Remi Fronzes

List of Publications by Year
in descending order

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38 papers	3,494 citations	236925 25 h-index	315739 38 g-index
42 all docs	42 docs citations	42 times ranked	3961 citing authors

#	Article	IF	Citations
1	The mycoplasma surface proteins MIB and MIP promote the dissociation of the antibody-antigen interaction. Science Advances, 2021, 7, .	10.3	15
2	Mounting, structure and autocleavage of a type VI secretion-associated Rhs polymorphic toxin. Nature Communications, 2021, 12, 6998.	12.8	27
3	Binding mechanisms of therapeutic antibodies to human CD20. Science, 2020, 369, 793-799.	12.6	79
4	Structural basis for loading and inhibition of a bacterial T6 <scp>SS</scp> phospholipase effector by the VgrG spike. EMBO Journal, 2020, 39, e104129.	7.8	31
5	Filamentation of the bacterial bi-functional alcohol/aldehyde dehydrogenase AdhE is essential for substrate channeling and enzymatic regulation. Nature Communications, 2020, 11, 1426.	12.8	28
6	In situ and highâ€resolution cryoâ€•<scp>EM</scp> structure of a bacterial type <scp>VI</scp> secretion system membrane complex. EMBO Journal, 2019, 38, .	7.8	72
7	BAmSA: Visualising transmembrane regions in protein complexes using biotinylated amphipols and electron microscopy. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 466-477.	2.6	7
8	Biogenesis and structure of a type VI secretion baseplate. Nature Microbiology, 2018, 3, 1404-1416.	13.3	76
9	Using Cryo-EM to Investigate Bacterial Secretion Systems. Annual Review of Microbiology, 2018, 72, 231-254.	7.3	18
10	Secretion Systems Used by Bacteria to Subvert Host Functions. Current Issues in Molecular Biology, 2018, 25, 1-42.	2.4	44
11	Bacterial transformation: ComFA is a DNAâ€dependent ATPase that forms complexes with ComFC and DprA. Molecular Microbiology, 2017, 105, 741-754.	2.5	42
12	Bacterial RadA is a DnaB-type helicase interacting with RecA to promote bidirectional D-loop extension. Nature Communications, 2017, 8, 15638.	12.8	101
13	Molecular dissection of proteinâ€“protein interactions between integrin Î±5Î²1 and the Helicobacter pylori Cag type <scp>IV</scp> secretion system. FEBS Journal, 2017, 284, 4143-4157.	4.7	29
14	Labeling of Membrane Complexes for Electron Microscopy. Methods in Molecular Biology, 2017, 1635, 125-138.	0.9	1
15	Insights into the structure and assembly of a bacterial cellulose secretion system. Nature Communications, 2017, 8, 2065.	12.8	90
16	Structural basis of the signalling through a bacterial membrane receptor HasR deciphered by an integrative approach. Biochemical Journal, 2016, 473, 2239-2248.	3.7	13
17	Priming and polymerization of a bacterial contractile tail structure. Nature, 2016, 531, 59-63.	27.8	127
18	Probing a cell-embedded megadalton protein complex by DNP-supported solid-state NMR. Nature Methods, 2015, 12, 649-652.	19.0	124

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19	Biogenesis and structure of a type VI secretion membrane core complex. Nature, 2015, 523, 555-560.	27.8	241
20	Conserved Streptococcus pneumoniae Spirosomes Suggest a Single Type of Transformation Pilus in Competence. PLoS Pathogens, 2015, 11, e1004835.	4.7	26
21	Structural and mechanistic insights into the bacterial amyloid secretion channel CsgG. Nature, 2014, 516, 250-253.	27.8	246
22	Structure of a type IV secretion system. Nature, 2014, 508, 550-553.	27.8	280
23	Structure of a bacterial type IV secretion core complex at subnanometre resolution. EMBO Journal, 2013, 32, 1195-1204.	7.8	85
24	A Type IV Pilus Mediates DNA Binding during Natural Transformation in Streptococcus pneumoniae. PLoS Pathogens, 2013, 9, e1003473.	4.7	147
25	SbsB structure and lattice reconstruction unveil Ca2+ triggered S-layer assembly. Nature, 2012, 487, 119-122.	27.8	125
26	Molecular architecture of bacterial type IV secretion systems. Trends in Biochemical Sciences, 2010, 35, 691-698.	7.5	46
27	SnapShot: Bacterial Appendages I. Cell, 2010, 140, 162-162.e1.	28.9	2
28	SnapShot: Bacterial Appendages II. Cell, 2010, 140, 294-294.e1.	28.9	1
29	Structure of the outer membrane complex of a type IV secretion system. Nature, 2009, 462, 1011-1015.	27.8	283
30	The structural biology of type IV secretion systems. Nature Reviews Microbiology, 2009, 7, 703-714.	28.6	364
31	Protein oligomerization in the bacterial outer membrane (Review). Molecular Membrane Biology, 2009, 26, 136-145.	2.0	31
32	Structure of a Type IV Secretion System Core Complex. Science, 2009, 323, 266-268.	12.6	277
33	Architectures and biogenesis of non-flagellar protein appendages in Gram-negative bacteria. EMBO Journal, 2008, 27, 2271-2280.	7.8	156
34	VirB2 and VirB5 proteins: specialized adhesins in bacterial type-IV secretion systems?. Trends in Microbiology, 2008, 16, 409-413.	7.7	110
35	Yeast Cells Depleted in Atp14p Fail to Assemble Atp6p within the ATP Synthase and Exhibit Altered Mitochondrial Cristae Morphology. Journal of Biological Chemistry, 2008, 283, 9749-9758.	3.4	20
36	NMR structure of a complex between the VirB9/VirB7 interaction domains of the pKM101 type IV secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1673-1678.	7.1	48

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37	The Peripheral Stalk Participates in the Yeast ATP Synthase Dimerization Independently of e and g Subunits. Biochemistry, 2006, 45, 6715-6723.	2.5	51
38	Topological and Functional Study of Subunit h of the F1Fo ATP Synthase Complex in YeastSaccharomyces cerevisiaeâ€. Biochemistry, 2003, 42, 12038-12049.	2.5	22