

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

CNVVdb - Copy Number Variations across Vertebrate genomes

RRID:SCR_007194

Type: Tool

Proper Citation

CNVVdb - Copy Number Variations across Vertebrate genomes (RRID:SCR_007194)

Resource Information

URL: <http://cnvvdb.genomics.sinica.edu.tw/>

Proper Citation: CNVVdb - Copy Number Variations across Vertebrate genomes (RRID:SCR_007194)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 17, 2013. A web interface for identification of potential inter-species CNV information by finding duplicated regions within a genome (paralogues) and between different genomes (orthologues). The paralogues/orthologues are inferred from pairwise sequence alignments between 16 vertebrate species. Note that the CNVs referred here are not equal to copy number polymorphisms of a population. Further experimental evidence is needed to support the polymorphism status of the inferred CNVs in this database.

Abbreviations: CNVVdb

Synonyms: Copy Number Variations across Vertebrate genomes

Resource Type: database, data or information resource, service resource

Funding: National Health Research Institutes; Zhunan; Taiwan

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CNVVdb - Copy Number Variations across Vertebrate genomes

Resource ID: SCR_007194

Alternate IDs: nlx_94129

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260808T190402+0000

Ratings and Alerts

No rating or validation information has been found for CNVVdb - Copy Number Variations across Vertebrate genomes.

No alerts have been found for CNVVdb - Copy Number Variations across Vertebrate genomes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Ostrovskaya I, et al. (2010) A classification model for distinguishing copy number variants from cancer-related alterations. BMC bioinformatics, 11, 297.