Resource Summary Report

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Stanley Medical Research Institute Online Genomics Database

RRID:SCR_004859
Type: Tool

Proper Citation

Stanley Medical Research Institute Online Genomics Database (RRID:SCR_004859)

Resource Information

URL: https://www.stanleygenomics.org/

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Description: The Stanley Online Genomics Database uses samples from the Stanley Medical Research Institute (SMRI) Brain Bank. These samples were processed and run on gene expression arrays by a variety of researchers in collaboration with the SMRI. These researchers have performed analyses on their respective studies using a range of analytic approaches. All of the genomic data have been aggregated in this online database, and a consistent set of analyses have been applied to each study. Additionally, a comprehensive set of cross-study analyses have been performed. A thorough collection of gene expression summaries are provided, inclusive of patient demographics, disease subclasses, regulated biological pathways, and functional classifications. Raw data is also available to download. The database is derived from two sets of brain samples, the Stanley Array collection and the Stanley Consortium collection. The Stanley Array collection contains 105 patients, and the Stanley Consortium collection contains 60 patients. Multiple genomic studies have been conducted using these brain samples. From these studies, twelve were selected for inclusion in the database on the basis of number of patients studied, genomic platform used, and data quality. The Consortium collection studies have fewer patients but more diversity in brain regions and array platforms, while the Array collection studies are more homogenous. There are tradeoffs, the Consortium results will be more variable, but findings may be more broadly representative. The collections contain brain samples from subjects in four main groups: Bipolar Schizophrenia, Depression, and Controls Brain regions used in the studies include: Broadman Area 6, Broadman Area 8/9, Broadman Area 10, Broadman Area 46, Cerebellum The 12 studies encompass a range of microarray platforms: Affymetrix HG-U95Av2, Affymetrix HG-U133A, Affymetrix HG-U133 2.0+, Codelink Human 20K, Agilent Human I, Custom cDNA Publications based on any of the clinical or genomic data should credit the Stanley Medical Research Institute, as well as any individual SMRI collaborators

whose data is being used. Publications which make use of analytic results/methods in the database should additionally cite Dr. Michael Elashoff. Registration is required to access the data.

Abbreviations: Stanley Online Genomics Database

Synonyms: SMRI Online Genomics Database

Resource Type: database, data or information resource

Defining Citation: PMID:16594998

Keywords: clinical, genomic, gene expression, microarray, bipolar disorder, schizophrenia, depressive disorder, control, brain, brodmann area 6, brodmann area 8, brodmann area 9, brodmann (1909) area 10, brodmann area 46, cerebellum, FASEB list

Resource Name: Stanley Medical Research Institute Online Genomics Database

Resource ID: SCR_004859

Alternate IDs: nlx_143935

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260725T191132+0000

Ratings and Alerts

No rating or validation information has been found for Stanley Medical Research Institute Online Genomics Database.

No alerts have been found for Stanley Medical Research Institute Online Genomics Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Pocivavsek A, et al. (2024) Neuroactive Kynurenines as Pharmacological Targets: New Experimental Tools and Exciting Therapeutic Opportunities. Pharmacological reviews, 76(6), 978.

Hagihara H, et al. (2024) Postmortem evidence of decreased brain pH in major depressive disorder: a systematic review and meta-analysis. Translational psychiatry, 14(1), 460.

Zhang X, et al. (2024) Differentially Altered Metabolic Pathways in the Amygdala of Subjects with Schizophrenia, Bipolar Disorder and Major Depressive Disorder. medRxiv : the preprint server for health sciences.

Belaish S, et al. (2021) Genome wide analysis implicates upregulation of proteasome pathway in major depressive disorder. Translational psychiatry, 11(1), 409.

Bakshi K, et al. (2020) Two Thalamic Regions Screened Using Laser Capture Microdissection with Whole Human Genome Microarray in Schizophrenia Postmortem Samples. Schizophrenia research and treatment, 2020, 5176834.

Duan J, et al. (2018) Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. Translational psychiatry, 8(1), 158.

Hagihara H, et al. (2018) Decreased Brain pH as a Shared Endophenotype of Psychiatric Disorders. Neuropsychopharmacology : official publication of the American College of Neuropsychopharmacology, 43(3), 459.

Mancarci BO, et al. (2017) Cross-Laboratory Analysis of Brain Cell Type Transcriptomes with Applications to Interpretation of Bulk Tissue Data. eNeuro, 4(6).

Sellgren CM, et al. (2016) A genome-wide association study of kynurenic acid in cerebrospinal fluid: implications for psychosis and cognitive impairment in bipolar disorder. Molecular psychiatry, 21(10), 1342.

Duong A, et al. (2016) Regulators of mitochondrial complex I activity: A review of literature and evaluation in postmortem prefrontal cortex from patients with bipolar disorder. Psychiatry research, 236, 148.

Witt SH, et al. (2014) Investigation of manic and euthymic episodes identifies state- and trait-specific gene expression and STAB1 as a new candidate gene for bipolar disorder. Translational psychiatry, 4(8), e426.

Mehta D, et al. (2014) Comprehensive survey of CNVs influencing gene expression in the human brain and its implications for pathophysiology. Neuroscience research, 79, 22.

Kubota-Sakashita M, et al. (2014) A role of ADAR2 and RNA editing of glutamate receptors in mood disorders and schizophrenia. Molecular brain, 7, 5.

Ib????ez K, et al. (2014) Molecular evidence for the inverse comorbidity between central nervous system disorders and cancers detected by transcriptomic meta-analyses. PLoS genetics, 10(2), e1004173.

Ojeda DA, et al. (2014) Study of five novel non-synonymous polymorphisms in human brain-expressed genes in a Colombian sample. Annals of neurosciences, 21(4), 138.

Lavebratt C, et al. (2014) The KMO allele encoding Arg452 is associated with psychotic features in bipolar disorder type 1, and with increased CSF KYNA level and reduced KMO expression. Molecular psychiatry, 19(3), 334.

Umeda-Yano S, et al. (2014) Expression analysis of the genes identified in GWAS of the postmortem brain tissues from patients with schizophrenia. Neuroscience letters, 568, 12.

Seifuddin F, et al. (2013) Systematic review of genome-wide gene expression studies of bipolar disorder. BMC psychiatry, 13, 213.

Mistry M, et al. (2013) Meta-analysis of gene coexpression networks in the post-mortem prefrontal cortex of patients with schizophrenia and unaffected controls. BMC neuroscience, 14, 105.

Willour VL, et al. (2012) A genome-wide association study of attempted suicide. Molecular psychiatry, 17(4), 433.