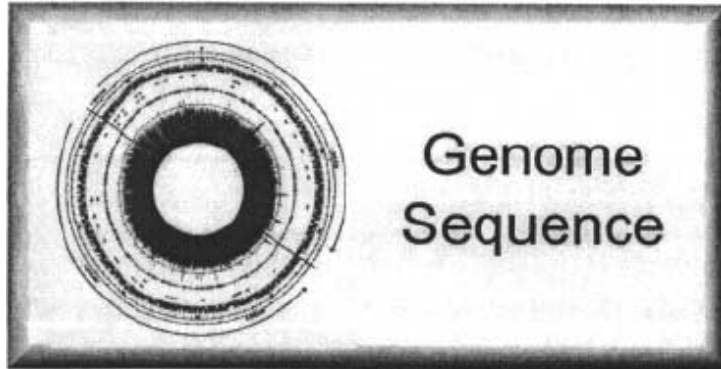
2. Miao B, Degterev A.
Autophagy. 2011 Jun 1;7(6). [Epub ahead of print]
PMID: 21460619 [PubMed - as supplied by publisher]
[Related citations](#)

☐ [eEF-2 kinase, another meddler in the "Yin and Yang" of Akt-mediated cell fate?](#)

3. Cheng Y, Yan L, Ren X, Yang JM.
Autophagy. 2011 Jun 1;7(6). [Epub ahead of print]
PMID: 21460616 [PubMed - as supplied by publisher]
[Related citations](#)

81030 ссылок на ключевые слова “metabolic pathway”

От генома до фенотипа



Пример аминокислотной последовательности

MAALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTNTNHGHILVDYSKNLV
TEDVMRMLVDLAKSRGVEAARERMFNGEKINYTEGRAVLHVALRNRSNTPILVDGKDVMMP
EVNKVLDKMKSFCQRVRSGDWKGYTGKTITDVINIGIGGSDDLGPLMVTEALKPYSSGGPR
VWYVSNIDGTHIAKTLAQLNPESSLFIIASKTFTTQETITNAETAKEWFLQAAKDPSAVA
KHFVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGA
HWMDQHFRTTPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDMESN
GKYITKSGTRVDHQTGPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPIRKGL
HHKILLANFLAQTEALMRGKSTEEARKELQAAGKSPEDLERLLPHKVFEGNRPTNSIVFT
KLTPFMLGALVAMYEHKIFVQGGIWDINSFDQWGVELGKQLAKKIEPELDGSAQVTSHDA
STNGLINFIKQQREARVQ

BLAST База данных по сравнению последовательностей

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

**BLAST**
Basic Local Alignment Search Tool

HomeRecent ResultsSaved StrategiesHelp

My NCBI
[Sign In] [Register]

NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)New Aligning Multiple Protein Sequences? Try the [COBALT Multiple Alignment Tool](#). [Go](#)

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

Human	Oryza sativa	Gallus gallus
Mouse	Bos taurus	Pan troglodytes
Rat	Danio rerio	Microbes
Arabidopsis thaliana	Drosophila melanogaster	Apis mellifera

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms: blastn, megablast, discontinuous megablast</i>
protein blast	Search protein database using a protein query <i>Algorithms: blastp, psi-blast, phi-blast</i>
blastx	Search protein database using a translated nucleotide query
tblastn	Search translated nucleotide database using a protein query
tblastx	Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with [Primer-BLAST](#)
- Search [trace archives](#)

Your Recent Results **New!**

- [Protein Sequence \(558 letters\)](#)
- [Protein Sequence \(60 letters\)](#)

News

[BLAST 2.2.25 release](#)

A new version of the stand-alone applications is available.
Thu, 24 Mar 2011 09:00:00 EST

[More BLAST news...](#)

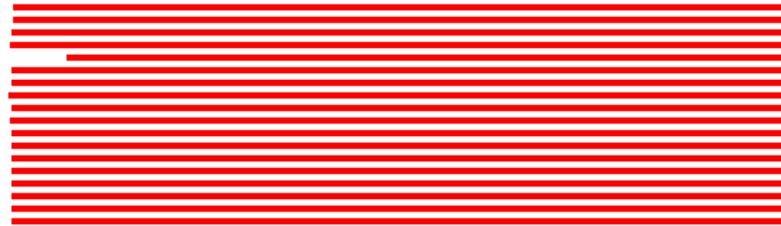
Tip of the Day

[How to do Batch BLAST jobs.](#)

BLAST makes it easy to examine a large group of potential gene candidates.

[More tips...](#)

BLAST База данных по сравнению последовательностей



▼ Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
AAP36518.1	Homo sapiens glucose phosphate isomerase [synthetic construct]	1169	1169	100%	0.0	
NP_000166.2	<u>glucose-6-phosphate isomerase</u> isoform 2 [Homo sapiens] >sp P06	1169	1169	100%	0.0	U G M
1JLH_A	Chain A, Human Glucose-6-Phosphate Isomerase >pdb 1JLH B Cha	1167	1167	100%	0.0	S
AAF22645.1	sperm antigen-36 [Homo sapiens]	1167	1167	100%	0.0	
1IAT_A	Chain A, Crystal Structure Of Human Phosphoglucose IsomeraseNE	1166	1166	99%	0.0	S
AAA36368.1	neuroleukin [Homo sapiens] >gb AAB36062.1 glucose phosphate i	1165	1165	100%	0.0	G
NP_001126984.1	glucose-6-phosphate isomerase [Pongo abelii] >sp Q5R4E3.3 G6PI	1158	1158	100%	0.0	G M
Q4R591.3	RecName: Full=Glucose-6-phosphate isomerase; Short=GPI; AltNar	1155	1155	100%	0.0	
NP_001075538.1	glucose-6-phosphate isomerase [Oryctolagus cuniculus] >sp Q9N1	1100	1100	100%	0.0	U G M
NP_999495.1	glucose-6-phosphate isomerase [Sus scrofa] >sp P08059.3 G6PI_I	1099	1099	100%	0.0	U G M
1N8T_A	Chain A, The Crystal Structure Of Phosphoglucose Isomerase From	1098	1098	99%	0.0	S
1G98_A	Chain A, Crystal Structure Analysis Of Rabbit Phosphoglucose Isom	1098	1098	100%	0.0	S P
1GZD_A	Chain A, Crystal Structure Of Pig Phosphoglucose Isomerase >pdb	1098	1098	99%	0.0	S P
NP_001171651.1	glucose-6-phosphate isomerase isoform 1 [Homo sapiens] >dbj BA	1097	1097	100%	0.0	U G M
BAG56947.1	unnamed protein product [Homo sapiens]	1096	1096	100%	0.0	G

Определили фермент, соответствующий выбранной последовательности:
glucose-6-phosphate isomerase

Базы данных по метаболическим путям

KEGG Pathway Database:

<http://www.genome.jp/kegg/pathway.html>

MetaCyc:

<http://metacyc.org/>

KEGG База данных по метаболическим путям



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions, and relations

KEGG2 PATHWAY BRITE MODULE DISEASE DRUG GENES GENOME LIGAND DBGET

Select prefix

map

Organism

Enter keywords

Go

[Help](#)

Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps (see [new maps](#), [change history](#), and [last updates](#)) representing our knowledge on the molecular interaction and reaction networks for:

0. Global Map

1. Metabolism

[Carbohydrate](#) [Energy](#) [Lipid](#) [Nucleotide](#) [Amino acid](#) [Other amino acid](#) [Glycan](#)
[Cofactor/vitamin](#) [Terpenoid/PK](#) [Other secondary metabolite](#) [Xenobiotics](#) [Overview](#)

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

6. Human Diseases

and also on the structure relationships (KEGG drug structure maps) in:

7. Drug Development

KEGG База данных по метаболическим путям



Search

ENZYME



for

glucose-6-phosphate isomerase

Go

Clear

Database: ENZYME - Search term: glucose-6-phosphate isomerase (Total 1 hit)

5.3.1.9

glucose-6-phosphate isomerase; phosphohexose isomerase; phosphohexomutase; oxoisomerase;
hexosephosphate isomerase; phosphosaccharomutase; phosphoglucoisomerase;
phosphohexoisomerase; phosphoglucose isomerase; glucose phosphate isomerase; hexose pho • • •

DBGET integrated database retrieval system

KEGG База данных по метаболическим путям



ENZYME: 5.3.1.9

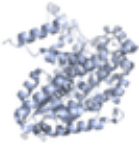
Help

Entry	EC 5.3.1.9 Enzyme
Name	glucose-6-phosphate isomerase; phosphohexose isomerase; phosphohexomutase; oxoisomerase; hexosephosphate isomerase; phosphosaccharomutase; phosphoglucosomerase; phosphohexoisomerase; phosphoglucose isomerase; glucose phosphate isomerase; hexose phosphate isomerase; D-glucose-6-phosphate ketol-isomerase
Class	Isomerases; Intramolecular oxidoreductases; Interconverting aldoses and ketoses, and related compounds BRITE hierarchy
Sysname	D-glucose-6-phosphate aldose-ketose-isomerase
Reaction(IUBMB)	D-glucose 6-phosphate = D-fructose 6-phosphate [RN:R00771]
Reaction(KEGG)	R00771 > R02740 R03321; (other) R02739 Show all
Substrate	D-glucose 6-phosphate [CPD:C00092]
Product	D-fructose 6-phosphate [CPD:C00085]
Comment	Also catalyses the anomerization of D-glucose 6-phosphate.
Pathway	ec00010 Glycolysis / Gluconeogenesis ec00030 Pentose phosphate pathway ec00500 Starch and sucrose metabolism ec00520 Amino sugar and nucleotide sugar metabolism ec01100 Metabolic pathways ec01110 Biosynthesis of secondary metabolites ec01120 Microbial metabolism in diverse environments
Orthology	K01810 glucose-6-phosphate isomerase K06859 glucose-6-phosphate isomerase, archaeal K13810 transaldolase / glucose-6-phosphate isomerase
Genes	HS: 2821(GPI) PTR: 455941(GPI) PON: 100174006(GPI) MCC: 717980

All links

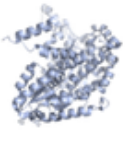
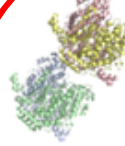
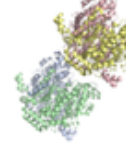
[Ontology \(5\)](#)
 [KEGG BRITE \(5\)](#)
[Pathway \(8421\)](#)
 [KEGG PATHWAY \(5587\)](#)
 [KEGG MODULE \(2834\)](#)
[Disease \(1\)](#)
 [OMIM \(1\)](#)
[Chemical substance \(5\)](#)
 [KEGG COMPOUND \(5\)](#)
[Chemical reaction \(14\)](#)
 [KEGG ENZYME \(1\)](#)
 [KEGG REACTION \(5\)](#)
 [KEGG RPAIR \(4\)](#)
 [KEGG RCLASS \(4\)](#)
[Genome \(3\)](#)
 [KEGG GENOME \(3\)](#)
[Gene \(2209\)](#)
 [KEGG ORTHOLOGY \(3\)](#)
 [KEGG GENES \(1494\)](#)
 [KEGG DGENES \(27\)](#)
 [KEGG EGENES \(450\)](#)
 [KEGG MGENES \(235\)](#)
[Protein sequence \(6112\)](#)
 [UniProt \(3930\)](#)
 [PRF \(180\)](#)
 [RefSeq\(pep\) \(1868\)](#)
 [PDBSTR \(126\)](#)
 [PMD \(8\)](#)
[DNA sequence \(4921\)](#)
 [RefSeq\(nuc\) \(1843\)](#)
 [GenBank \(1541\)](#)
 [EMBL \(1537\)](#)
[3D Structure \(64\)](#)
 [PDB \(64\)](#)
[Protein domain \(11\)](#)
 [InterPro \(7\)](#)
 [Pfam \(3\)](#)
 [PROSITE\(LOC\) \(1\)](#)
[Literature \(5\)](#)
 [PubMed \(5\)](#)
[Enzyme \(4\)](#)
 [BRENDA \(1\)](#)
 [EXPASY-ENZYME \(1\)](#)
 [EXPLORENZ \(1\)](#)
 [IUBMB \(1\)](#)
[All databases \(21775\)](#)

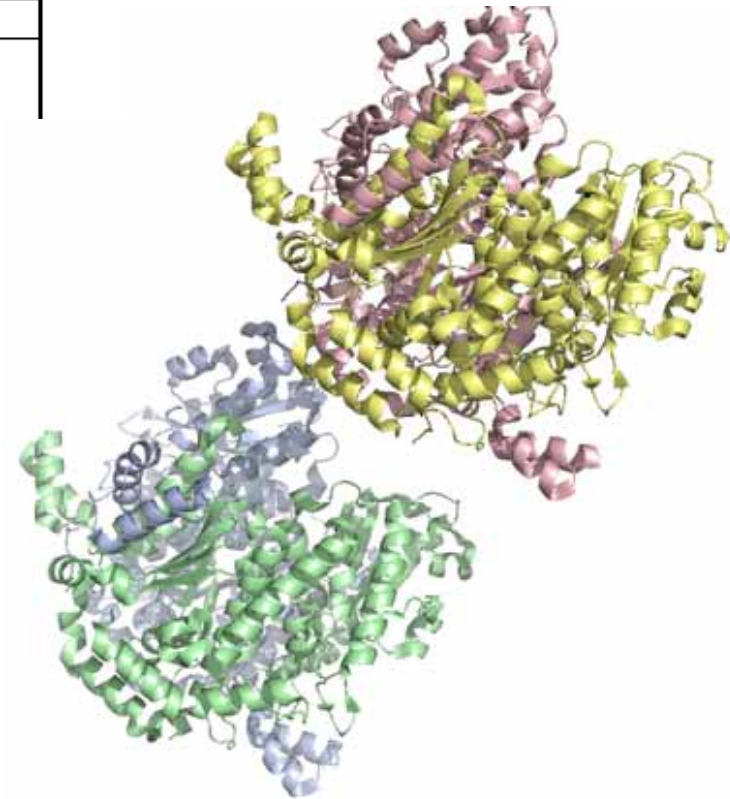
KEGG База данных по метаболическим путям

	HPRD: 01394 Ensembl: ENSG00000105220 UniProt: P06744 B4DG39
Structure	PDB: 1IAT 1JIQ 1JLH 1IRI 1NUH Thumbnails  Jmol
Position	19q13.1
AA seq	558 aa AA seq DB search MAALTRDPQFQKLQQWYREHRSEINLRRLFDANKDRFNHFSLTNTNHGHILVDYSKNLV



KEGG Homo sapiens (human) : 2821 5 PDB structures

 PDB:1IAT 1.62 Å SO4 BME Jmol	 PDB:1JIQ 1.90 Å Jmol	 PDB:1JLH 2.10 Å Jmol	 PDB:1IRI 2.40 Å E4P Jmol	 PDB:1NUH 2.51 Å SO4 PA5 Jmol
---	--	--	---	---



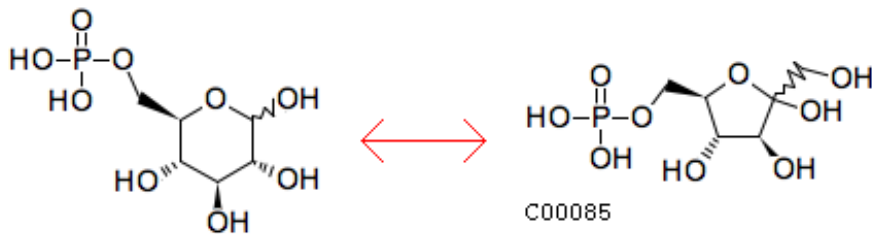
Определили структуру белка

KEGG База данных по метаболическим путям



REACTION: R00771

Help

Entry	R00771	Reaction
Name	D-glucose-6-phosphate aldose-ketose-isomerase	
Definition	D-Glucose 6-phosphate <=> D-Fructose 6-phosphate	
Equation	C00092 <=> C00085	
	 C00092	
RPair	RP01093 C00085_C00092 main	
Enzyme	5.3.1.9	

All links

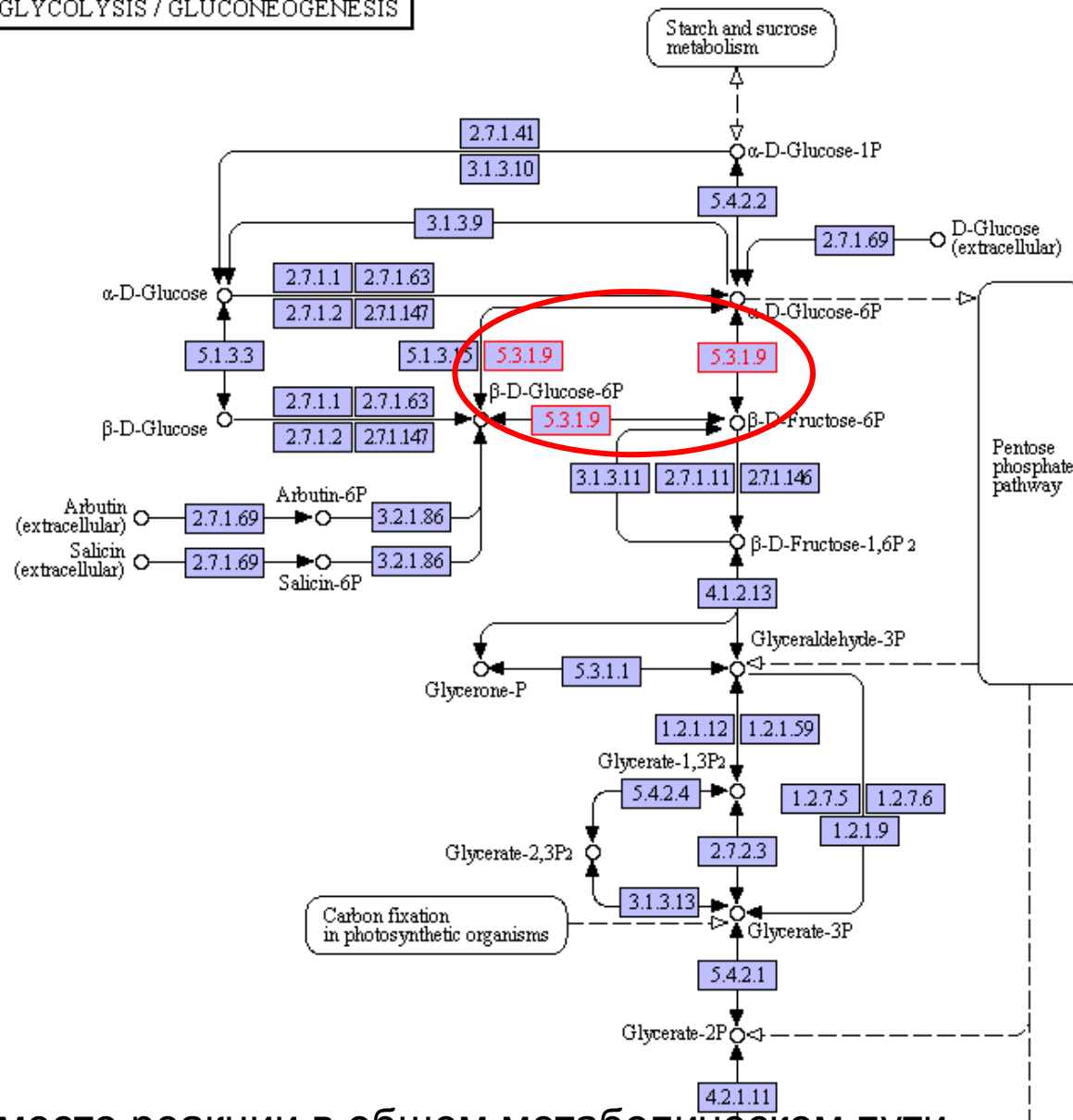
Ontology (2)
KEGG BRITE (2)
Chemical substance (2)
KEGG COMPOUND (2)
Chemical reaction (3)
KEGG ENZYME (1)
KEGG RPAIR (1)
KEGG RCLASS (1)
All databases (7)

DBGET integrated database retrieval system

Определили метаболическую реакцию

KEGG База данных по метаболическим путям

GLYCOLYSIS / GLUCONEOGENESIS



Определили место реакции в общем метаболическом пути

MetaCyc База данных по метаболическим путям



[Pathway Tools Tutorial](#)
[April 25 - 27, 2011](#)
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	Quick Search	Gene Search
Searching <i>MetaCyc</i> change organism database		

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METACYC OVERVIEW

MetaCyc is a database of nonredundant, experimentally elucidated metabolic pathways. MetaCyc contains more than 1670 pathways from more than 2100 different organisms [\[more\]](#), and is curated from the scientific experimental literature. [\[more\]](#)

MetaCyc contains pathways involved in both primary [\[def\]](#) and secondary [\[def\]](#) metabolism, as well as associated compounds, enzymes, and genes. [\[more\]](#)

Motivations

The goal of MetaCyc is to catalog the universe of metabolism by storing a representative sample of each experimentally elucidated pathway. [\[MetaCyc mission\]](#)

MetaCyc is used in a variety of scientific applications, such as providing a reference data set for computationally predicting the metabolic pathways of organisms from their sequenced genomes, supporting metabolic engineering, helping to compare biochemical networks, and serving as an encyclopedia of metabolism. [\[scientific applications\]](#)

Recent Publication

- [The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases](#), *Nucleic Acids Research* 38:D473-D479 2010.

Query and Visualization

MetaCyc pathways can be browsed from a list, from ontologies [\[def\]](#), or queried directly when searching for pathways, proteins, reactions or compounds. [\[more\]](#) MetaCyc can also be queried programmatically using [Java](#) or [PERL](#) when installed locally. [\[more\]](#)

New Users

Get a bird's eye view of the MetaCyc web site [here](#).

MetaCyc База данных по метаболическим путям

Search Results for **glucose-6-phosphate isomerase** using database *MetaCyc* [what is this?](#)

[Proteins](#) (12) | [Gene Ontology Terms](#) (1) | [Reactions](#) (1)

Proteins Gene/Gene Product pages contain: chromosomal location of gene; depiction of its operon; link to genome browser; detailed summaries and citations; subunit structure (for protein complexes); cofactors, activators, and inhibitors (for enzymes), depiction of regulon (for transcriptional regulators), protein features.

- [glucose 6-phosphate isomerase - *Mycoplasma pneumoniae*](#)
- [glucose-6-phosphate isomerase - *Bifidobacterium bifidum*](#)
- [glucose-6-phosphate isomerase - *Lactobacillus fermentum*](#)
- [glucose-6-phosphate isomerase - *Lactococcus lactis*](#)
- [glucose-6-phosphate isomerase - *Pisum sativum* \(polypeptide\)](#)
- [glucose-6-phosphate isomerase - *Pisum sativum* \(protein complex\)](#)
- [glucose-6-phosphate isomerase - *Saccharomyces cerevisiae*](#)
- [glucose-6-phosphate isomerase - *Spinacia oleracea*](#)
- [glucose-6-phosphate isomerase - *Thermotoga maritima*](#)
- [glucosamine-6-phosphate deaminase \(2-amino-2-deoxy-D-glucose-6-phosphate ketol isomerase \(deaminating\)\) - *Escherichia coli*](#)
- [phosphoglucose isomerase \(*glucose-6-phosphate isomerase*\) - *Escherichia coli*](#)
- [phosphoglucose isomerase \(*glucose-6-phosphate isomerase*\) - *Pyrococcus furiosus*](#)

Gene Ontology Terms GO term pages contain: Parent and child terms, and lists of matching gene products. Note that only those terms that have one or more associated genes in the selected organism (or that have children with one or more associated genes) are listed.

Molecular Function

- [Class: GO:0004347 - glucose-6-phosphate isomerase activity](#)

Reactions Reaction pages contain: reaction equation with chemical structures, links to all enzymes that catalyze the reaction, and all pathways in which the reaction participates.

- [8-D-glucose-6-phosphate = D-fructose-6-phosphate \(*glucose-6-phosphate isomerase*\)](#)

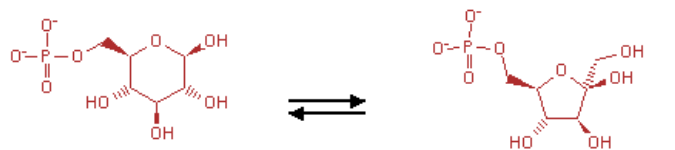
Alternative searches:

- [Full text search](#) for glucose-6-phosphate isomerase on all pages in this database using [Google](#)

Определили реакцию

MetaСус База данных по метаболическим путям

In Pathway: [sorbitol biosynthesis I](#), [starch biosynthesis](#), [sucrose degradation IV](#), [sucrose degradation III](#), [heterolactic fermentation](#), [gluconeogenesis I](#), [formaldehyde oxidation I](#), [glycolysis V \(Pyrococcus\)](#), [glycolysis III](#), [glycolysis I](#), [GDP-mannose biosynthesis](#), [Bifidobacterium shunt](#), [homolactic fermentation](#), [mannitol cycle](#), [gluconeogenesis II \(Methanobacterium thermoautotrophicum\)](#)



β -D-glucose-6-phosphate

D-fructose-6-phosphate

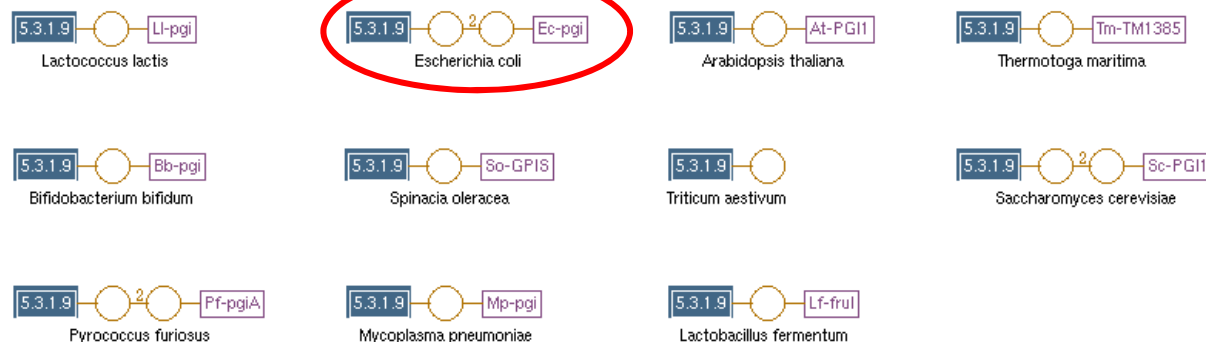
The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the Enzyme Commission system.

Enzyme Commission Primary Name for this Reaction: glucose-6-phosphate isomerase

Enzyme Commission Synonyms for this Reaction: phosphohexose isomerase, phosphohexomutase, oxoisomerase, hexosephosphate isomerase, phosphosaccharomutase, phosphoglucoisomerase, phosphohexoisomerase, phosphoglucose isomerase, glucose phosphate isomerase, hexose phosphate isomerase, D-glucose-6-phosphate ketol-isomerase

ΔG° (kcal/mol): 0.4 KCAL/MOLE [[Stryer88](#)]

Gene-Reaction Schematic:



Unification Links: [BRENDA:5.3.1.9](#), [ENZYME:5.3.1.9](#), [ExplorEnz:5.3.1.9](#), [KEGG:R00771](#)

Relationship Links: [UniProt:RELATED-TO:O25781](#), [UniProt:RELATED-TO:O61113](#), [UniProt:RELATED-TO:O82058](#), [UniProt:RELATED-TO:O82059](#), [UniProt:RELATED-TO:O83488](#), [UniProt:RELATED-TO:O84382](#), [UniProt:RELATED-TO:P06744](#), [UniProt:RELATED-TO:P06745](#), [UniProt:RELATED-TO:P08059](#), [UniProt:RELATED-TO:P0A6T1](#), [UniProt:RELATED-TO:P12341](#), [UniProt:RELATED-TO:P12709](#), [UniProt:RELATED-TO:P13375](#), [UniProt:RELATED-TO:P13376](#), [UniProt:RELATED-TO:P13377](#), [UniProt:RELATED-TO:P18240](#), [UniProt:RELATED-TO:P28718](#), [UniProt:RELATED-TO:P29333](#), [UniProt:RELATED-TO:P34796](#), [UniProt:RELATED-TO:P34797](#), [UniProt:RELATED-TO:P42862](#), [UniProt:RELATED-TO:P42863](#), [UniProt:RELATED-TO:P49105](#), [UniProt:RELATED-TO:P50309](#), [UniProt:RELATED-TO:P52983](#), [UniProt:RELATED-TO:P54240](#), [UniProt:RELATED-TO:P54242](#), [UniProt:RELATED-TO:P78033](#), [UniProt:RELATED-TO:P78917](#), [UniProt:RELATED-TO:P81181](#), [UniProt:RELATED-TO:Q7LZP0](#), [UniProt:RELATED-TO:Q9JSS6](#), [UniProt:RELATED-TO:Q9JTW1](#), [UniProt:RELATED-TO:Q9PMD4](#), [UniProt:RELATED-TO:Q9RMC1](#), [UniProt:RELATED-TO:Q9S857](#), [UniProt:RELATED-TO:Q9X670](#), [UniProt:RELATED-TO:Q59000](#), [UniProt:RELATED-TO:Q59088](#)

Выбрали интересующий организм

MetaСус База данных по метаболическим путям

Enzymatic reaction of: phosphoglucose isomerase

Synonyms: glucose-6-phosphate isomerase, D-glucose-6-phosphate-ketol-isomerase

[β-D-glucose-6-phosphate <=> D-fructose-6-phosphate](#)

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

This reaction is reversible. [[Ishii07](#)]

In Pathways: [gluconeogenesis I](#), [glycolysis I](#), [GDP-mannose biosynthesis](#)

Summary:

The equilibrium constant for the reaction is 0.30 [[Ishii07](#)].

Citations: [[Klungsoyr64](#)]

Inhibitors (Competitive): [phosphoenolpyruvate](#) [[Ogawa07](#)]

Inhibitors (Unknown Mechanism): [6-phospho-D-gluconate](#) [[Schreyer80](#)]

K_M for D-fructose-6-phosphate: 78 μM [[Ogawa07](#)]

K_M for β-D-glucose-6-phosphate: 1018 μM [[Ogawa07](#)]

$\text{pH}_{(\text{opt})}$: 8 [[Schreyer80](#)]

Определили кинетические константы для уравнения скорости для *E.coli*

MetaСус База данных по метаболическим путям

In Pathway: [sorbitol biosynthesis I](#), [starch biosynthesis](#), [sucrose degradation IV](#), [sucrose degradation III](#), [heterolactic fermentation](#), [gluconeogenesis I](#), [formaldehyde oxidation I](#), [glycolysis V \(Pyrococcus\)](#), [glycolysis III](#), [glycolysis I](#), [GDP-mannose biosynthesis](#), [Bifidobacterium shunt](#), [homolactic fermentation](#), [mannitol cycle](#), [gluconeogenesis II \(Methanobacterium thermoautotrophicum\)](#)



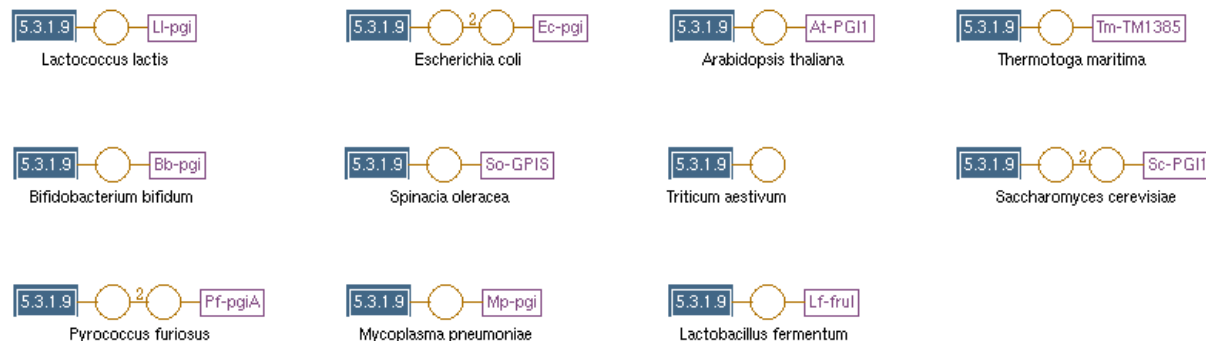
The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the Enzyme Commission system.

Enzyme Commission Primary Name for this Reaction: glucose-6-phosphate isomerase

Enzyme Commission Synonyms for this Reaction: phosphohexose isomerase, phosphohexomutase, oxoisomerase, hexosephosphate isomerase, phosphosaccharomutase, phosphoglucoisomerase, phosphohexoisomerase, phosphoglucose isomerase, glucose phosphate isomerase, hexose phosphate isomerase, D-glucose-6-phosphate ketol-isomerase

ΔG^0 (kcal/mol): 0.4 KCAL/MOLE [[Stryer88](#)]

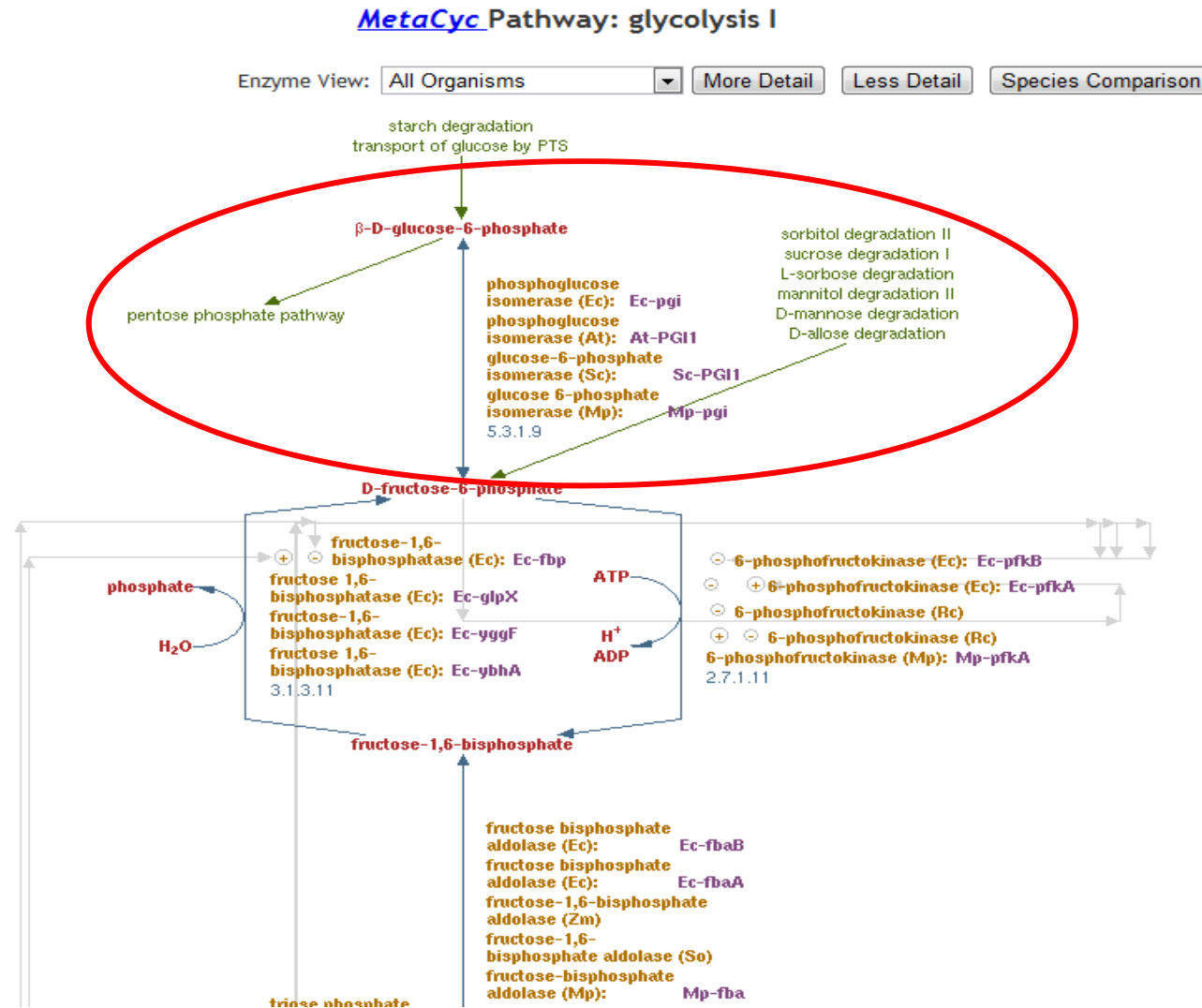
Gene-Reaction Schematic: [?](#)



Unification Links: [BRENDA:5.3.1.9](#), [ENZYME:5.3.1.9](#), [ExplorEnz:5.3.1.9](#), [KEGG:R00771](#)

Relationship Links: [UniProt:RELATED-TO:O25781](#), [UniProt:RELATED-TO:O61113](#), [UniProt:RELATED-TO:O82058](#), [UniProt:RELATED-TO:O82059](#), [UniProt:RELATED-TO:O83488](#), [UniProt:RELATED-TO:O84382](#), [UniProt:RELATED-TO:P06744](#), [UniProt:RELATED-TO:P06745](#), [UniProt:RELATED-TO:P08059](#), [UniProt:RELATED-TO:P0A6T1](#), [UniProt:RELATED-TO:P12341](#), [UniProt:RELATED-TO:P12709](#), [UniProt:RELATED-TO:P13375](#), [UniProt:RELATED-TO:P13376](#), [UniProt:RELATED-TO:P13377](#), [UniProt:RELATED-TO:P18240](#), [UniProt:RELATED-TO:P28718](#), [UniProt:RELATED-TO:P29333](#), [UniProt:RELATED-TO:P34796](#), [UniProt:RELATED-TO:P34797](#), [UniProt:RELATED-TO:P42862](#), [UniProt:RELATED-TO:P42863](#), [UniProt:RELATED-TO:P49105](#), [UniProt:RELATED-TO:P50309](#), [UniProt:RELATED-TO:P52983](#), [UniProt:RELATED-TO:P54240](#), [UniProt:RELATED-TO:P54242](#), [UniProt:RELATED-TO:P78033](#), [UniProt:RELATED-TO:P78917](#), [UniProt:RELATED-TO:P81181](#), [UniProt:RELATED-TO:Q7LZP0](#), [UniProt:RELATED-TO:Q9JSS6](#), [UniProt:RELATED-TO:Q9JTW1](#), [UniProt:RELATED-TO:Q9PMD4](#), [UniProt:RELATED-TO:Q9RMC1](#), [UniProt:RELATED-TO:Q9S857](#), [UniProt:RELATED-TO:Q9X670](#), [UniProt:RELATED-TO:Q59000](#), [UniProt:RELATED-TO:Q59088](#)

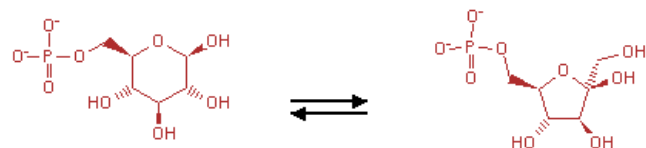
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Определили место реакции в метаболическом пути

MetaСус База данных по метаболическим путям

In Pathway: [sorbitol biosynthesis I](#), [starch biosynthesis](#), [sucrose degradation IV](#), [sucrose degradation III](#), [heterolactic fermentation](#), [gluconeogenesis I](#), [formaldehyde oxidation I](#), [glycolysis V \(Pyrococcus\)](#), [glycolysis III](#), [glycolysis I](#), [GDP-mannose biosynthesis](#), [Bifidobacterium shunt](#), [homolactic fermentation](#), [mannitol cycle](#), [gluconeogenesis II \(Methanobacterium thermoautotrophicum\)](#)



β -D-glucose-6-phosphate

D-fructose-6-phosphate

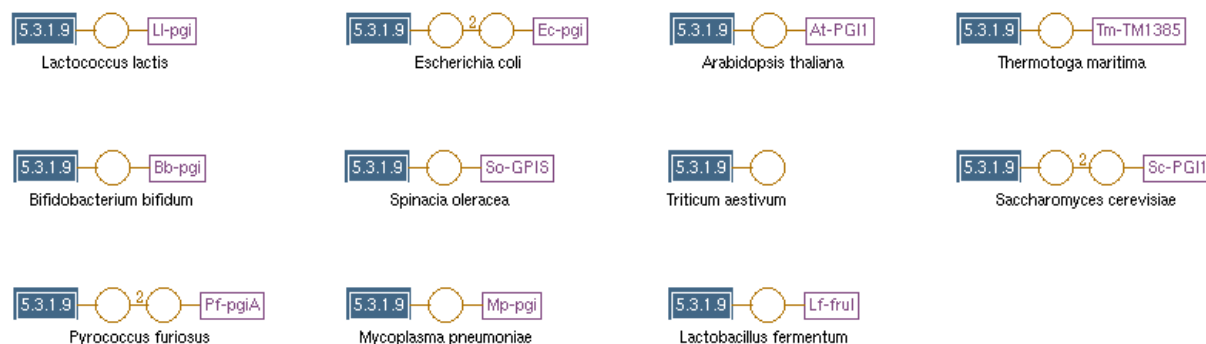
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ΔG^0 (kcal/mol): 0.4 KCAL/MOLE [[Stryer88](#)]

Gene-Reaction Schematic:



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BRENDA База данных по белкам

<http://www.brenda-enzymes.info/index.php4>

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Enzyme Nomenclature
EC number
Recommended Name
Reaction
Reaction Type
Pathway
Systematic Name
Synonyms
CAS Registry Number
Enzyme-Ligand Interactions
Substrate/Product
Natural Substrates
Cofactor
Metals and Ions
Inhibitors
Activating Compound
Functional Parameters
KM Value
Turnover Number
kcat/KM Value
KI Value
IC50 Value
Specific Activity
pH Optimum
pH Range
Temperature Optimum
Temperature Range
pI Value
Organism related Information
Source Tissue
Localization
Organism
General Information
Enzyme Structure
AA Sequence
PDB and Structure Links
Molecular Weight
Subunits
Posttranslational Modification

 BRENDA
The Comprehensive Enzyme Information System
EC 5.3.1.9 - Glucose-6-phosphate isomerase

Information on EC 5.3.1.9 - Glucose-6-phosphate isomerase:

Mark a special word or phrase in this record:

Select one or more organisms in this record:

All organisms
Aeropyrum pernix
Apis mellifera
Arabidopsis thaliana
Archaeoglobus fulgidus

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- ☒ Do not include text mining results
☐ Include **AMENDA** (text mining) results ^{new!} ([more...](#))
☐ Include **FRENDA** results ^{new!} (AMENDA + additional results, but less precise; [more...](#))

 [Please login to have access to the AMENDA and FRENDA data](#)

EC NUMBER	COMMENTARY
5.3.1.9	-

RECOMMENDED NAME	GeneOntology No.
Glucose-6-phosphate isomerase	GO:0004347

REACTION	REACTION DIAGRAM	COMMENTARY	ORGANISM	LITERATURE
D-Glucose 6-phosphate = D-fructose 6-phosphate		-	-	-
D-Glucose 6-phosphate = D-fructose 6-phosphate		push-pull mechanism of ring opening in which H388 breaks the O5-C1 bond by donating a proton, and simultaneously, K518 abstracts a proton from the C1 hydroxyl group	Mus musculus	662633
D-Glucose 6-phosphate = D-fructose 6-phosphate		mechanism is based on an enediol intermediate	Pyrococcus furiosus	662637
D-Glucose 6-phosphate = D-fructose 6-phosphate		multistep catalytic mechanism, model including catalytically active amino acids	Oryctolagus cuniculus	663346

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[Unreleased Entries](#)
[Browse Database](#)
[Histograms](#)

Explorer:

Last Structure: 1IAT

Summary

Sequence

Annotations

Seq. Similarity

3D Similarity

Literature

Biol. & Chem.

Methods

Geometry

Links

CRYSTAL STRUCTURE OF HUMAN PHOSPHOGLUCOSE ISOMERASE/NEUROLEUKIN/AUTOCRINE MOTILITY FACTOR/MATURATION FACTOR

DOI:10.2210/pdb1iat/pdb

1IAT

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Primary Citation

The crystal structure of human phosphoglucose isomerase at 1.6 Å resolution: implications for catalytic mechanism, cytokine activity and haemolytic anaemia.

Read, J. , Pearce, J. , Li, X. , Muirhead, H. , Chirgwin, J. , Davies, C. 

Journal: (2001) J.Mol.Biol. 309: 447-463

PubMed: 11371164 

DOI: 10.1006/jmbi.2001.4680 

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PubMed Abstract:

Phosphoglucose isomerase (PGI) is a multifunctional protein, which, inside the cell, functions as a housekeeping enzyme of glycolysis and gluconeogenesis and, outside the cell, exerts wholly unrelated cytokine properties. We have determined the structure of human PGI to a resolution...

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Molecular Description

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Classification: Isomerase 

Structure Weight: 63369.64

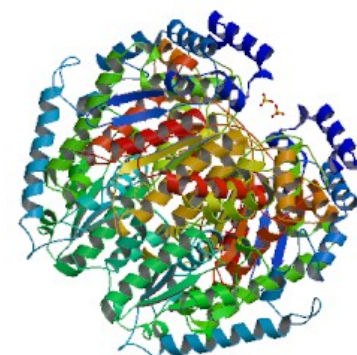
Molecule: PHOSPHOGLUCOSE ISOMERASE

Polymer: 1 Type: polypeptide(L)

Chains: A

Length: 557

Biological Assembly ?



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[Other Viewers](#) ▾

[Protein Workshop](#)

Biological assembly assigned by authors

PDB База данных по структуре белков

Read, J.¹, Pearce, J.², Li, X.³, Muirhead, H.², Chirgwin, J.², Davies, C.²
Journal: (2001) J.Mol.Biol. 309: 447-463
PubMed: 1137116
DOI: 10.1006/jmb.2001.2511
Search Related Articles

PubMed Abstract:
Phosphoglucose isomerase is a housekeeping enzyme with cytokine properties. [Read More & See Full Text]

Classification:
Structure Weight:
Molecule: PHOSPHOGLUCOSE ISOMERASE/NEUROLEUKIN/AUTOCRINE MOTILITY FACTOR/MATURATION FACTOR
Polymer: 1
Chains: A
EC#: 5.3.1.9

Source:
Polymer: 1
Scientific Name: Homo sapiens

Related PDB Entries:
Id: 1DQR

Ligand Chemical:
Identifier: BME
Formula: C_2H_5OS
Name: BETA-MERCAPTOETHANOL
Interactions: [Ligand Explorer](#)

Biological Assembly Image for 1IAT
CRYSTAL STRUCTURE OF HUMAN PHOSPHOGLUCOSE ISOMERASE/NEUROLEUKIN/AUTOCRINE MOTILITY FACTOR/MATURATION FACTOR
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Other Viewers
Biological assembly as

MyPDB Personal
To save personal annotations, login to your MyPDB account

Deposition Summary
Authors: Read, J.A., Pearce, J., Li, X., Muirhead, H., Chirgwin, J., Davies, C.
Deposition: 2001-01-01
Release: 2001-01-01
Last Modified (REVDAT): 2001-01-01

Experimental Data
Method: X-RAY DIFFRACTION
Exp. Data: 2.00 Å
[Structure Factors](#)
[EDS](#)

BRENDA База данных по белкам

metals and ions							
Inhibitors							
Activating Compound							
Functional Parameters							
KM Value	0.031	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant S278L	702456	● 2D-image
Turnover Number	0.034	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant I525T	702456	● 2D-image
kcat/KM Value	0.037	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant wild-type enzyme	702456	● 2D-image
Ki Value	0.038	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant R347H; pH 7.5, 30°C, recombinant mutant R75G	702456	● 2D-image
IC50 Value	0.039	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant L487F	702456	● 2D-image
Specific Activity	0.04	-	D-fructose 6-phosphate	Methanocaldococcus jannaschii	50°C, pH 6.3	649517	● 2D-image
pH Optimum	0.045	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant A300P; pH 7.5, 30°C, recombinant mutant L339P	702456	● 2D-image
pH Range	0.046	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant R347C; pH 7.5, 30°C, recombinant mutant T375R	702456	● 2D-image
Temperature Optimum	0.05	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant E495K	702456	● 2D-image
Temperature Range	0.06	-	D-fructose 6-phosphate	Pyrobaculum aerophilum	pH 7.4, 80°C	661679	● 2D-image
pI Value	0.061	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant R83W	702456	● 2D-image
Organism related Information	0.063	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant T195I; pH 7.5, 30°C, recombinant mutant V101M	702456	● 2D-image
Source Tissue	0.068	-	D-fructose 6-phosphate	Homo sapiens	pH 7.5, 30°C, recombinant mutant R472H	702456	● 2D-image
Localization	0.147	-	D-fructose 6-phosphate	Escherichia coli	22°C, pH 7.4	661902	● 2D-image
Organism	0.2	-	D-fructose 6-phosphate	Thermoplasma acidophilum	80°C, pH 7.4	662220	● 2D-image
General Information	0.21	-	D-fructose 6-phosphate	Aeropyrum pernix	50°C, pH 7.4	662220	● 2D-image
Enzyme Structure	0.27	-	D-fructose 6-phosphate	Mycobacterium tuberculosis	pH 7.6, 25°C	682664	● 2D-image
AA Sequence							
PDB and Structure Links							
Molecular Weight							
Subunits							
Posttranslational Modification							
Crystallization							
Molecular Properties							
pH Stability							
Temperature Stability							
General Stability							
Organic Solvent Stability							
Oxidation Stability							
Storage Stability							
Purification							
Cloned							
Expression							

Определили кинетические константы для уравнения скорости

База данных по публикациям в биологии и медицине

Effects of inherited mutations on catalytic activity and structural stability of human glucose-6-phosphate isomerase expressed in *Escherichia coli*

Lin, H.; Kao, Y.; Chen, S.; Meng, M.; *Biochim. Biophys. Acta* 1794, 315-323 (2009)



Data extracted from this reference:

Cloned(Commentary)

Commentary Organism
expression of wild-type and mutant enzymes in *Escherichia coli* strain DF2145Homo sapiens

Engineering

Amino acid exchange	Commentary	Organism
A300P	the mutation may affect the folding efficiency of the enzyme protein, the mutant shows reduced expression level and barely detectable activity	Homo sapiens
E495K	the mutation may affect the folding efficiency of the enzyme protein, the mutant shows reduced expression level and barely detectable activity; the mutation weakens network bonding of the enzyme	Homo sapiens
H389R	the mutation at or near the active site highly affects the catalytic efficiency of the enzyme, the mutant shows barely detectable activity	Homo sapiens
I525T	the mutation decreases the enzyme tolerance to heat or SDS by mechanisms of decreasing packing efficiency; the mutation destabilizes the ternary structure of the enzyme	Homo sapiens

the mutation decreases the enzyme tolerance to heat or SDS by mechanisms of decreasing packing efficiency; the mutation may affect the folding efficiency of the enzyme protein, the mutant shows reduced expression level and barely detectable activity

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Biochim Biophys Acta. 2009 Feb;1794(2):315-23. Epub 2008 Nov 21.

Effects of inherited mutations on catalytic activity and structural stability of human glucose-6-phosphate isomerase expressed in *Escherichia coli*.

Lin HY, Kao YH, Chen ST, Meng M.

Graduate Institute of Biotechnology, National Chung Hsing University, Taichung, Taiwan 40227, Republic of China.

Abstract

Glucose-6-phosphate isomerase (GPI), a homodimeric enzyme, catalyzes the interconversion between glucose-6-phosphate and fructose-6-phosphate. In mammals, it can also act as an autocrine motility factor, neuroleukin, and maturation factor. Deficiency of the enzymatic activity in red blood cells causes nonspherocytic hemolytic anemia in human. To gain a more complete understanding of the molecular basis for the hemolytic anemia due to the GPI-deficiency, the wild-type enzyme and sixteen genetic variants were expressed in *Escherichia coli* and functionally characterized. Conclusions are as follows: (1) mutations usually have negative influences on catalytic parameters, particularly k_{cat} , as well as structure stability; (2) mutations at or close to the active site, including R273H, H389R, and S278L, cause great damage to the catalytic function, yet

Related citations

Erythrocyte pyruvate kinase- and glucose phosphate isomerase deficiency [Biophys Chem. 1997]

Expression and enzymatic characterization of human glucose phosphate isomerase deficiency [Blood Cells Mol Dis. 1998]

Molecular basis of neurological dysfunction coupled with haemolytic anaemia [Hum Genet. 1998]

Review Glucose-6-phosphate isomerase deficiency [Baillieres Best Pract Res Clin Haematol. 2000]

Review Red cell glycolytic enzyme disorders [Cardiovasc Hematol Disord Drug Targets. 2000]

Нашли ссылки на сходные публикации