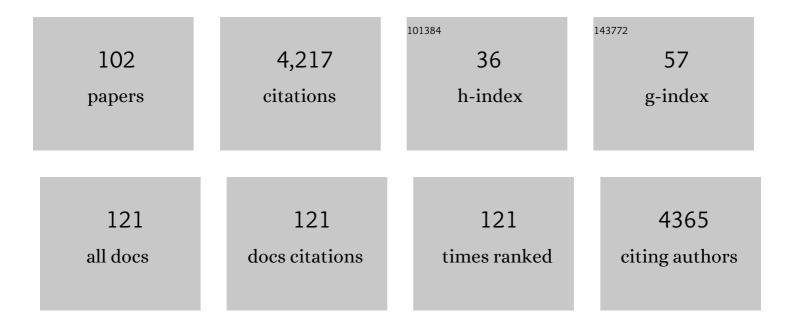
List of Publications by Year in descending order

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CEDT RANCE

#	Article	IF	CITATIONS
1	The magic dance of the alarmones (p)ppGpp. Molecular Microbiology, 2016, 101, 531-544.	1.2	171
2	Visualizing the Assembly Pathway of Nucleolar Pre-60S Ribosomes. Cell, 2017, 171, 1599-1610.e14.	13.5	162
3	PAM identification by CRISPR-Cas effector complexes: diversified mechanisms and structures. RNA Biology, 2019, 16, 504-517.	1.5	160
4	FlhA provides the adaptor for coordinated delivery of late flagella building blocks to the type III secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11295-11300.	3.3	154
5	ParB-type DNA Segregation Proteins Are CTP-Dependent Molecular Switches. Cell, 2019, 179, 1512-1524.e15.	13.5	136
6	Protein targeting by the signal recognition particle. Biological Chemistry, 2009, 390, 775-782.	1.2	134
7	How bacteria maintain location and number of flagella?. FEMS Microbiology Reviews, 2015, 39, 812-822.	3.9	128
8	60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle. Nature Communications, 2014, 5, 3491.	5.8	117
9	Catalytic mechanism and allosteric regulation of an oligomeric (p)ppGpp synthetase by an alarmone. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13348-13353.	3.3	111
10	The Ustilago maydis repetitive effector Rsp3 blocks the antifungal activity of mannose-binding maize proteins. Nature Communications, 2018, 9, 1711.	5.8	102
11	Synchronizing Nuclear Import of Ribosomal Proteins with Ribosome Assembly. Science, 2012, 338, 666-671.	6.0	95
12	Escherichia coli Signal Recognition Particle Receptor FtsY Contains an Essential and Autonomous Membrane-binding Amphipathic Helix. Journal of Biological Chemistry, 2007, 282, 32176-32184.	1.6	93
13	MinD-like ATPase FlhG effects location and number of bacterial flagella during C-ring assembly. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3092-3097.	3.3	86
14	Structural characterization of a eukaryotic chaperone—the ribosome-associated complex. Nature Structural and Molecular Biology, 2013, 20, 23-28.	3.6	79
15	Structure of the <i>Bacillus subtilis</i> hibernating 100S ribosome reveals the basis for 70S dimerization. EMBO Journal, 2017, 36, 2061-2072.	3.5	74
16	(p)ppGpp: Magic Modulators of Bacterial Physiology and Metabolism. Frontiers in Microbiology, 2020, 11, 2072.	1.5	72
17	SIMIBI twins in protein targeting and localization. Nature Structural and Molecular Biology, 2013, 20, 776-780.	3.6	71
18	Type IV CRISPR RNA processing and effector complex formation in Aromatoleum aromaticum. Nature Microbiology, 2019, 4, 89-96.	5.9	70

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19	Structural Variation of Type I-F CRISPR RNA Guided DNA Surveillance. Molecular Cell, 2017, 67, 622-632.e4.	4.5	67
20	Regulation of the opposing (p)ppGpp synthetase and hydrolase activities in a bifunctional RelA/SpoT homologue from Staphylococcus aureus. PLoS Genetics, 2018, 14, e1007514.	1.5	67
21	Co-translational capturing of nascent ribosomal proteins by their dedicated chaperones. Nature Communications, 2015, 6, 7494.	5.8	63
22	The crystal structure of the third signal-recognition particle GTPase FlhF reveals a homodimer with bound GTP. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13621-13625.	3.3	60
23	Consistent mutational paths predict eukaryotic thermostability. BMC Evolutionary Biology, 2013, 13, 7.	3.2	60
24	Structural basis for the molecular evolution of SRP-GTPase activation by protein. Nature Structural and Molecular Biology, 2011, 18, 1376-1380.	3.6	59
25	The Dedicated Chaperone Acl4 Escorts Ribosomal Protein Rpl4 to Its Nuclear Pre-60S Assembly Site. PLoS Genetics, 2015, 11, e1005565.	1.5	59
26	AraC-like transcriptional activator CuxR binds c-di-GMP by a PilZ-like mechanism to regulate extracellular polysaccharide production. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4822-E4831.	3.3	58
27	Modulating the Cascade architecture of a minimal Type I-F CRISPR-Cas system. Nucleic Acids Research, 2016, 44, 5872-5882.	6.5	57
28	The crystal structure of Ebp1 reveals a methionine aminopeptidase fold as binding platform for multiple interactions. FEBS Letters, 2007, 581, 4450-4454.	1.3	55
29	The alarmones (p)ppGpp are part of the heat shock response of Bacillus subtilis. PLoS Genetics, 2020, 16, e1008275.	1.5	52
30	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. Nature Communications, 2015, 6, 6510.	5.8	51
31	Structural and mechanistic divergence of the small (p)ppGpp synthetases RelP and RelQ. Scientific Reports, 2018, 8, 2195.	1.6	51
32	Collapse of genetic division of labour and evolution of autonomy in pellicle biofilms. Nature Microbiology, 2018, 3, 1451-1460.	5.9	51
33	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. Nature, 2019, 565, 650-653.	13.7	48
34	Structural basis of HypK regulating N-terminal acetylation by the NatA complex. Nature Communications, 2017, 8, 15726.	5.8	44
35	A redox-mediated Kemp eliminase. Nature Communications, 2017, 8, 14876.	5.8	44
36	The role of <scp>FlhF</scp> and <scp>HubP</scp> as polar landmark proteins in <scp><i>S</i></scp> <i>hewanella putrefaciens</i> â€ <scp>CN</scp> â€32. Molecular Microbiology, 2015, 98, 727-742.	1.2	43

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37	Structure and function of the archaeal response regulator CheY. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1259-E1268.	3.3	43
38	Formin-like 2 Promotes β1-Integrin Trafficking and Invasive Motility Downstream of PKCα. Developmental Cell, 2015, 34, 475-483.	3.1	42
39	Undiscovered regions on the molecular landscape of flagellar assembly. Current Opinion in Microbiology, 2015, 28, 98-105.	2.3	41
40	Structural basis for the CsrA-dependent modulation of translation initiation by an ancient regulatory protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10168-10173.	3.3	41
41	Structural basis for (p)ppGpp-mediated inhibition of the GTPase RbgA. Journal of Biological Chemistry, 2018, 293, 19699-19709.	1.6	41
42	Lipids Trigger a Conformational Switch That Regulates Signal Recognition Particle (SRP)-mediated Protein Targeting. Journal of Biological Chemistry, 2011, 286, 23489-23497.	1.6	39
43	Structural Basis for Conserved Regulation and Adaptation of the Signal Recognition Particle Targeting Complex. Journal of Molecular Biology, 2016, 428, 2880-2897.	2.0	39
44	Biosynthesis of the Stress-Protectant and Chemical Chaperon Ectoine: Biochemistry of the Transaminase EctB. Frontiers in Microbiology, 2019, 10, 2811.	1.5	39
45	Structural Basis for Regulation of the Opposing (p)ppGpp Synthetase and Hydrolase within the Stringent Response Orchestrator Rel. Cell Reports, 2020, 32, 108157.	2.9	39
46	The CTPase activity of ParB determines the size and dynamics of prokaryotic DNA partition complexes. Molecular Cell, 2021, 81, 3992-4007.e10.	4.5	37
47	The multicatalytic compartment of propionyl-CoA synthase sequesters a toxic metabolite. Nature Chemical Biology, 2018, 14, 1127-1132.	3.9	34
48	From molecular evolution to biobricks and synthetic modules: a lesson by the bacterial flagellum. Biotechnology and Genetic Engineering Reviews, 2014, 30, 49-64.	2.4	33
49	Metabolism of non-growing bacteria. Biological Chemistry, 2020, 401, 1479-1485.	1.2	33
50	Architecture of the active postâ€ŧranslational Sec translocon. EMBO Journal, 2021, 40, e105643.	3.5	33
51	FlhG employs diverse intrinsic domains and influences FlhF GTPase activity to numerically regulate polar flagellar biogenesis in <i>Campylobacter jejuni</i> . Molecular Microbiology, 2016, 99, 291-306.	1.2	32
52	Two P or Not Two P: Understanding Regulation by the Bacterial Second Messengers (p)ppGpp. Annual Review of Microbiology, 2021, 75, 383-406.	2.9	32
53	Computational method allowing Hydrogen-Deuterium Exchange Mass Spectrometry at single amide Resolution. Scientific Reports, 2017, 7, 3789.	1.6	31
54	Flagellar number governs bacterial spreading and transport efficiency. Science Advances, 2018, 4, eaar6425.	4.7	31

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55	Structure and Mechanism of the Sphingopyxinâ€I Lasso Peptide Isopeptidase. Angewandte Chemie - International Edition, 2016, 55, 12717-12721.	7.2	27
56	New twist to nuclear import: When two travel together. Communicative and Integrative Biology, 2013, 6, e24792.	0.6	26
57	The ups and downs of ectoine: structural enzymology of a major microbial stress protectant and versatile nutrient. Biological Chemistry, 2020, 401, 1443-1468.	1.2	25
58	Crystal Structure of Bacillus subtilis Cysteine Desulfurase SufS and Its Dynamic Interaction with Frataxin and Scaffold Protein SufU. PLoS ONE, 2016, 11, e0158749.	1.1	24
59	FliS/flagellin/FliW heterotrimer couples type III secretion and flagellin homeostasis. Scientific Reports, 2018, 8, 11552.	1.6	23
60	Interaction studies on bacterial stringent response protein RelA with uncharged tRNA provide evidence for its prerequisite complex for ribosome binding. Current Genetics, 2019, 65, 1173-1184.	0.8	23
61	Molecular architecture of the DNA-binding sites of the P-loop ATPases MipZ and ParA from Caulobacter crescentus. Nucleic Acids Research, 2020, 48, 4769-4779.	6.5	23
62	The GGDEF Domain of the Phosphodiesterase PdeB in <i>Shewanella putrefaciens</i> Mediates Recruitment by the Polar Landmark Protein HubP. Journal of Bacteriology, 2019, 201, .	1.0	20
63	Tol-Pal System and Rgs Proteins Interact to Promote Unipolar Growth and Cell Division in Sinorhizobium meliloti. MBio, 2020, 11, .	1.8	18
64	Dual role of a (p)ppGpp―and (p)ppAppâ€degrading enzyme in biofilm formation and interbacterial antagonism. Molecular Microbiology, 2021, 115, 1339-1356.	1.2	18
65	Bistable Photoswitch Allows in Vivo Control of Hematopoiesis. ACS Central Science, 2022, 8, 57-66.	5.3	18
66	An ATP-dependent partner switch links flagellar C-ring assembly with gene expression. Proceedings of the United States of America, 2020, 117, 20826-20835.	3.3	17
67	Carbon Source-Dependent Reprogramming of Anaerobic Metabolism in <i>Staphylococcus aureus</i> . Journal of Bacteriology, 2021, 203, .	1.0	17
68	Hampered motility promotes the evolution of wrinkly phenotype in Bacillus subtilis. BMC Evolutionary Biology, 2018, 18, 155.	3.2	16
69	CdbA is a DNA-binding protein and c-di-GMP receptor important for nucleoid organization and segregation in Myxococcus xanthus. Nature Communications, 2020, 11, 1791.	5.8	16
70	Inhibition of SRP-dependent protein secretion by the bacterial alarmone (p)ppGpp. Nature Communications, 2022, 13, 1069.	5.8	16
71	Structural insights into the assembly of the human and archaeal signal recognition particles. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 295-303.	2.5	15
72	Bacillus subtilis Bactofilins Are Essential for Flagellar Hook- and Filament Assembly and Dynamically Localize into Structures of Less than 100 nm Diameter underneath the Cell Membrane. PLoS ONE, 2015, 10, e0141546.	1.1	15

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73	ZomB is essential for flagellar motor reversals in <i>Shewanella putrefaciens</i> and <i>Vibrio parahaemolyticus</i> . Molecular Microbiology, 2018, 109, 694-709.	1.2	15
74	Degradation of the microbial stress protectants and chemical chaperones ectoine and hydroxyectoine by a bacterial hydrolase–deacetylase complex. Journal of Biological Chemistry, 2020, 295, 9087-9104.	1.6	15
75	Structure and mechanistic features of the prokaryotic minimal RNase P. ELife, 2021, 10, .	2.8	15
76	Engineered PQQ-Dependent Alcohol Dehydrogenase for the Oxidation of 5-(Hydroxymethyl)furoic Acid. ACS Catalysis, 2020, 10, 7836-7842.	5.5	14
77	Dynamics of Bacterial Signal Recognition Particle at a Single Molecule Level. Frontiers in Microbiology, 2021, 12, 663747.	1.5	12
78	Diversification of 4′-Methylated Nucleosides by Nucleoside Phosphorylases. ACS Catalysis, 2021, 11, 10830-10835.	5.5	11
79	The two paralogous kiwellin proteins KWL1 and KWL1-b from maize are structurally related and have overlapping functions in plant defense. Journal of Biological Chemistry, 2020, 295, 7816-7825.	1.6	9
80	The Stand-Alone PilZ-Domain Protein MotL Specifically Regulates the Activity of the Secondary Lateral Flagellar System in Shewanella putrefaciens. Frontiers in Microbiology, 2021, 12, 668892.	1.5	9
81	Physiology of guanosine-based second messenger signaling in Bacillus subtilis. Biological Chemistry, 2020, 401, 1307-1322.	1.2	9
82	GTP-Dependent FlhF Homodimer Supports Secretion of a Hemolysin in Bacillus cereus. Frontiers in Microbiology, 2020, 11, 879.	1.5	9
83	In Vitro Activity of Amphotericin B in Combination with Colistin against Fungi Responsible for Invasive Infections. Journal of Fungi (Basel, Switzerland), 2022, 8, 115.	1.5	9
84	How to save a bacterial ribosome in times of stress. Seminars in Cell and Developmental Biology, 2023, 136, 3-12.	2.3	9
85	GGDEF domain as spatial on-switch for a phosphodiesterase by interaction with landmark protein HubP. Npj Biofilms and Microbiomes, 2022, 8, 35.	2.9	9
86	Co-translational Folding Intermediate Dictates Membrane Targeting of the Signal Recognition Particle Receptor. Journal of Molecular Biology, 2018, 430, 1607-1620.	2.0	8
87	Plants strike back: Kiwellin proteins as a modular toolbox for plant defense mechanisms. Communicative and Integrative Biology, 2019, 12, 31-33.	0.6	8
88	Non-invasive and label-free 3D-visualization shows in vivo oligomerization of the staphylococcal alkaline shock protein 23 (Asp23). Scientific Reports, 2020, 10, 125.	1.6	8
89	The Vibrio vulnificus stressosome is an oxygen-sensor involved in regulating iron metabolism. Communications Biology, 2022, 5, .	2.0	6
90	Swimming of bacterium Bacillus subtilis with multiple bundles of flagella. Soft Matter, 2019, 15, 10029-10034.	1.2	4

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91	Structural and functional characterization of the bacterial biofilm activator RemA. Nature Communications, 2021, 12, 5707.	5.8	4
92	A Proline-Rich Element in the Type III Secretion Protein FlhB Contributes to Flagellar Biogenesis in the Beta- and Gamma-Proteobacteria. Frontiers in Microbiology, 2020, 11, 564161.	1.5	3
93	A Synthetic Adenylationâ€Domainâ€Based tRNAâ€Aminoacylation Catalyst. Angewandte Chemie, 2015, 127, 2522-2526.	1.6	2
94	Structure and Mechanism of the Sphingopyxinâ€I Lasso Peptide Isopeptidase. Angewandte Chemie, 2016, 128, 12909-12913.	1.6	2
95	The many faces of the unusual biofilm activator RemA. BioEssays, 2022, 44, e2200009.	1.2	2
96	In Vitro Synergy of Isavuconazole Combined With Colistin Against Common Candida Species. Frontiers in Cellular and Infection Microbiology, 2022, 12, 892893.	1.8	1
97	Structural insights into the mechanism of archaellar rotational switching. Nature Communications, 2022, 13, .	5.8	1
98	Editorial overview: Synthetic biology – From understanding to engineering biology and back. Current Opinion in Chemical Biology, 2016, 34, A151-A153.	2.8	0
99	Ausrottung der Anopheles-Mücken durch CRISPR-Cas9?. BioSpektrum, 2018, 24, 712-716.	0.0	0
100	Cloning and characterization of a novel druggable fusion kinase in acute myeloid leukemia. Haematologica, 2020, 105, e395-e398.	1.7	0
101	Editorial: (p)ppGpp and Its Homologs: Enzymatic and Mechanistic Diversity Among the Microbes. Frontiers in Microbiology, 2021, 12, 658282.	1.5	0
102	Synergistic In Vitro Interaction of Isavuconazole and Isoquercitrin against Candida glabrata. Journal of Fungi (Basel, Switzerland), 2022, 8, 525.	1.5	0