

Gert Bange

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

4,217
citations

101496

36
h-index

143943

57
g-index

121
all docs

121
docs citations

121
times ranked

4365
citing authors

#	ARTICLE	IF	CITATIONS
1	How to save a bacterial ribosome in times of stress. <i>Seminars in Cell and Developmental Biology</i> , 2023, 136, 3-12.	2.3	9
2	In Vitro Activity of Amphotericin B in Combination with Colistin against Fungi Responsible for Invasive Infections. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 115.	1.5	9
3	Inhibition of SRP-dependent protein secretion by the bacterial alarmone (p)ppGpp. <i>Nature Communications</i> , 2022, 13, 1069.	5.8	16
4	The many faces of the unusual biofilm activator RemA. <i>BioEssays</i> , 2022, 44, e2200009.	1.2	2
5	Bistable Photoswitch Allows in Vivo Control of Hematopoiesis. <i>ACS Central Science</i> , 2022, 8, 57-66.	5.3	18
6	In Vitro Synergy of Isavuconazole Combined With Colistin Against Common Candida Species. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 892893.	1.8	1
7	GGDEF domain as spatial on-switch for a phosphodiesterase by interaction with landmark protein HubP. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 35.	2.9	9
8	Structural insights into the mechanism of archaeellar rotational switching. <i>Nature Communications</i> , 2022, 13, .	5.8	1
9	Synergistic In Vitro Interaction of Isavuconazole and Isoquercitrin against <i>Candida glabrata</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 525.	1.5	0
10	The <i>Vibrio vulnificus</i> stressosome is an oxygen-sensor involved in regulating iron metabolism. <i>Communications Biology</i> , 2022, 5, .	2.0	6
11	Dual role of a (p)ppGpp and (p)ppApp degrading enzyme in biofilm formation and interbacterial antagonism. <i>Molecular Microbiology</i> , 2021, 115, 1339-1356.	1.2	18
12	Carbon Source-Dependent Reprogramming of Anaerobic Metabolism in <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	17
13	Editorial: (p)ppGpp and Its Homologs: Enzymatic and Mechanistic Diversity Among the Microbes. <i>Frontiers in Microbiology</i> , 2021, 12, 658282.	1.5	0
14	Dynamics of Bacterial Signal Recognition Particle at a Single Molecule Level. <i>Frontiers in Microbiology</i> , 2021, 12, 663747.	1.5	12
15	Structure and mechanistic features of the prokaryotic minimal RNase P. <i>ELife</i> , 2021, 10, .	2.8	15
16	The Stand-Alone PilZ-Domain Protein MotL Specifically Regulates the Activity of the Secondary Lateral Flagellar System in <i>Shewanella putrefaciens</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 668892.	1.5	9
17	Two P or Not Two P: Understanding Regulation by the Bacterial Second Messengers (p)ppGpp. <i>Annual Review of Microbiology</i> , 2021, 75, 383-406.	2.9	32
18	Diversification of 4-Methylated Nucleosides by Nucleoside Phosphorylases. <i>ACS Catalysis</i> , 2021, 11, 10830-10835.	5.5	11

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19	Structural and functional characterization of the bacterial biofilm activator RemA. <i>Nature Communications</i> , 2021, 12, 5707.	5.8	4
20	The CTPase activity of ParB determines the size and dynamics of prokaryotic DNA partition complexes. <i>Molecular Cell</i> , 2021, 81, 3992-4007.e10.	4.5	37
21	Architecture of the active post-translational Sec translocon. <i>EMBO Journal</i> , 2021, 40, e105643.	3.5	33
22	Structural Basis for Regulation of the Opposing (p)ppGpp Synthetase and Hydrolase within the Stringent Response Orchestrator Rel. <i>Cell Reports</i> , 2020, 32, 108157.	2.9	39
23	An ATP-dependent partner switch links flagellar C-ring assembly with gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20826-20835.	3.3	17
24	Tol-Pal System and Rgs Proteins Interact to Promote Unipolar Growth and Cell Division in <i>Sinorhizobium meliloti</i> . <i>MBio</i> , 2020, 11, .	1.8	18
25	Cloning and characterization of a novel druggable fusion kinase in acute myeloid leukemia. <i>Haematologica</i> , 2020, 105, e395-e398.	1.7	0
26	(p)ppGpp: Magic Modulators of Bacterial Physiology and Metabolism. <i>Frontiers in Microbiology</i> , 2020, 11, 2072.	1.5	72
27	Molecular architecture of the DNA-binding sites of the P-loop ATPases MipZ and ParA from <i>Caulobacter crescentus</i> . <i>Nucleic Acids Research</i> , 2020, 48, 4769-4779.	6.5	23
28	The two paralogous kiwellin proteins KWL1 and KWL1-b from maize are structurally related and have overlapping functions in plant defense. <i>Journal of Biological Chemistry</i> , 2020, 295, 7816-7825.	1.6	9
29	Degradation of the microbial stress protectants and chemical chaperones ectoine and hydroxyectoine by a bacterial hydrolase-deacetylase complex. <i>Journal of Biological Chemistry</i> , 2020, 295, 9087-9104.	1.6	15
30	Engineered PQQ-Dependent Alcohol Dehydrogenase for the Oxidation of 5-(Hydroxymethyl)furoic Acid. <i>ACS Catalysis</i> , 2020, 10, 7836-7842.	5.5	14
31	The alarmones (p)ppGpp are part of the heat shock response of <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2020, 16, e1008275.	1.5	52
32	Non-invasive and label-free 3D-visualization shows in vivo oligomerization of the staphylococcal alkaline shock protein 23 (Asp23). <i>Scientific Reports</i> , 2020, 10, 125.	1.6	8
33	CdbA is a DNA-binding protein and c-di-GMP receptor important for nucleoid organization and segregation in <i>Myxococcus xanthus</i> . <i>Nature Communications</i> , 2020, 11, 1791.	5.8	16
34	Metabolism of non-growing bacteria. <i>Biological Chemistry</i> , 2020, 401, 1479-1485.	1.2	33
35	The ups and downs of ectoine: structural enzymology of a major microbial stress protectant and versatile nutrient. <i>Biological Chemistry</i> , 2020, 401, 1443-1468.	1.2	25
36	Physiology of guanosine-based second messenger signaling in <i>Bacillus subtilis</i> . <i>Biological Chemistry</i> , 2020, 401, 1307-1322.	1.2	9

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37	GTP-Dependent FlhF Homodimer Supports Secretion of a Hemolysin in <i>Bacillus cereus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 879.	1.5	9
38	A Proline-Rich Element in the Type III Secretion Protein FlhB Contributes to Flagellar Biogenesis in the Beta- and Gamma-Proteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 564161.	1.5	3
39	PAM identification by CRISPR-Cas effector complexes: diversified mechanisms and structures. <i>RNA Biology</i> , 2019, 16, 504-517.	1.5	160
40	The GGDEF Domain of the Phosphodiesterase PdeB in <i>Shewanella putrefaciens</i> Mediates Recruitment by the Polar Landmark Protein HubP. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	20
41	Plants strike back: Kiwellin proteins as a modular toolbox for plant defense mechanisms. <i>Communicative and Integrative Biology</i> , 2019, 12, 31-33.	0.6	8
42	Interaction studies on bacterial stringent response protein RelA with uncharged tRNA provide evidence for its prerequisite complex for ribosome binding. <i>Current Genetics</i> , 2019, 65, 1173-1184.	0.8	23
43	Swimming of bacterium <i>Bacillus subtilis</i> with multiple bundles of flagella. <i>Soft Matter</i> , 2019, 15, 10029-10034.	1.2	4
44	ParB-type DNA Segregation Proteins Are CTP-Dependent Molecular Switches. <i>Cell</i> , 2019, 179, 1512-1524.e15.	13.5	136
45	Biosynthesis of the Stress-Protectant and Chemical Chaperon Ectoine: Biochemistry of the Transaminase EctB. <i>Frontiers in Microbiology</i> , 2019, 10, 2811.	1.5	39
46	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. <i>Nature</i> , 2019, 565, 650-653.	13.7	48
47	Type IV CRISPR RNA processing and effector complex formation in <i>Aromatoleum aromaticum</i> . <i>Nature Microbiology</i> , 2019, 4, 89-96.	5.9	70
48	Structural and mechanistic divergence of the small (p)ppGpp synthetases RelP and RelQ. <i>Scientific Reports</i> , 2018, 8, 2195.	1.6	51
49	Structure and function of the archaeal response regulator CheY. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1259-E1268.	3.3	43
50	Co-translational Folding Intermediate Dictates Membrane Targeting of the Signal Recognition Particle Receptor. <i>Journal of Molecular Biology</i> , 2018, 430, 1607-1620.	2.0	8
51	The <i>Ustilago maydis</i> repetitive effector Rsp3 blocks the antifungal activity of mannose-binding maize proteins. <i>Nature Communications</i> , 2018, 9, 1711.	5.8	102
52	Ausrottung der Anopheles-Mücken durch CRISPR-Cas9?. <i>BioSpektrum</i> , 2018, 24, 712-716.	0.0	0
53	Collapse of genetic division of labour and evolution of autonomy in pellicle biofilms. <i>Nature Microbiology</i> , 2018, 3, 1451-1460.	5.9	51
54	Flagellar number governs bacterial spreading and transport efficiency. <i>Science Advances</i> , 2018, 4, eaar6425.	4.7	31

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55	Hampered motility promotes the evolution of wrinkly phenotype in <i>Bacillus subtilis</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 155.	3.2	16
56	Structural basis for (p)ppGpp-mediated inhibition of the GTPase RbgA. <i>Journal of Biological Chemistry</i> , 2018, 293, 19699-19709.	1.6	41
57	The multicatalytic compartment of propionyl-CoA synthase sequesters a toxic metabolite. <i>Nature Chemical Biology</i> , 2018, 14, 1127-1132.	3.9	34
58	ZomB is essential for flagellar motor reversals in <i>Shewanella putrefaciens</i> and <i>Vibrio parahaemolyticus</i> . <i>Molecular Microbiology</i> , 2018, 109, 694-709.	1.2	15
59	FliS/flagellin/FliW heterotrimer couples type III secretion and flagellin homeostasis. <i>Scientific Reports</i> , 2018, 8, 11552.	1.6	23
60	Regulation of the opposing (p)ppGpp synthetase and hydrolase activities in a bifunctional RelA/SpoT homologue from <i>Staphylococcus aureus</i> . <i>PLoS Genetics</i> , 2018, 14, e1007514.	1.5	67
61	Structure of the <i>Bacillus subtilis</i> hibernating 100S ribosome reveals the basis for 70S dimerization. <i>EMBO Journal</i> , 2017, 36, 2061-2072.	3.5	74
62	Structural basis of HypK regulating N-terminal acetylation by the NatA complex. <i>Nature Communications</i> , 2017, 8, 15726.	5.8	44
63	AraC-like transcriptional activator CuxR binds c-di-GMP by a PilZ-like mechanism to regulate extracellular polysaccharide production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4822-E4831.	3.3	58
64	A redox-mediated Kemp eliminase. <i>Nature Communications</i> , 2017, 8, 14876.	5.8	44
65	Structural Variation of Type I-F CRISPR RNA Guided DNA Surveillance. <i>Molecular Cell</i> , 2017, 67, 622-632.e4.	4.5	67
66	Visualizing the Assembly Pathway of Nucleolar Pre-60S Ribosomes. <i>Cell</i> , 2017, 171, 1599-1610.e14.	13.5	162
67	Computational method allowing Hydrogen-Deuterium Exchange Mass Spectrometry at single amide Resolution. <i>Scientific Reports</i> , 2017, 7, 3789.	1.6	31
68	Crystal Structure of <i>Bacillus subtilis</i> Cysteine Desulfurase SufS and Its Dynamic Interaction with Frataxin and Scaffold Protein SufU. <i>PLoS ONE</i> , 2016, 11, e0158749.	1.1	24
69	Structural Basis for Conserved Regulation and Adaptation of the Signal Recognition Particle Targeting Complex. <i>Journal of Molecular Biology</i> , 2016, 428, 2880-2897.	2.0	39
70	FlhG employs diverse intrinsic domains and influences FlhF GTPase activity to numerically regulate polar flagellar biogenesis in <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2016, 99, 291-306.	1.2	32
71	The magic dance of the alarmones (p)ppGpp. <i>Molecular Microbiology</i> , 2016, 101, 531-544.	1.2	171
72	Modulating the Cascade architecture of a minimal Type I-F CRISPR-Cas system. <i>Nucleic Acids Research</i> , 2016, 44, 5872-5882.	6.5	57

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73	Structure and Mechanism of the Sphingopyxinâ€¦Lasso Peptide Isopeptidase. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 12717-12721.	7.2	27
74	Editorial overview: Synthetic biology â€œ From understanding to engineering biology and back. <i>Current Opinion in Chemical Biology</i> , 2016, 34, A151-A153.	2.8	0
75	Structural basis for the CsrA-dependent modulation of translation initiation by an ancient regulatory protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10168-10173.	3.3	41
76	Structure and Mechanism of the Sphingopyxinâ€¦Lasso Peptide Isopeptidase. <i>Angewandte Chemie</i> , 2016, 128, 12909-12913.	1.6	2
77	A Synthetic Adenylationâ€Domainâ€Based tRNAâ€Aminoacylation Catalyst. <i>Angewandte Chemie</i> , 2015, 127, 2522-2526.	1.6	2
78	The role of <scp>FlhF</scp> and <scp>HubP</scp> as polar landmark proteins in <scp><i>S</i></scp><i>hewanella putrefaciens</i></scp>â€¦<scp>CN</scp>â€³2. <i>Molecular Microbiology</i> , 2015, 98, 727-742.	1.2	43
79	<i>Bacillus subtilis</i> Bactofilins Are Essential for Flagellar Hook- and Filament Assembly and Dynamically Localize into Structures of Less than 100 nm Diameter underneath the Cell Membrane. <i>PLoS ONE</i> , 2015, 10, e0141546.	1.1	15
80	Formin-like 2 Promotes Î²1-Integrin Trafficking and Invasive Motility Downstream of PKCÎ±. <i>Developmental Cell</i> , 2015, 34, 475-483.	3.1	42
81	Co-translational capturing of nascent ribosomal proteins by their dedicated chaperones. <i>Nature Communications</i> , 2015, 6, 7494.	5.8	63
82	How bacteria maintain location and number of flagella?. <i>FEMS Microbiology Reviews</i> , 2015, 39, 812-822.	3.9	128
83	Undiscovered regions on the molecular landscape of flagellar assembly. <i>Current Opinion in Microbiology</i> , 2015, 28, 98-105.	2.3	41
84	Symportin 1 chaperones 5S RNP assembly during ribosome biogenesis by occupying an essential rRNA-binding site. <i>Nature Communications</i> , 2015, 6, 6510.	5.8	51
85	Catalytic mechanism and allosteric regulation of an oligomeric (p)ppGpp synthetase by an alarmone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13348-13353.	3.3	111
86	MinD-like ATPase FlhG effects location and number of bacterial flagella during C-ring assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3092-3097.	3.3	86
87	The Dedicated Chaperone Acl4 Escorts Ribosomal Protein Rpl4 to Its Nuclear Pre-60S Assembly Site. <i>PLoS Genetics</i> , 2015, 11, e1005565.	1.5	59
88	From molecular evolution to biobricks and synthetic modules: a lesson by the bacterial flagellum. <i>Biotechnology and Genetic Engineering Reviews</i> , 2014, 30, 49-64.	2.4	33
89	60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle. <i>Nature Communications</i> , 2014, 5, 3491.	5.8	117
90	Structural characterization of a eukaryotic chaperoneâ€”the ribosome-associated complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 23-28.	3.6	79

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91	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
92	SIMIBI twins in protein targeting and localization. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 776-780.	3.6	71
93	New twist to nuclear import: When two travel together. <i>Communicative and Integrative Biology</i> , 2013, 6, e24792.	0.6	26
94	Synchronizing Nuclear Import of Ribosomal Proteins with Ribosome Assembly. <i>Science</i> , 2012, 338, 666-671.	6.0	95
95	Structural basis for the molecular evolution of SRP-GTPase activation by protein. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1376-1380.	3.6	59
96	Lipids Trigger a Conformational Switch That Regulates Signal Recognition Particle (SRP)-mediated Protein Targeting. <i>Journal of Biological Chemistry</i> , 2011, 286, 23489-23497.	1.6	39
97	Structural insights into the assembly of the human and archaeal signal recognition particles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 295-303.	2.5	15
98	FlhA provides the adaptor for coordinated delivery of late flagella building blocks to the type III secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11295-11300.	3.3	154
99	Protein targeting by the signal recognition particle. <i>Biological Chemistry</i> , 2009, 390, 775-782.	1.2	134
100	The crystal structure of the third signal-recognition particle GTPase FlhF reveals a homodimer with bound GTP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13621-13625.	3.3	60
101	<i>Escherichia coli</i> Signal Recognition Particle Receptor FtsY Contains an Essential and Autonomous Membrane-binding Amphipathic Helix. <i>Journal of Biological Chemistry</i> , 2007, 282, 32176-32184.	1.6	93
102	The crystal structure of Ebp1 reveals a methionine aminopeptidase fold as binding platform for multiple interactions. <i>FEBS Letters</i> , 2007, 581, 4450-4454.	1.3	55