

Pathway Databases

Shatakshi Kulkarni

Introduction

- ❑ Pathway databases are repositories of curated information about biological pathways, which are sequences of biochemical reactions and interactions that occur within cells or organisms.
- ❑ Facilitates research in molecular biology and biochemistry
- ❑ Databases:
 - 1) KEGG
 - 2) Reactome
 - 3) WikiPathway

KEGG

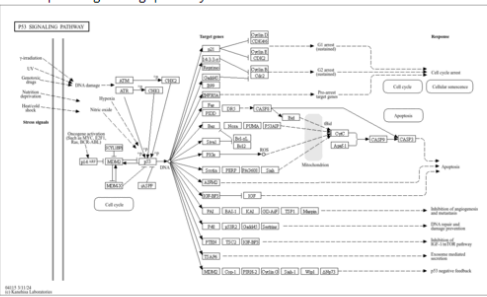
- ❑ <https://www.genome.jp/kegg/>
- ❑ The Kyoto Encyclopedia of Genes and Genomes (KEGG) collects individual genomes, gene products and their functions.
- ❑ It focuses on interactions: molecular assemblies, and metabolic and regulatory networks.
- ❑ KEGG organizes five types of data into a comprehensive system:
 1. Gene catalogues: information about particular molecules or sequences
 2. Genome maps
 3. Pathway maps: describe potential networks of molecular activities, both metabolic and regulatory. A metabolic pathway in KEGG is an idealization corresponding to a large number of possible metabolic cascades. It can generate a real metabolic pathway of a particular organism, by matching the proteins of that organism to enzymes within the reference pathways.
 4. Orthologue tables: One enzyme in one organism would be referred to in KEGG in its orthologue tables, which link the enzyme to related ones in other organisms. This permits analysis of relationships between the metabolic pathways of different organisms.

KEGG

- ❑ Searching the pathway catalogue for sets of enzymes that share a folding pattern will reveal clusters of paralogues.
- ❑ It can take the set of enzymes from some organism and check whether they can be integrated into known metabolic pathways. A gap in a pathway suggests a missing enzyme or an unexpected alternative pathway.

PATHWAY: map04115 [Help](#)

Entry	map04115	Pathway
Name	p53 signaling pathway	
Description	p53 activation is induced by a number of stress signals, including DNA damage, oxidative stress and activated oncogenes. The p53 protein is employed as a transcriptional activator of p53-regulated genes. This results in three major outputs; cell cycle arrest, cellular senescence or apoptosis. Other p53-regulated gene functions communicate with adjacent cells, repair the damaged DNA or set up positive and negative feedback loops that enhance or attenuate the functions of the p53 protein and integrate these stress responses with other signal transduction pathways.	
Class	Cellular Processes; Cell growth and death BRITE hierarchy	
Pathway map	map04115 p53 signaling pathway	



[Ortholog table](#)

All links

[Gene \(140110\)](#)
[KEGG ORTHOLOGY \(69\)](#)
[RefGene \(140841\)](#)
[Literature \(15\)](#)
[Pubmed \(15\)](#)
[All databases \(140125\)](#)
[Download RDF](#)

Ortholog table

Grp	Genus	Organism	K04728 (ATM) [393]	K06641 (CHEK2) [409]	K06640 (ATR) [399]	K02216 (CHEK1) [385]	K19748 (GORAB) [405]	K06621 (CDKN2A) [136]	K06643 (MDM2) [447]
E.Anim Homo	hsa	472	11200	545	1111	92344	1029	4193	
E.Anim Pan	ptr	451530	458733	460745	739836	469578	465021	742141	
E.Anim Pan	pps	100982830	100987687	100975153	100982317	100988290	100975637	100968756	

[Brite menu](#) | [Copy URL](#) | [Help](#)]

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Option

☐ One-click mode
☐ Row border ☐ shading
☒ Pruning neighbor

Search

ko04115 [Go](#) ✕

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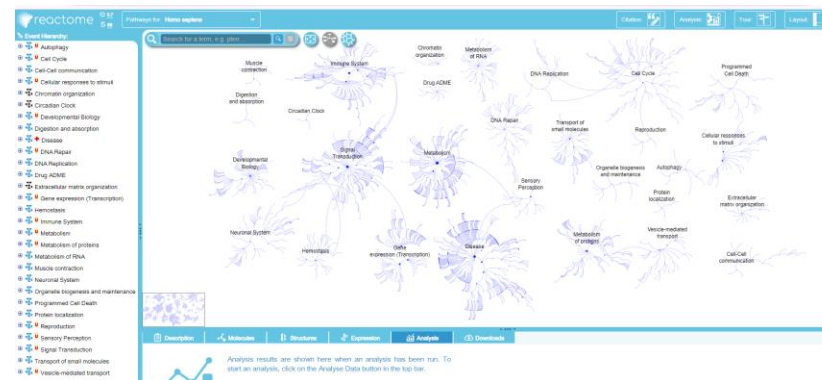
Join

[Go](#)

- 09100 Metabolism
- 09120 Genetic Information Processing
- 09130 Environmental Information Processing
- 09140 Cellular Processes
 - 09141 Transport and catabolism
 - 09143 Cell growth and death
 - 04110 Cell cycle [PATH:ko04110]
 - 04111 Cell cycle - yeast [PATH:ko04111]
 - 04112 Cell cycle - Caulobacter [PATH:ko04112]
 - 04113 Meiosis - yeast [PATH:ko04113]
 - 04114 Oocyte meiosis [PATH:ko04114]
 - 04210 Apoptosis [PATH:ko04210]
 - 04214 Apoptosis - fly [PATH:ko04214]
 - 04215 Apoptosis - multiple species [PATH:ko04215]
 - 04216 Ferroptosis [PATH:ko04216]
 - 04217 Necroptosis [PATH:ko04217]
 - 04115 p53 signaling pathway [PATH:ko04115]
 - 04218 Cellular senescence [PATH:ko04218]
- 09144 Cellular community - eukaryotes
- 09145 Cellular community - prokaryotes
- 09142 Cell motility
- 09150 Organismal Systems
- 09160 Human Diseases
- 09180 Brite Hierarchies
- 09190 Not Included in Pathway or Brite

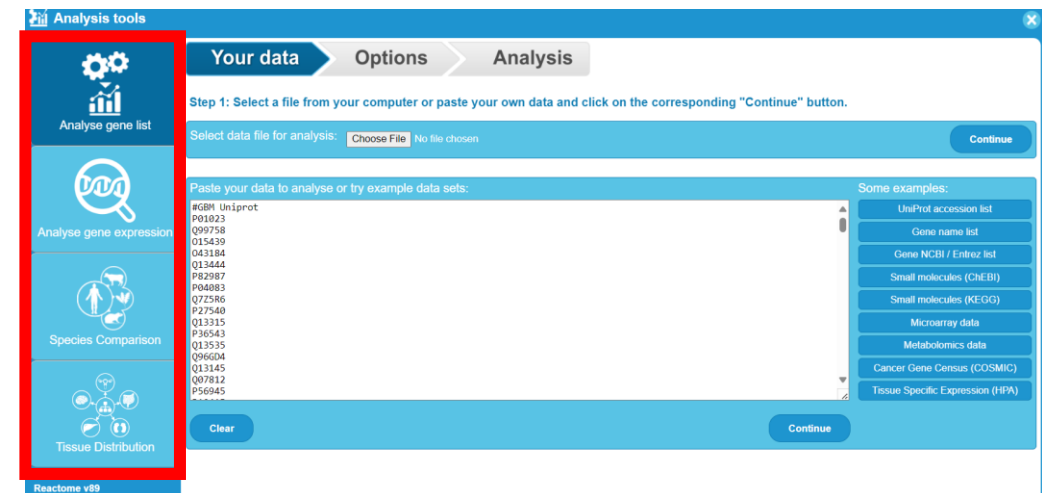
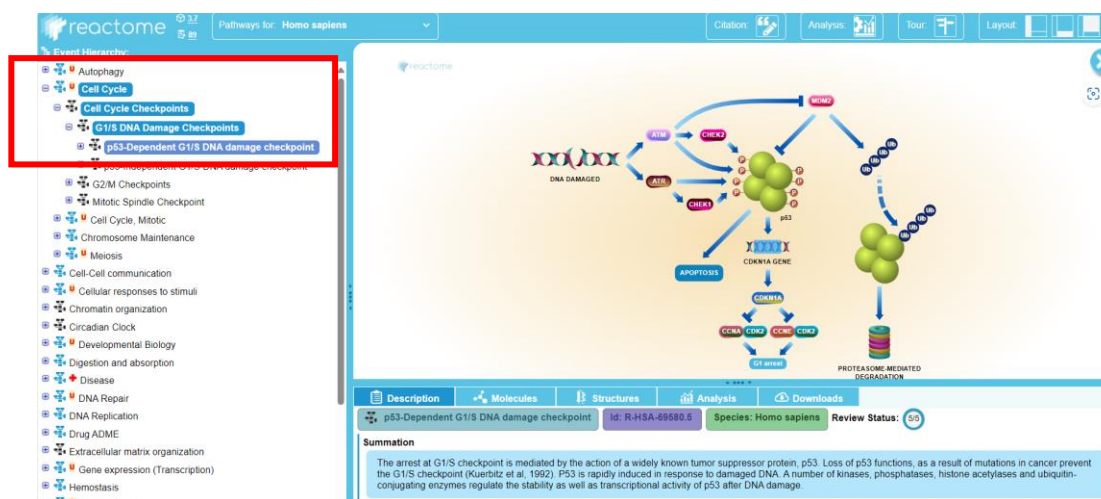
Reactome

- ❑ reactome.org
- ❑ Reactome is a curated, open-source database designed to provide a comprehensive resource for the exploration of molecular pathways and reactions in human biology.
- ❑ Contains a vast collection of pathways that represent various biological processes, such as metabolism, signal transduction, and the cell cycle.
- ❑ Offers insights into gene ontology and the molecular mechanisms driving biological functions
- ❑ Supports the comparison of pathways across different species
- ❑ Differential gene expression



Reactome

- ❑ Reactome database provides pathway browser and analysis tool
- ❑ In pathway browser, a hierarchy of pathways is provided which can be used to search for pathway of interest and to view the diagrammatic representation of pathway.
- ❑ The analysis tool helps in analyzing pathways related to a list of proteins/genes, compare pathways between different species and to view pathways in different human tissues based on RNA/Protein expression.

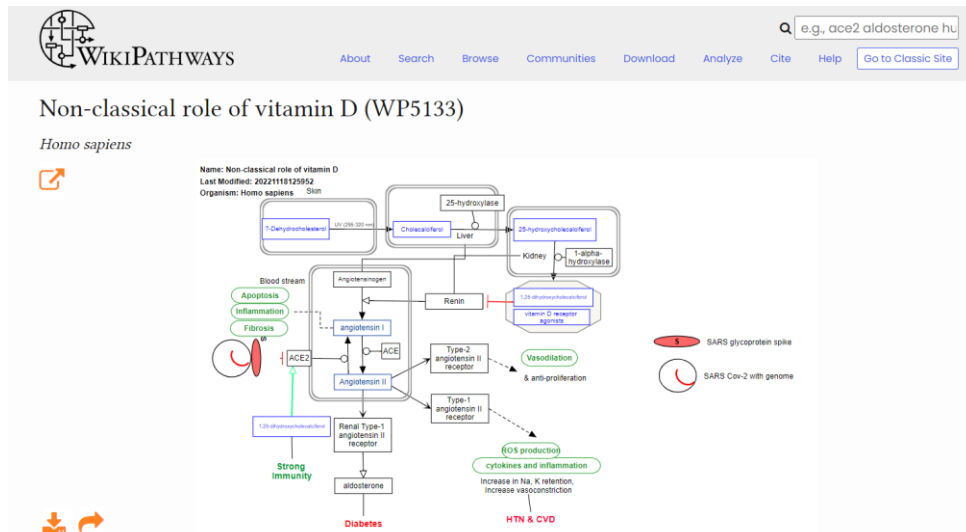


WikiPathways

- ❑ <https://www.wikipathways.org/>
- ❑ Wikipathways is a community-based resource dedicated to the collection and curation of biological pathways. It aims to facilitate the sharing and utilization of pathway knowledge by providing open and freely available content created by the research community.
- ❑ Molecular interactions, gene regulatory networks, and metabolic processes.
- ❑ Tools for visualizing and editing pathways are available, making it easier to understand complex biological interactions.
- ❑ Browse for gene, disease or biological processes
- ❑ Search by applying filter according to organisms, authors, disease/pathway ontology
- ❑ Detailed information about pathway, mechanism of particular biological activity
- ❑ Pathways can be downloaded in various formats such as GPML, PNG, or SVG for offline use and further analysis.
- ❑ PathVisio for data visualization and analysis. PathVisio can map your experimental data onto WikiPathways diagrams.
- ❑ Engage with the community by discussing pathways, suggesting edits, and collaborating on pathway curation.

WikiPathways

- ❑ Along with description of pathway, in which other disease mechanism pathways or metabolic pathways i.e., the ontologies it is involved in, can be studied in WikiPathways
- ❑ Participants in the pathway and literature references are also provided



Annotations

Pathway Ontology

vitamin D signaling pathway vitamin D metabolic pathway

Disease Ontology

hypertension diabetes mellitus COVID-19

Participants

Label	Type	Compact URI	Comment
aldosterone	Metabolite	wikidata:Q184564	
1,25-dihydroxycholecalciferol	Metabolite	chebi:17823	
vitamin D receptor agonists	Metabolite	chebi:139503	
25-hydroxycholecalciferol	Metabolite	chebi:17933	
angiotensin I	Metabolite	chebi:2718	

[more rows](#)

References

1. Vitamin D and its effects on cardiovascular diseases: a comprehensive review. Pérez-Hernández N, Aptilon-Duque G, Nostrza-Hernández MC, Vargas-Alarcón G, Rodríguez-Pérez JM, Blachman-Braun R. Korean J Intern Med. 2016 Nov;31(6):1018–29. [PubMed Europe PMC Scholia](#)
2. Vitamin D deficiency and diabetes. Berridge MJ. Biochem J. 2017 Mar 24;474(8):1321–32. [PubMed Europe PMC Scholia](#)
3. A brief review of interplay between vitamin D and angiotensin-converting enzyme 2: Implications for a potential treatment for COVID-19. Malek Mahdavi A. Rev Med Virol. 2020 Sep;30(5):e2119. [PubMed Europe PMC Scholia](#)
4. The angiotensin-converting enzyme 2 (ACE2) receptor in the prevention and treatment of COVID-19 are distinctly different paradigms. McLachlan CS. Clin Hypertens. 2020 Jul 15;26:14. [PubMed Europe PMC Scholia](#)

Application

- ❑ Understanding Biological Processes:

Provides detailed maps of molecular interactions and reactions within cells, tissues, or organisms.

- ❑ Disease Research and Biomarker Discovery:

Underlying mechanisms of diseases like cancer, cardiovascular diseases, and metabolic disorders.

- ❑ Drug Discovery and Development:

Target identification, drug mechanism

- ❑ Network Analysis:

Analyzes interactions and dependencies within biological networks to predict biological outcomes and responses to interventions.