Rolf Hilgenfeld

List of Publications by Year
in descending order

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96 papers	13,698 citations	50276 46 h-index	37204 96 g-index
113 all docs	113 docs citations	113 times ranked	15292 citing authors

#	Article	IF	Citations
1	Crystal structure of SARS-CoV-2 main protease provides a basis for design of improved Î±-ketoamide inhibitors. Science, 2020, 368, 409-412.	12.6	2,527
2	Coronavirus Main Proteinase (3CLpro) Structure: Basis for Design of Anti-SARS Drugs. Science, 2003, 300, 1763-1767.	12.6	1,514
3	The crystal structures of severe acute respiratory syndrome virus main protease and its complex with an inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13190-13195.	7.1	879
4	Crystal structure of active elongation factor Tu reveals major domain rearrangements. Nature, 1993, 365, 126-132.	27.8	569
5	Design of Wide-Spectrum Inhibitors Targeting Coronavirus Main Proteases. PLoS Biology, 2005, 3, e324.	5.6	547
6	Nsp3 of coronaviruses: Structures and functions of a large multi-domain protein. Antiviral Research, 2018, 149, 58-74.	4.1	542
7	Structure of coronavirus main proteinase reveals combination of a chymotrypsin fold with an extra alpha-helical domain. EMBO Journal, 2002, 21, 3213-3224.	7.8	538
8	From <scp>SARS</scp> to <scp>MERS</scp>: crystallographic studies on coronaviral proteases enable antiviral drug design. FEBS Journal, 2014, 281, 4085-4096.	4.7	537
9	Î±-Ketoamides as Broad-Spectrum Inhibitors of Coronavirus and Enterovirus Replication: Structure-Based Design, Synthesis, and Activity Assessment. Journal of Medicinal Chemistry, 2020, 63, 4562-4578.	6.4	437
10	The SARS-Coronavirus-Host Interactome: Identification of Cyclophilins as Target for Pan-Coronavirus Inhibitors. PLoS Pathogens, 2011, 7, e1002331.	4.7	367
11	Accessory proteins of SARS-CoV and other coronaviruses. Antiviral Research, 2014, 109, 97-109.	4.1	339
12	From SARS to MERS: 10 years of research on highly pathogenic human coronaviruses. Antiviral Research, 2013, 100, 286-295.	4.1	292
13	Crystal structure of Zika virus NS2B-NS3 protease in complex with a boronate inhibitor. Science, 2016, 353, 503-505.	12.6	285
14	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. Science, 2021, 372, 642-646.	12.6	240
15	SARS-CoV-2 Mpro inhibitors and activity-based probes for patient-sample imaging. Nature Chemical Biology, 2021, 17, 222-228.	8.0	215
16	pH-dependent Conformational Flexibility of the SARS-CoV Main Proteinase (Mpro) Dimer: Molecular Dynamics Simulations and Multiple X-ray Structure Analyses. Journal of Molecular Biology, 2005, 354, 25-40.	4.2	175
17	p53 down-regulates SARS coronavirus replication and is targeted by the SARS-unique domain and PL ^{pro} via E3 ubiquitin ligase RCHY1. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5192-201.	7.1	172
18	The SARS-CoV-2 main protease Mpro causes microvascular brain pathology by cleaving NEMO in brain endothelial cells. Nature Neuroscience, 2021, 24, 1522-1533.	14.8	164

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19	The SARS-Unique Domain (SUD) of SARS Coronavirus Contains Two Macrodomains That Bind G-Quadruplexes. PLoS Pathogens, 2009, 5, e1000428.	4.7	156
20	Two non-prolinecispeptide bonds may be important for factor XIII function. FEBS Letters, 1998, 423, 291-296.	2.8	138
21	Peptide aldehyde inhibitors challenge the substrate specificity of the SARS-coronavirus main protease. Antiviral Research, 2011, 92, 204-212.	4.1	112
22	A G-quadruplex-binding macrodomain within the â€œSARS-unique domainâ€•is essential for the activity of the SARS-coronavirus replicationâ€“transcription complex. Virology, 2015, 484, 313-322.	2.4	112
23	Crystal structure of Mip, a prolylisomerase from Legionella pneumophila. Nature Structural Biology, 2001, 8, 779-783.	9.7	105
24	Peptideâ€“Boronic Acid Inhibitors of Flaviviral Proteases: Medicinal Chemistry and Structural Biology. Journal of Medicinal Chemistry, 2017, 60, 511-516.	6.4	105
25	Nucleocapsid protein of SARS coronavirus tightly binds to human cyclophilin A. Biochemical and Biophysical Research Communications, 2004, 321, 557-565.	2.1	104
26	3C Protease of Enterovirus 68: Structure-Based Design of Michael Acceptor Inhibitors and Their Broad-Spectrum Antiviral Effects against Picornaviruses. Journal of Virology, 2013, 87, 4339-4351.	3.4	91
27	Processing of the SARS-CoV pp1a/ab nsp7â€“10 region. Biochemical Journal, 2020, 477, 1009-1019.	3.7	90
28	The Evolution of Insulin Glargine and its Continuing Contribution to Diabetes Care. Drugs, 2014, 74, 911-927.	10.9	81
29	A Structural View of the Inactivation of the SARS Coronavirus Main Proteinase by Benzotriazole Esters. Chemistry and Biology, 2008, 15, 597-606.	6.0	79
30	Molecular mechanisms of severe acute respiratory syndrome (SARS). Respiratory Research, 2005, 6, 8.	3.6	78
31	Picornavirus non-structural proteins as targets for new anti-virals with broad activity. Antiviral Research, 2011, 89, 204-218.	4.1	76
32	Crystal structure of the papain-like protease of MERS coronavirus reveals unusual, potentially druggable active-site features. Antiviral Research, 2014, 109, 72-82.	4.1	74
33	Nonstructural Proteins 7 and 8 of Feline Coronavirus Form a 2:1 Heterotrimer That Exhibits Primer-Independent RNA Polymerase Activity. Journal of Virology, 2012, 86, 4444-4454.	3.4	73
34	Structure and Cleavage Specificity of the Chymotrypsin-Like Serine Protease (3CLSP/nsp4) of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV). Journal of Molecular Biology, 2009, 392, 977-993.	4.2	66
35	A common core for binding single-stranded DNA: structural comparison of the single-stranded DNA-binding proteins (SSB) fromE. coliand human mitochondria. FEBS Letters, 1997, 411, 313-316.	2.8	64
36	Sensitized Detection of Inhibitory Fragments and Iterative Development of Nonâ€Peptidic Protease Inhibitors by Dynamic Ligation Screening. Angewandte Chemie - International Edition, 2008, 47, 3275-3278.	13.8	64

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37	<scp>RNA</scp>â€virus proteases counteracting host innate immunity. FEBS Letters, 2017, 591, 3190-3210.	2.8	64
38	Development and Characterization of New Peptidomimetic Inhibitors of the West Nile Virus NS2Bâ€“NS3 Protease. ChemMedChem, 2013, 8, 231-241.	3.2	63
39	The Capsid Binder Vapendavir and the Novel Protease Inhibitor SG85 Inhibit Enterovirus 71 Replication. Antimicrobial Agents and Chemotherapy, 2014, 58, 6990-6992.	3.2	60
40	Liberation of SARS-CoV main protease from the viral polyprotein: N-terminal autocleavage does not depend on the mature dimerization mode. Protein and Cell, 2010, 1, 59-74.	11.0	58
41	Crystal Structure of the Peroxo-diiron(III) Intermediate of Deoxyhypusine Hydroxylase, an Oxygenase Involved in Hypusination. Structure, 2015, 23, 882-892.	3.3	55
42	Extended substrate specificity and first potent irreversible inhibitor/activity-based probe design for Zika virus NS2B-NS3 protease. Antiviral Research, 2017, 139, 88-94.	4.1	55
43	Antiviral Activity of Broad-Spectrum and Enterovirus-Specific Inhibitors against Clinical Isolates of Enterovirus D68. Antimicrobial Agents and Chemotherapy, 2015, 59, 7782-7785.	3.2	54
44	Binding of phenol to R6 insulin hexamers*. Biopolymers, 1999, 51, 165-172.	2.4	52
45	Thiazolidone derivatives as inhibitors of chikungunya virus. European Journal of Medicinal Chemistry, 2015, 89, 172-178.	5.5	52
46	Zika virus <scp>NS</scp>1, a pathogenicity factor with many faces. EMBO Journal, 2016, 35, 2631-2633.	7.8	52
47	Design, Synthesis, and Biological Evaluation of Peptidomimetic Aldehydes as Broad-Spectrum Inhibitors against Enterovirus and SARS-CoV-2. Journal of Medicinal Chemistry, 2022, 65, 2794-2808.	6.4	52
48	An Efficient Method for the Synthesis of Peptide Aldehyde Libraries Employed in the Discovery of Reversible SARS Coronavirus Main Protease (SARSâ€CoV M pro) Inhibitors. ChemBioChem, 2006, 7, 1048-1055.	2.6	50
49	Recent Advances in Targeting Viral Proteases for the Discovery of Novel Antivirals. Current Topics in Medicinal Chemistry, 2010, 10, 323-345.	2.1	48
50	Variable Oligomerization Modes in Coronavirus Non-structural Protein 9. Journal of Molecular Biology, 2008, 383, 1081-1096.	4.2	47
51	The â€œSARS-unique domainâ€•(SUD) of SARS coronavirus is an oligo(G)-binding protein. Biochemical and Biophysical Research Communications, 2007, 364, 877-882.	2.1	46
52	An overview on 2-methyl-2,4-pentanediol in crystallization and in crystals of biological macromolecules. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1722-1728.	2.5	43
53	Virusâ€“host interactomes â€” antiviral drug discovery. Current Opinion in Virology, 2012, 2, 614-621.	5.4	40
54	The non-structural protein Nsp10 of mouse hepatitis virus binds zinc ions and nucleic acids. FEBS Letters, 2006, 580, 4143-4149.	2.8	36

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55	Crystal structures of the Xâ€domains of a Groupâ€1 and a Groupâ€3 coronavirus reveal that ADPâ€ribioseâ€binding may not be a conserved property. Protein Science, 2009, 18, 6-16.	7.6	36
56	Effects of NS2B-NS3 protease and furin inhibition on West Nile and Dengue virus replication. Journal of Enzyme Inhibition and Medicinal Chemistry, 2017, 32, 712-721.	5.2	34
57	WaaA of the Hyperthermophilic Bacterium Aquifex aeolicus Is a Monofunctional 3-Deoxy-d-manno-oct-2-ulosonic Acid Transferase Involved in Lipopolysaccharide Biosynthesis. Journal of Biological Chemistry, 2009, 284, 22248-22262.	3.4	33
58	Calcium Binding of Transglutaminases: A⁴³Ca NMR Study Combined with Surface Polarity Analysis. Journal of Biomolecular Structure and Dynamics, 2001, 19, 59-74.	3.5	32
59	How do the GTPases really work?. Nature Structural Biology, 1995, 2, 3-6.	9.7	31
60	Irreversible inhibitors of the 3C protease of Coxsackie virus through templated assembly of protein-binding fragments. Nature Communications, 2016, 7, 12761.	12.8	30
61	Structural and mutational analysis of the interaction between the Middle-East respiratory syndrome coronavirus (MERS-CoV) papain-like protease and human ubiquitin. Virologica Sinica, 2016, 31, 288-299.	3.0	30
62	The Structure of the Zika Virus Protease, NS2B/NS3pro. Advances in Experimental Medicine and Biology, 2018, 1062, 131-145.	1.6	28
63	The SARSâ€unique domain (SUD) of SARSâ€CoV and SARSâ€CoVâ€2 interacts with human Paip1 to enhance viral RNA translation. EMBO Journal, 2021, 40, e102277.	7.8	26
64	Structure of the GTPase and GDI domains of FeoB, the ferrous iron transporter of Legionella pneumophila. FEBS Letters, 2010, 584, 733-738.	2.8	25
65	Coronavirus main proteinase: target for antiviral drug therapy. , 2005, , 173-199.		20
66	Acquisition of new protein domains by coronaviruses: analysis of overlapping genes coding for proteins N and 9b in SARS coronavirus. Virus Genes, 2015, 50, 29-38.	1.6	20
67	Structural biology in the fight against COVID-19. Nature Structural and Molecular Biology, 2021, 28, 2-7.	8.2	20
68	Structures of DegQ from Legionella pneumophila Define Distinct ON and OFF States. Journal of Molecular Biology, 2015, 427, 2840-2851.	4.2	19
69	The Enterovirus 3C Protease Inhibitor SG85 Efficiently Blocks Rhinovirus Replication and Is Not Cross-Resistant with Rupintrivir. Antimicrobial Agents and Chemotherapy, 2015, 59, 5814-5818.	3.2	18
70	Viral enzymes. Current Opinion in Structural Biology, 2006, 16, 776-786.	5.7	17
71	Application of a cell-based protease assay for testing inhibitors of picornavirus 3C proteases. Antiviral Research, 2014, 103, 17-24.	4.1	17
72	Structure of the X (ADRP) domain of nsp3 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1292-1300.	2.5	16

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73	Profiling of flaviviral NS2B-NS3 protease specificity provides a structural basis for the development of selective chemical tools that differentiate Dengue from Zika and West Nile viruses. Antiviral Research, 2020, 175, 104731.	4.1	14
74	A method to detect nonprolinecis peptide bonds in proteins. Biopolymers, 1999, 50, 536-544.	2.4	13
75	Lybatides from Lycium barbarum Contain An Unusual Cystine-stapled Helical Peptide Scaffold. Scientific Reports, 2017, 7, 5194.	3.3	13
76	Structure and Dynamics of Sars Coronavirus Main Proteinase (MPRO). Advances in Experimental Medicine and Biology, 2006, 581, 585-591.	1.6	12
77	Coxsackievirus B3 protease 3C: expression, purification, crystallization and preliminary structural insights. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 877-884.	0.8	11
78	Crystal structure of the C-terminal fragment of NS1 protein from yellow fever virus. Science China Life Sciences, 2017, 60, 1403-1406.	4.9	11
79	From Repurposing to Redesign: Optimization of Boceprevir to Highly Potent Inhibitors of the SARS-CoV-2 Main Protease. Molecules, 2022, 27, 4292.	3.8	10
80	Perspectives on Single Molecule Diffraction Using the X-Ray Free Electron Laser. Single Molecules, 2002, 3, 63-68.	0.9	9
81	Structural Basis of the Proteolytic and Chaperone Activity of Chlamydia trachomatis CT441. Journal of Bacteriology, 2015, 197, 211-218.	2.2	9
82	Insights into the GTPase Mechanism of EF-Tu from Structural Studies. , 0, , 347-357.		7
83	STD-NMR experiments identify a structural motif with novel second-site activity against West Nile virus NS2B-NS3 protease. Antiviral Research, 2017, 146, 174-183.	4.1	6
84	Crystal structure of the middle domain of human poly(A)-binding protein-interacting protein 1. Biochemical and Biophysical Research Communications, 2011, 408, 680-685.	2.1	5
85	Sometimes Intermediates Do the Job!. Chemistry and Biology, 2006, 13, 235-236.	6.0	4
86	Viral Entry and NS1 as Potential Antiviral Drug Targets. Advances in Experimental Medicine and Biology, 2018, 1062, 107-113.	1.6	4
87	Structural Proteomics of Emerging Viruses: The Examples of SARS-CoV and Other Coronaviruses. , 2008, , 361-433.		4
88	Computer-Aided Structure Based Drug Design Approaches for the Discovery of New Anti-CHIKV Agents. Current Computer-Aided Drug Design, 2017, 13, 346-361.	1.2	4
89	Synthesis, Structureâ€“Activity Relationships, and Antiviral Profiling of 1-Heteroaryl-2-Alkoxyphenyl Analogs as Inhibitors of SARS-CoV-2 Replication. Molecules, 2022, 27, 1052.	3.8	4
90	Characterization of an Allosteric Pocket in Zika Virus NS2B-NS3 Protease. Journal of Chemical Information and Modeling, 2022, 62, 945-957.	5.4	4

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91	Structure-based antivirals for emerging and neglected RNA viruses: an emerging field for medicinal chemistry in academia. Future Medicinal Chemistry, 2010, 2, 1061-1067.	2.3	3
92	Third Tofo Advanced Study Week on Emerging and Re-emerging Viruses, 2018. Antiviral Research, 2019, 162, 142-150.	4.1	3
93	Identification of non-covalent SARS-CoV-2 main protease inhibitors by a virtual screen of commercially available drug-like compounds. Bioorganic and Medicinal Chemistry Letters, 2021, 41, 127990.	2.2	2
94	Non Structural Proteins 8 and 9 of Human Coronavirus 229E. Advances in Experimental Medicine and Biology, 2006, 581, 49-54.	1.6	2
95	Production, crystallization and X-ray diffraction analysis of the protease CT441 fromChlamydia trachomatis. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1454-1458.	0.8	1
96	Production of Coronavirus Nonstructural Proteins in Soluble Form for Crystallization. Methods in Molecular Biology, 2008, 454, 139-159.	0.9	1