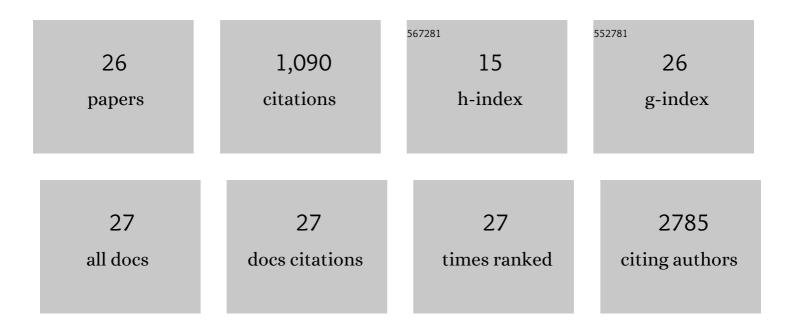
## Phil Barnett

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1158721/publications.pdf Version: 2024-02-01



**Ομίι Βλονεττ** 

#	Article	IF	CITATIONS
1	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. Nature Genetics, 2013, 45, 822-824.	21.4	123
2	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
3	Follistatin-like 1 in development and human diseases. Cellular and Molecular Life Sciences, 2018, 75, 2339-2354.	5.4	110
4	<i>Saccharomyces cerevisiae</i> PTS1 Receptor Pex5p Interacts with the SH3 Domain of the Peroxisomal Membrane Protein Pex13p in an Unconventional, Non-PXXP–related Manner. Molecular Biology of the Cell, 2000, 11, 3963-3976.	2.1	102
5	Structure and function of the Nppa–Nppb cluster locus during heart development and disease. Cellular and Molecular Life Sciences, 2018, 75, 1435-1444.	5.4	91
6	GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. Nature Communications, 2014, 5, 3680.	12.8	78
7	Conserved <i>NPPB</i> + Border Zone Switches From MEF2- to AP-1–Driven Gene Program. Circulation, 2019, 140, 864-879.	1.6	70
8	Identification of atrial fibrillation associated genes and functional non-coding variants. Nature Communications, 2019, 10, 4755.	12.8	64
9	Genetic Determinants of P Wave Duration and PR Segment. Circulation: Cardiovascular Genetics, 2014, 7, 475-481.	5.1	45
10	A Large Permissive Regulatory Domain Exclusively Controls Tbx3 Expression in the Cardiac Conduction System. Circulation Research, 2014, 115, 432-441.	4.5	44
11	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. Circulation Research, 2020, 127, 229-243.	4.5	33
12	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	2.9	24
13	An enhancer cluster controls gene activity and topology of the SCN5A-SCN10A locus in vivo. Nature Communications, 2019, 10, 4943.	12.8	24
14	Variants in the <i>SCN5A</i> Promoter Associated With Various Arrhythmia Phenotypes. Journal of the American Heart Association, 2016, 5, .	3.7	22
15	Variant Intronic Enhancer Controls <i>SCN10A-short</i> Expression and Heart Conduction. Circulation, 2021, 144, 229-242.	1.6	20
16	T-box transcription factor 3 governs a transcriptional program for the function of the mouse atrioventricular conduction system. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18617-18626.	7.1	19
17	Identification and Characterization of a Transcribed Distal Enhancer Involved in Cardiac Kcnh2 Regulation. Cell Reports, 2019, 28, 2704-2714.e5.	6.4	15
18	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. Circulation Research, 2022, 130, 166-180.	4.5	15

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#	Article	IF	CITATIONS
19	Patient-Specific TBX5-G125R Variant Induces Profound Transcriptional Deregulation and Atrial Dysfunction. Circulation, 2022, 145, 606-619.	1.6	15
20	Cardiac regeneration: different cells same goal. Medical and Biological Engineering and Computing, 2011, 49, 723-732.	2.8	14
21	Localized and Temporal Gene Regulation in Heart Development. Current Topics in Developmental Biology, 2012, 100, 171-201.	2.2	11
22	OccuPeak: ChIP-Seq Peak Calling Based on Internal Background Modelling. PLoS ONE, 2014, 9, e99844.	2.5	11
23	From GWAS to function: Genetic variation in sodium channel gene enhancer influences electrical patterning. Trends in Cardiovascular Medicine, 2014, 24, 99-104.	4.9	9
24	Trait-associated noncoding variant regions affect TBX3 regulation and cardiac conduction. ELife, 2020, 9, .	6.0	7
25	Genetics of congenital heart disease: Beyond half-measures. Trends in Cardiovascular Medicine, 2015, 25, 302-304.	4.9	4
26	Epigenetic State Changes Underlie Metabolic Switch in Mouse Post-Infarction Border Zone Cardiomyocytes. Journal of Cardiovascular Development and Disease, 2021, 8, 134.	1.6	3