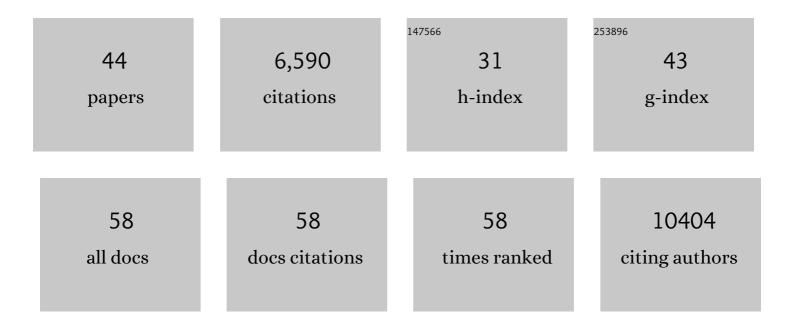
Eric B Fauman

List of Publications by Year in descending order

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FRIC R FALIMAN

#	Article	IF	CITATIONS
1	An effector index to predict target genes at GWAS loci. Human Genetics, 2022, 141, 1431-1447.	1.8	28
2	Effector membrane translocation biosensors reveal G protein and \hat{I}^2 arrestin coupling profiles of 100 therapeutically relevant GPCRs. ELife, 2022, 11, .	2.8	101
3	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
4	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge. Molecular Psychiatry, 2022, 27, 3095-3106.	4.1	4
5	An optimal variant to gene distance window derived from an empirical definition of cis and trans protein QTLs. BMC Bioinformatics, 2022, 23, 169.	1.2	22
6	Largeâ€scale profiling of physiologically relevant naturally occurring rare GPCR variants using the bioSensAll® technology. FASEB Journal, 2022, 36, .	0.2	0
7	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	9.4	117
8	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci. BMC Medicine, 2021, 19, 232.	2.3	25
9	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533.	9.4	208
10	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
11	Current Techniques for Complex Phenotypes: GWAS of the Electrocardiogram. Trends in Genetics, 2020, 36, 897-899.	2.9	3
12	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
13	Insights into genetic variants associated with NASH-fibrosis from metabolite profiling. Human Molecular Genetics, 2020, 29, 3451-3463.	1.4	27
14	Characterising a healthy adult with a rare HAO1 knockout to support a therapeutic strategy for primary hyperoxaluria. ELife, 2020, 9, .	2.8	45
15	An Unbiased Lipid Phenotyping Approach To Study the Genetic Determinants of Lipids and Their Association with Coronary Heart Disease Risk Factors. Journal of Proteome Research, 2019, 18, 2397-2410.	1.8	55
16	ProGeM: a framework for the prioritization of candidate causal genes at molecular quantitative trait loci. Nucleic Acids Research, 2019, 47, e3-e3.	6.5	90
17	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.3	136
18	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260

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19	The Genetic Landscape of Renal Complications in Type 1 Diabetes. Journal of the American Society of Nephrology: JASN, 2017, 28, 557-574.	3.0	101
20	GWAS of self-reported mosquito bite size, itch intensity and attractiveness to mosquitoes implicates immune-related predisposition loci. Human Molecular Genetics, 2017, 26, 1391-1406.	1.4	32
21	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194
22	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	9.4	1,084
23	Biomarkers for Type 2 Diabetes and Impaired Fasting Glucose Using a Nontargeted Metabolomics Approach. Diabetes, 2013, 62, 4270-4276.	0.3	356
24	GeneTopics - interpretation of gene sets via literature-driven topic models. BMC Systems Biology, 2013, 7, S10.	3.0	10
25	Structure-based druggability assessment—identifying suitable targets for small molecule therapeutics. Current Opinion in Chemical Biology, 2011, 15, 463-468.	2.8	160
26	Rational protein engineering in action: The first crystal structure of a phenylalanine tRNA synthetase from Staphylococcus haemolyticus. Journal of Structural Biology, 2008, 162, 152-169.	1.3	17
27	Pharmacology and mechanism of action of pregabalin: The calcium channel α2–δ (alpha2–delta) subunit as a target for antiepileptic drug discovery. Epilepsy Research, 2007, 73, 137-150.	0.8	492
28	Structural Bioinformatics in Drug Discovery. Methods of Biochemical Analysis, 2005, 44, 477-497.	0.2	9
29	Identification of a Novel Mitogen-Activated Protein Kinase Kinase Activation Domain Recognized by the Inhibitor PD 184352. Molecular and Cellular Biology, 2002, 22, 7593-7602.	1.1	64
30	RNA Methylation under Heat Shock Control. Molecular Cell, 2000, 6, 349-360.	4.5	228
31	Crystal Structure of the Catalytic Domain of the Human Cell Cycle Control Phosphatase, Cdc25A. Cell, 1998, 93, 617-625.	13.5	265
32	Structure and function of theprotein tyrosine phosphatases. Trends in Biochemical Sciences, 1996, 21, 413-417.	3.7	342
33	Contribution of a salt bridge to binding affinity and dUMP orientation to catalytic rate: mutation of a substrate-binding arginine in thymidylate synthase. Protein Engineering, Design and Selection, 1996, 9, 69-75.	1.0	6
34	The X-ray Crystal Structures of Yersinia Tyrosine Phosphatase with Bound Tungstate and Nitrate. Journal of Biological Chemistry, 1996, 271, 18780-18788.	1.6	106
35	A ligand-induced conformational change in the <i>yersinia</i> protein tyrosine phosphatase. Protein Science, 1995, 4, 1904-1913.	3.1	116
36	Significance of structural changes in proteins: Expected errors in refined protein structures. Protein Science, 1995, 4, 2392-2404.	3.1	43

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37	Crystal structure of Yersinia protein tyrosine phosphatase at 2.5 Ã and the complex with tungstate. Nature, 1994, 370, 571-575.	13.7	423
38	The Cys(X)5Arg Catalytic Motif in Phosphoester Hydrolysis. Biochemistry, 1994, 33, 15266-15270.	1.2	179
39	Water-mediated substrate/product discrimination: The product complex of thymidylate synthase at 1.83 .ANG Biochemistry, 1994, 33, 1502-1511.	1.2	74
40	Refined Structures of Substrate-bound and Phosphate-bound Thymidylate Synthase from Lactobacillus casei. Journal of Molecular Biology, 1993, 232, 1101-1116.	2.0	85
41	Tracking conformational states in allosteric transitions of phosphorylase. Biochemistry, 1992, 31, 11297-11304.	1.2	25
42	1.59 Ã structure of trypsin at 120 K: Comparison of low temperature and room temperature structures. Proteins: Structure, Function and Bioinformatics, 1991, 10, 171-187.	1.5	39
43	Plastic adaptation toward mutations in proteins: Structural comparison of thymidylate synthases. Proteins: Structure, Function and Bioinformatics, 1990, 8, 315-333.	1.5	154
44	Structure, multiple site binding, and segmental accommodation in thymidylate synthase on binding dUMP and an anti-folate. Biochemistry, 1990, 29, 6964-6977.	1.2	262