

研究成果の刊行に関する一覧表

書籍

著者氏名	論文タイトル名	書籍全体の編集者名	書籍名	出版社名	出版地	出版年	ページ
尾崎浩一	Genetics of Coronary Artery Diseases.	Tatsuhiko Tsunoda, Toshihiro Tanaka, Yusuke Nakamura	<i>Genome Wide Association Studies.</i>	Springer Nature	アメリカ	2019	Chapter 2 p21-36.
尾崎浩一 新飯田俊平	アルツハイマー病の遺伝的背景		<i>BRAIN and NERVE</i>	医学書院	東京	2019	71巻10号, p1039-1051

雑誌

発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
Shigemizu D, Mitsumori R, Akiyama S, Miyashita A, Morizono T, Higaki S, Asanomi Y, Hara N, Tamiya G, Kinoshita K, Ikeuchi T, Niida S, Ozaki K.	Ethnic and trans-ethnic genome-wide association studies identify new loci influencing Japanese Alzheimer's disease risk.	Translational Psychiatry	11	151	2021
Shigemizu D, Akiyama S, Higaki S, Sugimoto T, Sakurai T, Boroevich KA, Sharma A, Tsunoda T, Ochiya T, Niida S, Ozaki K	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimer's disease created by integrative analysis of multi-omics data.	Alzheimer's Research & Therapy	12	145	2020
Johnson T, Mashimo Y, Wu JY, Yoon D, Hata A, Kubo M, Takahashi A, Tsunoda T, Ozaki K, Tanaka T, Ito K, Suzuki H, Hamada H, Kobayashi T, Hara T, Chen CH, Lee YC, Liu YM, Chang LC, Chang CP, Hong YM, Jang G, Yun S, Yu J, Lee KY, Kim JJ, Park T, Lee JK, Chen YT, Oouchi Y.	Published Online 26 October (2020). doi: 10.1038/s10038-020-00864-z. Association of an IGHV3-66 gene variant with Kawasaki disease.	Journal of Human Genetics	Published Online		2020

Koyama S, Ito K, Terao C, Akiyama M, Horikoshi M, Momozawa Y, Matsunaga H, Ieki H, <u>Ozaki K</u> , Onouchi Y, et al.	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease.	Nature Genetics	52	1169-1177	2020
Ishigaki K, Akiyama M, Kanai M, Takahashi A, Kawakami E, Sugishita H, Sakaue S, Matoba N, Low SK, Okada Y, Terao C, Amariuta T, Gazal S, Kochi Y, Horikoshi M, Suzuki K, Ito K, Koyama S, <u>Ozaki K</u> , Niida S. et al.	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases.	Nature Genetics	52 (7)	669-679	2020
Matsunaga H, Akiyama M, Takahashi A, Nomura S, <u>Ozaki K</u> , Onouchi Y, Suna S, Ogishima S, Yamamoto M, Satoh M, Sasaki M, Yamaji T, Iwasaki M, Tsugane S, Tanaka K, Naito M, Akai W, Tanaka H, Sakata Y, Morita H, Matsuda K, Murakami Y, Akazawa H, Kubo M, Kamatani Y, Komuro I, Ito K.	Transethnic meta-analysis of genome-wide association studies identifies three new loci for coronary artery disease.	Circulation: Genomics and Precision Medicine.	13(3)	e002670	2020
<u>Shigemizu D</u> , Akiyama S, Asanomi Y, Boroevich KA, Sharma A, Tsunoda T, Smakurai T, <u>Ozaki K</u> , Ochiya T, <u>Niida S</u> .	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data.	BMC Medical Genomics.	30;12(1)	150	2019
Asanomi Y, <u>Shigemizu D</u> , Miyashita A, Mitsumori R, Mori T, Hara N, Ito K, <u>Niida S</u> , Ikeuchi T, <u>Ozaki K</u> .	A rare functional variant of <i>SHARPIN</i> attenuates the inflammatory response and associates with increased risk of late-onset Alzheimer's disease.	Molecular Medicine.	25(1)	20	2019
Ebana Y, Sun Y, Yang X, Watanabe T, Makita S, <u>Ozaki K</u> , Tanaka T, Arai H, Furukawa T.	Pathway analysis with genome-wide association study (GWAS) data detected the association of atrial fibrillation with the mTOR signaling pathway.	International Journal of Cardiology. Heart & Vascular Medicine.	24	100383	2019

Shigemizu D, Akiyama S, Asanomi Y, Boroevich KA, Sharma A, Tsunoda T, Matsukuma K, Ichikawa M, Takizawa S, Sakurai T, Ozaki K, Ochiya T, Niida S.	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data.	Communications in Biology.	2	77	2019
Shigemizu D, Miya F, Akiyama S, Okuda S, Boroevich K, Fujimoto A, Nakagawa H, Ozaki K, Niida S, Kanemura Y, Okamoto N, Saitoh S, Kato M, Yamasaki M, Matsunaga T, Mutai H, Kosaki K, Tsunoda T.	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis.	Scientific Reports.	8 (1)	5608	2018
Nagata Y, Hirayama A, Ikeda S, Shirahata A, Shoji F, Maruyama M, Kayano M, Bundo M, Hattori K, Yoshida S, Gotto Y, Urakami K, Soga T, Ozaki K, Niida S.	Comparative analysis of cerebrospinal fluid metabolites in an Alzheimer's disease and idiopathic normal pressure hydrocephalus in a Japanese cohort.	Biomarker Research	6	5	2018
Saji N, Niida S, Murotani K, Hisada T, Tsuduki T, Sugimoto T, Kimura A, Toba K, Sakurai T.	Analysis of the relationship between the gut microbiome and dementia: a cross-sectional study conducted in Japan.	Scientific Reports.	9	1008	2019
Yamaguchi-Kabata Y, Morihara T, Ohara T, Ninomiya T, Takahashi A, Akatsu H, Hashizume Y, Hayashi N, Shigemizu D, Boroevich KA, Ikeda M, Kubo M, Takeda M, Tsunoda	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid- β accumulation in Alzheimer's disease.	Hum Genet.	137	521-533.	2018
Nishino J, Kochi Y, Shigemizu D, Kato M, Ikari K, Ochi H, Noma H, Matsui K, Morizono T, Boroevich K, Tsunoda T, and Matsui S:	Empirical Bayes estimation of semi-parametric hierarchical mixture models for unbiased characterization of polygenic disease architectures.	Frontiers in Genetics	9	115	2018