Alessandro Muzzi

List of Publications by Year in descending order

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44	2,987	172386	243529
papers	citations	29 h-index	44 g-index

45	45	45	2904
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolution of strain coverage by the multicomponent meningococcal serogroup B vaccine (4CMenB) in France. Human Vaccines and Immunotherapeutics, 2024, 17, 5614-5622.	1.4	5
2	Deconvolution of intergenic polymorphisms determining high expression of Factor H binding protein in meningococcus and their association with invasive disease. PLoS Pathogens, 2021, 17, e1009461.	2.1	4
3	High coverage of diverse invasive meningococcal serogroup B strains by the 4-component vaccine 4CMenB in Australia, 2007â€“2011: Concordant predictions between MATS and genetic MATS. Human Vaccines and Immunotherapeutics, 2021, 17, 3230-3238.	1.4	7
4	Genomic Characterization of Invasive Meningococcal Serogroup B Isolates and Estimation of 4CMenB Vaccine Coverage in Finland. MSphere, 2020, 5, .	1.3	5
5	The global meningitis genome partnership. Journal of Infection, 2020, 81, 510-520.	1.7	13
6	Genetic Meningococcal Antigen Typing System (gMATS): A genotyping tool that predicts 4CMenB strain coverage worldwide. Vaccine, 2019, 37, 991-1000.	1.7	64
7	PIPE-chipSAD: A Pipeline for the Analysis of High Density Arrays of Bacterial Transcriptomes. Frontiers in Molecular Biosciences, 2016, 3, 82.	1.6	0
8	Predicted Strain Coverage of a New Meningococcal Multicomponent Vaccine (4CMenB) in Spain: Analysis of the Differences with Other European Countries. PLoS ONE, 2016, 11, e0150721.	1.1	41
9	Expression of factor H binding protein in meningococcal strains can vary at least 15-fold and is genetically determined. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2714-2719.	3.3	73
10	Dual RNA-seq of Nontypeable Haemophilus influenzae and Host Cell Transcriptomes Reveals Novel Insights into Host-Pathogen Cross Talk. MBio, 2015, 6, e01765-15.	1.8	123
11	Global Transcriptome Analysis Reveals Small RNAs Affecting Neisseria meningitidis Bacteremia. PLoS ONE, 2015, 10, e0126325.	1.1	23
12	Neisseria Adhesin A Variation and Revised Nomenclature Scheme. Vaccine Journal, 2014, 21, 966-971.	3.2	54
13	Analysis of Two-Component Systems in Group B Streptococcus Shows That RgfAC and the Novel FspSR Modulate Virulence and Bacterial Fitness. MBio, 2014, 5, e00870-14.	1.8	67
14	Genome sequencing of disease and carriage isolates of nontypeable Haemophilus influenzae identifies discrete population structure. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5439-5444.	3.3	104
15	Diversity of greek meningococcal serogroup B isolates and estimated coverage of the 4CMenB meningococcal vaccine. BMC Microbiology, 2014, 14, 111.	1.3	40
16	An extended multi-locus molecular typing schema for Streptococcus pneumoniae demonstrates that a limited number of capsular switch events is responsible for serotype heterogeneity of closely related strains from different countries. Infection, Genetics and Evolution, 2013, 13, 151-161.	1.0	9
17	Predicted strain coverage of a meningococcal multicomponent vaccine (4CMenB) in Europe: a qualitative and quantitative assessment. Lancet Infectious Diseases, The, 2013, 13, 416-425.	4.6	261
18	Conservation of Meningococcal Antigens in the Genus Neisseria. MBio, 2013, 4, e00163-13.	1.8	50

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19	Sequence Analysis of 96 Genomic Regions Identifies Distinct Evolutionary Lineages within CC156, the Largest Streptococcus pneumoniae Clonal Complex in the MLST Database. PLoS ONE, 2013, 8, e61003.	1.1	8
20	Adaptive Response of Group B Streptococcus to High Glucose Conditions: New Insights on the CovRS Regulation Network. PLoS ONE, 2013, 8, e61294.	1.1	31
21	An Analysis of the Sequence Variability of Meningococcal fHbp, NadA and NHBA over a 50-Year Period in the Netherlands. PLoS ONE, 2013, 8, e65043.	1.1	47
22	MF59 and Pam3CSK4 Boost Adaptive Responses to Influenza Subunit Vaccine through an IFN Type I-Independent Mechanism of Action. Journal of Immunology, 2012, 188, 3088-3098.	0.4	129
23	Analysis of the Regulated Transcriptome of Neisseria meningitidis in Human Blood Using a Tiling Array. Journal of Bacteriology, 2012, 194, 6217-6232.	1.0	24
24	The Streptococcus pneumoniae Pilus-1 Displays a Biphasic Expression Pattern. PLoS ONE, 2011, 6, e21269.	1.1	42
25	Population genetics and evolution of the pan-genome of Streptococcus pneumoniae. International Journal of Medical Microbiology, 2011, 301, 619-622.	1.5	46
26	A novel Hfqâ€dependent sRNA that is under FNR control and is synthesized in oxygen limitation in Neisseria meningitidis. Molecular Microbiology, 2011, 80, 507-523.	1.2	34
27	A novel epigenetic regulator associated with the hypervirulent Neisseria meningitidis clonal complex 41/44. FASEB Journal, 2011, 25, 3622-3633.	0.2	39
28	Transcriptome Analysis of Neisseria meningitidis in Human Whole Blood and Mutagenesis Studies Identify Virulence Factors Involved in Blood Survival. PLoS Pathogens, 2011, 7, e1002027.	2.1	129
29	Characterization of Diverse Subvariants of the Meningococcal Factor H (fH) Binding Protein for Their Ability To Bind fH, To Mediate Serum Resistance, and To Induce Bactericidal Antibodies. Infection and Immunity, 2011, 79, 970-981.	1.0	64
30	Characterization of fHbp , nhba (gna2132), nadA , porA , and Sequence Type in Group B Meningococcal Case Isolates Collected in England and Wales during January 2008 and Potential Coverage of an Investigational Group B Meningococcal Vaccine. Vaccine Journal, 2010, 17, 919-929.	3.2	95
31	Qualitative and quantitative assessment of meningococcal antigens to evaluate the potential strain coverage of protein-based vaccines. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19490-19495.	3.3	267
32	Intranasal Administration of CpG Induces a Rapid and Transient Cytokine Response Followed by Dendritic and Natural Killer Cell Activation and Recruitment in the Mouse Lung. Journal of Innate Immunity, 2010, 2, 144-159.	1.8	26
33	Src Kinases Are Required for a Balanced Production of IL-12/IL-23 in Human Dendritic Cells Activated by Toll-Like Receptor Agonists. PLoS ONE, 2010, 5, e11491.	1.1	17
34	Characterization of fHbp , nhba (gna2132), nadA , porA , Sequence Type (ST), and Genomic Presence of IS 1301 in Group B Meningococcal ST269 Clonal Complex Isolates from England and Wales. Journal of Clinical Microbiology, 2009, 47, 3577-3585.	1.8	71
35	The Hfq-Dependent Small Noncoding RNA NrrF Directly Mediates Fur-Dependent Positive Regulation of Succinate Dehydrogenase in Neisseria meningitidis. Journal of Bacteriology, 2009, 191, 1330-1342.	1.0	54
36	Distribution and genetic variability of three vaccine components in a panel of strains representative of the diversity of serogroup B meningococcus. Vaccine, 2009, 27, 2794-2803.	1.7	111

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37	A Second Pilus Type in Streptococcus pneumoniae Is Prevalent in Emerging Serotypes and Mediates Adhesion to Host Cells. Journal of Bacteriology, 2008, 190, 5480-5492.	1.0	159
38	Pilus Operon Evolution in Streptococcus pneumoniae Is Driven by Positive Selection and Recombination. PLoS ONE, 2008, 3, e3660.	1.1	21
39	The Acquired Immune Response to the Mucosal Adjuvant LTK63 Imprints the Mouse Lung with a Protective Signature. Journal of Immunology, 2007, 179, 5346-5357.	0.4	29
40	The pan-genome: towards a knowledge-based discovery of novel targets for vaccines and antibacterials. Drug Discovery Today, 2007, 12, 429-439.	3.2	110
41	Identification of iron-activated and -repressed Fur-dependent genes by transcriptome analysis of Neisseria meningitidis group B. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9542-9547.	3.3	191
42	Previously unrecognized vaccine candidates against group B meningococcus identified by DNA microarrays. Nature Biotechnology, 2002, 20, 914-921.	9.4	205
43	Time-resolved experiments on light diffusion in anisotropic random media. Physical Review E, 2000, 62, 6681-6687.	0.8	27
44	Time-Resolved Anisotropic Multiple Light Scattering in Nematic Liquid Crystals. Physical Review Letters, 1999, 83, 4321-4324.	2.9	56