Elisabeth A Rosenthal

List of Publications by Year
in descending order

28 papers	1,348 citations	687363 13 h-index	526287 27 g-index
28 all docs	28 docs citations	28 times ranked	3827 citing authors

#	Article	IF	Citations
1	Loci identified by a genomeâ€wide association study of carotid artery stenosis in the eMERGE network. Genetic Epidemiology, 2021, 45, 4-15.	1.3	6
2	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	1.5	4
3	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	6.2	5
4	Penetrance of Breast Cancer Susceptibility Genes from the eMERGE III Network. JNCI Cancer Spectrum, 2021, 5, pkab044.	2.9	14
5	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. Circulation Genomic and Precision Medicine, 2021, 14, e003354.	3.6	21
6	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
7	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
8	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
9	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis. Human Genetics and Genomics Advances, 2020, 1, 100010.	1.7	3
10	Rates of Actionable Genetic Findings in Individuals with Colorectal Cancer or Polyps Ascertained from a Community Medical Setting. American Journal of Human Genetics, 2019, 105, 526-533.	6.2	4
11	Clinical exome sequencing vs. usual care for hereditary colorectal cancer diagnosis: A pilot comparative effectiveness study. Contemporary Clinical Trials, 2019, 84, 105820.	1.8	6
12	Unfolding of hidden white blood cell count phenotypes for gene discovery using latent class mixed modeling. Genes and Immunity, 2019, 20, 555-565.	4.1	4
13	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
14	A comparison of cosegregation analysis methods for the clinical setting. Familial Cancer, 2018, 17, 295-302.	1.9	19
15	Rare loss of function variants in candidate genes and risk of colorectal cancer. Human Genetics, 2018, 137, 795-806.	3.8	10
16	Power of pedigree likelihood analysis in extended pedigrees to classify rare variants of uncertain significance in cancer risk genes. Familial Cancer, 2017, 16, 611-620.	1.9	7
17	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. Genetic Epidemiology, 2016, 40, 470-474.	1.3	11
18	Family Studies for Classification of Variants of Uncertain Classification: Current Laboratory Clinical Practice and a New Webâ€Based Educational Tool. Journal of Genetic Counseling, 2016, 25, 1146-1156.	1.6	26

#	Article	IF	Citations
19	Next-generation gene discovery for variants of large impact on lipid traits. Current Opinion in Lipidology, 2015, 26, 114-119.	2.7	5
20	PLTP activity inversely correlates with CAAD: effects of PON1 enzyme activity and genetic variants on PLTP activity. Journal of Lipid Research, 2015, 56, 1351-1362.	4.2	15
21	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	5.5	313
22	HDLâ€3 is a Superior Predictor of Carotid Artery Disease in a Caseâ€Control Cohort of 1725 Participants. Journal of the American Heart Association, 2014, 3, e000902.	3.7	35
23	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	2.5	35
24	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
25	Joint Linkage and Association Analysis with Exome Sequence Data Implicates SLC25A40 in Hypertriglyceridemia. American Journal of Human Genetics, 2013, 93, 1035-1045.	6.2	36
26	TCIRG1 Associated Congenital Neutropenia. Blood, 2013, 122, 440-440.	1.4	0
27	Linkage and association of phospholipid transfer protein activity to LASS4. Journal of Lipid Research, 2011, 52, 1837-1846.	4.2	23
28	Joint linkage and segregation analysis under multiallelic trait inheritance: simplifying interpretations for complex traits. Genetic Epidemiology, 2010, 34, 344-353.	1.3	9