

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](#) .

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.

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.

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.

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

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.

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.

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).

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).

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).

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

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

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

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

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

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).

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.