

Han Remaut

List of Publications by Year in descending order

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79
papers

5,032
citations

81900

39
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98798

67
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docs citations

86
times ranked

6632
citing authors

#	ARTICLE	IF	CITATIONS
1	β -Barrels covalently link peptidoglycan and the outer membrane in the β -proteobacterium <i>Brucella abortus</i> . <i>Nature Microbiology</i> , 2021, 6, 27-33.	13.3	34
2	Endospore Appendages: a novel pilus superfamily from the endospores of pathogenic <i>Bacilli</i> . <i>EMBO Journal</i> , 2021, 40, e106887.	7.8	10
3	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. <i>Nature Methods</i> , 2021, 18, 60-68.	19.0	79
4	The <i>Bacillus anthracis</i> Cell Envelope: Composition, Physiological Role, and Clinical Relevance. <i>Microorganisms</i> , 2020, 8, 1864.	3.6	11
5	An embedded lipid in the multidrug transporter LmrP suggests a mechanism for polyspecificity. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 829-835.	8.2	57
6	Structural insight into the formation of lipoprotein- β -barrel complexes. <i>Nature Chemical Biology</i> , 2020, 16, 1019-1025.	8.0	34
7	A dual-constriction biological nanopore resolves homonucleotide sequences with high fidelity. <i>Nature Biotechnology</i> , 2020, 38, 1415-1420.	17.5	84
8	Cysteine Residues in <i>Helicobacter pylori</i> Adhesin HopQ are Required for CEACAM-HopQ Interaction and Subsequent CagA Translocation. <i>Microorganisms</i> , 2020, 8, 465.	3.6	12
9	Synthesis of Fucose Derivatives with Thiol Motifs towards Suicide Inhibition of <i>Helicobacter pylori</i> . <i>Molecules</i> , 2020, 25, 4281.	3.8	0
10	Structure of S-layer protein Sap reveals a mechanism for therapeutic intervention in anthrax. <i>Nature Microbiology</i> , 2019, 4, 1805-1814.	13.3	23
11	The Biosynthesis and Structures of Bacterial Pili. <i>Sub-Cellular Biochemistry</i> , 2019, 92, 369-413.	2.4	40
12	Curli Biogenesis: Bacterial Amyloid Assembly by the Type VIII Secretion Pathway. <i>EcoSal Plus</i> , 2019, 8, .	5.4	41
13	Curli Biogenesis: Bacterial Amyloid Assembly by the Type VIII Secretion Pathway. , 2019, , 163-171.		3
14	Selective Engagement of Fc γ 3RIV by a M2e-Specific Single Domain Antibody Construct Protects Against Influenza A Virus Infection. <i>Frontiers in Immunology</i> , 2019, 10, 2920.	4.8	14
15	In silico proteomic and phylogenetic analysis of the outer membrane protein repertoire of gastric <i>Helicobacter</i> species. <i>Scientific Reports</i> , 2018, 8, 15453.	3.3	22
16	<i>Helicobacter pylori</i> adhesin HopQ disrupts trans dimerization in human <i>CEACAM3</i> . <i>EMBO Journal</i> , 2018, 37, .	7.8	73
17	Future perspective for potential <i>Helicobacter pylori</i> eradication therapies. <i>Future Microbiology</i> , 2018, 13, 671-687.	2.0	64
18	The Role of Functional Amyloids in Bacterial Virulence. <i>Journal of Molecular Biology</i> , 2018, 430, 3657-3684.	4.2	127

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19	Hop family <i>Helicobacter</i> outer membrane adhesins form a novel class of Type V secretion proteins with an interrupted β -barrel domain. <i>Molecular Microbiology</i> , 2018, 110, 33-46.	2.5	24
20	<i>Helicobacter pylori</i> Adapts to Chronic Infection and Gastric Disease via pH-Responsive BabA-Mediated Adherence. <i>Cell Host and Microbe</i> , 2017, 21, 376-389.	11.0	104
21	Structural analysis of the interaction between spiroisoxazoline SMART-420 and the <i>Mycobacterium tuberculosis</i> repressor EthR2. <i>Biochemical and Biophysical Research Communications</i> , 2017, 487, 403-408.	2.1	9
22	Nucleation and growth of a bacterial functional amyloid at single-fiber resolution. <i>Nature Chemical Biology</i> , 2017, 13, 902-908.	8.0	58
23	Bacterial RadA is a DnaB-type helicase interacting with RecA to promote bidirectional D-loop extension. <i>Nature Communications</i> , 2017, 8, 15638.	12.8	101
24	Selective depletion of uropathogenic <i>E. coli</i> from the gut by a FimH antagonist. <i>Nature</i> , 2017, 546, 528-532.	27.8	231
25	Evolution and structural dynamics of bacterial glycan binding adhesins. <i>Current Opinion in Structural Biology</i> , 2017, 44, 48-58.	5.7	34
26	<i>Helicobacter pylori</i> adhesin HopQ engages in a virulence-enhancing interaction with human CEACAMs. <i>Nature Microbiology</i> , 2017, 2, 16189.	13.3	188
27	Inflammation-Induced Adhesin-Receptor Interaction Provides a Fitness Advantage to Uropathogenic <i>E. coli</i> during Chronic Infection. <i>Cell Host and Microbe</i> , 2016, 20, 482-492.	11.0	53
28	Structural Insights into Polymorphic ABO Glycan Binding by <i>Helicobacter pylori</i> . <i>Cell Host and Microbe</i> , 2016, 19, 55-66.	11.0	88
29	Crystal Structure of the Conserved Amino Terminus of the Extracellular Domain of Matrix Protein 2 of Influenza A Virus Grippped by an Antibody. <i>Journal of Virology</i> , 2016, 90, 611-615.	3.4	36
30	Virulence-Targeted Antibacterials: Concept, Promise, and Susceptibility to Resistance Mechanisms. <i>Chemical Biology and Drug Design</i> , 2015, 86, 379-399.	3.2	66
31	Structural insight in the inhibition of adherence of F4 fimbriae producing enterotoxigenic <i>Escherichia coli</i> by llama single domain antibodies. <i>Veterinary Research</i> , 2015, 46, 14.	3.0	17
32	Insights in peptide diffusion channels from the bacterial amyloid secretor CsgG. <i>Channels</i> , 2015, 9, 65-67.	2.8	7
33	Structural and Functional Insight into the Carbohydrate Receptor Binding of F4 Fimbriae-producing Enterotoxigenic <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 8409-8419.	3.4	26
34	Production, purification and crystallization of atrans-sialidase from <i>Trypanosoma vivax</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 577-585.	0.8	5
35	Structural and adhesive properties of the long polar fimbriae protein LpfD from adherent-invasive <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1615-1626.	2.5	8
36	Bacterial Amyloid Formation: Structural Insights into Curli Biogenesis. <i>Trends in Microbiology</i> , 2015, 23, 693-706.	7.7	148

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37	S-layer Structure in Bacteria and Archaea. , 2014, , 11-37.		4
38	Structural and mechanistic insights into the bacterial amyloid secretion channel CsgG. Nature, 2014, 516, 250-253.	27.8	246
39	Secretion and functional display of fusion proteins through the curli biogenesis pathway. Molecular Microbiology, 2014, 91, 1022-1035.	2.5	37
40	Bacterial surface appendages as targets for novel antibacterial therapeutics. Future Microbiology, 2014, 9, 887-900.	2.0	26
41	Expression, purification and X-ray crystallographic analysis of the <i>Helicobacter pylori</i> blood group antigen-binding adhesin BabA. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1631-1635.	0.8	11
42	The Molecular Mechanism of Shiga Toxin Stx2e Neutralization by a Single-domain Antibody Targeting the Cell Receptor-binding Domain. Journal of Biological Chemistry, 2014, 289, 25374-25381.	3.4	26
43	Suppression of type 1 pilus assembly in uropathogenic Escherichia coli by chemical inhibition of subunit polymerization. Journal of Antimicrobial Chemotherapy, 2014, 69, 1017-1026.	3.0	41
44	Nanobody Mediated Inhibition of Attachment of F18 Fimbriae Expressing Escherichia coli. PLoS ONE, 2014, 9, e114691.	2.5	23
45	Lifting the lid on pilus assembly. ELife, 2014, 3, .	6.0	4
46	Chemical attenuation of pilus function and assembly in Gram-negative bacteria. Current Opinion in Microbiology, 2013, 16, 85-92.	5.1	20
47	Structure of a bacterial type IV secretion core complex at subnanometre resolution. EMBO Journal, 2013, 32, 1195-1204.	7.8	85
48	The crystal structure of the cell division amidase <i>AmiC</i> reveals the fold of the <i>AMIN</i> domain, a new peptidoglycan binding domain. Molecular Microbiology, 2013, 90, 267-277.	2.5	60
49	Crystallization and preliminary X-ray crystallographic analysis of the curli transporter CsgG. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1349-1353.	0.7	7
50	d-Aminopeptidase DppA. , 2013, , 1667-1669.		0
51	Structural insights into <i>Helicobacter pylori</i> oncoprotein CagA interaction with β 1 integrin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14640-14645.	7.1	114
52	Structural insight in histone blood group binding by the F18 fimbrial adhesin FedF. Molecular Microbiology, 2012, 86, 82-95.	2.5	46
53	SAMBA, a plant-specific anaphase-promoting complex/cyclosome regulator is involved in early development and A-type cyclin stabilization. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13853-13858.	7.1	80
54	The Tyrosine Gate as a Potential Entropic Lever in the Receptor-Binding Site of the Bacterial Adhesin FimH. Biochemistry, 2012, 51, 4790-4799.	2.5	67

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55	A bacterial glycosidase enables mannose-6-phosphate modification and improved cellular uptake of yeast-produced recombinant human lysosomal enzymes. <i>Nature Biotechnology</i> , 2012, 30, 1225-1231.	17.5	95
56	SbsB structure and lattice reconstruction unveil Ca ²⁺ triggered S-layer assembly. <i>Nature</i> , 2012, 487, 119-122.	27.8	125
57	Pili and Flagella. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 103, 21-72.	1.7	25
58	Crystal structure of the FimD usher bound to its cognate FimCâ€“FimH substrate. <i>Nature</i> , 2011, 474, 49-53.	27.8	170
59	Small Heat-Shock Protein HSPB1 Mutants Stabilize Microtubules in Charcot-Marie-Tooth Neuropathy. <i>Journal of Neuroscience</i> , 2011, 31, 15320-15328.	3.6	95
60	Design and Synthesis of C-2 Substituted Thiazolo and Dihydrothiazolo Ring-Fused 2-Pyridones: Pilocides with Increased Antivirulence Activity. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 5690-5695.	6.4	82
61	Protein oligomerization in the bacterial outer membrane (Review). <i>Molecular Membrane Biology</i> , 2009, 26, 136-145.	2.0	31
62	Architectures and biogenesis of non-flagellar protein appendages in Gram-negative bacteria. <i>EMBO Journal</i> , 2008, 27, 2271-2280.	7.8	156
63	Structural Determinants of Polymerization Reactivity of the P pilus Adaptor Subunit PapF. <i>Structure</i> , 2008, 16, 1724-1731.	3.3	22
64	Structural Analysis of the Saf Pilus by Electron Microscopy and Image Processing. <i>Journal of Molecular Biology</i> , 2008, 379, 174-187.	4.2	31
65	Fiber Formation across the Bacterial Outer Membrane by the Chaperone/Usher Pathway. <i>Cell</i> , 2008, 133, 640-652.	28.9	194
66	Unraveling the molecular basis of subunit specificity in P pilus assembly by mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12873-12878.	7.1	54
67	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted Î² Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	9.7	159
68	Molecular mechanism of P pilus termination in uropathogenic <i>Escherichia coli</i> . <i>EMBO Reports</i> , 2006, 7, 1228-1232.	4.5	70
69	Proteinâ€“protein interaction through Î²-strand addition. <i>Trends in Biochemical Sciences</i> , 2006, 31, 436-444.	7.5	176
70	Rationally designed small compounds inhibit pilus biogenesis in uropathogenic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17897-17902.	7.1	257
71	Structural biology of bacterial pathogenesis. <i>Current Opinion in Structural Biology</i> , 2004, 14, 161-170.	5.7	53
72	Fiber assembly by the chaperoneâ€“usher pathway. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004, 1694, 259-267.	4.1	166

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73	Crystal Structure of T State Aspartate Carbamoyltransferase of the Hyperthermophilic Archaeon <i>Sulfolobus acidocaldarius</i> . <i>Journal of Molecular Biology</i> , 2004, 339, 887-900.	4.2	11
74	d-Aminopeptidase DppA. , 2004, , 992-994.		0
75	Molecular characterization of <i>Bacillus pasteurii</i> UreE, a metal-binding chaperone for the assembly of the urease active site. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 623-631.	2.6	39
76	Crystallization and preliminary X-ray crystallographic analysis of glutathione amide reductase from <i>Chromatium gracile</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 339-340.	2.5	2
77	Structure of the <i>Bacillus subtilis</i> D-aminopeptidase DppA reveals a novel self-compartmentalizing protease. <i>Nature Structural Biology</i> , 2001, 8, 674-678.	9.7	42
78	Structural Basis for Ni ²⁺ Transport and Assembly of the Urease Active Site by the Metallochaperone UreE from <i>Bacillus pasteurii</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 49365-49370.	3.4	74
79	Crystal structure of a d-aminopeptidase from <i>Ochrobactrum anthropi</i> , a new member of the α -penicillin-recognizing enzyme family. <i>Structure</i> , 2000, 8, 971-980.	3.3	41