Guangshun Wang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4713640/publications.pdf

Version: 2024-02-01

99 papers	8,447 citations	57631 44 h-index	46693 89 g-index
100 all docs	100 docs citations	100 times ranked	8336 citing authors

#	Article	IF	Citations
1	The evolution of the antimicrobial peptide database over 18â€‰years: Milestones and new features. Protein Science, 2022, 31, 92-106.	3.1	34
2	Realistic and critical review of the state of systemic antimicrobial peptides. ADMET and DMPK, 2022, 10, 91-105.	1.1	0
3	Unifying the classification of antimicrobial peptides in the antimicrobial peptide database. Methods in Enzymology, 2022, 663, 1-18.	0.4	20
4	Machine Learning Prediction of Antimicrobial Peptides. Methods in Molecular Biology, 2022, 2405, 1-37.	0.4	22
5	Linearized teixobactin is inactive and after sequence enhancement, kills methicillinâ€resistant Staphylococcus aureus via a different mechanism. Peptide Science, 2022, 114, .	1.0	1
6	Improved Database Filtering Technology Enables More Efficient Ab Initio Design of Potent Peptides against Ebola Viruses. Pharmaceuticals, 2022, 15, 521.	1.7	2
7	Simultaneous Delivery of Multiple Antimicrobial Agents by Biphasic Scaffolds for Effective Treatment of Wound Biofilms. Advanced Healthcare Materials, 2021, 10, e2100135.	3.9	29
8	Short and Robust Anti-Infective Lipopeptides Engineered Based on the Minimal Antimicrobial Peptide KR12 of Human LL-37. ACS Infectious Diseases, 2021, 7, 1795-1808.	1.8	24
9	Designing novel antimicrobial peptides against multi-drug resistant bacteria. , 2021, , .		0
10	Natural antimicrobial peptides as a source of new antiviral agents. Journal of General Virology, 2021, 102, .	1.3	22
11	Structure and Activity of a Selective Antibiofilm Peptide SK-24 Derived from the NMR Structure of Human Cathelicidin LL-37. Pharmaceuticals, 2021, 14, 1245.	1.7	11
12	The antimicrobial peptide database provides a platform for decoding the design principles of naturally occurring antimicrobial peptides. Protein Science, 2020, 29, 8-18.	3.1	52
13	Two distinct amphipathic peptide antibiotics with systemic efficacy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19446-19454.	3.3	61
14	Engineered Human Cathelicidin Antimicrobial Peptides Inhibit Ebola Virus Infection. IScience, 2020, 23, 100999.	1.9	40
15	Bioinformatic Analysis of 1000 Amphibian Antimicrobial Peptides Uncovers Multiple Length-Dependent Correlations for Peptide Design and Prediction. Antibiotics, 2020, 9, 491.	1.5	36
16	Dissolvable Microneedles Coupled with Nanofiber Dressings Eradicate Biofilms via Effectively Delivering a Database-Designed Antimicrobial Peptide. ACS Nano, 2020, 14, 11775-11786.	7.3	129
17	Membrane activity of two short Trp-rich amphipathic peptides. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183280.	1.4	8
18	Resistome of Staphylococcus aureus in Response to Human Cathelicidin LL-37 and Its Engineered Antimicrobial Peptides. ACS Infectious Diseases, 2020, 6, 1866-1881.	1.8	15

#	Article	IF	Citations
19	Spotlight on the Selected New Antimicrobial Innate Immune Peptides Discovered During 2015-2019. Current Topics in Medicinal Chemistry, 2020, 20, 2984-2998.	1.0	7
20	Sequence Permutation Generates Peptides with Different Antimicrobial and Antibiofilm Activities. Pharmaceuticals, 2020, 13, 271.	1.7	8
21	Modulation of antimicrobial potency of human cathelicidin peptides against the ESKAPE pathogens and in vivo efficacy in a murine catheter-associated biofilm model. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 1592-1602.	1.4	27
22	Low cationicity is important for systemic in vivo efficacy of database-derived peptides against drug-resistant Gram-positive pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13517-13522.	3.3	89
23	Nanofiber Dressings Topically Delivering Molecularly Engineered Human Cathelicidin Peptides for the Treatment of Biofilms in Chronic Wounds. Molecular Pharmaceutics, 2019, 16, 2011-2020.	2.3	42
24	Design of Antimicrobial Peptides: Progress Made with Human Cathelicidin LL-37. Advances in Experimental Medicine and Biology, 2019, 1117, 215-240.	0.8	91
25	Amino Acid Composition Determines Peptide Activity Spectrum and Hotâ€Spotâ€Based Design of Merecidin. Advanced Biology, 2018, 2, 1700259.	3.0	35
26	Antimicrobial peptide LL-37 and its truncated forms, GI-20 and GF-17, exert spermicidal effects and microbicidal activity against Neisseria gonorrhoeae. Human Reproduction, 2018, 33, 2175-2183.	0.4	14
27	Antibacterial, antifungal, anticancer activities and structural bioinformatics analysis of six naturally occurring temporins. Peptides, 2018, 106, 9-20.	1.2	46
28	Cathelicidin-Derived Antimicrobial Peptides Inhibit Zika Virus Through Direct Inactivation and Interferon Pathway. Frontiers in Immunology, 2018, 9, 722.	2.2	79
29	Mechanism of Action of Tethered Antimicrobial Peptides. , 2018, , 559-566.		0
30	Host defense antimicrobial peptides as antibiotics: design and application strategies. Current Opinion in Chemical Biology, 2017, 38, 87-96.	2.8	249
31	Arginine-lysine positional swap of the LL-37 peptides reveals evolutional advantages of the native sequence and leads to bacterial probes. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1350-1361.	1.4	27
32	Design and surface immobilization of short anti-biofilm peptides. Acta Biomaterialia, 2017, 49, 316-328.	4.1	66
33	Small molecule mimics of DFTamP1, a database designed anti-Staphylococcal peptide. Bioorganic and Medicinal Chemistry, 2017, 25, 864-869.	1.4	12
34	The Ï€ Configuration of the WWW Motif of a Short Trp-Rich Peptide Is Critical for Targeting Bacterial Membranes, Disrupting Preformed Biofilms, and Killing Methicillin-Resistant Staphylococcus aureus. Biochemistry, 2017, 56, 4039-4043.	1.2	30
35	Titanium surfaces immobilized with the major antimicrobial fragment FK-16 of human cathelicidin LL-37 are potent against multiple antibiotic-resistant bacteria. Biofouling, 2017, 33, 544-555.	0.8	47
36	Collectins, H-ficolin and LL-37 reduce influence viral replication in human monocytes and modulate virus-induced cytokine production. Innate Immunity, 2017, 23, 77-88.	1.1	21

#	Article	IF	Citations
37	Individual and Combined Effects of Engineered Peptides and Antibiotics on Pseudomonas aeruginosa Biofilms. Pharmaceuticals, 2017, 10, 58.	1.7	55
38	Membrane-Active Epithelial Keratin 6A Fragments (KAMPs) Are Unique Human Antimicrobial Peptides with a Non-Î±Î² Structure. Frontiers in Microbiology, 2016, 7, 1799.	1.5	16
39	Potential Use of Antimicrobial Peptides as Vaginal Spermicides/Microbicides. Pharmaceuticals, 2016, 9, 13.	1.7	41
40	Structural Analysis of Amphibian, Insect, and Plant Host Defense Peptides Inspires the Design of Novel Therapeutic Molecules. , 2016, , 229-252.		0
41	Structure of the NPr:EINNtr Complex: Mechanism for Specificity in Paralogous Phosphotransferase Systems. Structure, 2016, 24, 2127-2137.	1.6	16
42	Anti-Staphylococcal Biofilm Effects of Human Cathelicidin Peptides. ACS Medicinal Chemistry Letters, 2016, 7, 117-121.	1.3	68
43	APD3: the antimicrobial peptide database as a tool for research and education. Nucleic Acids Research, 2016, 44, D1087-D1093.	6.5	1,537
44	Insights into Antimicrobial Peptides from Spiders and Scorpions. Protein and Peptide Letters, 2016, 23, 707-721.	0.4	41
45	Identifying the Critical Domain of LL-37 Involved in Mediating Neutrophil Activation in the Presence of Influenza Virus: Functional and Structural Analysis. PLoS ONE, 2015, 10, e0133454.	1.1	21
46	Antiviral Activity of the Human Cathelicidin, LL-37, and Derived Peptides on Seasonal and Pandemic Influenza A Viruses. PLoS ONE, 2015, 10, e0124706.	1.1	72
47	Improved Methods for Classification, Prediction, and Design of Antimicrobial Peptides. Methods in Molecular Biology, 2015, 1268, 43-66.	0.4	136
48	Small lipopeptides possess anti-biofilm capability comparable to daptomycin and vancomycin. RSC Advances, 2015, 5, 59758-59769.	1.7	28
49	Database Resources Dedicated to Antimicrobial Peptides. , 2015, , 365-384.		6
50	Antimicrobial Peptides in 2014. Pharmaceuticals, 2015, 8, 123-150.	1.7	168
51	Interaction of the core fragments of the LL-37 host defense peptide with actin. RSC Advances, 2015, 5, 9361-9367.	1.7	9
52	Anti-tumor effect of a series of engineered peptides in N-MYC amplified Neuroblastoma.. Journal of Clinical Oncology, 2015, 33, e21013-e21013.	0.8	0
53	Human Antimicrobial Peptides and Proteins. Pharmaceuticals, 2014, 7, 545-594.	1.7	402
54	High-quality 3D structures shine light on antibacterial, anti-biofilm and antiviral activities of human cathelicidin LL-37 and its fragments. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 2160-2172.	1.4	142

#	Article	IF	Citations
55	Transformation of Human Cathelicidin LL-37 into Selective, Stable, and Potent Antimicrobial Compounds. ACS Chemical Biology, 2014, 9, 1997-2002.	1.6	110
56	Structural location determines functional roles of the basic amino acids of KR-12, the smallest antimicrobial peptide from human cathelicidin LL-37. RSC Advances, 2013, 3, 19560.	1.7	52
57	Database-Guided Discovery of Potent Peptides to Combat HIV-1 or Superbugs. Pharmaceuticals, 2013, 6, 728-758.	1.7	90
58	Decoding the Functional Roles of Cationic Side Chains of the Major Antimicrobial Region of Human Cathelicidin LL-37. Antimicrobial Agents and Chemotherapy, 2012, 56, 845-856.	1.4	88
59	Ab Initio Design of Potent Anti-MRSA Peptides Based on Database Filtering Technology. Journal of the American Chemical Society, 2012, 134, 12426-12429.	6.6	147
60	Database screening and in vivo efficacy of antimicrobial peptides against methicillin-resistant Staphylococcus aureus USA300. International Journal of Antimicrobial Agents, 2012, 39, 402-406.	1.1	81
61	Structure, Dynamics, and Antimicrobial and Immune Modulatory Activities of Human LL-23 and Its Single-Residue Variants Mutated on the Basis of Homologous Primate Cathelicidins. Biochemistry, 2012, 51, 653-664.	1.2	55
62	The Importance of Amino Acid Composition in Natural AMPs: An Evolutional, Structural, and Functional Perspective. Frontiers in Immunology, 2012, 3, 221.	2.2	63
63	Post-Translational Modifications of Natural Antimicrobial Peptides and Strategies for Peptide Engineering. Current Biotechnology, 2012, 1, 72-79.	0.2	103
64	Natural antimicrobial peptides as promising anti-HIV candidates. Current Topics in Peptide and Protein Research, 2012, 13, 93-110.	1.0	21
65	Emerging roles of the host defense peptide LLâ€37 in human cancer and its potential therapeutic applications. International Journal of Cancer, 2010, 127, 1741-1747.	2.3	109
66	Identification of Novel Human Immunodeficiency Virus Type 1-Inhibitory Peptides Based on the Antimicrobial Peptide Database. Antimicrobial Agents and Chemotherapy, 2010, 54, 1343-1346.	1.4	108
67	Structure, dynamics and mapping of membrane-binding residues of micelle-bound antimicrobial peptides by natural abundance 13C NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 114-121.	1.4	12
68	Lipid clustering by three homologous arginine-rich antimicrobial peptides is insensitive to amino acid arrangement and induced secondary structure. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 1272-1280.	1.4	62
69	Lipid Segregation Explains Selective Toxicity of a Series of Fragments Derived from the Human Cathelicidin LL-37. Antimicrobial Agents and Chemotherapy, 2009, 53, 3705-3714.	1.4	81
70	APD2: the updated antimicrobial peptide database and its application in peptide design. Nucleic Acids Research, 2009, 37, D933-D937.	6.5	816
71	Solution structure of NPr, a bacterial signal-transducing protein that controls the phosphorylation state of the potassium transporter-regulating protein IIANtr. Amino Acids, 2008, 35, 531-539.	1.2	15
72	Structures of Human Host Defense Cathelicidin LL-37 and Its Smallest Antimicrobial Peptide KR-12 in Lipid Micelles. Journal of Biological Chemistry, 2008, 283, 32637-32643.	1.6	371

#	Article	IF	Citations
73	Anti-Human Immunodeficiency Virus Type 1 Activities of Antimicrobial Peptides Derived from Human and Bovine Cathelicidins. Antimicrobial Agents and Chemotherapy, 2008, 52, 3438-3440.	1.4	109
74	NMR of Membrane-Associated Peptides and Proteins. Current Protein and Peptide Science, 2008, 9, 50-69.	0.7	58
75	NMR Studies of a Model Antimicrobial Peptide in the Micelles of SDS, Dodecylphosphocholine, or Dioctanoylphosphatidylglycerol. The Open Magnetic Resonance Journal, 2008, 1, 9-15.	0.5	12
76	Tool Developments for Structure-Function Studies of Host Defense Peptides. Protein and Peptide Letters, 2007, 14, 57-69.	0.4	27
77	A novel method for purifying recombinant human host defense cathelicidin LL-37 by utilizing its inherent property of aggregation. Protein Expression and Purification, 2007, 54, 157-165.	0.6	43
78	On-resin cleavage of bacterially expressed fusion proteins for purification of active recombinant peptides SK-29, KR-20, LL-29, and LL-23 from human sweat or skin. Protein Expression and Purification, 2007, 55, 395-405.	0.6	10
79	Determination of solution structure and lipid micelle location of an engineered membrane peptide by using one NMR experiment and one sample. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3271-3281.	1.4	44
80	Solution Structures of Human LL-37 Fragments and NMR-Based Identification of a Minimal Membrane-Targeting Antimicrobial and Anticancer Region. Journal of the American Chemical Society, 2006, 128, 5776-5785.	6.6	252
81	Parallel PTS systems. Archives of Biochemistry and Biophysics, 2006, 453, 101-107.	1.4	24
82	NMR studies of aurein 1.2 analogs. Biochimica Et Biophysica Acta - Biomembranes, 2006, 1758, 1203-1214.	1.4	46
83	Cloning, expression, isotope labeling, and purification of human antimicrobial peptide LL-37 in Escherichia coli for NMR studies. Protein Expression and Purification, 2006, 47, 498-505.	0.6	62
84	Structural Biology of Antimicrobial Peptides by NMR Spectroscopy. Current Organic Chemistry, 2006, 10, 569-581.	0.9	28
85	Correlation of Three-dimensional Structures with the Antibacterial Activity of a Group of Peptides Designed Based on a Nontoxic Bacterial Membrane Anchor. Journal of Biological Chemistry, 2005, 280, 5803-5811.	1.6	83
86	NMR characterization of the Escherichia coli nitrogen regulatory protein IIANtr in solution and interaction with its partner protein, NPr. Protein Science, 2005, 14, 1082-1090.	3.1	19
87	Shortâ€'chain diacyl phosphatidylglycerols: which one to choose for the NMR structural determination of a membraneâ€'associated peptide fromEscherichia coli?. Spectroscopy, 2004, 18, 257-264.	0.8	14
88	APD: the Antimicrobial Peptide Database. Nucleic Acids Research, 2004, 32, 590D-592.	6.5	651
89	Effects of detergent alkyl chain length and chemical structure on the properties of a micelle-bound bacterial membrane targeting peptide. Analytical Biochemistry, 2004, 331, 33-39.	1.1	11
90	1H, 15N, and 13C chemical shift assignments of the Escherichia coli nitrogen regulatory phosphocarrier IIA(Ntr). Journal of Biomolecular NMR, 2003, 27, 401-402.	1.6	3

#	Article	IF	Citations
91	Solution structure of the N-terminal amphitropic domain ofEscherichia coliglucose-specific enzyme IIA in membrane-mimetic micelles. Protein Science, 2003, 12, 1087-1096.	3.1	47
92	Solution Structure of the Phosphoryl Transfer Complex between the Signal-transducing Protein IIAGlucose and the Cytoplasmic Domain of the Glucose Transporter IICBGlucose of the Escherichia coli Glucose Phosphotransferase System. Journal of Biological Chemistry, 2003, 278, 25191-25206.	1.6	61
93	Solution Structure of the Phosphoryl Transfer Complex between the Cytoplasmic A Domain of the Mannitol Transporter IIMannitol and HPr of the Escherichia coliPhosphotransferase System. Journal of Biological Chemistry, 2002, 277, 42289-42298.	1.6	61
94	How the lipid-free structure of the N-terminal truncated human apoA-I converts to the lipid-bound form: new insights from NMR and X-ray structural comparison. FEBS Letters, 2002, 529, 157-161.	1.3	17
95	A Novel Membrane Anchor Function for the N-terminal Amphipathic Sequence of the Signal-transducing Protein IIAGlucose of the Escherichia coli Phosphotransferase System. Journal of Biological Chemistry, 2000, 275, 39811-39814.	1.6	39
96	A Common Interface on Histidine-containing Phosphocarrier Protein for Interaction with Its Partner Proteins. Journal of Biological Chemistry, 2000, 275, 16401-16403.	1.6	27
97	The Helix-Hinge-Helix Structural Motif in Human Apolipoprotein A-I Determined by NMR Spectroscopy,. Biochemistry, 1997, 36, 13657-13666.	1.2	53
98	Conformations of Human Apolipoprotein E(263â˜286) and E(267â˜289) in Aqueous Solutions of Sodium Dodecyl Sulfate by CD and1H NMRâ€,â€¡. Biochemistry, 1996, 35, 10358-10366.	1.2	52
99	Conformation of human serum apolipoprotein A-I(166â€“185) in the presence of sodium dodecyl sulfate or dodecylphosphocholine by 1H-NMR and CD. Evidence for specific peptide-SDS interactions. Lipids and Lipid Metabolism, 1996, 1301, 174-184.	2.6	56