

# CellBase Home

Cellbase is a centralised database that integrates lots of information from several main genomic and biological databases used for genomic annotation and clinical variant prioritisation. See [Overview](#) for details.

CellBase is open-source and freely available at <https://github.com/opencb/cellbase>

You can search CellBase using your favourite programming language:

	installation	API	docs	tutorials
REST API			<a href="#">RESTful Web Services</a>	
Python	<a href="#">pypi</a>			
R	<a href="#">Bioconductor</a>			<a href="#">Vignette</a>
Java	<a href="#">Installation</a>	<a href="#">Javadoc</a>		

## Recent space activity



[Julie Sullivan](#)

[Data sources and species](#) updated Jun 02, 2020 • [view change](#)

[Installation](#) updated Mar 10, 2020 • [view change](#)

[CellBase Versions](#) updated Feb 20, 2020 • [view change](#)

[CellBase Home](#) updated Jan 06, 2020 • [view change](#)

[Building the CellBase database](#) updated Jan 06, 2020 • [view change](#)



[CellBase 4.5.3 released](#)

[Javier Lopez](#) posted on Nov 22, 2017

Some important fixes made, please check

<https://github.com/opencb/cellbase/releases/tag/v4.5.2>

<https://github.com/opencb/cellbase/releases/tag/v4.5.3>

Web services updated and accessible at:

<http://bioinfo.hpc.cam.ac.uk/cellbase/webservices>



[CellBase 4.5.1 released](#)

[Javier Lopez](#) posted on Oct 11, 2017

Some important fixes made, please check

<https://github.com/opencb/cellbase/releases/tag/v4.5.1>

Web services updated and accessible at:

<http://bioinfo.hpc.cam.ac.uk/cellbase/webservices>



[CellBase v4.5.0 Released](#)

[Javier Lopez](#) posted on Sep 25, 2017

New data sources, new web services and many variant annotation improvements (structural variants annotation, new population frequencies datasets and much more).

Accessible now at

<http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

Please, have a look to the release notes document at

<https://github.com/opencb/cellbase/releases/tag/v4.5.0>



#### [Updated variation downloads](#)

[Javier Lopez](#) posted on Jun 12, 2017

variation\_chr\*.full.json.gz GRCh37 files in our http download server have been updated to include gnomAD frequencies:

[http://bioinfo.hpc.cam.ac.uk/downloads/cellbase/v4/homo\\_sapiens\\_grch37/variation/json/](http://bioinfo.hpc.cam.ac.uk/downloads/cellbase/v4/homo_sapiens_grch37/variation/json/)



#### [CellBaseR Bioconductor](#)

[Javier Lopez](#) posted on Jun 12, 2017

An R CellBase client (CellBaseR) is now distributed by Bioconductor

<https://bioconductor.org/packages/release/bioc/html/cellbaseR.html>



#### [gnomAD population frequencies](#)

[Javier Lopez](#) posted on Jun 02, 2017

gnomAD exomes and genomes population frequencies (GRCh37) are now provided as part of the variant annotation results:

<http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/rest/v4/hsapiens/genomic/variant/19:45411941:T:C/annotation>

<http://gnomad.broadinstitute.org/>

## Space contributors

- [Julie Sullivan](#) (803 days ago)
- [Nacho Medina](#) (986 days ago)
- [Javier Lopez](#) (1040 days ago)
- [Daniel Perez](#) (1518 days ago)