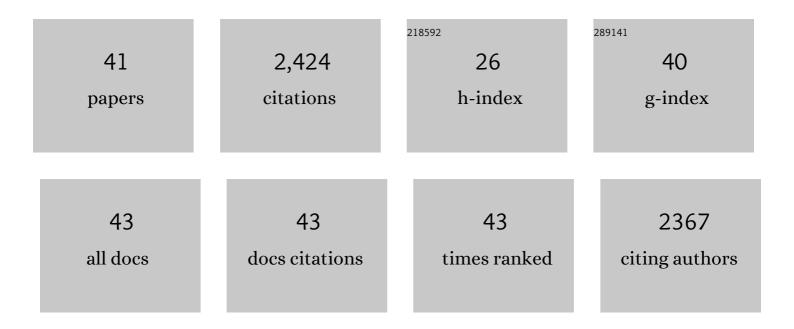
Uwe H Stroeher

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The StkSR Two-Component System Influences Colistin Resistance in Acinetobacter baumannii. Microorganisms, 2022, 10, 985.	1.6	5
2	Resistance to pentamidine is mediated by AdeAB, regulated by AdeRS, and influenced by growth conditions in Acinetobacter baumannii ATCC 17978. PLoS ONE, 2018, 13, e0197412.	1.1	27
3	Microencapsulation of bacterial strains in graphene oxide nano-sheets using vortex fluidics. RSC Advances, 2015, 5, 37424-37430.	1.7	19
4	Identification of genes essential for pellicle formation in Acinetobacter baumannii. BMC Microbiology, 2015, 15, 116.	1.3	90
5	Aqueous based synthesis of antimicrobial-decorated graphene. Journal of Colloid and Interface Science, 2015, 443, 88-96.	5.0	20
6	A new antibiotic with potent activity targets MscL. Journal of Antibiotics, 2015, 68, 453-462.	1.0	46
7	Clonal expansion of hepatocytes with a selective advantage occurs during all stages of chronic hepatitis <scp>B</scp> virus infection. Journal of Viral Hepatitis, 2015, 22, 737-753.	1.0	73
8	Continuous flow vortex fluidic synthesis of silica xerogel as a delivery vehicle for curcumin. RSC Advances, 2015, 5, 7953-7958.	1.7	16
9	Comparative analysis of surface-exposed virulence factors of Acinetobacter baumannii. BMC Genomics, 2014, 15, 1020.	1.2	149
10	H-NS Plays a Role in Expression of Acinetobacter baumannii Virulence Features. Infection and Immunity, 2013, 81, 2574-2583.	1.0	100
11	Contribution of a Genomic Accessory Region Encoding a Putative Cellobiose Phosphotransferase System to Virulence of Streptococcus pneumoniae. PLoS ONE, 2012, 7, e32385.	1.1	27
12	A Variable Region within the Genome of Streptococcus pneumoniae Contributes to Strain-Strain Variation in Virulence. PLoS ONE, 2011, 6, e19650.	1.1	43
13	Adherence and motility characteristics of clinical Acinetobacter baumannii isolates. FEMS Microbiology Letters, 2011, 323, 44-51.	0.7	168
14	The Conformation and Function of a Multimodular Glycogen-Degrading Pneumococcal Virulence Factor. Structure, 2011, 19, 640-651.	1.6	42
15	Contribution of Serotype and Genetic Background to Virulence of Serotype 3 and Serogroup 11 Pneumococcal Isolates. Infection and Immunity, 2011, 79, 4839-4849.	1.0	25
16	Contributions of Pneumolysin, Pneumococcal Surface Protein A (PspA), and PspC to Pathogenicity of Streptococcus pneumoniae D39 in a Mouse Model. Infection and Immunity, 2007, 75, 1843-1851.	1.0	86
17	A Pneumococcal MerRâ€Like Regulator and <i>S</i> â€nitrosoglutathione Reductase Are Required for Systemic Virulence. Journal of Infectious Diseases, 2007, 196, 1820-1826.	1.9	47
18	The Pneumococcal Two-Component Signal Transduction System RR/HK06 Regulates CbpA and PspA by Two Distinct Mechanisms. Journal of Bacteriology, 2007, 189, 5591-5600.	1.0	19

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19	Albomycin is an effective antibiotic, as exemplified with Yersinia enterocolitica and Streptococcus pneumoniae. International Journal of Medical Microbiology, 2007, 297, 459-469.	1.5	66
20	The two-component signal transduction system RR06/HK06 regulates expression of cbpA in Streptococcus pneumoniae. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7701-7706.	3.3	41
21	Mutation of luxS of Streptococcus pneumoniae Affects Virulence in a Mouse Model. Infection and Immunity, 2003, 71, 3206-3212.	1.0	84
22	The Human Complement Regulator Factor H Binds Pneumococcal Surface Protein PspC via Short Consensus Repeats 13 to 15. Infection and Immunity, 2002, 70, 5604-5611.	1.0	76
23	Isolation and characterization of bacteriophage-resistant mutants of Vibrio cholerae O139. Microbial Pathogenesis, 2001, 30, 237-246.	1.3	27
24	Surface Signaling in Ferric Citrate Transport Gene Induction: Interaction of the FecA, FecR, and FecI Regulatory Proteins. Journal of Bacteriology, 2000, 182, 637-646.	1.0	112
25	Distribution of IS1358 and linkage to rfb-related genes in Vibrio anguillarum The GenBank accession numbers for the IS1358 sequences are U93587–U93597 Microbiology (United Kingdom), 2000, 146, 323-331.	0.7	10
26	Genetic organization of the regions associated with surface polysaccharide synthesis in Vibrio cholerae O1, O139 and Vibrio anguillarum O1 and O2: a review1Published in conjunction with A Wisconsin Gathering Honoring Waclaw Szybalski on the occasion of his 75th year and 20 years of Editorship-in-Chief of Gene, 10–11 August 1997, University of Wisconsin, Madison, WI, USA.1. Gene, 1998, 223, 269-282.	1.0	57
27	Lipopolysaccharide O-antigen expression and the effect of its absence on virulence in rfb mutants of Vibrio cholerae O1. FEMS Immunology and Medical Microbiology, 1998, 20, 45-54.	2.7	16
28	Novel Vibrio cholerae O139 genes involved in lipopolysaccharide biosynthesis. Journal of Bacteriology, 1997, 179, 2740-2747.	1.0	79
29	Vibrio cholerae serotype 0139: Swapping genes for surface polysaccharide biosynthesis. Trends in Microbiology, 1997, 5, 178-180.	3.5	33
30	Genetic rearrangements in the rfb regions of Vibrio cholerae O1 and O139 Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 10374-10378.	3.3	107
31	Putative O-antigen transport genes within the rfb region of Vibrio cholerae O1 are homologous to those for capsule transport. Gene, 1995, 158, 1-7.	1.0	37
32	A putative pathway for biosynthesis of the O-antigen component, 3-deoxy-L-glycero-tetronic acid, based on the sequence of the Vibrio cholerae 01 rfb region. Gene, 1995, 166, 19-31.	1.0	13
33	A putative pathway for perosamine biosynthesis is the first function encoded within the rfb region of Vibrio cholerae O1. Gene, 1995, 166, 33-42.	1.0	55
34	Gene sequence of recA + and construction of recA mutants of Vibrio cholerae. Molecular Genetics and Genomics, 1994, 244, 295-302.	2.4	11
35	Characterization and sequence of a 33-kDa enterohemolysin (Ehly1)-associated protein in Escherichia coli. Gene, 1993, 132, 89-94.	1.0	28
36	Isolation of enterohemolysin (Ehly2)-associated sequences encoded on temperate phages of Escherichia coli. Gene, 1993, 132, 95-99.	1.0	39

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37Serotype conversion in Vibrio cholerae O1 Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 2566-2570.3.319938Nucleotide sequence of the structural gene, tcpA, for a major pilin subunit of Vibrio choleras. Gene, 1989, 85, 227-231.1.08039The toxin-coregulated pilus (TCP) of Vibrio cholerae: molecular cloning of genes involved in pilus biosynthesis and evaluation of TCP as a protective antigen in the infant mouse model. Microbial Pathogenesis, 1989, 7, 437-448.1.35840Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structural gene (hlyA) for the haemolytic classical strain 569B. Molecular Microbiology, 1988, 2, 481-488.1.211841Molecular Basis for O-Antigen Biosynthesis in <i>Vibrio cholerae74</i>	#	Article	IF	CITATIONS
38 1989, 85, 227-231. 1.0 80 39 The toxin-coregulated pilus (TCP) of Vibrio cholerae: molecular cloning of genes involved in pilus biosynthesis and evaluation of TCP as a protective antigen in the infant mouse model. Microbial 1.3 58 39 Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structural gene (hlyA) for the haemolysin of the haemolytic El Tor strain 017 and characterization of the hlyA mutation in the non-haemolytic classical strain 569B. Molecular Microbiology, 1988, 2, 481-488. 1.2 118 40 Molecular Basis for O-Antigen Biosynthesis in <i>Vibrio cholerae 1/2 12 118</i>	37		3.3	199
 biosynthesis and evaluation of TCP as a protective antigen in the infant mouse model. Microbial 1.3 58 Pathogenesis, 1989, 7, 437-448. Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structural gene (hlyA) for the haemolysin of the haemolytic El Tor strain 017 and characterization of the hlyA mutation in the non-haemolytic classical strain 569B. Molecular Microbiology, 1988, 2, 481-488. Molecular Basis for O-Antigen Biosynthesis in<i>Vibrio cholerae</i> 	38		1.0	80
40haemolysin of the haemolytic El Tor strain 017 and characterization of the hlyA mutation in the non-haemolytic classical strain 569B. Molecular Microbiology, 1988, 2, 481-488.1.211841Molecular Basis for O-Antigen Biosynthesis in <i>Vibrio cholerae </i> 01: Ogawa-Inaba Switching. , 0, ,74	39	biosynthesis and evaluation of TCP as a protective antigen in the infant mouse model. Microbial	1.3	58
	40	haemolysin of the haemolytic El Tor strain 017 and characterization of the hlyA mutation in the	1.2	118
	41			74