# 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 | 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 |
| 2 | 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 |
| 3 | Characterization of an Allosteric Pocket in Zika Virus NS2B-NS3 Protease. Journal of Chemical Information and Modeling, 2022, 62, 945-957. | 5.4 | 4 |
| 4 | 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 |
| 5 | SARS-CoV-2 Mpro inhibitors and activity-based probes for patient-sample imaging. Nature Chemical Biology, 2021, 17, 222-228. | 8.0 | 215 |
| 6 | 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 |
| 7 | X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. Science, 2021, 372, 642-646. | 12.6 | 240 |
| 8 | 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 |
| 9 | Structural biology in the fight against COVID-19. Nature Structural and Molecular Biology, 2021, 28, 2-7. | 8.2 | 20 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Processing of the SARS-CoV pp1a/ab nsp7â€“10 region. Biochemical Journal, 2020, 477, 1009-1019. | 3.7 | 90 |
| 15 | Third Tofo Advanced Study Week on Emerging and Re-emerging Viruses, 2018. Antiviral Research, 2019, 162, 142-150. | 4.1 | 3 |
| 16 | Nsp3 of coronaviruses: Structures and functions of a large multi-domain protein. Antiviral Research, 2018, 149, 58-74. | 4.1 | 542 |
| 17 | The Structure of the Zika Virus Protease, NS2B/NS3pro. Advances in Experimental Medicine and Biology, 2018, 1062, 131-145. | 1.6 | 28 |
| 18 | Viral Entry and NS1 as Potential Antiviral Drug Targets. Advances in Experimental Medicine and Biology, 2018, 1062, 107-113. | 1.6 | 4 |

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|---|---|---|---|
| 19 | Peptideâ€“Boronic Acid Inhibitors of Flaviviral Proteases: Medicinal Chemistry and Structural Biology. Journal of Medicinal Chemistry, 2017, 60, 511-516. | 6.4 | 105 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | <scp>RNA</scp>â€virus proteases counteracting host innate immunity. FEBS Letters, 2017, 591, 3190-3210. | 2.8 | 64 |
| 24 | Lybatides from Lycium barbarum Contain An Unusual Cystine-stapled Helical Peptide Scaffold. Scientific Reports, 2017, 7, 5194. | 3.3 | 13 |
| 25 | 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 |
| 26 | 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 |
| 27 | Crystal structure of Zika virus NS2B-NS3 protease in complex with a boronate inhibitor. Science, 2016, 353, 503-505. | 12.6 | 285 |
| 28 | 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 |
| 29 | p53 down-regulates SARS coronavirus replication and is targeted by the SARS-unique domain and PL <sup>pro</sup> 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 |
| 30 | Zika virus <scp>NS</scp>1, a pathogenicity factor with many faces. EMBO Journal, 2016, 35, 2631-2633. | 7.8 | 52 |
| 31 | Irreversible inhibitors of the 3C protease of Coxsackie virus through templated assembly of protein-binding fragments. Nature Communications, 2016, 7, 12761. | 12.8 | 30 |
| 32 | 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 |
| 33 | 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 |
| 34 | Structures of DegQ from Legionella pneumophila Define Distinct ON and OFF States. Journal of Molecular Biology, 2015, 427, 2840-2851. | 4.2 | 19 |
| 35 | 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 |
| 36 | Crystal Structure of the Peroxo-diiron(III) Intermediate of Deoxyhypusine Hydroxylase, an Oxygenase Involved in Hypusination. Structure, 2015, 23, 882-892. | 3.3 | 55 |

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| 37 | 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 |
| 38 | 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 |
| 39 | Structural Basis of the Proteolytic and Chaperone Activity of Chlamydia trachomatis CT441. Journal of Bacteriology, 2015, 197, 211-218. | 2.2 | 9 |
| 40 | Thiazolidone derivatives as inhibitors of chikungunya virus. European Journal of Medicinal Chemistry, 2015, 89, 172-178. | 5.5 | 52 |
| 41 | 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 |
| 42 | 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 |
| 43 | Application of a cell-based protease assay for testing inhibitors of picornavirus 3C proteases. Antiviral Research, 2014, 103, 17-24. | 4.1 | 17 |
| 44 | 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 |
| 45 | Accessory proteins of SARS-CoV and other coronaviruses. Antiviral Research, 2014, 109, 97-109. | 4.1 | 339 |
| 46 | 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 |
| 47 | The Evolution of Insulin Glargine and its Continuing Contribution to Diabetes Care. Drugs, 2014, 74, 911-927. | 10.9 | 81 |
| 48 | From SARS to MERS: 10 years of research on highly pathogenic human coronaviruses. Antiviral Research, 2013, 100, 286-295. | 4.1 | 292 |
| 49 | Development and Characterization of New Peptidomimetic Inhibitors of the West Nile Virus NS2Bâ€“NS3 Protease. ChemMedChem, 2013, 8, 231-241. | 3.2 | 63 |
| 50 | 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 |
| 51 | 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 |
| 52 | Virusâ€“host interactomes â€” antiviral drug discovery. Current Opinion in Virology, 2012, 2, 614-621. | 5.4 | 40 |
| 53 | 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 |
| 54 | Picornavirus non-structural proteins as targets for new anti-virals with broad activity. Antiviral Research, 2011, 89, 204-218. | 4.1 | 76 |

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| 55 | Peptide aldehyde inhibitors challenge the substrate specificity of the SARS-coronavirus main protease. Antiviral Research, 2011, 92, 204-212. | 4.1 | 112 |
| 56 | The SARS-Coronavirus-Host Interactome: Identification of Cyclophilins as Target for Pan-Coronavirus Inhibitors. PLoS Pathogens, 2011, 7, e1002331. | 4.7 | 367 |
| 57 | Recent Advances in Targeting Viral Proteases for the Discovery of Novel Antivirals. Current Topics in Medicinal Chemistry, 2010, 10, 323-345. | 2.1 | 48 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | Crystal structures of the Xâ€domains of a Groupâ€1 and a Groupâ€3 coronavirus reveal that ADPâ€riboseâ€binding may not be a conserved property. Protein Science, 2009, 18, 6-16. | 7.6 | 36 |
| 62 | 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 |
| 63 | The SARS-Unique Domain (SUD) of SARS Coronavirus Contains Two Macrodomains That Bind G-Quadruplexes. PLoS Pathogens, 2009, 5, e1000428. | 4.7 | 156 |
| 64 | Structure of the X (ADRP) domain of nsp3 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1292-1300. | 2.5 | 16 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | Variable Oligomerization Modes in Coronavirus Non-structural Protein 9. Journal of Molecular Biology, 2008, 383, 1081-1096. | 4.2 | 47 |
| 69 | Production of Coronavirus Nonstructural Proteins in Soluble Form for Crystallization. Methods in Molecular Biology, 2008, 454, 139-159. | 0.9 | 1 |
| 70 | Structural Proteomics of Emerging Viruses: The Examples of SARS-CoV and Other Coronaviruses. , 2008, , 361-433. | | 4 |
| 71 | 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 |
| 72 | 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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| 73 | Sometimes Intermediates Do the Job!. Chemistry and Biology, 2006, 13, 235-236. | 6.0 | 4 |
| 74 | Viral enzymes. Current Opinion in Structural Biology, 2006, 16, 776-786. | 5.7 | 17 |
| 75 | 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 |
| 76 | Structure and Dynamics of Sars Coronavirus Main Proteinase (MPRO). Advances in Experimental Medicine and Biology, 2006, 581, 585-591. | 1.6 | 12 |
| 77 | Non Structural Proteins 8 and 9 of Human Coronavirus 229E. Advances in Experimental Medicine and Biology, 2006, 581, 49-54. | 1.6 | 2 |
| 78 | Coronavirus main proteinase: target for antiviral drug therapy. , 2005, , 173-199. | | 20 |
| 79 | Design of Wide-Spectrum Inhibitors Targeting Coronavirus Main Proteases. PLoS Biology, 2005, 3, e324. | 5.6 | 547 |
| 80 | 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 |
| 81 | Molecular mechanisms of severe acute respiratory syndrome (SARS). Respiratory Research, 2005, 6, 8. | 3.6 | 78 |
| 82 | Nucleocapsid protein of SARS coronavirus tightly binds to human cyclophilin A. Biochemical and Biophysical Research Communications, 2004, 321, 557-565. | 2.1 | 104 |
| 83 | Coronavirus Main Proteinase (3CLpro) Structure: Basis for Design of Anti-SARS Drugs. Science, 2003, 300, 1763-1767. | 12.6 | 1,514 |
| 84 | 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 |
| 85 | Perspectives on Single Molecule Diffraction Using the X-Ray Free Electron Laser. Single Molecules, 2002, 3, 63-68. | 0.9 | 9 |
| 86 | 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 |
| 87 | 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 |
| 88 | Crystal structure of Mip, a prolylisomerase from Legionella pneumophila. Nature Structural Biology, 2001, 8, 779-783. | 9.7 | 105 |
| 89 | Calcium Binding of Transglutaminases: A<sup>43</sup>Ca NMR Study Combined with Surface Polarity Analysis. Journal of Biomolecular Structure and Dynamics, 2001, 19, 59-74. | 3.5 | 32 |
| 90 | Binding of phenol to R6 insulin hexamers*. Biopolymers, 1999, 51, 165-172. | 2.4 | 52 |

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| 91 | A method to detect nonprolinecis peptide bonds in proteins. Biopolymers, 1999, 50, 536-544. | 2.4 | 13 |
| 92 | Two non-prolinecispeptide bonds may be important for factor XIII function. FEBS Letters, 1998, 423, 291-296. | 2.8 | 138 |
| 93 | 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 |
| 94 | How do the GTPases really work?. Nature Structural Biology, 1995, 2, 3-6. | 9.7 | 31 |
| 95 | Crystal structure of active elongation factor Tu reveals major domain rearrangements. Nature, 1993, 365, 126-132. | 27.8 | 569 |
| 96 | Insights into the GTPase Mechanism of EF-Tu from Structural Studies. , 0, , 347-357. | | 7 |