

Haitao Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3293478/publications.pdf>

Version: 2024-02-01

69
papers

11,423
citations

159585

30
h-index

98798

67
g-index

78
all docs

78
docs citations

78
times ranked

14000
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Mpro from SARS-CoV-2 and discovery of its inhibitors. <i>Nature</i> , 2020, 582, 289-293.	27.8	3,133
2	Structure of the RNA-dependent RNA polymerase from COVID-19 virus. <i>Science</i> , 2020, 368, 779-782.	12.6	1,228
3	Structure-based design of antiviral drug candidates targeting the SARS-CoV-2 main protease. <i>Science</i> , 2020, 368, 1331-1335.	12.6	1,135
4	The crystal structures of severe acute respiratory syndrome virus main protease and its complex with an inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13190-13195.	7.1	879
5	Structural Basis for RNA Replication by the SARS-CoV-2 Polymerase. <i>Cell</i> , 2020, 182, 417-428.e13.	28.9	672
6	Design of Wide-Spectrum Inhibitors Targeting Coronavirus Main Proteases. <i>PLoS Biology</i> , 2005, 3, e324.	5.6	547
7	Structures of Two Coronavirus Main Proteases: Implications for Substrate Binding and Antiviral Drug Design. <i>Journal of Virology</i> , 2008, 82, 2515-2527.	3.4	388
8	Structural basis for the inhibition of SARS-CoV-2 main protease by antineoplastic drug carmofur. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 529-532.	8.2	339
9	Structural biology of SARS-CoV-2 and implications for therapeutic development. <i>Nature Reviews Microbiology</i> , 2021, 19, 685-700.	28.6	259
10	Production of Authentic SARS-CoV Mpro with Enhanced Activity: Application as a Novel Tag-cleavage Endopeptidase for Protein Overproduction. <i>Journal of Molecular Biology</i> , 2007, 366, 965-975.	4.2	221
11	Crystal Structures of Membrane Transporter MmpL3, an Anti-TB Drug Target. <i>Cell</i> , 2019, 176, 636-648.e13.	28.9	172
12	Zika virus evades interferon-mediated antiviral response through the co-operation of multiple nonstructural proteins in vitro. <i>Cell Discovery</i> , 2017, 3, 17006.	6.7	166
13	Inhibition mechanism of SARS-CoV-2 main protease by ebselen and its derivatives. <i>Nature Communications</i> , 2021, 12, 3061.	12.8	149
14	Drug Design Targeting the Main Protease, the Achilles Heel of Coronaviruses. <i>Current Pharmaceutical Design</i> , 2006, 12, 4573-4590.	1.9	145
15	Structure of Main Protease from Human Coronavirus NL63: Insights for Wide Spectrum Anti-Coronavirus Drug Design. <i>Scientific Reports</i> , 2016, 6, 22677.	3.3	145
16	Crystal structure of SARS-CoV-2 main protease in complex with protease inhibitor PF-07321332. <i>Protein and Cell</i> , 2022, 13, 689-693.	11.0	136
17	Efficient biodegradation of highly crystallized polyethylene terephthalate through cell surface display of bacterial PETase. <i>Science of the Total Environment</i> , 2020, 709, 136138.	8.0	103
18	High-throughput screening identifies established drugs as SARS-CoV-2 PLpro inhibitors. <i>Protein and Cell</i> , 2021, 12, 877-888.	11.0	95

#	ARTICLE	IF	CITATIONS
19	Recent Progress in the Drug Development Targeting SARS-CoV-2 Main Protease as Treatment for COVID-19. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 616341.	3.5	83
20	Structures of cell wall arabinosyltransferases with the anti-tuberculosis drug ethambutol. <i>Science</i> , 2020, 368, 1211-1219.	12.6	82
21	Antivirals with common targets against highly pathogenic viruses. <i>Cell</i> , 2021, 184, 1604-1620.	28.9	78
22	Discovery of unsymmetrical aromatic disulfides as novel inhibitors of SARS-CoV main protease: Chemical synthesis, biological evaluation, molecular docking and 3D-QSAR study. <i>European Journal of Medicinal Chemistry</i> , 2017, 137, 450-461.	5.5	75
23	The crystal structure of Zika virus helicase: basis for antiviral drug design. <i>Protein and Cell</i> , 2016, 7, 450-454.	11.0	72
24	Structural basis of Zika virus helicase in recognizing its substrates. <i>Protein and Cell</i> , 2016, 7, 562-570.	11.0	72
25	Mechanisms of activation and inhibition of Zika virus NS2B-NS3 protease. <i>Cell Research</i> , 2016, 26, 1260-1263.	12.0	71
26	Structural basis for replicase polyprotein cleavage and substrate specificity of main protease from SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2117142119.	7.1	64
27	Hypersonic Poration: A New Versatile Cell Poration Method to Enhance Cellular Uptake Using a Piezoelectric Nano-Electromechanical Device. <i>Small</i> , 2017, 13, 1602962.	10.0	53
28	Structures of Omicron spike complexes and implications for neutralizing antibody development. <i>Cell Reports</i> , 2022, 39, 110770.	6.4	47
29	Parabrachial neuron types categorically encode thermoregulation variables during heat defense. <i>Science Advances</i> , 2020, 6, .	10.3	44
30	Recent progress in the discovery of inhibitors targeting coronavirus proteases. <i>Virologica Sinica</i> , 2016, 31, 24-30.	3.0	43
31	Potent SARS-CoV-2 neutralizing antibodies with protective efficacy against newly emerged mutational variants. <i>Nature Communications</i> , 2021, 12, 6304.	12.8	42
32	Structural basis for dimerization and RNA binding of avian infectious bronchitis virus nsp9. <i>Protein Science</i> , 2017, 26, 1037-1048.	7.6	35
33	Mass spectrometry reveals potential of β -lactams as SARS-CoV-2 M ^{pro} inhibitors. <i>Chemical Communications</i> , 2021, 57, 1430-1433.	4.1	35
34	Structural and mechanistic insights into the complexes formed by <i>Wolbachia</i> cytoplasmic incompatibility factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	33
35	The main protease and RNA-dependent RNA polymerase are two prime targets for SARS-CoV-2. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 63-71.	2.1	30
36	Crystal Structure of Feline Infectious Peritonitis Virus Main Protease in Complex with Synergetic Dual Inhibitors. <i>Journal of Virology</i> , 2016, 90, 1910-1917.	3.4	29

#	ARTICLE	IF	CITATIONS
37	Effective Bioactivity Retention of Low-Concentration Antibodies on HFBI-Modified Fluorescence ICTS for Sensitive and Rapid Detection of PSA. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 14549-14558.	8.0	29
38	A Mutation Identified in Neonatal Microcephaly Destabilizes Zika Virus NS1 Assembly in Vitro. <i>Scientific Reports</i> , 2017, 7, 42580.	3.3	28
39	Structural basis for GTP-induced dimerization and antiviral function of guanylate-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
40	Structural insight into the Zika virus capsid encapsulating the viral genome. <i>Cell Research</i> , 2018, 28, 497-499.	12.0	26
41	Molecular Mechanism of SARS-CoVs Orf6 Targeting the Rae1–Nup98 Complex to Compete With mRNA Nuclear Export. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 813248.	3.5	26
42	The crystal structure of main protease from mouse hepatitis virus A59 in complex with an inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2019, 511, 794-799.	2.1	25
43	Michael Acceptor-Based Peptidomimetic Inhibitor of Main Protease from Porcine Epidemic Diarrhea Virus. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 3212-3216.	6.4	24
44	The conformational changes of Zika virus methyltransferase upon converting SAM to SAH. <i>Oncotarget</i> , 2017, 8, 14830-14834.	1.8	24
45	Mechanism of ATP hydrolysis by the Zika virus helicase. <i>FASEB Journal</i> , 2018, 32, 5250-5257.	0.5	20
46	Structures of <i>Mycobacterium tuberculosis</i> Penicillin-Binding Protein 3 in Complex with Five β -Lactam Antibiotics Reveal Mechanism of Inactivation. <i>Molecular Pharmacology</i> , 2020, 97, 287-294.	2.3	20
47	Structural basis of trehalose recycling by the ABC transporter LpqY-SugABC. <i>Science Advances</i> , 2020, 6, .	10.3	19
48	Dual-functional protein for one-step production of a soluble and targeted fluorescent dye. <i>Theranostics</i> , 2018, 8, 3111-3125.	10.0	17
49	Identification of proteasome and caspase inhibitors targeting SARS-CoV-2 Mpro. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 214.	17.1	17
50	Crystal Structures of Wolbachia CidA and CidB Reveal Determinants of Bacteria-induced Cytoplasmic Incompatibility and Rescue. <i>Nature Communications</i> , 2022, 13, 1608.	12.8	15
51	Self-assembled hydrophobin for producing water-soluble and membrane permeable fluorescent dye. <i>Scientific Reports</i> , 2016, 6, 23061.	3.3	14
52	Cryo-EM snapshots of mycobacterial arabinosyltransferase complex EmbB2-AcpM2. <i>Protein and Cell</i> , 2020, 11, 505-517.	11.0	13
53	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21242-21251.	3.4	9
54	A Rapid and Ultrasensitive Thrombin Biosensor Based on a Rationally Designed Trifunctional Protein. <i>Advanced Healthcare Materials</i> , 2020, 9, e2000364.	7.6	9

#	ARTICLE	IF	CITATIONS
55	Structural characterization of the HCoV-229E fusion core. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 705-712.	2.1	8
56	Crystal structure of the apurinic/apyrimidinic endonuclease IV from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 111-118.	2.1	7
57	Discovery of the first macrolide antibiotic binding protein in <i>Mycobacterium tuberculosis</i> : a new antibiotic resistance drug target. <i>Protein and Cell</i> , 2018, 9, 971-975.	11.0	6
58	Structural Insight into the Activation of PknI Kinase from <i>M. tuberculosis</i> via Dimerization of the Extracellular Sensor Domain. <i>Structure</i> , 2017, 25, 1286-1294.e4.	3.3	5
59	Crystal structure of the NS3 helicase of tick-borne encephalitis virus. <i>Biochemical and Biophysical Research Communications</i> , 2020, 528, 601-606.	2.1	4
60	An ultra-red fluorescent biosensor for highly sensitive and rapid detection of biliverdin. <i>Analytica Chimica Acta</i> , 2021, 1174, 338709.	5.4	3
61	The Structure of the Porcine Deltacoronavirus Main Protease Reveals a Conserved Target for the Design of Antivirals. <i>Viruses</i> , 2022, 14, 486.	3.3	3
62	Crystallization and preliminary crystallographic study of human coronavirus NL63 main protease in complex with an inhibitor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1068-1071.	0.8	2
63	Soluble hydrophobin mutants produced in <i>Escherichia coli</i> can self-assemble at various interfaces. <i>Journal of Colloid and Interface Science</i> , 2020, 573, 384-395.	9.4	2
64	Crystallization and preliminary crystallographic study of Feline infectious peritonitis virus main protease in complex with an inhibitor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1612-1615.	0.8	1
65	Crystal structure and biochemical study on argininosuccinate lyase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 510, 116-121.	2.1	1
66	Crystallization and preliminary crystallographic study of Porcine epidemic diarrhea virus main protease in complex with an inhibitor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1608-1611.	0.8	0
67	Expression, crystallization and preliminary crystallographic study of the functional mutant (N60K) of nonstructural protein 9 from Human coronavirus HKU1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1620-1623.	0.8	0
68	Conformational Changes in a Macrolide Antibiotic Binding Protein From <i>Mycobacterium smegmatis</i> Upon ADP Binding. <i>Frontiers in Microbiology</i> , 2021, 12, 780954.	3.5	0
69	Structural Basis of Zika Virus Helicase in RNA Unwinding and ATP Hydrolysis. <i>ACS Infectious Diseases</i> , 2022, 8, 150-158.	3.8	0