

# Duccio Medini

## List of Publications by Year in descending order

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46  
papers

7,141  
citations

279798

23  
h-index

265206

42  
g-index

49  
all docs

49  
docs citations

49  
times ranked

7755  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : Implications for the microbial "pan-genome". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13950-13955.	7.1	2,161
2	The microbial pan-genome. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 589-594.	3.3	1,151
3	Comparative genomics: the bacterial pan-genome. <i>Current Opinion in Microbiology</i> , 2008, 11, 472-477.	5.1	868
4	Ten years of pan-genome analyses. <i>Current Opinion in Microbiology</i> , 2015, 23, 148-154.	5.1	498
5	Microbiology in the post-genomic era. <i>Nature Reviews Microbiology</i> , 2008, 6, 419-430.	28.6	324
6	Qualitative and quantitative assessment of meningococcal antigens to evaluate the potential strain coverage of protein-based vaccines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19490-19495.	7.1	267
7	Predicted strain coverage of a meningococcal multicomponent vaccine (4CMenB) in Europe: a qualitative and quantitative assessment. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 416-425.	9.1	261
8	Adjuvanted H5N1 vaccine induces early CD4 <sup>+</sup> T cell response that predicts long-term persistence of protective antibody levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3877-3882.	7.1	242
9	<i>Neisseria meningitidis</i> is structured in clades associated with restriction modification systems that modulate homologous recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4494-4499.	7.1	198
10	Bactericidal antibody against a representative epidemiological meningococcal serogroup B panel confirms that MATS underestimates 4CMenB vaccine strain coverage. <i>Vaccine</i> , 2013, 31, 4968-4974.	3.8	123
11	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	1.8	116
12	Comparison of Open-Source Reverse Vaccinology Programs for Bacterial Vaccine Antigen Discovery. <i>Frontiers in Immunology</i> , 2019, 10, 113.	4.8	107
13	MATS: Global coverage estimates for 4CMenB, a novel multicomponent meningococcal B vaccine. <i>Vaccine</i> , 2015, 33, 2629-2636.	3.8	95
14	Bexsero® chronicle. <i>Pathogens and Global Health</i> , 2014, 108, 305-316.	2.3	89
15	Diversity of Canadian meningococcal serogroup B isolates and estimated coverage by an investigational meningococcal serogroup B vaccine (4CMenB). <i>Vaccine</i> , 2013, 32, 124-130.	3.8	81
16	Microbial genomes and vaccine design: refinements to the classical reverse vaccinology approach. <i>Current Opinion in Microbiology</i> , 2006, 9, 532-536.	5.1	76
17	Genetic Meningococcal Antigen Typing System (gMATS): A genotyping tool that predicts 4CMenB strain coverage worldwide. <i>Vaccine</i> , 2019, 37, 991-1000.	3.8	64
18	Interlaboratory Standardization of the Sandwich Enzyme-Linked Immunosorbent Assay Designed for MATS, a Rapid, Reproducible Method for Estimating the Strain Coverage of Investigational Vaccines. <i>Vaccine Journal</i> , 2012, 19, 1609-1617.	3.1	59

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19	Protein Homology Network Families Reveal Step-Wise Diversification of Type III and Type IV Secretion Systems. <i>PLoS Computational Biology</i> , 2006, 2, e173.	3.2	51
20	Early Rise of Blood T Follicular Helper Cell Subsets and Baseline Immunity as Predictors of Persisting Late Functional Antibody Responses to Vaccination in Humans. <i>PLoS ONE</i> , 2016, 11, e0157066.	2.5	43
21	Meningococcal Antigen Typing System (MATS)-Based <i>Neisseria meningitidis</i> Serogroup B Coverage Prediction for the MenB-4C Vaccine in the United States. <i>MSphere</i> , 2017, 2, .	2.9	37
22	Towards a universal group B <i>Streptococcus</i> vaccine using multistrain genome analysis. <i>Expert Review of Vaccines</i> , 2006, 5, 687-694.	4.4	27
23	The challenge of post-implementation surveillance for novel meningococcal vaccines. <i>Vaccine</i> , 2012, 30, B67-B72.	3.8	25
24	In-silico prediction and deep-DNA sequencing validation indicate phase variation in 115 <i>Neisseria meningitidis</i> genes. <i>BMC Genomics</i> , 2016, 17, 843.	2.8	22
25	Pooled-sera hSBA titres predict individual seroprotection in infants and toddlers vaccinated with 4CMenB. <i>Vaccine</i> , 2016, 34, 2579-2584.	3.8	22
26	Potential Coverage of the 4CMenB Vaccine against Invasive Serogroup B <i>Neisseria meningitidis</i> Isolated from 2009 to 2013 in the Republic of Ireland. <i>MSphere</i> , 2018, 3, .	2.9	18
27	Adjuvant effect of TLR7 agonist adsorbed on aluminum hydroxide (AS37): A phase I randomized, dose escalation study of an AS37-adjuvanted meningococcal C conjugated vaccine. <i>Clinical Immunology</i> , 2019, 209, 108275.	3.2	18
28	Interplay Between Virulence and Variability Factors as a Potential Driver of Invasive Meningococcal Disease. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 61-69.	4.1	14
29	The Pangenome: A Data-Driven Discovery in Biology. , 2020, , 3-20.		11
30	Fast and accurate dynamic estimation of field effectiveness of meningococcal vaccines. <i>BMC Medicine</i> , 2016, 14, 98.	5.5	10
31	A quantitative systems pharmacology approach to support mRNA vaccine development and optimization. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2021, 10, 1448-1451.	2.5	8
32	High coverage of diverse invasive meningococcal serogroup B strains by the 4-component vaccine 4CMenB in Australia, 2007–2011: Concordant predictions between MATS and genetic MATS. <i>Human Vaccines and Immunotherapeutics</i> , 2021, 17, 3230-3238.	3.3	7
33	Genomic Characterization of Invasive Meningococcal Serogroup B Isolates and Estimation of 4CMenB Vaccine Coverage in Finland. <i>MSphere</i> , 2020, 5, .	2.9	5
34	Potential impact of the 4CMenB vaccine on oropharyngeal carriage of <i>Neisseria meningitidis</i> . <i>Journal of Infection</i> , 2017, 75, 511-520.	3.3	4
35	Literature Mining and Mechanistic Graphical Modelling to Improve mRNA Vaccine Platforms. <i>Frontiers in Immunology</i> , 2021, 12, 738388.	4.8	4
36	Computational modeling of microfluidic data provides high-throughput affinity estimates for monoclonal antibodies. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3664-3672.	4.1	3

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37	Single-Cell Analysis of Antigen-Specific CD8+ T-Cell Transcripts Reveals Profiles Specific to mRNA or Adjuvanted Protein Vaccines. <i>Frontiers in Immunology</i> , 2021, 12, 757151.	4.8	3
38	Exploring the Limitations of Peripheral Blood Transcriptional Biomarkers in Predicting Influenza Vaccine Responsiveness. <i>Complexity</i> , 2017, 2017, 1-9.	1.6	2
39	A re-assessment of 4CMenB vaccine effectiveness against serogroup B invasive meningococcal disease in England based on an incidence model. <i>BMC Infectious Diseases</i> , 2021, 21, 1244.	2.9	2
40	Atomic scale fractal dimensionality in proteins. <i>Journal of Chemical Physics</i> , 2003, 118, 2405-2410.	3.0	1
41	Horizontal Gene Transfer and the Role of Restriction-Modification Systems in Bacterial Population Dynamics. , 2014, , 169-190.		1
42	Pangenomic Reverse Vaccinology. , 2010, , 203-221.		1
43	OUP accepted manuscript. <i>American Journal of Epidemiology</i> , 2021, , .	3.4	1
44	Building an insurance against modern pandemics. <i>Current Opinion in Investigational Drugs</i> , 2010, 11, 126-30.	2.3	1
45	STRAIN: an R package for multi-locus sequence typing from whole genome sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 347.	2.6	0
46	Systematic characterization of human response to H1N1 influenza vaccination through the construction and integration of personalized transcriptome response profiles. <i>Scientific Reports</i> , 2021, 11, 20821.	3.3	0