Resource Summary Report

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An Open Access On-Line Breast Cancer Mutation Data Base

RRID:SCR_008432
Type: Tool

Proper Citation

An Open Access On-Line Breast Cancer Mutation Data Base (RRID:SCR_008432)

Resource Information

URL: http://research.nhgri.nih.gov/bic/

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Description: When the BRCA1 gene was cloned, a Steering Committee was initiated to help coordinate the formation of a Breast Cancer Information Core (BIC) that could act as such a central repository. NHGRI has chosen as the most accessible format for the BIC this World Wide Web site. The recent identification of mutations in breast cancer susceptibility genes has provided the exciting opportunity to help identify women who are at high risk to develop breast cancer. One of the serious impediments to achieving clinical benefits from this information however, is finding and assessing the significance of mutations in these new susceptibility genes. It is imperative that the detection and interpretation of these mutations is coordinated and that this information is made available to as many qualified investigators as possible. There are many sites on the web that contain general as well as scientific information relevant to breast cancer. A partial list of these can be found here. Having participated in the poorly coordinated analysis of other cancer susceptibility genes, we consider it important to create and maintain a central repository for information regarding mutations and polymorphisms. NHGRI also think it critical to make available the reagents necessary to carry out many different techniques for the detection of such mutations. Sponsors: This resource is supported by the National Human Genome Research Institute (NHGRI). Keywords: Breast, Cancer, Mutation, Clincial, Polymorphism, Gene, Scientific,

Synonyms: Breast Cancer Information Core

Resource Type: data or information resource, database

Keywords: FASEB list

Funding:

Resource Name: An Open Access On-Line Breast Cancer Mutation Data Base

Resource ID: SCR_008432

Alternate IDs: nif-0000-30219

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250422T055453+0000

Ratings and Alerts

No rating or validation information has been found for An Open Access On-Line Breast Cancer Mutation Data Base.

No alerts have been found for An Open Access On-Line Breast Cancer Mutation Data Base.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 141 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Al Amri WS, et al. (2024) BRCA1/2 mutations and outcomes among Middle Eastern patients with early-onset breast cancer in Oman. The oncologist, 29(12), e1714.

Artioli G, et al. (2021) Characteristics and outcome of BRCA mutated epithelial ovarian cancer patients in Italy: A retrospective multicenter study (MITO 21). Gynecologic oncology, 161(3), 755.

Matos-Rodrigues G, et al. (2021) Mouse Models for Deciphering the Impact of Homologous Recombination on Tumorigenesis. Cancers, 13(9).

Ben Ayed-Guerfali D, et al. (2021) Novel and recurrent BRCA1/BRCA2 germline mutations in patients with breast/ovarian cancer: a series from the south of Tunisia. Journal of translational medicine, 19(1), 108.

Wang N, et al. (2020) Efficacy of platinum in advanced triple-negative breast cancer with

germline BRCA mutation determined by next generation sequencing. Chinese journal of cancer research = Chung-kuo yen cheng yen chiu, 32(2), 149.

Lee YJ, et al. (2020) Germline BRCA, chemotherapy response scores, and survival in the neoadjuvant treatment of ovarian cancer. BMC cancer, 20(1), 185.

Ndiaye R, et al. (2020) Evidence for an ancient BRCA1 pathogenic variant in inherited breast cancer patients from Senegal. NPJ genomic medicine, 5, 8.

Park HS, et al. (2020) Clinicopathological Features of Patients with the BRCA1 c.5339T>C (p.Leu1780Pro) Variant. Cancer research and treatment, 52(3), 680.

Incorvaia L, et al. (2020) BRCA1/2 pathogenic variants in triple-negative versus luminal-like breast cancers: genotype-phenotype correlation in a cohort of 531 patients. Therapeutic advances in medical oncology, 12, 1758835920975326.

Incorvaia L, et al. (2020) Hereditary Breast and Ovarian Cancer in Families from Southern Italy (Sicily)-Prevalence and Geographic Distribution of Pathogenic Variants in BRCA1/2 Genes. Cancers, 12(5).

Wappenschmidt B, et al. (2020) Criteria of the German Consortium for Hereditary Breast and Ovarian Cancer for the Classification of Germline Sequence Variants in Risk Genes for Hereditary Breast and Ovarian Cancer. Geburtshilfe und Frauenheilkunde, 80(4), 410.

Jeon HJ, et al. (2019) Trends in contralateral prophylactic mastectomy rate according to clinicopathologic and socioeconomic status. Annals of surgical treatment and research, 97(3), 113.

Kim HN, et al. (2019) Novel Germline Mutations of BRCA1 and BRCA2 in Korean Familial Breast Cancer Patients. Chonnam medical journal, 55(2), 99.

Wang X, et al. (2019) Prevalence of BRCA1 and BRCA2 gene mutations in Chinese patients with high-risk breast cancer. Molecular genetics & genomic medicine, 7(6), e677.

Cui Y, et al. (2019) Novel loss-of-function mutation in BRCA2 gene identified in a Chinese female with a family history of ovarian cancer: A case report. Oncology letters, 17(3), 3350.

Al Hannan F, et al. (2019) Characterization of BRCA1 and BRCA2 genetic variants in a cohort of Bahraini breast cancer patients using next-generation sequencing. Molecular genetics & genomic medicine, 7(7), e00771.

Deng H, et al. (2019) Comprehensive analysis of serum tumor markers and BRCA1/2 germline mutations in Chinese ovarian cancer patients. Molecular genetics & genomic medicine, 7(6), e672.

Macedo GS, et al. (2019) Reviewing the characteristics of BRCA and PALB2-related cancers in the precision medicine era. Genetics and molecular biology, 42(1 suppl 1), 215.

Diop JPD, et al. (2019) Novel BRCA2 pathogenic variant c.5219 T > G; p.(Leu1740Ter) in a

consanguineous Senegalese family with hereditary breast cancer. BMC medical genetics, 20(1), 73.

Annunziato S, et al. (2019) Comparative oncogenomics identifies combinations of driver genes and drug targets in BRCA1-mutated breast cancer. Nature communications, 10(1), 397.