

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>

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

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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Availability: Free, Available for download, Freely available

Resource Name: Recombination Detection Program

Resource ID: SCR_018537

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260912T195902+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 507 mentions in open access literature.

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

Cao HT, et al. (2026) Molecular characterization and evolutionary dynamics of a recombinant PDCoV strain in a swine diarrhea epidemic with SADS-CoV co-infection. *Frontiers in veterinary science*, 13, 1749819.

Bourgikos E, et al. (2026) Evolutionary history of Jamestown Canyon virus disentangles complex multi-vector ecology. *bioRxiv : the preprint server for biology*.

Luan Q, et al. (2026) Genetic variability and phylogenetic analysis of the VP2 gene of feline parvovirus in Harbin. *Frontiers in veterinary science*, 13, 1783463.

Xu W, et al. (2026) Structural diversity of Ym2, a gene conferring resistance against Wheat yellow mosaic virus. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(2), 57.

Cao L, et al. (2026) Highly divergent virome in wild rodents of Xinjiang, China: Implications for rodent origin of porcine reproductive and respiratory syndrome virus 1. *Zoological research*, 47(1), 72.

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.

Kwak M, et al. (2026) High-throughput sequencing-based virome analysis reveals genomic diversity and recombination of tomato-infecting viruses in Korea. *Scientific reports*, 16(1).

Zhang H, et al. (2026) Evolutionary dynamics of endogenous densoviruses NS1 proteins reveal ancient codivergence with their Platyhelminth hosts. *Microbiology spectrum*, 14(4), e0344125.

Ma W, et al. (2026) Whole-genome analysis of CVA4 in children with herpangina in two cities of Shandong, China. *Scientific reports*, 16(1).

Hu X, et al. (2026) Full-genome analysis of emerging Coxsackievirus B4 genotype D strains associated with herpangina in eastern China. *Microbial genomics*, 12(2).

Xiong T, et al. (2026) Characterization of the Genomics and Antigenicity of a Naturally Attenuated Gammacoronavirus Infectious Bronchitis Virus Strain in the Genotype GVI-1 Lineage. *Viruses*, 18(2).

Li C, et al. (2026) Genetic Evolutionary Analysis and Characterization of Bovine Viral Diarrhea Virus in Gansu Province, China. *Viruses*, 18(6).

Mauriello MA, et al. (2026) Begomovirus species demarcation based on genome-sequence identity yields non-monophyletic species: a case study of sweet potato-infecting begomoviruses. *Virus evolution*, 12(1), veag007.

Lee ES, et al. (2026) Reclassification and Recombination Analysis of Porcine Epidemic Diarrhea Virus Strains in South Korea Based on Spike Gene Analysis. *Veterinary sciences*, 13(3).

El-Duah P, et al. (2026) Detection and complete genome characterisation of bat coronaviruses from Ghana. *Archives of virology*, 171(6).

Lagrange A, et al. (2026) Retrospective Phylogenetic Analysis of Mayaro Virus, French Guiana, 1996-2024. *Emerging infectious diseases*, 32(5), 740.

Shen Q, et al. (2026) Viral communities and identification of a parvovirus and two picornaviruses in geese with gout. *The Journal of veterinary medical science*, 88(2), 341.

Chen J, et al. (2026) Molecular epidemiology and genetic characteristics of enterovirus A identified in pediatric patients with hand, foot, and mouth disease and herpangina in Linyi, China, 2023-2024, following the relaxation of COVID-19 policies. *BMC infectious diseases*, 26(1).

Santos-Silva S, et al. (2026) Molecular surveillance and genomic characterization of enterovirus D68 in southern Portugal, 2024-2025. *Archives of virology*, 171(6).

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).