

Resource Summary Report

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Recombination Detection Program

RRID:SCR_018537

Type: Tool

Proper Citation

Recombination Detection Program (RRID:SCR_018537)

Resource Information

URL: <http://web.cbio.uct.ac.za/~darren/rdp.html>

Proper Citation: Recombination Detection Program (RRID:SCR_018537)

Description: Software package to analyse nucleotide sequence data and identify evidence of genetic recombination. RDP3 is version of RDP program for characterizing recombination events in DNA-sequence alignments. RDP4 is version of RDP program for detection and analysis of recombination patterns in virus genomes.

Abbreviations: RDP

Synonyms: Recombination Detection Program, RDP4, RDP3

Resource Type: software resource, data processing software, software application, data analysis software

Defining Citation: [PMID:27774277](#), [PMID:20798170](#)

Keywords: DNA sequence, alignment, phylogenetic tree, nucleotide analysis, sequence data analysis, genetic recombination identification, DNA sequence alignment, recombinant pattern analysis, virus genome

Funding: Wellcome Trust ;
Fund for Scientific Research Flanders ;
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NIAID AI090970;
NIGMS U01 GM110749;

NIAID AI100665

Availability: Free, Available for download, Freely available

Resource Name: Recombination Detection Program

Resource ID: SCR_018537

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260804T043717+0000

Ratings and Alerts

No rating or validation information has been found for Recombination Detection Program.

No alerts have been found for Recombination Detection Program.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 483 mentions in open access literature.

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

Wang Y, et al. (2026) Molecular characterization and pathogenicity of a novel Chinese porcine deltacoronavirus strain CH/HLJ/20 isolated from diarrheic piglets. *Virulence*, 17(1), 2605366.

Wirten M, et al. (2025) Benefits of HIV-1 transmission cluster surveillance: a French retrospective observational study of the molecular and epidemiological co-evolution of recent circulating recombinant forms 94 and 132. *Journal of the International AIDS Society*, 28(2), e26416.

Suvanto MT, et al. (2025) Isolation and genetic characterization of a novel Kevo orbivirus and a strain of Mobuck virus from Ochlerotatus communis mosquitoes in Finland. *The Journal of general virology*, 106(6).

Wangui J, et al. (2025) Molecular Analysis of Human Respiratory Syncytial Virus Group B Strains Isolated in Kenya Before and During the Emergence of Pandemic Influenza A/H1N1. *Influenza and other respiratory viruses*, 19(2), e70082.

McClure CP, et al. (2025) 'Vivaldi': an amplicon-based whole-genome sequencing method for the four seasonal human coronaviruses, 229E, NL63, OC43 and HKU1, alongside SARS-CoV-2. *Microbial genomics*, 11(7).

- Chen Y, et al. (2025) Genomic, Evolutionary, and Pathogenic Characterization of a New Polerovirus in Traditional Chinese Medicine *Viola philippica*. *Viruses*, 17(1).
- Wei C, et al. (2025) Genetic characterization and pathogenicity of two recombinant PRRSV-2 strains from lineages 1, 3, 5, and 8 emerged in China. *BMC veterinary research*, 21(1), 341.
- Fu QL, et al. (2025) Novel avian metapneumovirus subtype C variant is a newly emerged pathogen causing hydrosalpinx fluid syndrome in Sheldrake ducks in China. *Virulence*, 16(1), 2590254.
- Tolentino JE, et al. (2025) Structural and phenotypic plasticity of the RBD loop2 region is a key determinant for HKU5r-CoVs' emergence in mink. *bioRxiv : the preprint server for biology*.
- Mauriello MA, et al. (2025) Begomovirus species demarcation based on genome-sequence identity often yields non-monophyletic species: A case study of sweet potato-infecting begomoviruses. *bioRxiv : the preprint server for biology*.
- Zhang XL, et al. (2025) Research note: Genetically diverse avian hepatitis E virus identified in chickens with hepatitis-splenomegaly syndrome in Guangdong Province, China. *Poultry science*, 104(1), 104557.
- Zhang Z, et al. (2025) First report of inter-species recombinant Gyroviruses in Chinese urban companion animals with cross-species transmission risks. *Frontiers in veterinary science*, 12, 1619325.
- Li M, et al. (2025) Evolutionary and genotypic analyses of goose astrovirus. *Poultry science*, 104(10), 105511.
- Zang J, et al. (2025) Molecular characteristics of human adenovirus isolated from the 2024 influenza-like illness outbreaks in Suzhou City, China. *Virology journal*, 22(1), 243.
- Shukla B, et al. (2025) Molecular genetic analyses of the N, NSm and NSs genes of a local population of Orthotospovirus tomatomaculae reveal purifying selection in crops in the southeastern USA. *The Journal of general virology*, 106(7).
- Yuan N, et al. (2025) Molecular Epidemiology and Genetic Evolution of Porcine Reproductive and Respiratory Syndrome Virus in Northern China During 2021-2023. *Viruses*, 17(1).
- Ren Y, et al. (2025) First isolation and characterization of a bovine parainfluenza virus type 3 genotype C strain from an aborted Holstein fetus. *Frontiers in veterinary science*, 12, 1598013.
- Škorić D, et al. (2025) Tomato spotted wilt virus in tomato from Croatia, Montenegro and Slovenia: genetic diversity and evolution. *Frontiers in microbiology*, 16, 1618327.
- Kim SJ, et al. (2025) Genetic, pathogenic, and antigenic characterization of GX-1, a novel infectious bronchitis virus genotype identified in South Korea. *Poultry science*, 105(2), 106217.

Zhang G, et al. (2025) Identification and phylogenetic characterization of novel hunnivirus recombinant strains in cattle from Guangxi, China. *Frontiers in cellular and infection microbiology*, 15, 1559722.