

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

FusionGDB2

RRID:SCR_025299

Type: Tool

Proper Citation

FusionGDB2 (RRID:SCR_025299)

Resource Information

URL: <https://compbio.uth.edu/FusionGDB2/>

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Description: Functional annotation database of human fusion genes. FusionGDB 2.0 has updates of contents such as up-to-date human fusion genes, fusion gene breakage tendency score with FusionAI deep learning model based on 20 kb DNA sequence around BP, investigation of overlapping between fusion breakpoints with human genomic features across cellular role's categories, transcribed chimeric sequence and following open reading frame analysis with coding potential based on deep learning approach with Ribo-seq read features, and rigorous investigation of protein feature retention of individual fusion partner genes in protein level.

Synonyms: FusionGDB 2.0

Resource Type: data or information resource, database

Defining Citation: [PMID:34755868](#)

Keywords: Functional annotation database, human fusion genes, fusion gene breakage tendency score,

Funding: NIGMS R35GM138184;
University of Texas

Availability: Free, Freely available

Resource Name: FusionGDB2

Resource ID: SCR_025299

Record Creation Time: 20240501T053247+0000

Record Last Update: 20260811T043751+0000

Ratings and Alerts

No rating or validation information has been found for FusionGDB2.

No alerts have been found for FusionGDB2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Ou-Yang Y, et al. (2025) Landscape of gene fusions in hormone receptor-positive breast cancer reveals ADK fusions as drivers of progression and potential therapeutic targets. Cell discovery, 11(1), 89.

Modestov A, et al. (2025) Regulatory Mechanisms and Functional Roles of Readthrough Transcripts in Tumorigenesis. International journal of molecular sciences, 26(20).

Gaziev I, et al. (2025) Accurate RET Fusion Detection in Solid Tumors Using RNA Sequencing Coverage Imbalance Analysis. International journal of molecular sciences, 26(23).

Plum PS, et al. (2024) Integrative genomic analyses of European intrahepatic cholangiocarcinoma: Novel ROS1 fusion gene and PBX1 as prognostic marker. Clinical and translational medicine, 14(6), e1723.