

# William J Lane

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2920692/publications.pdf>

Version: 2024-02-01

27  
papers

4,504  
citations

759190

12  
h-index

580810

25  
g-index

28  
all docs

28  
docs citations

28  
times ranked

6812  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recommendation for validation and quality assurance of non-invasive prenatal testing for foetal blood groups and implications for IVD risk classification according to EU regulations. <i>Vox Sanguinis</i> , 2022, 117, 157-165.	1.5	7
2	Novel or not? Reference alleles, genes, and genomes to unmask the true nature of the <i>ABO*AW.10</i> allele associated with weak A phenotype. <i>Transfusion</i> , 2022, 62, 721-724.	1.6	2
3	Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	10
4	PIGG defines the Emm blood group system. <i>Scientific Reports</i> , 2021, 11, 18545.	3.3	7
5	Blood Group Genotyping. <i>Advances in Molecular Pathology</i> , 2021, 4, 127-143.	0.4	3
6	A large peptidome dataset improves HLA class I epitope prediction across most of the human population. <i>Nature Biotechnology</i> , 2020, 38, 199-209.	17.5	324
7	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. <i>Blood Advances</i> , 2020, 4, 3495-3506.	5.2	31
8	Multiple <i>GYPB</i> gene deletions associated with the U <sup>+</sup> phenotype in those of African ancestry. <i>Transfusion</i> , 2020, 60, 1294-1307.	1.6	12
9	Overcoming the challenges of interpreting complex and uncommon RH alleles from whole genomes. <i>Vox Sanguinis</i> , 2020, 115, 790-801.	1.5	5
10	Automated typing of red blood cell and platelet antigens from whole exome sequences. <i>Transfusion</i> , 2019, 59, 3253-3263.	1.6	32
11	Recurrent genetic HLA loss in AML relapsed after matched unrelated allogeneic hematopoietic cell transplantation. <i>Blood Advances</i> , 2019, 3, 2199-2204.	5.2	52
12	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239.	27.8	956
13	A whole genome approach for discovering the genetic basis of blood group antigens: independent confirmation for P1 and X <sup>a</sup> . <i>Transfusion</i> , 2019, 59, 908-915.	1.6	13
14	Development of a Calculated Panel Reactive Antibody Web Service with Local Frequencies for Platelet Transfusion Refractoriness Risk Stratification. <i>Journal of Pathology Informatics</i> , 2019, 10, 26.	1.7	1
15	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. <i>Lancet Haematology</i> , 2018, 5, e241-e251.	4.6	70
16	A cloning and expression system to probe T-cell receptor specificity and assess functional avidity to neoantigens. <i>Blood</i> , 2018, 132, 1911-1921.	1.4	44
17	Molecular immunohaematology round table discussions at the AABB Annual Meeting, Orlando 2016. <i>Blood Transfusion</i> , 2018, 16, 447-456.	0.4	1
18	Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-allelic Cells Enables More Accurate Epitope Prediction. <i>Immunity</i> , 2017, 46, 315-326.	14.3	596

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19	An immunogenic personal neoantigen vaccine for patients with melanoma. <i>Nature</i> , 2017, 547, 217-221.	27.8	2,112
20	Comprehensive red blood cell and platelet antigen prediction from whole genome sequencing: proof of principle. <i>Transfusion</i> , 2016, 56, 743-754.	1.6	81
21	Next Generation Sequencing for Blood Group Antigen Profiling. <i>Blood</i> , 2016, 128, SCI-24-SCI-24.	1.4	0
22	Molecular immunohaematology round table discussions at the AABB Annual Meeting, Anaheim 2015. <i>Blood Transfusion</i> , 2016, 14, 557-565.	0.4	6
23	A One-Page Summary Report of Genome Sequencing for the Healthy Adult. <i>Public Health Genomics</i> , 2015, 18, 123-129.	1.0	37
24	Environmental components and methods for engaging pathology residents in informatics training. <i>Journal of Pathology Informatics</i> , 2015, 6, 42.	0.6	3
25	A systematic approach to the reporting of medically relevant findings from whole genome sequencing. <i>BMC Medical Genetics</i> , 2014, 15, 134.	2.1	84
26	The ongoing evolution of the core curriculum of a clinical fellowship in pathology informatics. <i>Journal of Pathology Informatics</i> , 2014, 5, 22.	1.7	9
27	Pathology informatics fellowship training: Focus on molecular pathology. <i>Journal of Pathology Informatics</i> , 2014, 5, 11.	1.7	6