

Dia da Propriedade Industrial

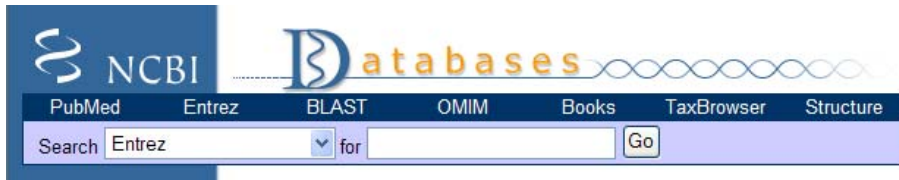
Vanessa Fatal

Examinadora de Patentes

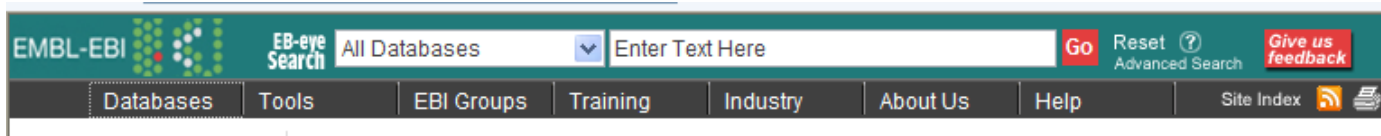


Bases de Dados de Biotecnologia

Universidade de Évora | 21.09.2010



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



<http://www.ebi.ac.uk/Tools/fast/index.html>



<http://chem.sis.nlm.nih.gov/chemidplus/>

The screenshot shows the NCBI homepage. On the left, a blue sidebar contains links to various resources. On the right, there are sections for 'What does NCBI do?', 'Hot Spots', 'NLN/NCBI H1N1 Flu Resources', and 'Genome Reference Consortium'. A search bar is at the top. Three orange arrows point from text labels on the left to specific parts of the website: 'Depósito de seqüências' points to the GenBank link, 'Bases de Dados de literatura biomédica' points to the Literature databases link, and 'Pesquisa de seqüências e estruturas; homologias' points to the Tools link.

NCBI

National Center for Biotechnology Information
[National Library of Medicine](#) [National Institutes of Health](#)

PubMed All Databases BLAST OMIM Books TaxBrowser Structure

Search for

SITE MAP
Alphabetical List
Resource Guide

About NCBI
An introduction to NCBI

GenBank
Sequence submission support and software

Literature databases
PubMed, OMIM, Books, and PubMed Central

Molecular databases
Sequences, structures, and taxonomy

Genomic biology
The human genome, whole genomes, and related resources

Tools
Data mining

Research at NCBI
People, projects, and seminars

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease. [More about NCBI...](#)

Hot Spots

- Clusters of orthologous groups
- Coffee Break, Genes & Disease, NCBI Handbook
- Electronic PCR
- Entrez Home
- Entrez Tools
- Gene expression omnibus (GEO)
- Human genome resources
- Influenza Virus Resource
- Map Viewer
- dbMHC
- Mouse genome resources
- My NCBI
- ORF finder
- Rat genome resources

NLM/NCBI H1N1 Flu Resources

- [Newest H1N1 influenza sequences](#)
- [Submit flu sequences to GenBank](#)
- [Latest H1N1 citations in PubMed](#)
- [MedlinePlus \(consumer health information\)](#)
- [Enviro-Health links](#)

KNOW
What to Do
About the Flu
www.flu.gov
Share this Widget



Genome Reference Consortium

The [Genome Reference Consortium](#) (GRC) has been formed to continue the improvement

Depósito de seqüências

Bases de Dados de
literatura biomédica







Pesquisa de seqüências e
estruturas; homologias































Entrez, The Life Sciences Search Engine

[HOME](#)
[SEARCH](#)
[SITE MAP](#)
[PubMed](#)
[All Databases](#)
[Human Genome](#)
[GenBank](#)
[Map Viewer](#)
[BLAST](#)

Search across databases

[Help](#)

 PubMed: biomedical literature citations and abstracts	 Books: online books
 PubMed Central: free, full text journal articles	 OMIM: online Mendelian Inheritance in Man
 Site Search: NCBI web and FTP sites	 OMIA: online Mendelian Inheritance in Animals

 Nucleotide: Core subset of nucleotide sequence records	 dbGaP: genotype and phenotype
 EST: Expressed Sequence Tag records	 UniGene: gene-oriented clusters of transcript sequences
 GSS: Genome Survey Sequence records	 CDD: conserved protein domain database
 Protein: sequence database	 3D Domains: domains from Entrez Structure
 Genome: whole genome sequences	 UniSTS: markers and mapping data
 Structure: three-dimensional macromolecular structures	 PopSet: population study data sets
 Taxonomy: organisms in GenBank	 GEO Profiles: expression and molecular abundance profiles
 SNP: single nucleotide polymorphism	 GEO DataSets: experimental sets of GEO data
 Gene: gene-centered information	 Cancer Chromosomes: cytogenetic databases
 SRA: Short Read Archive	 PubChem BioAssay: bioactivity screens of chemical substances
 BioSystems: Pathways and systems of interacting molecules	 PubChem Compound: unique small molecule chemical structures
 HomoloGene: eukaryotic homology groups	 PubChem Substance: deposited chemical substance records
 GENSAT: gene expression atlas of mouse central nervous system	 Protein Clusters: a collection of related protein sequences
 Probe: sequence-specific reagents	
 Genome Project: genome project information	

NCBI PubMed A service of the [U.S. National Library of Medicine](#) and the [National Institutes of Health](#) www.pubmed.gov

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search PubMed for [Advanced Search](#)

Preview/Index History Clipboard Details

started with PubMed, enter one or more search terms.

Terms may be [topics](#), [authors](#) or [journals](#).

NCBI H1N1 Flu Resources:

[Test 2009 H1N1 Flu Outbreak Sequences](#)

[Sequences recently added](#) to PubMed

[ePlus \(consumer health information\)](#)

[Pro-Health Links](#)

H1N1 Flu Info

U.S. Info •
Things You Can Do •
Plan & Prepare •
International Info •

HHS.gov CDC.gov

The NIH Public Access Policy May Affect You

Does NIH fund your work?

When your manuscript must be made available in PubMed Central

How?

If you publish in one of [these journals](#), they will take care of the whole process.

If you publish *anywhere else*, deposit the manuscript in PubMed Central via one of the options described at publicaccess.nih.gov.

Note: Other funding organizations, including [HHMI](#), [Wellcome Trust](#) and the [MRC](#) also require papers to be made freely available through PMC.

PubMed is a service of the [U.S. National Library of Medicine](#) that includes over 18 million citations from MEDLINE and other life science journals for biomedical articles back to 1948. PubMed includes links to full text articles and other related resources.

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

Department of Health & Human Services

[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)

NCBI MeSH A service of the National Library of Medicine and the National Institutes of Health

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search MeSH for phenobarbital Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Summary Show 20 Send to

All: 11

Items 1 - 11 of 11 One page.

- ☐ 1: **Phenobarbital** [Links](#)
A barbituric acid derivative that acts as a nonselective central nervous system depressant. It promotes binding to inhibitory GAMMA-AMINOBUTYRIC ACID subtype receptors, and modulates chloride currents through receptor channels. It also inhibits glutamate induced depolarizations.
- ☐ 2: **phenobarbital-N-glucoside** [\[Substance Name\]](#) [Links](#)
RN given refers to (beta-D)-isomer
Date introduced: January 28, 1985
- ☐ 3: **phenobarbital quinidine** [\[Substance Name\]](#) [Links](#)
drug combination consisting of the above cpds
Date introduced: February 26, 1982

<http://www.ncbi.nlm.nih.gov/mesh?itool=sidebar>

☐ 1: Phenobarbital

A barbituric acid derivative that acts as a nonselective central nervous system depressant. It promotes binding to inhibitory GAMMA-AMINOBUTYRIC ACID subtype receptors, and modulates chloride currents through receptor channels. It also inhibits glutamate induced depolarizations.

Subheadings: This list includes those paired at least once with this heading in MEDLINE and may not reflect current rules for allowable combinations.

☐ administration and dosage ☐ adverse effects ☐ analogs and derivatives ☐ analysis ☐ antagonists and inhibitors ☐ biosynthesis ☐ blood ☐ cerebrospinal fluid ☐ chemical synthesis ☐ chemistry ☐ classification ☐ contraindications ☐ diagnostic use ☐ drug therapy ☐ economics ☐ history ☐ immunology ☐ isolation and purification ☐ metabolism ☐ pharmacokinetics ☐ pharmacology ☐ physiology ☐ poisoning ☐ radiation effects ☐ secretion ☐ standards ☐ supply and distribution ☐ therapeutic use ☐ therapy ☐ toxicity ☐ urine

☐ Restrict Search to Major Topic headings only.

☐ Do Not Explode this term (i.e., do not include MeSH terms found below this term in the MeSH tree).

Registry Number: 50-06-6

Entry Terms:

- Phenylethylbarbituric Acid
- Acid, Phenylethylbarbituric
- Phenylbarbital
- Phenemal
- Phenobarbitone
- Phenobarbital Sodium
- Sodium, Phenobarbital
- Phenobarbital, Monosodium Salt
- Monosodium Salt Phenobarbital
- Luminal
- Gardenal
- Hysteps

Pharmacologic Action:

- [Hypnotics and Sedatives](#)
- [Excitatory Amino Acid Antagonists](#)
- [GABA Modulators](#)
- [Anticonvulsants](#)

[All MeSH Categories](#)

[Chemicals and Drugs Category](#)

[Heterocyclic Compounds](#)

[Heterocyclic Compounds, 1-Ring](#)

[Pyrimidines](#)

[Pyrimidinones](#)

[Barbiturates](#)

Phenobarbital

Os termos MeSH permitem alargar o âmbito da pesquisa ao estado da arte, através de uma hierarquia de categorização.

The screenshot shows the NCBI BLAST (Basic Local Alignment Search Tool) homepage. At the top, there's a blue header with the BLAST logo and navigation links: Home, Recent Results, Saved Strategies, and Help. Below the header, a text box explains that BLAST finds regions of similarity between biological sequences, with a 'more...' link. A red banner promotes 'Primer-BLAST' for designing or testing PCR primers. The 'BLAST Assembled Genomes' section allows users to choose a species genome to search, listing options like Human, Mouse, Rat, Arabidopsis thaliana, Oryza sativa, Bos taurus, Danio rerio, Drosophila melanogaster, Gallus gallus, Pan troglodytes, Microbes, and Apis mellifera. The 'Basic BLAST' section provides instructions to choose a BLAST program to run, listing six options: nucleotide blast (circled in orange), protein blast (circled in orange), blastx, tblastn, and tblastx, each with a brief description and the algorithms used.

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New Designing or Testing PCR Primers? Try your search in **Primer-BLAST**. [Go](#)

BLAST Assembled Genomes

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

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

Basic BLAST

Choose a BLAST program to run.

- [nucleotide blast](#) Search a nucleotide database using a nucleotide query
Algorithms: blastn, megablast, discontinuous megablast
- [protein blast](#) Search protein database using a protein query
Algorithms: blastp, psi-blast, phi-blast
- [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

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

BLAST

[Overview](#)
[FAQs](#)
[News](#)
[Manual](#)
[References](#)
[Retrieve results](#)

Genome Project

BLAST Drosophila melanogaster Sequences.

Enter an accession, gi, or a sequence in FASTA format:

agttaccttc gcacgatca actaaccaac tcagcctcag aatgatgaag
ttcatgtgca

Or, choose a file to upload

Set subsequence: (optional)

From: To:

Database:

6 sequences

Program:

megaBLAST: Compare highly related nucleotide sequences

Optional parameters

Expect	Filter	Descriptions	Alignments
0.01	default	100	100

Advanced options:

Introduzir a sequência a
pesquisar

agttaccttcgcacgatcaactaaccaactcagcctcagaatgatgaagttcatgtgca

Iniciar a pesquisa

BLAST *Basic Local Alignment Search Tool*

[Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

► [NCBI/BLAST/Format Request](#)

Query Nucleotide Sequence (60 letters)

Database dm_refc

Job title Nucleotide Sequence (60 letters)

Request ID WFA100TJ01R **View report** ☐ Show results in a new window

Format

Show	Alignment	as	HTML	<input type="checkbox"/> Advanced View	<input type="checkbox"/> Use old BLAST report format	Reset form to defaults
Alignment View	Pairwise					
Display	<input checked="" type="checkbox"/> Graphical Overview	<input checked="" type="checkbox"/> Linkout	<input checked="" type="checkbox"/> Sequence Retrieval	<input type="checkbox"/> NCBI-gi	<input type="checkbox"/> CDS feature	
	Masking Character:	Lower Case	Masking Color:	Grey		
Limit results	Descriptions:	100	Graphical overview:	100	Alignments:	100
	Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.					
	<input type="text" value="Enter organism name or id-completions will be suggested"/>					
	Entrez query: <input type="text"/>					
	Expect Min: <input type="text"/>		Expect Max: <input type="text"/>			

Inderego <http://blast.ncbi.nlm.nih.gov/Blast.cgi> Ir para Hiperligações

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/BLAST/Formatting Results - CVJWCYZE01S

[Formatting options](#) [Download](#)

Nucleotide Sequence (60 letters)

Query ID	Id 8085	Database Name	gp/7227.9554/dm_refc
Description	None	Description	Drosophila melanogaster genome (reference only)
Molecule type	nucleic acid	Program	BLASTN 2.2.22+ Citation
Query Length	60		

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Fruit fly genome view](#)

▼ [Graphic Summary](#)

Distribution of 1 Blast Hits on the Query Sequence ⓘ

Mouse over to see the define, click to show alignments

Color key for alignment scores

Score Range	Color
<40	Black
40-50	Blue
50-80	Green
80-200	Pink
>=200	Red

Query 0 10 20 30 40 50 60

▼ [Descriptions](#)

Sequences producing significant alignments:

	Score (Bits)	E Value
ref NT_037436.3 Drosophila melanogaster chromosome 3L, compl...	104	2e-22 E

Referências
bibliográficas

Sequência a
pesquisar

Resultado

▼ Alignments ☐ Select All [Get selected sequences](#) [Distance tree of results](#) [NEW](#)



> [ref|NT_037436.3|](#) **E D** Drosophila melanogaster chromosome 3L, complete sequence
Length=24543557






Features in this part of subject sequence:
[chorion protein 18](#)

Score = 104 bits (56), Expect = 2e-22
Identities = 56/56 (100%), Gaps = 0/56 (0%)
Strand: Plus/Plus


Query	AGTTACCTTCGCATCGATCAACTAACCAACTCAGCCTCAGAATGATGAAGTTCATG	56
Shjet	8719894 AGTTACCTTCGCATCGATCAACTAACCAACTCAGCCTCAGAATGATGAAGTTCATG	8719949


Percentagem
de identidade


Endereço  http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=Retrieve&db=nucleotide&dopt=GenBank&RID=CVJWCYZE015&log%24=nucdtop&blast_rank=1&list_uids=116010443  Ir para  Hiperligação


  **Nucleotide**   

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search Nucleotide  for

Format: GenBank [FASTA](#) [Graphics](#) [More Formats](#) 

 Try the [Graphics report](#) for a more informative view of the biological features.

 This record may be shown in an abbreviated form. Use 'Customize View' section for control.

NCBI Reference Sequence: NT_037436.3

Drosophila melanogaster chromosome 3L, complete sequence

[Comment](#) [Features](#)

LOCUS NT_037436 24543557 bp DNA linear INV 18-MAR-2009

DEFINITION Drosophila melanogaster chromosome 3L, complete sequence.

ACCESSION NT_037436

VERSION NT_037436.3 GI:116010443

DBLINK Project:164

KEYWORDS .

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM [Drosophila melanogaster](#)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila; Sophophora.

REFERENCE 1 (bases 1 to 24543557)

AUTHORS Hoskins,R.A., Carlson,J.W., Kennedy,C., Acevedo,D., Evans-Holm,M.,
Frise,E., Wan,K.H., Park,S., Mendez-Lago,M., Rossi,F.,
Villasante,A., Dimitri,P., Karpen,G.H. and Celniker,S.E.

TITLE Sequence finishing and mapping of Drosophila melanogaster
heterochromatin

JOURNAL Science 316 (5831), 1625-1628 (2007)

PUBMED [17569867](#)

REFERENCE 2 (bases 1 to 24543557)

AUTHORS Smith,C.D., Shu,S., Mungall,C.J. and Karpen,G.H.

TITLE The Release 5.1 annotation of Drosophila melanogaster
heterochromatin

JOURNAL Science 316 (5831), 1586-1591 (2007)


PUBMED [17569856](#)


REMARK Erratum:[Science. 2007 Sep 7;317(5843):1325]

REFERENCE 3 (bases 1 to 24543557)

AUTHORS Quesneville,H., Bergman,C.M., Andrieu,O., Autard,D., Nouaud,D.,
Ashburner,M. and Anxolabehere,D.

TITLE Combined evidence annotation of transposable elements in genome
sequences

Change Region Shown 

Customize View 

Basic Features

☐ Default features

☒ Gene, RNA, and CDS features only

Sequence display options


☐ Show sequence


☐ Show minus strand


Sequence Analysis Tools


► BLAST Sequence


► Pick Primers


Recent Activity 

 Drosophila melanogaster chromosome 3L,
complete sequence

 [Nucleotide Sequence \(60 l...](#)

 [Nucleotide Sequence \(60 l...](#)

 [Nucleotide Sequence \(60 l...](#) **BLAST**

 Homo sapiens breast cancer 2, early onset
(BRCA2), mRNA

» See more...



The screenshot shows the NCBI GenBank Overview page. At the top, the NCBI logo is on the left, and the title 'GenBank Overview' is in the center. Below the title is a navigation bar with links to PubMed, Entrez, BLAST, OMIM, Books, Taxonomy, and Structure. A search bar is located below the navigation bar, with 'Entrez' selected in the dropdown menu and a 'Go' button. On the left side, there is a vertical menu with links to NCBI Home, NCBI Site Map, Submit to GenBank, Submit an update, Search GenBank, GenBank and RefSeq: a comparison, and BLAST. The main content area on the right starts with a section titled 'What is GenBank?'. The text describes GenBank as the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences. It mentions that there are approximately 85,759,586,764 bases in 82,853,685 sequence records in the traditional GenBank divisions and 108,635,736,141 bases in 27,439,206 sequence records in the WGS division as of February 2008. It also states that the complete release notes for the current version of GenBank are available on the NCBI ftp site, and that a new release is made every two months. GenBank is part of the International Nucleotide Sequence Database Collaboration, which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI. These three organizations exchange data on a daily basis. Finally, it mentions that an example of a GenBank record may be viewed for a *Saccharomyces cerevisiae* gene.

NCBI **GenBank Overview**

PubMed Entrez BLAST OMIM Books Taxonomy Structure

Search Entrez for Go

NCBI Home
NCBI Site Map
Submit to GenBank
Submit an update
Search GenBank
GenBank and RefSeq: a comparison
BLAST

► **What is GenBank?**

GenBank® is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences ([Nucleic Acids Research, 2008 Jan;36\(Database issue\):D25-30](#)). There are approximately 85,759,586,764 bases in 82,853,685 sequence records in the traditional GenBank divisions and 108,635,736,141 bases in 27,439,206 sequence records in the WGS division as of February 2008.

The complete [release notes](#) for the current version of GenBank are available on the NCBI ftp site. A new release is made every two months. GenBank is part of the [International Nucleotide Sequence Database Collaboration](#), which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at NCBI. These three organizations exchange data on a daily basis.

An example of a GenBank [record](#) may be viewed for a *Saccharomyces cerevisiae* gene.

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



PubChem

PubMed | Entrez | Sitemap

PubChem Text Search

PubChem Compound 

GO

[Fill in a PubChem survey](#)

PubChem provides information on the biological activities of small molecules. It is a component of NIH's [Molecular Libraries Roadmap Initiative](#). If you would like to learn more about how to use the PubChem resources, please go to our [help page](#).



Structures from **Shanghai Sinofluoro Scientific Company** are now available in PubChem.



Structures from **Alinda Chemical** are now available in PubChem.

[More PubChem announcements ...](#)



PubChem Compound: Search unique chemical structures using names, synonyms or keywords. Links to available biological property information are provided for each compound.



PubChem Substance: Search deposited chemical substance records using names, synonyms or keywords. Links to biological property information and depositor web sites are provided.



PubChem BioAssay: Search bioassay records using terms from the bioassay description, for example "[cancer cell line](#)". Links to active compounds and bioassay results are provided.



Structure Search: Search PubChem's Compound database using a chemical structure as the query. Structures may be sketched or specified by SMILES, InChI, MOL files, or other formats.



BioAssay Services: BioAssay summary and bioactivity analysis tools.

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

NCBI PubChem Structure Search

Search By: **Name/Text** Identity/Similarity **Substructure/Superstructure** Molecular Formula Saved Search

Draw a Structure CID, SMILES/SMARTS, InChI Structure File

Launch the PubChem editor to make a structure

Options

Substructure

Filters

Clear

PubChem Server Side Structure Editor V1.21 - Microsoft Internet Explorer

Broadband SMILES C1=CC2C(CCC1)CNCC2

New Undo Cln Del Qry

H		?	?					He	
Li	Be			B	C	N	O	F	Ne
Na	Mg			Al	Si	P	S	Cl	Ar
K	Ca	Sc	Sc	Ga	Ge	As	Se	Br	Kr
Rb	Sr	Y	Y	In	Sn	Sb	Te	I	Xe
Cs	Ba	Lu	Lu	Tl	Pb	Bi	Po	At	Rn

Export SDF Done

Hydrogen Keep AsIs Help

Import Procurar...

NCBI **PubChem** Compound

Search PubChem Compound for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display [Summary](#) Show [20](#) Sort By [Name](#) Send to [Download](#)

Tools: [Structure](#) [BioAssay](#) [Literature](#) [Other Links](#)

All: 4988 BioAssay: 200 Protein3D: 2 Rule of 5: 2729

Items 1 - 20 of 4988 Page 1 of 250 [Next](#)

☐ 1: CID: 2599 [Related Structures](#)



[Caulibugulone E](#); UPCMLD00WCaulibugE; CID2599 ...

IUPAC: 5-amino-7-methyliminoisoquinolin-8-one

MW: 187.197960 g/mol | MF: C₁₀H₉N₃O

☐ 2: CID: 2600 [Related Structures](#)



[Caulibugulone F](#); NSC731588

IUPAC: 5-(2-hydroxyethylamino)-7-methyliminoisoquinolin-8-one

MW: 231.250520 g/mol | MF: C₁₂H₁₃N₃O₂

PubChem Compound

[PubMed](#) | [Entrez](#) | [S](#)

PubChem > Compound Summary

Caulibugulone E - Compound Summary (CID 2599)

Table of Contents

- Synonyms
- Properties
- Descriptors
- Compound Information
- Substance Information
 - Category
- Exports

Depositor-Supplied Synonyms: (Total: 8) [?](#)

Sort: Weight

Caulibugulone E
 UPCMLD00WCaulibugE
 CID2599
 NSC731587
 5-Imino-7-methylamino-5H-isoquinolin-8-one
 5-imino-7-(methylamino)isoquinolin-8(5H)-one
 8(5H)-isoquinolinone, 5-imino-7-(methylamino)-
 InChI=1/C10H9N3O/c1-12-9-4-8(11)6-2-3-13-5-7(6)10(9)14/h2-5,11-12H,1H

Properties Computed from Structure: [?](#)

Molecular Weight	187.19796 [g/mol]
Molecular Formula	C ₁₀ H ₉ N ₃ O
XLogP3-AA	-0.4
H-Bond Donor	1
H-Bond Acceptor	4
Rotatable Bond Count	0
Tautomer Count	3
Exact Mass	187.074562
Monoisotopic Mass	187.074562
Topological Polar Surface Area	68.3
Heavy Atom Count	14
Formal Charge	0
Complexity	319
Isotope Atom Count	0

Fill in a PubChem survey

Structure & Quick Link Bar

2D
 3D

[Pc3D Viewer](#)
[Download](#)

Compound ID	2599	?
Molecular Weight	187.19796 [g/mol]	?
Molecular Formula	C ₁₀ H ₉ N ₃ O	?
XLogP3-AA	-0.4	?
H-Bond Donor	1	?
H-Bond Acceptor	4	?

Links
[Chemical Structure Search](#) [?](#)

EMBL-EBI

EB-eye Search

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Literature

Microarray

Nucleotide

Pathways & Networks

Protein

Proteomic

Structure

Submissions

Downloads

Tools

UniProt

UniProt Databases:

UniProt

Q?

SRS

↓

UniRef

Q?

SRS

↓

UniParc

Q?

SRS

EBI > Databases

Databases at the EBI

The main missions of the European Bioinformatics Institute (EBI) centre on building, maintaining and providing biological databases and information services to support data deposition and exploitation.

Some of the databases we manage include:

EMBL Nucleotide Database

Europe's primary collection of nucleotide sequences is maintained in collaboration with [Genbank](#) (USA) and [DDBJ](#) (Japan)

UniProt Knowledgebase

- a complete annotated protein sequence database

Protein Databank in Europe Database

- European Project for the management and distribution of data on macromolecular structures

ArrayExpress

- for gene expression data

Ensembl

- Providing up to date completed metazoic genomes and the best possible automatic annotation.

IntAct

- Provides a freely available, open source database system and analysis tools for protein interaction data.

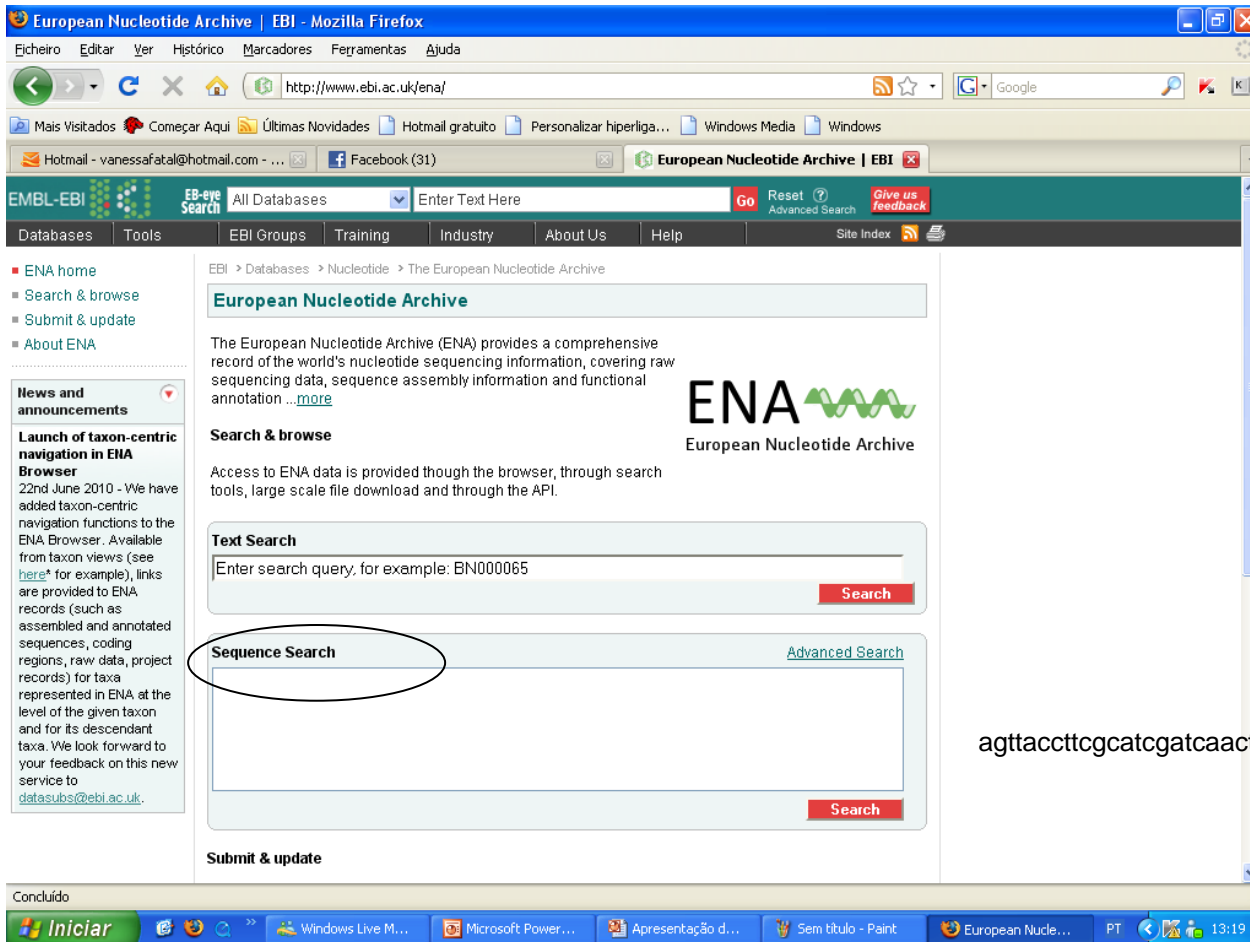
Databases A-Z

- A complete listing of all the EBI databases.

We have many other databases available including literature citation databases such as [Medline](#). You can browse the databases we have available by choosing the appropriate category on the left navigation column.

<http://www.ebi.ac.uk/Databases/>





European Nucleotide Archive | EBI - Mozilla Firefox

Ficheiro Editar Ver Histórico Marcadores Ferramentas Ajuda

http://www.ebi.ac.uk/ena/

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Hotmail - vanessafatal@hotmail.com - ... Facebook (31) European Nucleotide Archive | EBI

EMBL-EBI EB-eye Search All Databases Enter Text Here Go Reset Advanced Search Give us feedback

Databases Tools EBI Groups Training Industry About Us Help Site Index

■ ENA home

■ Search & browse

■ Submit & update

■ About ENA

News and announcements

Launch of taxon-centric navigation in ENA Browser

22nd June 2010 - We have added taxon-centric navigation functions to the ENA Browser. Available from taxon views (see [here](#) for example), links are provided to ENA records (such as assembled and annotated sequences, coding regions, raw data, project records) for taxa represented in ENA at the level of the given taxon and for its descendant taxa. We look forward to your feedback on this new service to datasubs@ebi.ac.uk.

EBI > Databases > Nucleotide > The European Nucleotide Archive

European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation [...more](#)

Search & browse

Access to ENA data is provided through the browser, through search tools, large scale file download and through the API.

Text Search

Enter search query, for example: BN000065

Search

Sequence Search

[Advanced Search](#)

Search


Submit & update



Concluido

Iniciar

Windows Live M... Microsoft Power... Apresentação d... Sem título - Paint European Nucle... PT 13:19

agttaccttcgcatcgatcaactaaccaactcagcctcagaatgatgaagttcatgtgca

EMBL-EBI  **EB-eye Search** All Databases

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- Proteomic Services
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at the EBI

The Bioinformatics Institute (EBI) toolbox area provides a comprehensive set of tools for the field of bioinformatics. These are subdivided into categories in order of convenience.


The EBI toolbox area has developed a large number of very useful bioinformatics tools.


Tools include:



- Similarity & Homology** - the [BLAST](#) or [FASTA](#) programs can be used to look for sequence similarity
- Protein Functional Analysis** - [InterProScan](#) can be used to search for motifs in your protein
- Proteomic Services** **NEW** - [UniProt DAS](#) server allows researchers to show their research results in the context of UniProtKB/Swiss-Prot annotation.
- Sequence Analysis** - [ClustalW2](#) a sequence alignment tool.
- Structural Analysis** - [MSDfold](#) can be used to query your protein structure and compare it to those in the Protein Data Bank (PDB).
- Web Services** - provide programmatic access to the various databases and retrieval/analysis services EBI provides.
- Tools Miscellaneous** - [Expression Profiler](#) a set of tools for clustering, analysis and visualisation of gene expression and other genomic data.

Web Services

Web services provide programmatic access to the various databases and retrieval/analysis services EBI provides...



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EBI > Tools


Toolbox at the EBI

The European Bioinformatics Institute (EBI) toolbox area provides a comprehensive range of tools for the field of bioinformatics. These are subdivided into categories in the left menu for convenience.


We have developed a large number of very useful bioinformatics tools.

A few examples include:

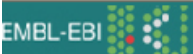

- Similarity & Homology** - the [BLAST](#) or [FASTA](#) programs can be used to look for sequence similarity and inter nomology.
- Protein Functional Analysis** - [InterProScan](#) can be used to search for motifs in your protein sequence.
- Proteomic Services** **NEW** - [UniProt DAS](#) server allows researchers to show their research results in the context of UniProtKB/Swiss-Prot annotation.
- Sequence Analysis** - [ClustalW2](#) a sequence alignment tool.
- Structural Analysis** - [MSDfold](#) or [DALI](#) can be used to query your protein structure and compare it to those in the Protein Data Bank (PDB).
- Web Services** - provide programmatic access to the various databases and retrieval/analysis services EBI provides.
- Tools Miscellaneous** - [Expression Profiler](#) a set of tools for clustering, analysis and visualisation of gene expression and other genomic data.



Web Services 

Web services provide programmatic access to the various databases and retrieval/analysis services EBI provides... [more](#)



Endereço  <http://www.ebi.ac.uk/Tools/blast/>

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- Structural Analysis
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NCBI-BLAST Related Literature

Search for NCBI-BLAST related literature in Medline... [more](#)

BLAST the UniProt Protein Resource

UniProt

- WU-BLAST2
- NCBI-BLAST2

UniParc

- WU-BLAST2
- NCBI-BLAST2

UniRef100

- WU-BLAST2
- NCBI-BLAST2

UniRef90

- WU-BLAST2
- NCBI-BLAST2

UniRef50

- WU-BLAST2
- NCBI-BLAST2

EBI > Tools > Similarity & Homology

BLAST @ EBI

BLAST stands for **B**asic **L**ocal **A**lignment **S**earch **T**ool. It is used to compare a novel sequence with those contained in nucleotide and protein databases by aligning the novel sequence with previously characterised genes. The emphasis of this tool is to find regions of sequence similarity, which will yield functional and evolutionary clues about the structure and function of this novel sequence. Regions of similarity detected via this type of alignment tool can be either local, where the region of similarity is based in 1 location, or global, where regions of similarity can be detected across otherwise unrelated genetic code.

Below is a list of all the BLAST's available at the EBI. Please note we also provide a '[Programmatic Access to BLAST](#)'.


General BLAST Programs



Tool	Description
WU-BLAST2 Protein ⓘ	Washington University BLAST2 for protein databases. (BLAST 2.0 with gaps)
WU-BLAST2 Nucleotide ⓘ	Washington University BLAST2 for nucleotide databases. (BLAST 2.0 with gaps)
NCBI-BLAST2 Protein ⓘ	NCBI BLAST2 (BLASTALL) program for protein databases.
NCBI-BLAST2 Nucleotide ⓘ	NCBI BLAST2 (BLASTALL) program for nucleotide databases.

Specialised BLAST Programs

Tool	Description
WU-BLAST2 ASD ⓘ	ASD BLAST server.
WU-BLAST2 Parasites ⓘ	Parasite Genomes BLAST server
NCBI-BLAST2 EVEC ⓘ	European BLAST2 Vector Searches. Check your sequences for vector contamination.
PSI-BLAST ⓘ [New Version]	Position specific iterative BLAST (PSI-BLAST) refers to a feature of BLAST 2.0 in which a profile is automatically constructed from the first set of BLAST alignments.
PSI-BLAST ⓘ [Old Version]	Position specific iterative BLAST (PSI-BLAST) refers to a feature of BLAST 2.0 in which a profile is automatically constructed from the first set of BLAST alignments.
PHI-BLAST ⓘ	Pattern Hit Initiated BLAST (PHI-BLAST) treats two occurrence of the same pattern within the query sequence as two independent sequences.

Endereço <http://www.ebi.ac.uk/Tools/blast2/nucleotide.html>

EMBL-EBI  **EB-eye Search** All Databases


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- Gaps
- Matrix
- References
- WU-BLAST2 Help
- MView Help
- DbClustal Help

- View all BLAST's at EBI
- WU-BLAST Programmatic Access

- Database Information
 - EMBL-Bank
 - IMG/HLA

- Similar Applications
 - FASTA
 - BLAST
 - GGSEARCH
 - GLSEARCH
 - MPsrch
 - ScanPS
 - SSEARCH


WU-BLAST Related Literature 

Search for WU-BLAST related literature

EBI > Tools > Similarity & Homology > BLAST > WU-BLAST2

WU-BLAST2 - Nucleotide Database Query

WU-BLAST2 stands for **W**ashington **U**niversity **B**asic **L**ocal **A**lignment **S**earch **T**ool Version 2.0. The emphasis of this tool is to find regions of sequence similarity or homology quickly, with minimum loss of sensitivity. This will yield functional and evolutionary clues about the structure and function of your novel sequence. [Dr Warren Gish](#) at [Washington University](#) released this first "gapped" version of [BLAST](#) allowing for gapped alignments and statistics.

 [Download Software](#)

PROGRAM	DATABASE	RESULTS	SEARCH TITLE	YOUR EMAIL
<input type="button" value="BLASTN"/>	<input type="button" value="Nucleic Acid"/>	<input type="button" value="interactive"/>	<input type="button" value="Sequence"/>	<input type="text"/>

MATRIX	EXP. THR	FILTER	VIEW FILTER	SENSITIVITY	DNA STRAND
<input type="button" value="default"/>	<input type="button" value="default"/>	<input type="button" value="dust"/>	<input type="button" value="no"/>	<input type="button" value="normal"/>	<input type="button" value="both"/>



SCORES	ALIGNMENTS	SORT	STATS	topcomboN	FORMAT
<input type="button" value="default"/>	<input type="button" value="default"/>	<input type="button" value="pvalue"/>	<input type="button" value="sump"/>	<input type="button" value="default"/>	<input type="button" value="Default"/>



Enter or Paste a Sequence in any format:

agttaccttcgcatcgatcaactaaccaactcagcctcagaatgatgaagttcatgtgca

Upload a file:

Endereço <http://www.ebi.ac.uk/Tools/blast2/nucleotide.html>

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- WU-BLAST Programmatic Access

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- EMBL-Bank
- IMGT/HLA

Similar Applications

- FASTA
- BLAST
- GGSEARCH
- GLSEARCH
- MPsrch
- ScanPS
- SSEARCH


WU-BLAST Related Literature

Search for WU-BLAST related literature in Medline... [more](#)

EBI > Tools > Similarity & Homology > BLAST > WU-BLAST2

WU-BLAST2 - Nucleotide Database Query

WU-BLAST2 stands for **W**ashington **U**niversity **B**asic **L**ocal **A**lignment **S**earch **T**ool Version 2.0. The emphasis of this tool is to find regions of sequence similarity or homology quickly, with minimum loss of sensitivity. This will yield functional and evolutionary clues about the structure and function of your novel sequence. [Dr Warren Gish](#) at [Washington University](#) released this first "gapped" version of [BLAST](#) allowing for gapped alignments and statistics.

 [Download Software](#)

PROGRAM	DATABASE	RESULTS	SEARCH TITLE	YOUR EMAIL
BLASTN	Nucleic Acid	interactive	Sequence	

MATRIX	SCORES	VIEW FILTER	SENSITIVITY	DNA STRAND
default	default	no	normal	both
		STATS	topcomboN	FORMAT
		sump	default	Default

Enter or Paste a sequence:

agttaccttgc

Upload a file:

Format:

during a course please [contact us](#).

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Endereço <http://www.ebi.ac.uk/Tools/es/cgi-bin/sumtab.cgi?tool=wublast&jobid=blast-20091008-1205592964>

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- UniParc

WU-BLAST2 Results

SUBMISSION PARAMETERS			
Title	Sequence	Database	em_rel_pat_inv
Sequence length	60	Sequence type	n
Program	WU-blastn	Version	2.0MP-WashU [04-May-2006]
Number of scores	100	Number of alignments	50
Expected threshold	10	Filter	dust

Alignment	DB:ID	Source	Length	Score	Identity%	Positives%	E()
1 <input type="checkbox"/>	EM_PAT:CQ586352	Sequence 14110 from Patent WO0171042.	2693	280	100	100	1.4e-06


**United States
National Library
of Medicine**

ChemIDplus Advanced


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Display 5 results

Substance Identification

Name/Synonym Equals

Data is available for 384,146 records.

Toxicity

Test: (any) between

(mg/kg or ppm)

Species: (any)

Route: (any)

Effect: (any)

Toxicity data is available for 139,354 records.

Physical Properties

Melting Point

between

Either Measurement Type

Physical property data was provided by [Syracuse Research Corporation](#) and is available for 25,461 records.

Locator Codes

Structure

[View](#) [Help](#)

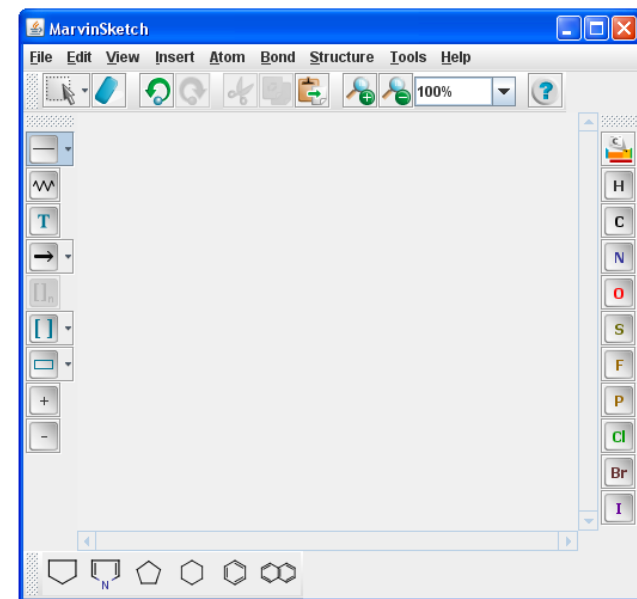
Powered by [ChemAxon Marvin](#)

Structure Search Options

- ☐ Substructure Search
- ☒ Similarity Search 80 %
- ☐ Exact (parent only)
- ☐ Flex (parent, salts, mixture) **NEW**
- ☐ Flexplus (parent, all variations) **NEW**

Display structures using

- ☒ Marvin
- ☐ Chime



<http://chem.sis.nlm.nih.gov/chemidplus/>

► [Env. Health & Toxicology](#)

Search

Clear

History

Help

Substance Identification

Name/Synonym

Equals

phenobarbital

Data is available for 389,463 records.

ChemIDplus Advanced - Mozilla Firefox

File Edit View History Markadores Ferramentas Ajuda

http://chem.sis.nlm.nih.gov/chemidplus/ProxyServlet?chemidheavy

Mais Visitados Começar Aqui Últimas Novidades Hotmail gratuito Personalizar hiperliga... Windows Media Windows

Start New Query

Modify Query

Show Query

Search History

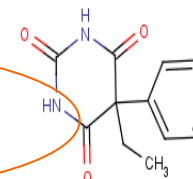
Go To Record Number

TOXNET Home

Results: 1 - 2 of 2

1

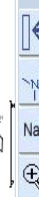
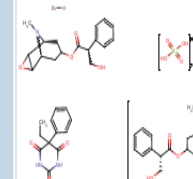
[Phenobarbital \(USAN:INN:JAN\)](#)
50-06-6



MMW: 232.2378

2

[Atropine sulfate mixture with phenobarbital and hyoscine sulfate and hyoscine hydrobromide](#)
8017-25-2



MMW: 1391.4066

Concluído

Iniciar

Windows Live Messe...

Microsoft PowerPoin...

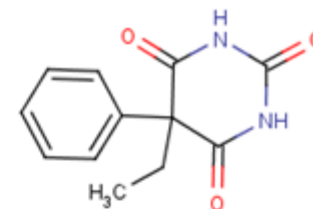
Sem título - Paint

ChemIDplus Advanc...

PT

12:20

NAME: Phenobarbital [USAN:INN:JAN]
RN: 50-06-6



MW: 232.238

[Enlarge Structure](#)

Basic Information

Full Record

Structure

Names & Synonyms

Formulas

Classification Codes

Registry Numbers

Notes

Toxicity

Physical Properties

For more information about this substance, you may select from the the links below.

File Locator

[CCRIS](#)
[ClinicalTrials.gov](#)

[DART](#)
[EINECS](#)

[EMIC](#)
[GENETOX](#)

[HSDB](#)
[LactMed](#)

[MeSH](#)
[MeSH Heading](#)

[MedlinePlusAll](#)
[MedlinePlusDrug](#)

[PubChem](#)
[PubMed](#)

[PubMed AIDS](#)
[PubMed Cancer](#)

[PubMed Toxicology](#)
[RTECS](#)

[TOXLINE](#)

[NCI Chem Carcino Res Info Sys](#)
[NIH ClinicalTrials.gov](#)
[Developmental and Reprod.Tox.](#)
[EU Inv of Exist. Comm. Chem Sub](#)
[Env. Mutagen Info. Center](#)
[EPA GENetic TOXicology](#)
[Hazardous Substances Data Bank](#)
[Drugs and Lactation Database](#)
[Medical Subject Headings File](#)
[Medical Subject Headings](#)
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[Consumer Drug Information](#)
[PubChem](#)
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[AIDS Citations from PubMed](#)
[Cancer Citations from PubMed](#)
[Toxicology Citations From PubMed](#)
[Reg. of Toxic Eff. of Chem. Sub.](#)
[NLM TOXLINE on TOXNET](#)

Search Navigation

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Modify Query

Show Query

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Structure Similarity Search

Structure Salt/Parent Search

Transfer Structure

Basic ChemIDplus Search

Classification Code

- [Anticonvulsant](#)
- [Anticonvulsants](#)
- [Central Nervous System Agents](#)
- [Central nervous system depressants](#)
- [Drug / Therapeutic Agent](#)
- [Excitatory Amino Acid Agents](#)
- [Excitatory amino acid antagonists](#)
- [GABA Agents](#)
- [GABA modulators](#)
- [Human Data](#)
- [Hypnotics and Sedatives](#)
- [Mutation data](#)
- [Neurotransmitter Agents](#)
- [Reproductive Effect](#)
- [Sedative-hypnotic](#)
- [Tumor data](#)

Superlist Classification Code

- [DEA Schedule IV](#)
- [Overall Carcinogenic Evaluation: Group 2B](#)



http://www.stn-international.de/stn_content.html?&L=class%3DI



<http://www.cas.org/expertise/cascontent/index.html>



The screenshot shows the STN International website. The header features the STN International logo and a navigation bar with links: Home, FIZ Karlsruhe Home, Press Room, Contact, Sitemap, and Print page. A search bar is located on the right. The main content area is divided into three columns. The left column contains a sidebar with categories: About STN, Solutions for, Products and Services, Customer Support, and Training Center, each with a list of sub-links. The middle column is titled 'Solutions for IP Professionals' and contains text about finding science and technology information, a list of services (Patentability, Prior art, Competitive intelligence, Legal status, Freedom-to-operate), and information about STN Express, STN on the Web, and STN Easy. The right column contains sections: Direct Access (Quicklinks), New on STN (updates for May 2009), Databases in Focus (Chemical Abstracts Plus, CAS REGISTRY, Derwent World Patents Index, INPAFAMDB), Meet us at (events in Erfurt and Ilmenau), and STN User Meetings. The footer includes a 'provided by' logo, legal notices, and a 'Top' link.

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- e-Seminars
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Solutions for IP Professionals

As an Intellectual Property (IP) professional, you can find science and technology information critical to your business needs - whether you do the searching or you let us search for you.

We offer patent and literature databases from all over the world for answering questions related to:

- Patentability
- Prior art
- Competitive intelligence
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To access the databases, you can use one or more of the following products:

STN - the online database service that connects you to patents, literature, substance information, and more

STN Express - comprehensive desktop access to the [STN Databases](#)

STN on the WebSM - comprehensive web access to STN

STN Easy - web access for the occasional or novice searcher

You can search patent data such as:

- Front page information, e.g., patent number, patent assignee, title
- Abstracts
- Full-text
- Legal status
- Patent family
- Database specific indexing, e.g., names and structures for specific or Markush structures, sequences, concepts

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- STN Express tools to easily mine large data sets, look for trends, and create graphical depictions of data for use in reports and presentations
- STN AnaVistTM features and capabilities for efficiently analyzing and interpreting information retrieved from scientific and patent databases
- STN ViewerTM features for simple management and evaluation of full-text patent documents from STN Express answer sets

Direct Access

Quicklinks

New on STN

May 2009
STN Express, Version 8.4, now available
[Read more](#)

May 2009
BEILSTEIN Database Update
[Read more](#)

May 2009
Legal Status Data for China now available in INPAFAMDB and INPADOCDB
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[More News Messages](#)

Databases in Focus

[Chemical Abstracts Plus \(CAplusSM\) and CAS REGISTRYSM](#)

[Derwent World Patents Index \(DWPI\)](#)

[INPAFAMDB](#)

Meet us at

98. Deutscher Bibliothekartag, Erfurt, Jun 02 - 05

Patinfo, Jun 18 - 19, Ilmenau

[More Information](#)

STN User Meetings

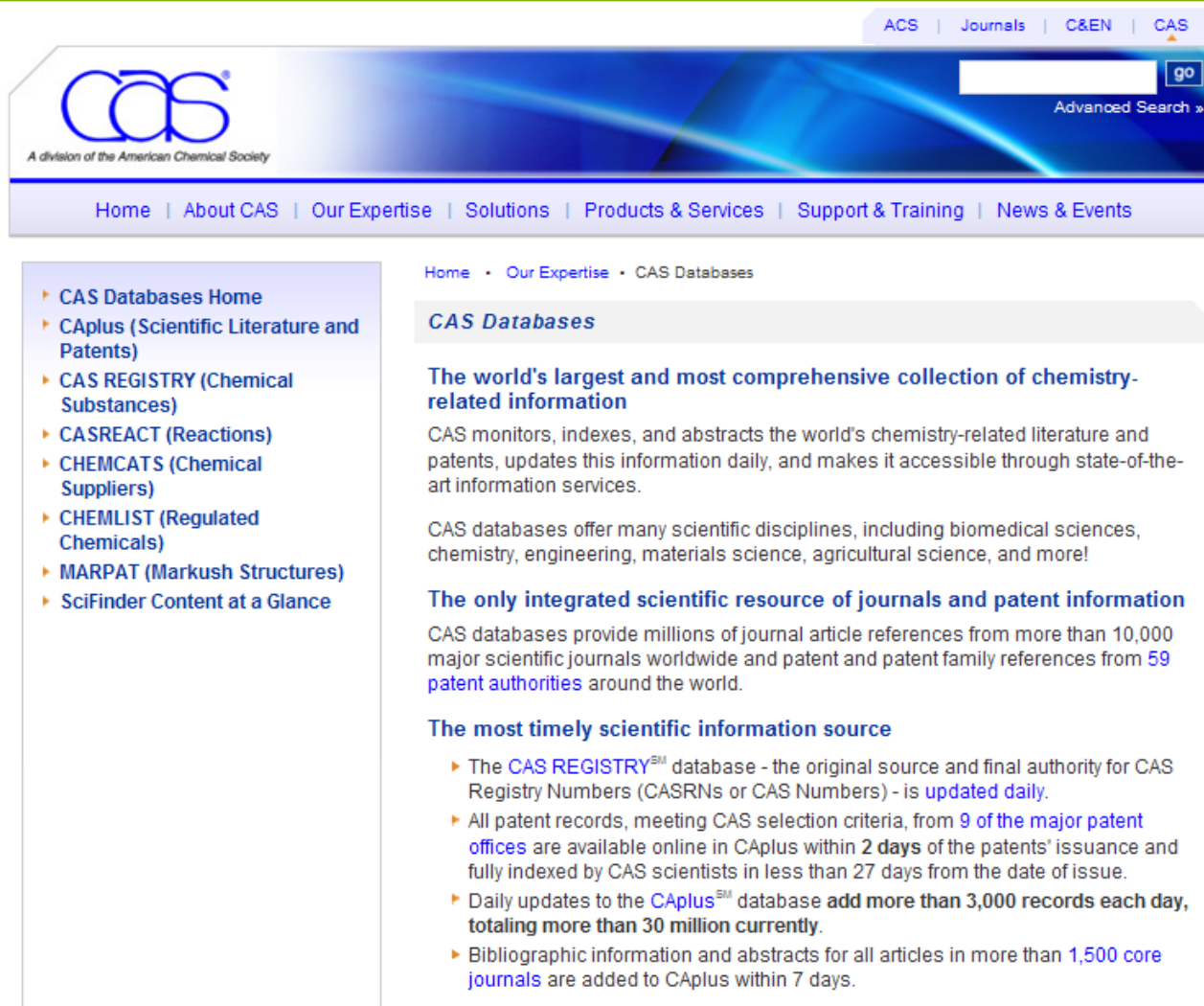
STN Benutzertreffen, München, Germany, June 16, 2009
STN User Meeting, Amsterdam, Netherland, June 30, 2009

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- ✓ Pesquisa por estrutura, CAS, sequência ou função em bases de dados científicas e de patentes
- ✓ Pesquisa de sequências homólogas em bases de dados científicas e de patentes



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A division of the American Chemical Society

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CAS databases offer many scientific disciplines, including biomedical sciences, chemistry, engineering, materials science, agricultural science, and more!

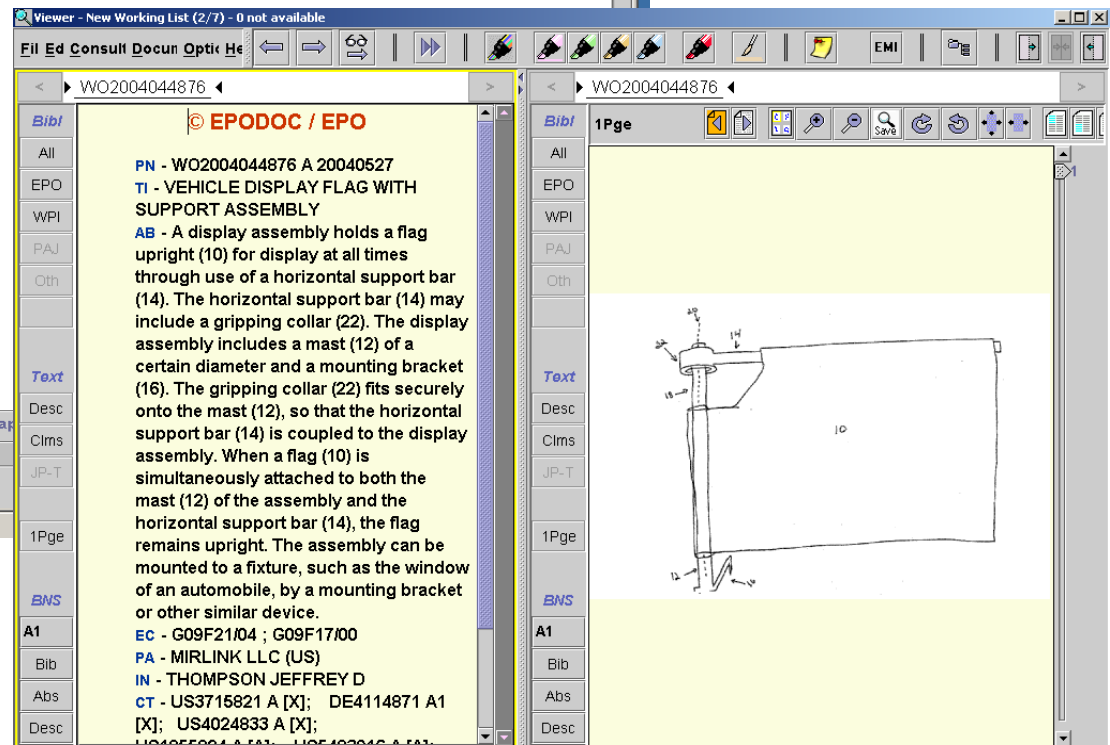
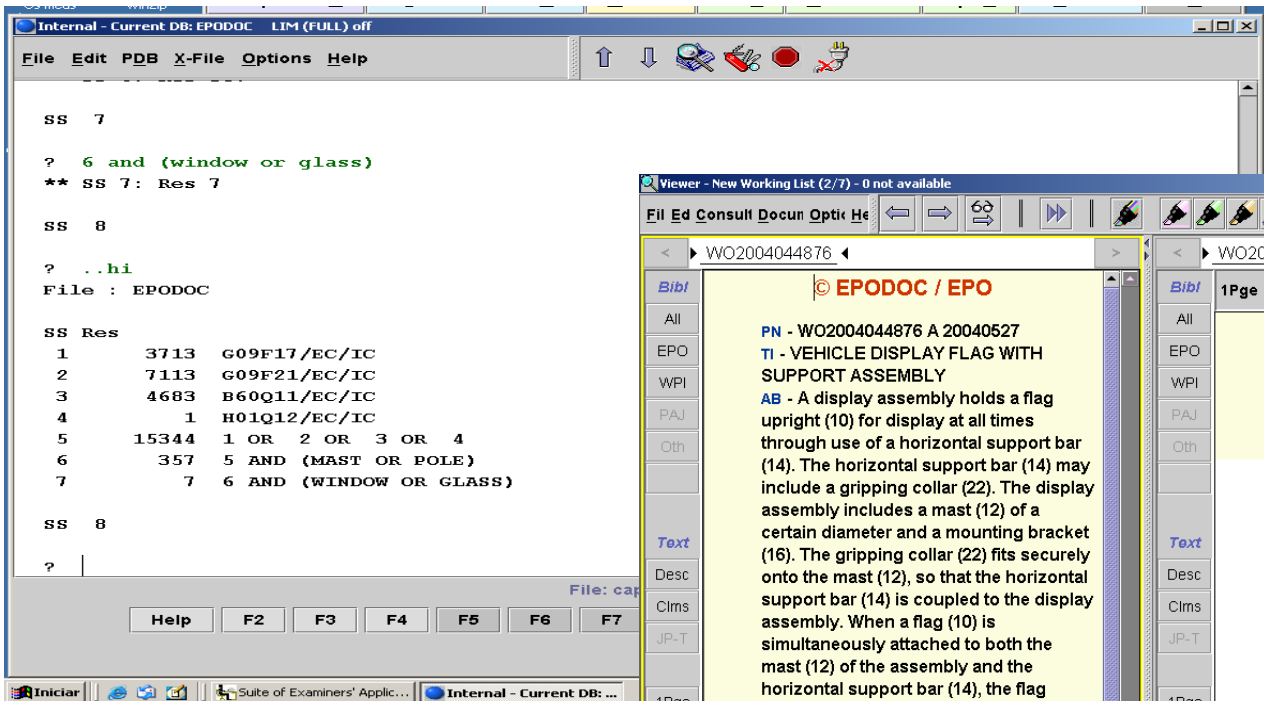
The only integrated scientific resource of journals and patent information

CAS databases provide millions of journal article references from more than 10,000 major scientific journals worldwide and patent and patent family references from **59 patent authorities** around the world.

The most timely scientific information source

- ▶ The **CAS REGISTRYSM** database - the original source and final authority for CAS Registry Numbers (CASRNs or CAS Numbers) - is **updated daily**.
- ▶ All patent records, meeting CAS selection criteria, from **9 of the major patent offices** are available online in CPlus within **2 days** of the patents' issuance and fully indexed by CAS scientists in less than 27 days from the date of issue.
- ▶ Daily updates to the **CPlusSM** database **add more than 3,000 records each day, totaling more than 30 million currently**.
- ▶ Bibliographic information and abstracts for all articles in more than **1,500 core journals** are added to CPlus within 7 days.

<http://www.cas.org/expertise/cascontent/index.html>



? ..fi

1	AKFU	Access file to USPTO Classification	
2	ALLOYS	Ferrous and non-ferrous alloys compositions	
3	APC	Board of Appeals decisions	
4	BIOSIS	Biological Abstracts	*LAE
5	BOCA	Book and magazine catalogue	
6	CIS	Complementary Information System	
7	COMPDX	Computerized engineering index	*LAE
8	CXCLA	COMPENDEX Classification	
9	ECLA	EPO Classification	
10	EMBASE	Biomedical and pharmacological data.	*LAE
11	EPODOC	EPO Documentation	
12	EPOS	EPO Synonyms	
13	EPUS	EPO-USPTO Class concordance	
14	EUREG	European Patent Register	
15	FICLA	JPO Classification	
16	FLDNAME	Field names of the EPOQUE databases	
17	FSTA	Food Science Technology Abstracts	*LAE
18	FTCLA	F-Terms Classification	
19	ICLA	INSPEC Classification	
20	IDT	Indeling Der Techniek Classification	
21	INSPEC	Physics Electronics Computing	*LAE
22	IPC	International Patent Classification vers.8	
23	IPC1	International Patent Classification vers.1	
24	IPC2	International Patent Classification vers.2	
25	IPC2006	International Patent Classification vers.8	
26	IPC3	International Patent Classification vers.3	
27	IPC4	International Patent Classification vers.4	
28	IPC5	International Patent Classification vers.5	
29	IPC6	International Patent Classification vers.6	
30	IPC7	International Patent Classification vers.7	
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32	MEDLINE	US National Library of Medicine	*LAE
33	NPL	Non Patent Literature	
34	PUBCHEM	Chemical structure and compound names	*LAE
35	RM13	Telephony	
36	RM18	Electric connectors	
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38	RM26	Laminates from 2000	

39	RM5N	Laminates up to 1971	
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43	SQEMOTH	Bib. data biological seq. EMBL Others	*LAE
44	SQEMWGS	Bib. data biological seq. WGS	*LAE
45	SQPRPUB	Bib. data biological seq. Uniprot+Prot	*LAE
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47	TCPAT	Correspondence and Flag Table	
48	TDB	IBM Technical Disclosure Bulletins	*LAE
49	TXAT1	Full-text of Austrian documents	*PFG
50	TXTAU1	Full-text of Australian documents	*PFE
51	TXTBED	Full-text of Dutch BE documents	*PFD
52	TXTBEF	Full-text of French BE documents	*PFF
53	TXTBEG	Full-text of German BE documents	*PFG
54	TXTCAF	Full-text of French CA documents	*PFF
55	TXTCAL	Full-text of English CA documents	*PFE
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74	WPI	World Patent Index (Derwent)	
75	WPICLA	WPI Classification	
76	XPAIP	American Institute of Physics documents	*LFE
77	XPESP	Full-text ELSEVIER Publications	*LFE
78	XPETSI	European Telecom Std Institute	*LFE
79	XPIEE	Inst. of Electrical Engineers (IEE)	*LFE
80	XPIETF	Internet Engineering Task Force	*LFE
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82	XPI3E	Inst. of Electrical /tronics Engineers	*LFE
83	XPJPEG	Joint Photographic Expert Group Std	*LFE
84	XPMISC	NPL Full-Text : Miscellaneous Providers	*LFE
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