

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

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Carnegie Corporation ;
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 diarrhetic piglets. *Virulence*, 17(1), 2605366.

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.

Chen Y, et al. (2025) Genomic, Evolutionary, and Pathogenic Characterization of a New Poliovirus 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.

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.

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).

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).

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.

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.

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.

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).

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.

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.

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).

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.