

# Chromozomy – jak zjistit kolik má daný druh chromozomů?

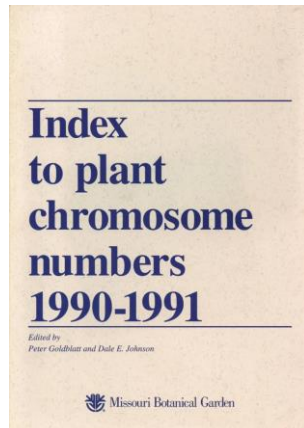
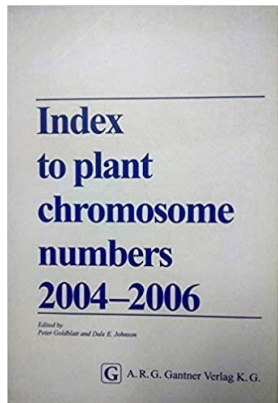
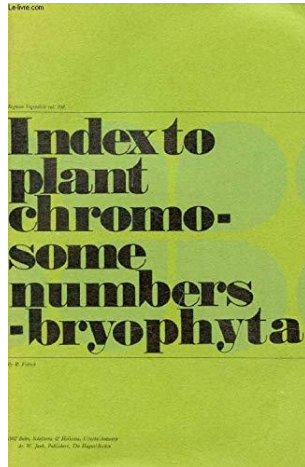
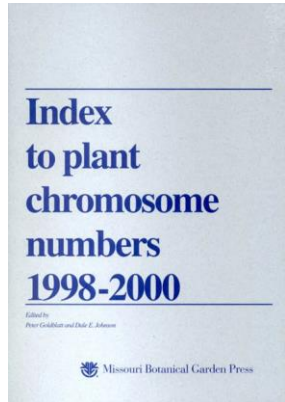


<http://ccdb.tau.ac.il/home/>

A screenshot of the CCDB (Chromosome Counts Database) website. The page features a green header with the CCDB logo and navigation links: Home, About, Browse, Services, Add new counts, Contact. Below the header, there is a search bar and a main text area. The main text describes the database as a comprehensive community resource for plant chromosome numbers, updated regularly. It encourages users to contribute by submitting new counts or reporting erroneous counts. A recommended citation is provided: Rice et al. 2015. The Chromosome Counts Database (CCDB) – a community resource of plant chromosome numbers. New Phytol. 206(1): 19-26. An abstract is also present. A 'Browse' section offers four categories: Flowering Plants (Angiosperms), Conifers, cycads and allies (Gymnosperms), Ferns and fern allies (Polypodiophytes and Lycophytes), and Mosses and liverworts (Bryophytes). A 'News' sidebar on the right lists recent updates, such as '12/18 6 New counts from Minareci2009' and '12/18 16 New counts from Yildiz2006'.

# Chromozomy – jak zjistit kolik má daný druh chromozomů?

<http://legacy.tropicos.org/Project/IPCN>



← → ↻ 🏠 legacy.tropicos.org/Project/IPCN 🔍 Vyhledat 📄 ⋮ ⭐ 🗨️

⚙️ Nejnavštěvovanější 🌐 Jak začít 📄 V negativním slova ... 🌐 ISI Web of Knowledge ... 📄 Electronic library. Dow... 🌐 Výsledek obrázku pro J... ➡️ 📁 Ostatní záložky

## 🌿 IPCN Chromosome Reports

Tropicos Names Specimens References Projects Images More Tools

MOBOT Sign In | Login | ?

Choose Project English

Home  
Name Search  
Browse Families  
Browse Genera  
Browse Species

### Index to Plant Chromosome Numbers (IPCN)

The *Index to Plant Chromosome Numbers* was an NSF funded project that aims to extract and index original plant chromosome numbers of naturally occurring and cultivated plants published throughout the world. A committee of voluntary contributing editors, located in various parts of the world, reviews sets of serial titles assigned to them and returns the information to the editors for collation in the *Index* and database. Chromosome indexes were published at two or three year intervals. The *Index to Plant Chromosome Numbers* project was based at the Missouri Botanical Garden since 1978. Data from published indexes from 1979 onward are available for consultation through this facility.

For additional information, see the last supplement by Goldblatt & Johnson 2006. *Index to Plant Chromosome Numbers 2001-2003. Monographs in Systematic Botany from the Missouri Botanical Garden* 106.

An Index covering the years 2004-2006 was published in 2010 as: Goldblatt & Johnson (eds) 2010. *Index to Plant Chromosome Numbers 2004-2006. Regnum Vegetabile*. Vol. 152.

Many but not all data in the printed version of the *Index to Plant Chromosome Numbers* (1979-- ) are available on the Web in the IPCN database. The printed indexes and the database provide references to chromosome counts reported in the original literature. We therefore request that the IPCN database itself not be cited as the source for chromosome counts. If there is a need to cite the IPCN database, we recommend the following:

*Index to plant chromosome numbers*. 1979-- . P. Goldblatt & D. E. Johnson, eds. Missouri Botanical Garden, St. Louis.

#### How to use the Chromosome Index.

The chromosome data is available in several different ways. First information is available on the Name screens as a tab for any taxon with counts – click on the 'chromosome counts' tab and see the reported counts with reference.

Second, under the System **project** tab (top yellow banner) there is a link to "IPCN Chromosome Reports" that provides a name search for direct display of counts for each taxon and Browse links for families, genera.

The Family and genera browse options provide links to included taxa on the page under 'lower taxa' (genera for families and species for genera) with counts. Click on the taxon link and see all of the species with counts – click on the taxon to see all of the counts for that taxon. The species browse screen provides an alphabetical list of species in the project and the link to displays the counts and references.

Last, next to each family/genus on the browse list or at the bottom of the lower taxa lists under families/genera is an (**export**) link. This will download a complete list of all the included taxa with counts and references, to the user pc. This '.dat' file is a tab delimited ascii file that can be saved and/or opened with Excel (or other similar programs) that can be used for searches or sorting on the users pc. Note that this may be a very large file if for example one exports all of the counts for Asteraceae rather than only the genera or species that are needed.

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Velikost genomu – jak velký genom má daný druh?

<https://pladias.cz/taxon/>

The screenshot shows the PLADIAS website. At the top, there is a navigation bar with the PLADIAS logo and menu items: Druhy, Vegetace, Určování, Ke stažení, Kontakty, and Přihlášení. Below this is a search bar with the text "Hledat" and a search box containing "Taxon zadejte jméno". Underneath the search bar is a table titled "Základní taxony" listing various plant groups and their corresponding Czech names.

Základní taxony	
<i>Lycopodiopsida</i>	plavuně
<i>Equisetopsida</i>	přesličky
<i>Psilotopsida</i>	prutovky
<i>Polypodiopsida</i>	kapradiny
<i>Ginkgoopsida</i>	jinany
<i>Coniferopsida</i>	jehličnany
<i>Magnoliopsida 1</i>	nižší dvouděložné
<i>Liliopsida</i>	jednoděložné
<i>Magnoliopsida 2</i>	vyšší dvouděložné

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Citace: Pladias – databáze české flóry a vegetace. [www.pladias.cz](http://www.pladias.cz)

<https://cvalues.science.kew.org/>

The screenshot shows the Kew Plant DNA C-values Database website. The header features the Kewscience logo and the text "Plant DNA C-values Database". Below the header is a navigation menu with items: Home, Introduction, Search, All Plant C-values, Angiosperm C-values, Gymnosperm C-values, Pteridophyte C-values, Bryophyte C-values, and Algal C-values. The main content area includes a "Home" section with the text "Plant DNA C-values Database" and "Release 7.1, April 2019. Leitch IJ, Johnston E, Pellicer J, Hidalgo O, Bennett MD". Below this is a row of six categories: All Plants, Angiosperm, Gymnosperm, Pteridophyte, Bryophyte, and Algae, each with a representative image. The text below the categories states: "The DNA amount in the unreplicated gametic nucleus of an organism is referred to as its C-value, irrespective of the ploidy level of the taxon. The Plant DNA C-values Database currently contains C-value data for 12,273 species comprising 10,770 angiosperms, 421 gymnosperms, 303 pteridophytes (246 ferns and fern allies and 57 lycophytes), 334 bryophytes, and 445 algae." At the bottom, there is a contact information section: "If you have comments and/or suggestions contact [dnac-value@kew.org](mailto:dnac-value@kew.org)". The footer features the Kew logo and the text "Royal Botanic Gardens Kew" along with links for Terms and Conditions, Cookie Policy, and Privacy Policy.

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# Velikost genomu – jak velký genom má daný druh?

<https://www.asteraceaegenomesize.com/>

**GSAD**  
Genome size in Asteraceae database  
release 3.0, July 2018

Search...

Author  Infrasp. author  Chrom. number  n/2n  Life cycle  Ploidy level  Standard **Advanced**  
Optional identification of the user: youremail@email.com

### Welcome to the GSAD: Genome Size in Asteraceae Database (Release 3.0) NEW

The GSAD is an exhaustive catalogue of genome size data for the family Asteraceae. Genome sizes are now available for 1,555 species based on 4,350 records from 198 publications released until July 2018. The current update represents around 40% increase of data entries with respect to release 2. There are 337 species (21.67%) and 46 genera (19.83%) recorded for the first time.

The main goal of the database is to serve as a tool aiming to make Asteraceae genome size information accessible to scientists interested in genome characterisation and evolution with basic (e.g. plant molecular systematics, NGS programs, evo-devo research) or applied (e.g. barcoding, breeding, races or raw material identification) focuses.

The database holds data from papers already published or in press up to July 2018. Regular updates are planned.

**Learn more...**

#### Data increment

Release	Percentage
Release 1.0	~55%
Release 2.0	~30%
Release 3.0	~15%

#### Methods

Method Group	Percentage
Group A	~75%
Group B	~15%
Group C	~5%
Group D	~5%
Group E	~2%
None	~2%

#### Legend

- Group A** (Flow cytometry with different fluorochromes)
- Group B** (Feulgen densitometry/ microdensitometry/ cytophotometry/ microspectrophotometry)
- Group C** (Feulgen image scanning or analysis)
- Group D** (Feulgen scanning densitometry or scanning microdensitometry)
- Group E** (biochemical method or chemical extraction)

© Design and programming by @iguannaweb and @bioscripts respectively for BioFIC-Planta / EtnobotCat -

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Visits since June 2013: 00012632 [Stats](#)

Velikost genomu – jak velký genom má daný druh?

<http://www.genomesize.com/>

The screenshot shows the homepage of the Animal Genome Size Database. At the top, the browser address bar displays [www.genomesize.com](http://www.genomesize.com/). The main header reads "ANIMAL GENOME SIZE DATABASE" with a "HOME" link on the right. A navigation menu on the left includes: Home, Search Data, Statistics, FAQ, References, Submit Data, and Links. A featured image shows a snail with the text: *Takifugu rubripes*, C-value: 0.40pg. A central box contains a French quote: "Il est hors de doute que l'étude systématique, de la teneur absolue du noyau en acide desoxyribonucleique, a travers de nombreuses especes animales, puisse fournir des suggestions interessantes en ce qui concerne le probleme de l'evolution." attributed to Vendrely and Vendrely, 1950, with a "Translate" link. Below this, a welcome message states: "Welcome to the *Animal Genome Size Database*, Release 2.0, a comprehensive catalogue of animal genome size data. Haploid DNA contents (C-values, in picograms) are currently available for 6222 species (3793 vertebrates and 2429 non-vertebrates) based on 8004 records from 786 published sources. You can navigate the database using the menu on the left. New features in Release 2.0 include enhanced [browsing and search](#) functions, data export capabilities, and up to the minute [summaries](#) of available data." The footer includes logos for Gregory Lab Genomic Diversity, University of Guelph, and the Biodiversity Institute of Ontario, along with a book cover titled "THE EVOLUTION OF THE GENOME" edited by T. Ryan Gregory.

# Sekvence nukleotidů – jsou k dispozici pro daný druh?

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

NCBI Home

Resource List (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

### Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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#### Submit

Deposit data or manuscripts into NCBI databases

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Transfer NCBI data to your computer

#### Learn

Find help documents, attend a class or watch a tutorial

#### Develop

Use NCBI APIs and code libraries to build applications

#### Analyze

Identify an NCBI tool for your data analysis task

#### Research

Explore NCBI research and collaborative projects

### Popular Resources

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

### NCBI News & Blog

NCBI at CSHL Biology of Genomes, May 11 – 14, 2021 07 May 2021

NCBI staff will be presenting virtual posters at the Cold Spring Harbor 06 May 2021

NCBI on YouTube: Tips for My Bibliography, Genome Data Viewer and more 06 May 2021

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GAATTTGCTATCCATAATCATTGTCATTTCTTTATTGACATGAAAAATATGATTTGATTGTTATTATGATCAA  
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ATACCAAGGCCAATCCAATGC

[http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE\\_TYPE=BlastSearch&LINK\\_LOC=blasthome](http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome)