

RNA-seq data.
Biological interpretation.

bio.tools <https://bio.tools/>

Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.



Communities in bio.tools

Explore **communities** in bio.tools and see what resources are used by different scientific communities.

Experts from scientific communities are key in identifying what are the methods and software resources used in their research activities. We rely upon scientific communities to improve the terminology and description of resources in different domains of the Life Sciences. This includes the **communities** being fostered by ELIXIR, and any other group of scientists with an interest to help out.

We strongly encourage everyone to take part in the community effort and contribute. [Email us](#) for more info.

Communities and domains

In bio.tools we try, with the help of the community, to create content domains or "slices" relevant to a specific community, research area or task (e.g. Proteomics, Rare diseases, COVID-19).

Explore and search bio.tools **domains** and **manage** your own domains. Read more about bio.tools domains [here](#).

What is bio.tools?

The use of bioinformatics is ubiquitous within the life sciences. In *bio.tools*, we are striving to provide a **comprehensive registry** of software and databases, facilitating researchers from across the spectrum of biological and biomedical science to **find, understand, utilise** and **cite** the resources they need in their day-to-day work.

Everything from simple command-line tools and online services, through to databases and complex, multi-functional analysis workflows is included. Resources are described in a rigorous semantics and syntax, providing end-users with the convenience of **concise, consistent** and therefore **comparable** information.

Each *bio.tools* entry is assigned a human-readable, **unique identifier** based on the resource name, e.g. **biotools:signalp**. These identifiers provide a persistent reference to our "Tool Cards" of essential information, as well as a means to trace resources and integrate *bio.tools* data with other resources.

All the *bio.tools* data and technical components are available under **open license** and we warmly welcome you to **get involved**. *bio.tools* development is supported by **ELIXIR** - the European infrastructure for life science information.



bio.tools is supported by ELIXIR through the ELIXIR-EXCELERATE grant, which is funded by the European Union Horizon 2020 program under grant agreement 676559.

Sequence analysis

Resources for the processing and analysis of [molecular sequences](#) including sequence editing and visualisation, molecular sequence [databases](#), [binding sites](#), [alignments](#) and [motifs](#) in nucleic acid and protein sequences.

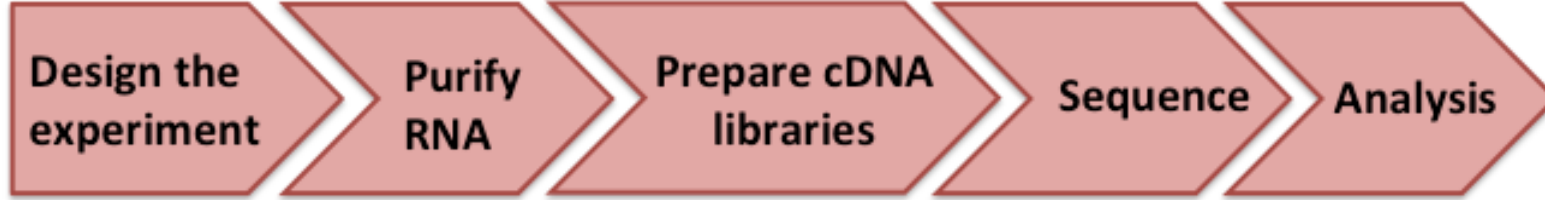
Sequence sites, features and motifs	▶	Sequence similarity search	▶
Sequence alignment	▶	Sequence motif recognition	▶
Sequence annotation	▶	Sequence visualisation	▶
Nucleic acid sequence analysis	▶	Nucleic acid feature detection	▶
Transcription factors and regulatory sites	▶	Protein sequence analysis	▶
Protein feature detection	▶	Sequence assembly	▶
Mapping	▶	Genome annotation	▶
PCR primer design	▶	Phylogenetics	▶

Genetics

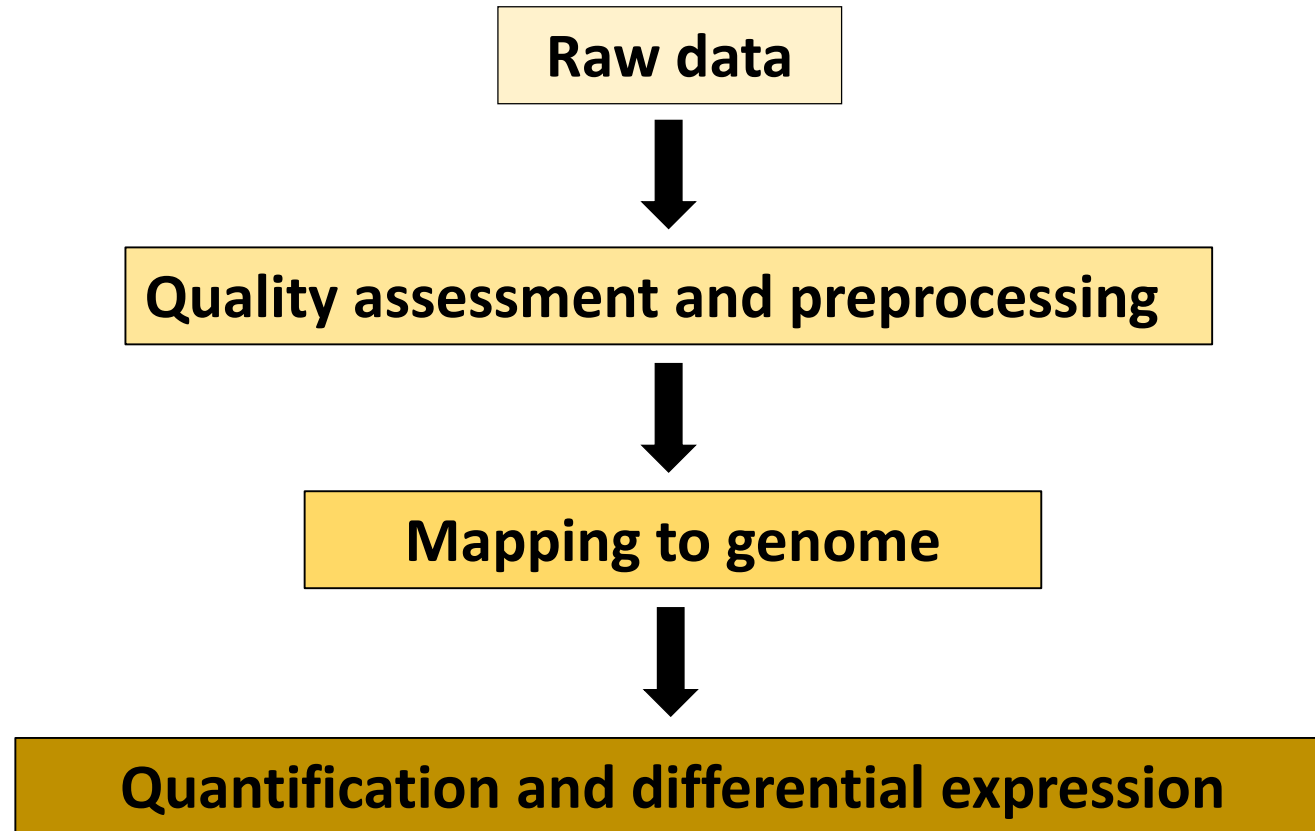
Resources for the study of [genes](#) and [heredity](#) in living organisms. They provide analytical approaches for studying [gene structure](#), [genetic variation](#), the [regulation of gene expression](#) and the relationships between organism [genotype](#) and [phenotype](#).

Genetics	▶	Gene expression	▶
Gene regulation	▶	Gene expression profiling	▶
Transcription factors and regulatory sites	▶	Functional, regulatory and non-coding RNA	▶
Genetic variation	▶	DNA polymorphism	▶
Genotyping	▶	Genotype and phenotype	▶
Population genetics	▶	Gene functional annotation	▶
Gene and protein families	▶	Gene prediction	▶
Enrichment analysis	▶	Genome visualisation	▶

RNA-seq data



Data analysis workflow





Search bio.tools

28190 tools

Explore ▾

Login

Sign-up

Sort by

Updated

Added

Name

Citation Count

Publication Date



Display as

Compact

Detailed



THE GENE ONTOLOGY RESOURCE

The mission of the GO Consortium is to develop a comprehensive, **computational model of biological systems**, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life.

The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research.

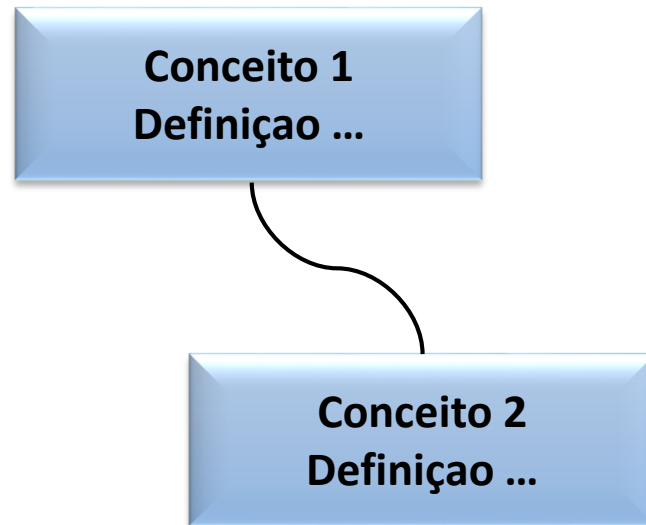


Any Ontology Gene Product

- O que é uma ontologia?
- O que é a ontologia GO?

- O que é a ontologia GO?

Uma ontologia é uma forma estruturada de conhecimento que fornece definições claras de conceitos e as relações entre eles.



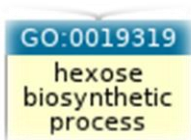
- O que é a ontologia GO?



biological_process

molecular_function

cellular_component



Term Information

Accession GO:0019319

Name hexose biosynthetic process

Ontology biological_process

Synonyms hexose anabolism, hexose biosynthesis, hexose formation, hexose synthesis

Alternate IDs None

Definition The chemical reactions and pathways resulting in the formation of hexose, any monosaccharide with a chain of six carbon atoms in the molecule. *Source:* [ISBN:0198506732](#)

Comment None


History See term [history for GO:0019319](#) at QuickGO

Subset None

Related [Link](#) to all **genes and gene products** annotated to hexose biosynthetic process (**excluding "regulates"**).

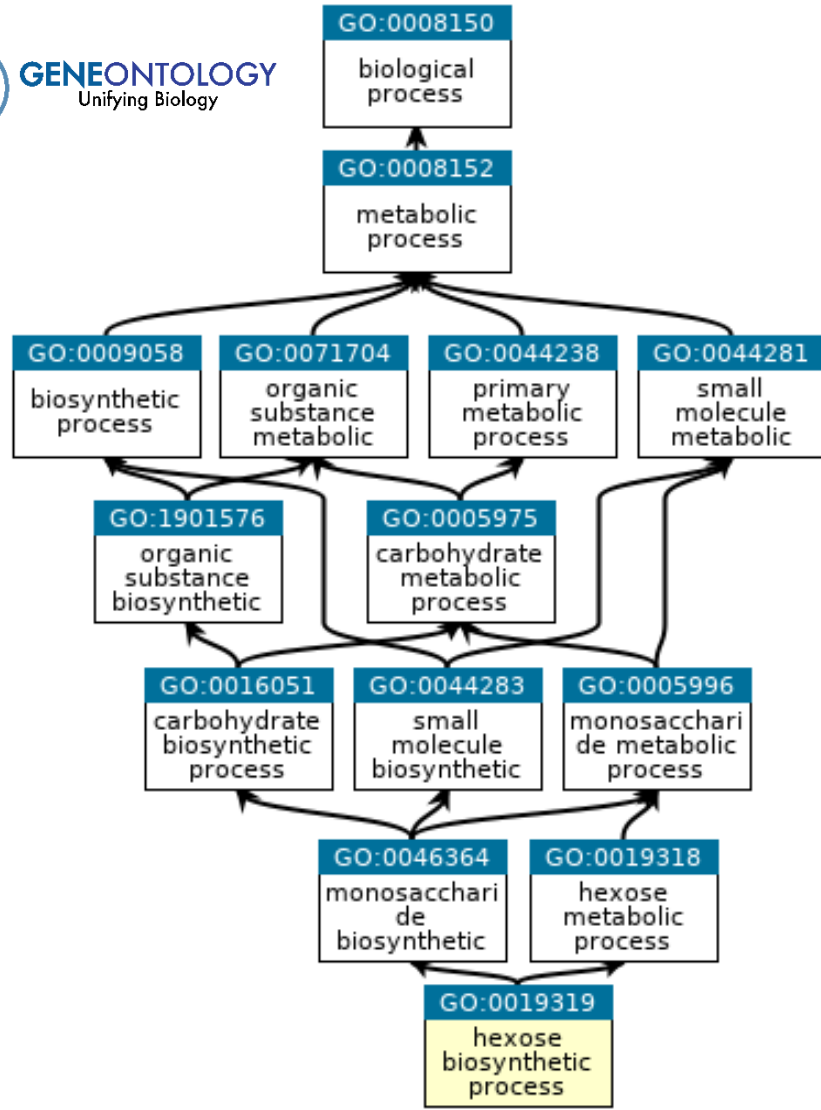
[Link](#) to all direct and indirect **annotations** to hexose biosynthetic process (**excluding "regulates"**).

[Link](#) to all direct and indirect **annotations download** (limited to first 10,000) for hexose biosynthetic process (**excluding "regulates"**).

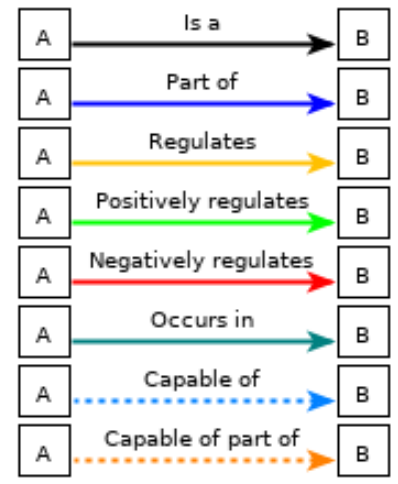
Data health 

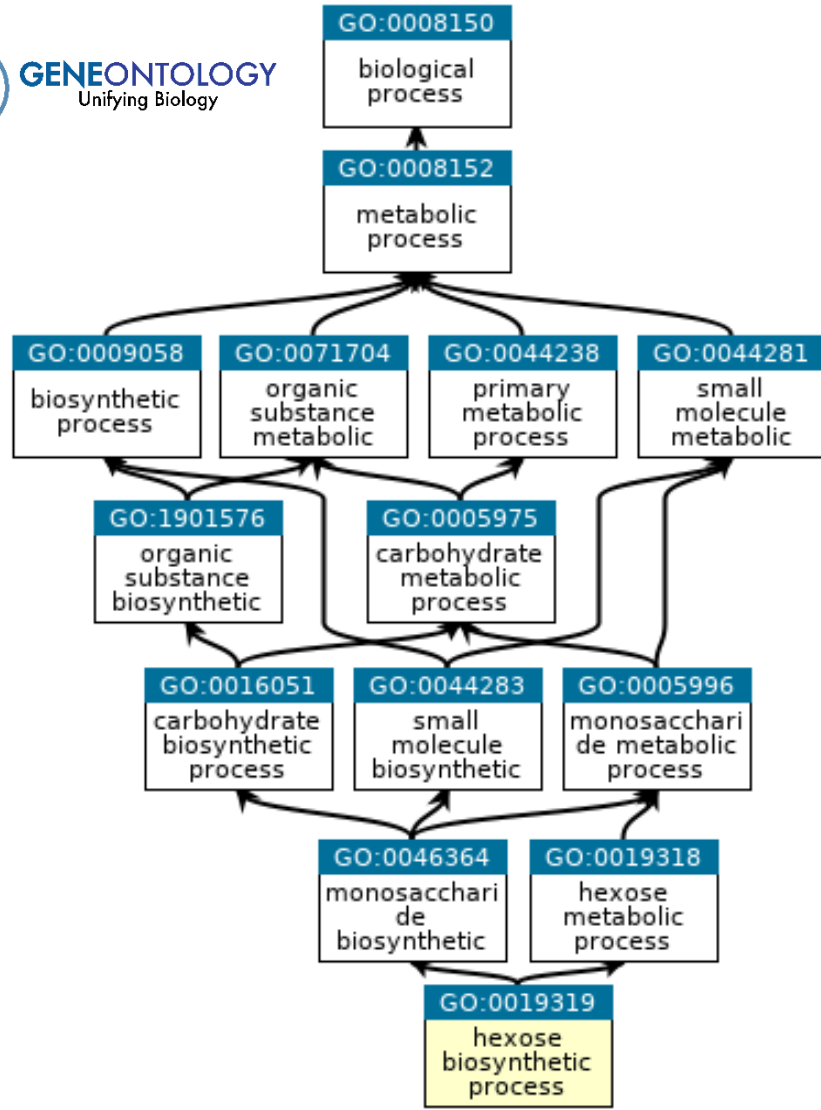
[Include "regulates"](#)

For more information, please see the [ontology relation documentation](#).

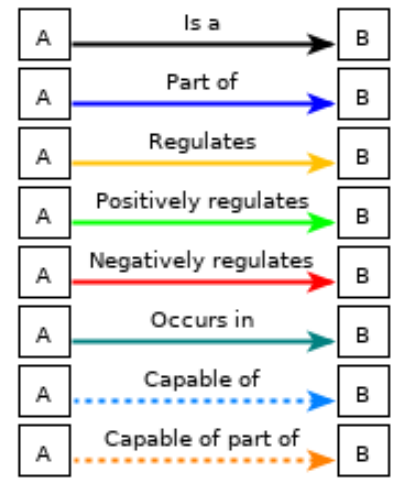


- Process
- Function
- Component





- Process
- Function
- Component



Child Term	Relationship to GO:0019319
GO:0046366 allose biosynthetic process	is_a
GO:0042353 fucose biosynthetic process	is_a
GO:0042847 sorbose biosynthetic process	is_a
GO:0046369 galactose biosynthetic process	is_a
GO:0019307 mannose biosynthetic process	is_a
GO:0006094 gluconeogenesis	is_a
GO:0019300 rhamnose biosynthetic process	is_a
GO:0046370 fructose biosynthetic process	is_a



Current Strain (Clear/Search All)

Pseudomonas aeruginosa PAO1 (Reference)

Gene/Product Name

Return

Exact matches



Complete Genomes Only

Current DB Version: 21.1 (2022-11-20)

The Pseudomonas Genome Database collaborates with an international panel of expert *Pseudomonas* researchers to provide high quality updates to the PAO1 genome annotation and make cutting edge genome analysis data available

Search Gene Annotations by Name

phospholipase C

Exact Name Name Contains

Choose a specific strain (optional)

Start typing and select from the list

OR choose a species (optional)

Start typing and select from the list

Complete genomes only

Include draft genomes

Search Annotations



Latest News

November 15, 2022

Pseudomonas Genome Database version 21.1 released.

128 curated [updates](#) to annotations.

4491 new *Pseudomonas* genomes added for a total of 14291.

Database now has 7960 *P. aeruginosa* genomes.

Updated antimicrobial resistance gene predictions based on the [Resistance Gene Identifier \(RGI\)](#) and [CARD](#) version 3.2.4.

NEW FEATURE: For *P. aeruginosa* PAO1, new links to predicted 3D structures in the [AlphaFold Protein Structure Database](#).

Updated functional domain predictions based on [InterPro](#) version 5.57-90.0.

[More news...](#)

Tweets from @pseudocap



Pseudomonas Database

@pseudocap · Nov 21, 2022



Replying to [@pseudocap](#)

For *P. aeruginosa* PAO1, new links to predicted protein structures in [AlphaFoldDB](#).



6

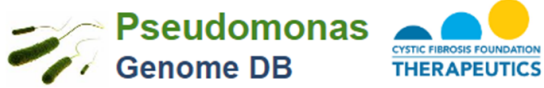


Pseudomonas Database

@pseudocap · Nov 21, 2022



Happy to announce that Pseudomonas Genome Database version 21.1 has been released. More details at:



Current Strain (Clear/Search All)

Search all strains or enter new strain here

Gene/Product Name

Return

Exact matches



Complete Genomes Only

Current DB Version: 21.1 (2022-11-20)

Options/Filter

Display 20 results per page Update

Columns 9 of 24 selected

Search Criteria Query Strain: All strains
Assemblies: Complete genomes only - Draft genomes omitted
Condition 1: name = phospholipase C

Filter results by organism name Enter any part of strain or species name Update Results

Download results TAB CSV GFF3 GTF

410 results were returned

1 2 3 4 5 6 7 8 9 10 .. 21 Next

★ = Popular strains (Ordered by popular strains first, then by strain name, ascending)

Strain	Assembly Status	Replicon	Locus Tag	Feature Type	Coordinates	Gene Length	Gene Name	Product Description	Clipboard
★ Pseudomonas aeruginosa PAK (Cain et al., 2019) - Assembly GCF_902172305.2	Complete Genome GCF_902172305.2 latest	chromosome1	PAKAF_RS00130	CDS	27156..28142 (+)	987	phospholipase C	phospholipase C	Add
★ Pseudomonas aeruginosa PAK - Assembly GCF_000568855.2	Complete Genome GCF_000568855.2 latest	chromosome	Y880_RS26715	CDS	5609232..5610218 (+)	987	phospholipase C	phospholipase C	Add
★ Pseudomonas aeruginosa CF39S	Complete Genome GCF_011466835.1 latest	chromosome	GIY05_RS00130	CDS	27635..28621 (+)	987	phospholipase C	phospholipase C	Add
Pseudomonas aeruginosa SE5381	Complete Genome GCF_024407345.4 latest	chromosome	HUK70_RS00130	CDS	27415..28401 (+)	987	phospholipase C	phospholipase C	Add



Current Strain (Clear/Search All)

Gene/Product Name

Return

Search all strains or enter new strain here

Search input field

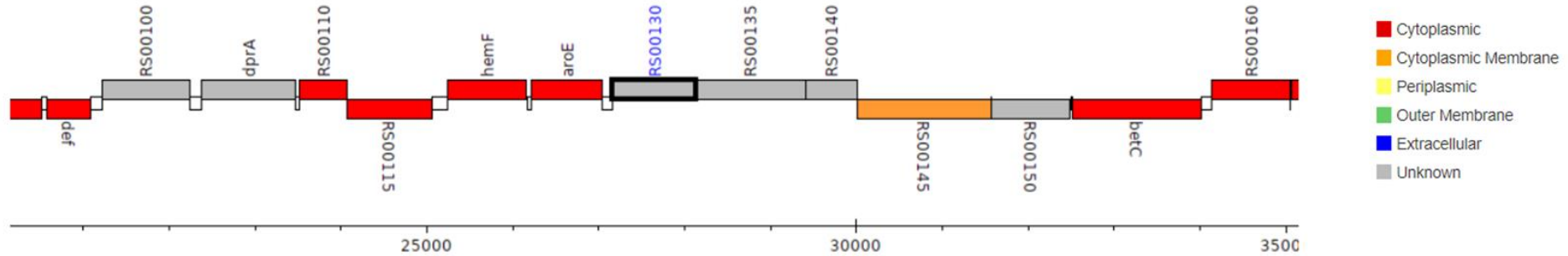
Exact matches



Complete Genomes Only

Current DB Version: 21.1 (2022-11-20)

Pseudomonas aeruginosa PAK, PAKAF_RS00130



View in JBrowse

Overview Sequences Function/Pathways/GO Motifs Save gene

Gene Feature Overview

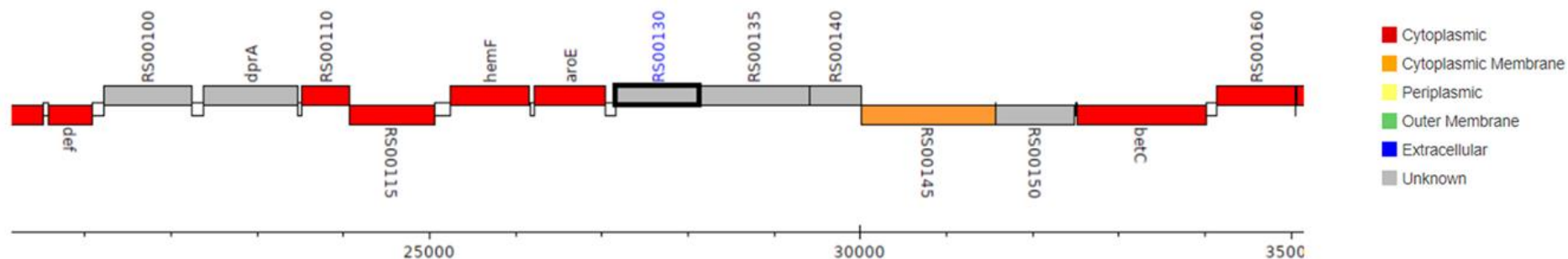
Strain	Pseudomonas aeruginosa PAK (Cain et al., 2019) - Assembly GCF_902172305.2 GCF_902172305.2 latest
Locus Tag	PAKAF_RS00130
Name	Synonym: PAKAF_00026
Replicon	chromosome1
Genomic location	27156 - 28142 (+ strand)

Product

Feature Type	CDS
Coding Frame	1
Product Name	phospholipase C
Evidence for Translation	
Charge (pH 7)	-10.94
Kyte-Doolittle Hydrophobicity Value	-0.433



Pseudomonas aeruginosa PAK, PAKAF_RS00130



[View in JBrowse](#)

[Overview](#)
[Sequences](#)
[Function/Pathways/GO](#)
[Motifs](#)
[Save gene](#)

Gene Ontology

Ontology	Accession	Term	GO Evidence	Evidence Ontology (ECO) Code	Reference	Comments
Molecular Function	GO:0016788	hydrolase activity, acting on ester bonds	ISM Inferred from Sequence Model Term mapped from: InterPro:SSF48537	ECO:0000259 match to InterPro signature evidence used in automatic assertion		
Molecular Function	GO:0008270	zinc ion binding	ISM Inferred from Sequence Model Term mapped from: InterPro:cd11009	ECO:0000259 match to InterPro signature evidence used in automatic assertion		
Molecular Function	GO:0004629	phospholipase C activity	ISM Inferred from Sequence Model Term mapped from: InterPro:cd11009	ECO:0000259 match to InterPro signature evidence used in automatic assertion		

Summary Sequence Protein Gene Ontology Phenotype Interactions Regulation Expression Literature Homology

HSP12 / YFL014W

Locus Overview

Sequence

Protein

Alleles

Gene Ontology

Phenotype

Interaction

Regulation

Expression

Literature

History

References

Resources



HSP12 / YFL014W Overview

Standard Name: HSP12¹

Systematic Name: YFL014W

SGD ID: SGD:S000001880

Aliases: GLP1², HOR5⁵

Feature Type: ORF , Verified

Description: Plasma membrane protein involved in maintaining membrane organization; involved in maintaining organization during stress conditions; induced by heat shock, oxidative stress, osmostress, stationary phase, glucose depletion, oleate and alcohol; protein abundance increased in response to DNA replication stress and dietary restriction; regulated by the HOG and Ras-Pka pathways; required for dietary restriction-induced lifespan extension^{1 2 3 4 5 6 7 8 9 10}

Name Description: Heat Shock Protein¹

Comparative Info:



Sequence

Sequence Details

Gene Ontology ?

HSP12 / YFL014W
Locus Overview
Sequence
Protein
Alleles
Gene Ontology
Phenotype
Interaction
Regulation
Expression
Literature
History
References
Resources

Summary: Lipid binding protein; involved in plasma membrane organization and response to oxidative, osmotic and heat stress; localized to plasma membrane

[View computational annotations](#)

Molecular Function

Manually Curated:

- enables lipid binding (IDA)

Biological Process

Manually Curated:

- involved in cell adhesion (IDA)
- involved in cellular response to heat (IMP)
- involved in cellular response to osmotic stress (IMP)
- involved in cellular response to oxidative stress (IMP)
- involved in plasma membrane organization (IMP)

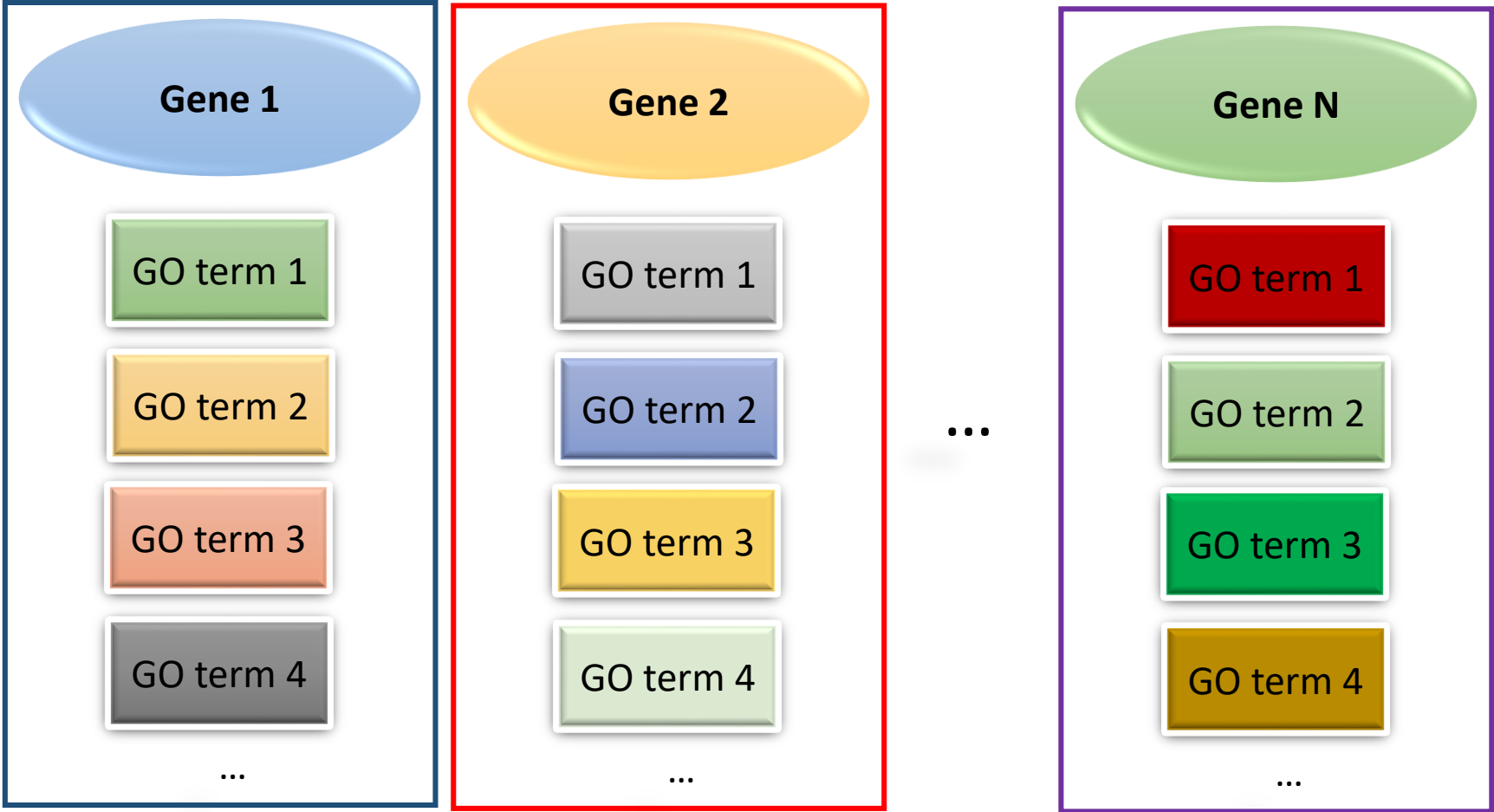
Cellular Component

Manually Curated:

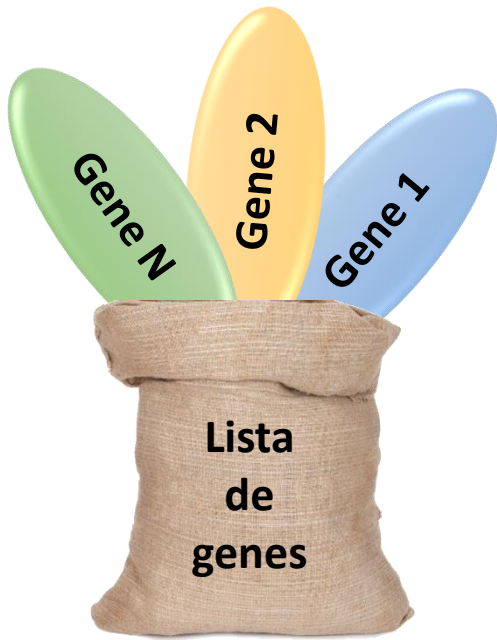
- part of cytosol (IDA)
- part of endosome (IDA)
- part of plasma membrane (IDA)

High-Throughput:

- part of cytoplasm (HDA)
- part of nucleus (HDA)
- part of plasma membrane (HDA)



S000000012	S000000375	S000001055	S000001538	S000002435	S000002993	S000003740	S000004409	S000005176	S000005833	S000006363
S000000014	S000000383	S000001068	S000001542	S000002472	S000003003	S000003746	S000004474	S000005180	S000005857	S000006364
S000000051	S000000397	S000001072	S000001563	S000002476	S000003026	S000003747	S000004590	S000005189	S000005858	S000006370
S000000070	S000000398	S000001083	S000001680	S000002487	S000003034	S000003772	S000004628	S000005224	S000005859	S000006377
S000000102	S000000404	S000001102	S000001732	S000002521	S000003038	S000003779	S000004641	S000005241	S000005923	S000006398
S000000103	S000000513	S000001107	S000001743	S000002522	S000003095	S000003786	S000004664	S000005251	S000005934	S000006433
S000000120	S000000514	S000001133	S000001866	S000002536	S000003103	S000003794	S000004682	S000005288	S000005952	S000007245
S000000121	S000000537	S000001142	S000001871	S000002545	S000003120	S000003804	S000004703	S000005289	S000005966	S000007603
S000000137	S000000541	S000001162	S000001925	S000002603	S000003121	S000003834	S000004750	S000005293	S000005996	S000028508
S000000175	S000000602	S000001190	S000002163	S000002615	S000003186	S000003836	S000004753	S000005309	S000005998	
S000000176	S000000612	S000001210	S000002198	S000002652	S000003188	S000003865	S000004811	S000005318	S000006005	
S000000186	S000000618	S000001230	S000002201	S000002653	S000003204	S000003866	S000004815	S000005319	S000006038	
S000000190	S000000659	S000001249	S000002205	S000002668	S000003206	S000003966	S000004816	S000005320	S000006082	
S000000199	S000000667	S000001250	S000002223	S000002672	S000003209	S000004015	S000004841	S000005334	S000006155	
S000000215	S000000735	S000001288	S000002273	S000002673	S000003213	S000004029	S000004844	S000005441	S000006162	
S000000239	S000000753	S000001360	S000002274	S000002701	S000003252	S000004138	S000004945	S000005503	S000006187	
S000000281	S000000762	S000001369	S000002319	S000002703	S000003309	S000004172	S000004951	S000005505	S000006192	
S000000299	S000000771	S000001379	S000002326	S000002706	S000003336	S000004184	S000004952	S000005534	S000006237	
S000000301	S000000772	S000001390	S000002351	S000002737	S000003337	S000004329	S000004970	S000005561	S000006240	
S000000305	S000000777	S000001403	S000002384	S000002800	S000003365	S000004330	S000004984	S000005562	S000006253	
S000000327	S000000924	S000001415	S000002385	S000002841	S000003379	S000004350	S000005000	S000005569	S000006303	
S000000330	S000000957	S000001450	S000002412	S000002878	S000003412	S000004361	S000005025	S000005641	S000006305	
S000000331	S000001003	S000001485	S000002415	S000002971	S000003484	S000004388	S000005028	S000005667	S000006308	
S000000336	S000001017	S000001520	S000002424	S000002988	S000003563	S000004395	S000005077	S000005679	S000006335	
S000000356	S000001050	S000001537	S000002434	S000002992	S000003716	S000004406	S000005083	S000005722	S000006343	



GENEONTOLOGY Unifying Biology
 PANTHER Classification System

[LOGIN](#)
[REGISTER](#)
[CONTACT US](#)

[Home](#)
[About](#)
[PANTHER Data](#)
[PANTHER Tools](#)
[PANTHER Services](#)
[Workspace](#)
[Downloads](#)
[Help/Tutorial](#)

[PANTHER17.0 Released.](#)

Analysis Summary: Please report in publication [?](#)

Analysis Type: PANTHER Overrepresentation Test (Released 20220202)

Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.6399963 Released 2022-03-22

Analyzed List: upload_1 (Homo sapiens) [Change](#)

Reference List: Homo sapiens (all genes in database) [Change](#)

Annotation Data Set: GO biological process complete [?](#)

Test Type: Fisher's Exact Binomial

Correction: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing [?](#) No correction

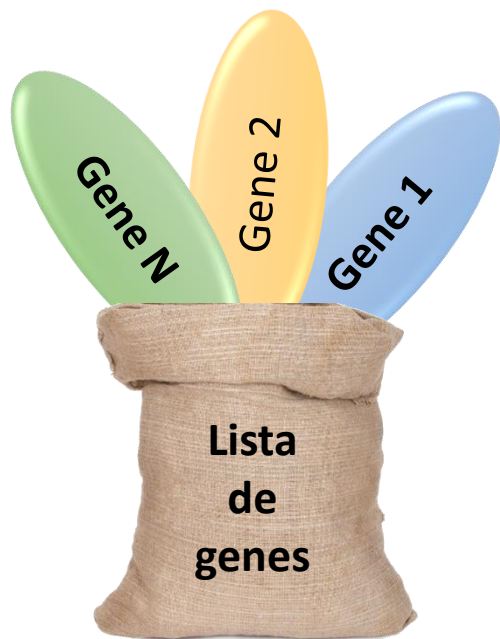
Results [?](#)


	Reference list	upload_1
Uniquely Mapped IDs:	20589 out of 20589	36 out of 39
Unmapped IDs:	0	0
Multiple mapping information:	0	3

Export [Table](#) [XML with user input ids](#) [JSON with user input ids](#)

Displaying only results for FDR P < 0.05, [click here to display all results](#)


	Homo sapiens (REF)	upload_1 (Hierarchy NEW! ?)					
	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
GO biological process complete							
VEGF-activated neuropilin signaling pathway	2	2	.00	> 100	+	2.08E-05	2.72E-03
↳ neuropilin signaling pathway	4	2	.01	> 100	+	5.20E-05	5.43E-03
↳ cell surface receptor signaling pathway	2106	17	3.99	4.26	+	8.49E-08	4.75E-05
↳ signal transduction	4820	22	9.13	2.41	+	9.64E-06	1.61E-03
↳ signaling	5163	22	9.78	2.25	+	4.31E-05	4.73E-03
↳ cell communication	5266	23	9.97	2.31	+	1.06E-05	1.69E-03
↳ cellular response to stimulus	6479	25	12.27	2.04	+	3.57E-05	4.18E-03
↳ response to stimulus	9096	22	15.24	2.09	+	6.22E-08	2.94E-05





DAVID Bioinformatics Resources (2021 Update)

Laboratory of Human Retrovirology and
Immunoinformatics (LHRI)



*** Welcome to DAVID (2021 Update) ***

*** If you are looking for [DAVID 6.8](#), it is still accessible on [this server](#) until retirement on [June 1, 2022](#). ***

Functional Annotation Chart

[Help and Manual](#)

Current Gene List: demolist1
Current Background: Homo sapiens
145 DAVID IDs

Options

Rerun Using Options Create Sublist

243 chart records [Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular space	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	37	25.5	9.9E-9	2.4E-6
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular region	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	38	26.2	4.5E-8	5.4E-6
<input type="checkbox"/>	GOTERM_BP_DIRECT	antimicrobial humoral immune response mediated by antimicrobial peptide	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	9	6.2	9.2E-7	7.8E-4
<input type="checkbox"/>	GOTERM_BP_DIRECT	innate immune response in mucosa	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	6	4.1	1.3E-6	7.8E-4
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Secreted	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	35	24.1	1.5E-6	5.2E-5
<input type="checkbox"/>	GOTERM_BP_DIRECT	antibacterial humoral response	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	7	4.8	3.0E-6	1.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to Gram-negative bacterium	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	8	5.5	3.8E-6	1.2E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	azurophil granule lumen	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	7	4.8	3.7E-5	2.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	defense response to fungus	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	5	3.4	7.8E-5	1.9E-2
<input type="checkbox"/>	UP_KW_DOMAIN	Signal	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	51	35.2	1.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	killing of cells of other organism	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	6	4.1	1.3E-4	2.5E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Chemotaxis	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	7	4.8	1.3E-4	8.5E-3
<input type="checkbox"/>	GOTERM_CC_DIRECT	apical plasma membrane	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	11	7.6	2.2E-4	1.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	chemotaxis	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	7	4.8	2.2E-4	3.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	positive regulation of gene expression	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	13	9.0	2.3E-4	3.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	monocyte chemotaxis	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	5	3.4	2.7E-4	3.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	Transcriptional misregulation in cancer	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	9	6.2	4.5E-4	5.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Gastric cancer	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	8	5.5	4.9E-4	5.5E-2
<input type="checkbox"/>	GOTERM_MF_DIRECT	heme binding	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	7	4.8	6.8E-4	1.6E-1
<input type="checkbox"/>	INTERPRO	Alpha-defensin	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	INTERPRO	Mammalian defensins	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	INTERPRO	Defensin propeptide	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	3	2.1	7.3E-4	9.1E-2
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Antibiotic	RT	<div style="width: 100%; height: 10px; background-color: #0056b3;"></div>	6	4.1	7.5E-4	5.1E-2

Exercício