Laurent Terradot

List of Publications by Year
in descending order

54	1,991	201674	254184
papers	citations	27 h-index	43 g-index

58	58	58	2424
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Paramagnetic Solidâ€State NMR to Localize the Metalâ€Ion Cofactor in an Oligomeric DnaB Helicase. Chemistry - A European Journal, 2021, 27, 7745-7755.	3.3	8
2	Nucleotide Binding Modes in a Motor Protein Revealed by ³¹Pâ€•and ¹Hâ€Detected MAS Solidâ€State NMR Spectroscopy. ChemBioChem, 2020, 21, 324-330.	2.6	20
3	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
4	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. PLoS Pathogens, 2020, 16, e1007979.	4.7	45
5	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
6	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
7	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
8	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
9	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
10	The TIR-domain containing effectors BtpA and BtpB from Brucella abortus impact NAD metabolism. , 2020, 16, e1007979.		0
11	A secreted metal-binding protein protects necrotrophic phytopathogens from reactive oxygen species. Nature Communications, 2019, 10, 4853.	12.8	16
12	The conformational changes coupling ATP hydrolysis and translocation in a bacterial DnaB helicase. Nature Communications, 2019, 10, 31.	12.8	45
13	Biochemical characterization of the Helicobacter pylori Cag Type 4 Secretion System protein CagN and its interaction partner CagM. International Journal of Medical Microbiology, 2018, 308, 425-437.	3.6	4
14	Structural and functional insight into serine hydroxymethyltransferase from Helicobacter pylori. PLoS ONE, 2018, 13, e0208850.	2.5	9
15	Integrin but not CEACAM receptors are dispensable for Helicobacter pylori CagA translocation. PLoS Pathogens, 2018, 14, e1007359.	4.7	49
16	Solidâ€state NMR and EPR Spectroscopy of Mn²⁺â€Substituted ATPâ€Fueled Protein Engines. Angewandte Chemie - International Edition, 2017, 56, 3369-3373.	13.8	49
17	A Pseudomonas aeruginosaÂ<scp>TIR</scp> effector mediates immune evasion by targetingÂ<scp>UBAP</scp>1 and <scp>TLR</scp> adaptors. EMBO Journal, 2017, 36, 1869-1887.	7.8	31
18	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

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19	FestkÃ¶rperâ€NMRâ€und EPRâ€Spektroskopie an Mn²⁺â€substituierten ATPâ€angetriebenen Proteinmaschinen. Angewandte Chemie, 2017, 129, 3418-3422.	2.0	5
20	Structural and Molecular Biology of Type IV Secretion Systems. Current Topics in Microbiology and Immunology, 2017, 413, 31-60.	1.1	13
21	Performance of a Multiplex Serological Helicobacter pylori Assay on a Novel Microfluidic Assay Platform. Proteomes, 2017, 5, 24.	3.5	7
22	Structural Insights into Helicobacter pylori Cag Protein Interactions with Host Cell Factors. Current Topics in Microbiology and Immunology, 2017, 400, 129-147.	1.1	13
23	Syndecans as Cell Surface Receptors in Cancer Biology. A Focus on their Interaction with PDZ Domain Proteins. Frontiers in Pharmacology, 2016, 7, 10.	3.5	35
24	Variability and conservation of structural domains in divide-and-conquer approaches. Journal of Biomolecular NMR, 2016, 65, 79-86.	2.8	15
25	Beobachtung von ssDNAâ€Bindung an die DnaBâ€Helikase von Helicobacter pylori mittels FestkÃ¶rperâ€NMRâ€Spektroskopie. Angewandte Chemie, 2016, 128, 14370-14375.	2.0	4
26	Monitoring ssDNA Binding to the DnaB Helicase from Helicobacter pylori by Solidâ€State NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 14164-14168.	13.8	22
27	Solid-state NMR chemical-shift perturbations indicate domain reorientation of the DnaG primase in the primosome of Helicobacter pylori. Journal of Biomolecular NMR, 2016, 64, 189-195.	2.8	15
28	Tetramerization and interdomain flexibility of the replication initiation controller YabA enables simultaneous binding to multiple partners. Nucleic Acids Research, 2016, 44, 449-463.	14.5	96
29	Solid-state NMR sequential assignments of the N-terminal domain of HpDnaB helicase. Biomolecular NMR Assignments, 2016, 10, 13-23.	0.8	16
30	Francisella tularensis IglG Belongs to a Novel Family of PAAR-Like T6SS Proteins and Harbors a Unique N-terminal Extension Required for Virulence. PLoS Pathogens, 2016, 12, e1005821.	4.7	41
31	Structure and primase-mediated activation of a bacterial dodecameric replicative helicase. Nucleic Acids Research, 2015, 43, 8564-8576.	14.5	42
32	The Brucella TIR domain containing proteins BtpA and BtpB have a structural WxxxE motif important for protection against microtubule depolymerisation. Cell Communication and Signaling, 2014, 12, 53.	6.5	36
33	Structure of the Toll/interleukin 1 receptor (TIR) domain of the immunosuppressive Brucella effector BtpA/Btp1/TcpB. FEBS Letters, 2013, 587, 3412-3416.	2.8	33
34	Structural insights into Helicobacter pylori oncoprotein CagA interaction with Î²1 integrin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14640-14645.	7.1	114
35	A Sedimented Sample of a 59â€…kDa Dodecameric Helicase Yields Highâ€Resolution Solidâ€State NMR Spectra. Angewandte Chemie - International Edition, 2012, 51, 7855-7858.	13.8	112
36	Architecture of a Dodecameric Bacterial Replicative Helicase. Structure, 2012, 20, 554-564.	3.3	42

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37	DiaA/HobA and DnaA: A Pair of Proteins Co-evolved to Cooperate During Bacterial Orisome Assembly. Journal of Molecular Biology, 2011, 408, 238-251.	4.2	34
38	The structure of the Helicobacter pylori ferric uptake regulator Fur reveals three functional metal binding sites. Molecular Microbiology, 2011, 79, 1260-1275.	2.5	109
39	Architecture of the Helicobacterâ€ƒpylori Cagâ€type IV secretion system. FEBS Journal, 2011, 278, 1213-1222.	4.7	83
40	Bacterial protein interaction networks: puzzle stones from solved complex structures add to a clearer picture. Integrative Biology (United Kingdom), 2011, 3, 645-652.	1.3	6
41	Crystal structure of HP0721, a novel secreted protein from Helicobacter pylori. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1678-1681.	2.6	6
42	Structural insight intoHelicobacter pyloriDNA replication initiation. Gut Microbes, 2010, 1, 330-334.	9.8	6
43	Helicobacter pylori Type IV Secretion Apparatus Exploits Î²1 Integrin in a Novel RGD-Independent Manner. PLoS Pathogens, 2009, 5, e1000684.	4.7	203
44	Structures of the tumor necrosis factor Î± inducing protein TipÎ±: A novel virulence factor from Helicobacter pylori. FEBS Letters, 2009, 583, 1581-1585.	2.8	19
45	Expression of Helicobacterâ€ƒpylori CagA domains by libraryâ€based construct screening. FEBS Journal, 2009, 276, 816-824.	4.7	33
46	The structure of a DnaA/HobA complex from Helicobacter pylori provides insight into regulation of DNA replication in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21115-21120.	7.1	48
47	Structural and enzymatic characterization of HP0496, a YbgC thioesterase from Helicobacter pylori. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1212-1221.	2.6	30
48	In HspA from Helicobacter pylori vicinal disulfide bridges are a key determinant of domain B structure. FEBS Letters, 2008, 582, 3537-3541.	2.8	12
49	Identification, structure and mode of action of a new regulator of the Helicobacter pylori HP0525 ATPase. EMBO Journal, 2007, 26, 4926-4934.	7.8	34
50	Structural similarity between the DnaAâ€binding proteins HobA (HP1230) from Helicobacter pylori and DiaA from Escherichia coli. Molecular Microbiology, 2007, 65, 995-1005.	2.5	42
51	Structural Basis of the Nickel Response in Helicobacter pylori: Crystal Structures of HpNikR in Apo and Nickel-bound States. Journal of Molecular Biology, 2006, 361, 715-730.	4.2	74
52	Structures of two core subunits of the bacterial type IV secretion system, VirB8 from Brucella suis and ComB10 from Helicobacter pylori. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4596-4601.	7.1	113
53	Biochemical Characterization of Protein Complexes from the Helicobacter pylori Protein Interaction Map. Molecular and Cellular Proteomics, 2004, 3, 809-819.	3.8	44
54	Structural Basis of 5-Nitroimidazole Antibiotic Resistance. Journal of Biological Chemistry, 2004, 279, 55840-55849.	3.4	71