Quentin K Kaas

List of Publications by Year
in descending order

#	Article	IF	Citations
1	IMGT unique numbering for immunoglobulin and T cell receptor constant domains and Ig superfamily C-like domains. Developmental and Comparative Immunology, 2005, 29, 185-203.	2.3	454
2	Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335.	27.8	327
3	ConoServer: updated content, knowledge, and discovery tools in the conopeptide database. Nucleic Acids Research, 2012, 40, D325-D330.	14.5	298
4	Discovery, Synthesis, and Structureâ€"Activity Relationships of Conotoxins. Chemical Reviews, 2014, 114, 5815-5847.	47.7	258
5	IMGT, the international ImMunoGeneTics information system(R). Nucleic Acids Research, 2004, 33, D593-D597.	14.5	251
6	CyBase: a database of cyclic protein sequences and structures, with applications in protein discovery and engineering. Nucleic Acids Research, 2007, 36, D206-D210.	14.5	242
7	IMGT/3Dstructure-DB and IMGT/DomainGapAlign: a database and a tool for immunoglobulins or antibodies, T cell receptors, MHC, IgSF and MhcSF. Nucleic Acids Research, 2010, 38, D301-D307.	14.5	232
8	Conopeptide characterization and classifications: An analysis using ConoServer. Toxicon, 2010, 55, 1491-1509.	1.6	198
9	ConoServer, a database for conopeptide sequences and structures. Bioinformatics, 2008, 24, 445-446.	4.1	193
10	Efficient backbone cyclization of linear peptides by a recombinant asparaginyl endopeptidase. Nature Communications, 2015, 6, 10199.	12.8	186
11	Deep Venomics Reveals the Mechanism for Expanded Peptide Diversity in Cone Snail Venom. Molecular and Cellular Proteomics, 2013, 12, 312-329.	3.8	180
12	Conotoxins: Chemistry and Biology. Chemical Reviews, 2019, 119, 11510-11549.	47.7	174
13	ArachnoServer 2.0, an updated online resource for spider toxin sequences and structures. Nucleic Acids Research, 2011, 39, D653-D657.	14.5	159
14	IMGT/3Dstructure-DB and IMGT/StructuralQuery, a database and a tool for immunoglobulin, T cell receptor and MHC structural data. Nucleic Acids Research, 2004, 32, 208D-210.	14.5	145
15	KNOTTIN: the knottin or inhibitor cystine knot scaffold in 2007. Nucleic Acids Research, 2007, 36, D314-D319.	14.5	140
16	High-affinity Cyclic Peptide Matriptase Inhibitors. Journal of Biological Chemistry, 2013, 288, 13885-13896.	3.4	122
17	IMGT-ONTOLOGY for immunogenetics and immunoinformatics. In Silico Biology, 2004, 4, 17-29.	0.9	119
18	IMGT-Kaleidoscope, the formal IMGT-ONTOLOGY paradigm. Biochimie, 2008, 90, 570-583.	2.6	107

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19	IMGT unique numbering for MHC groove G-DOMAIN and MHC superfamily (MhcSF) G-LIKE-DOMAIN. Developmental and Comparative Immunology, 2005, 29, 917-938.	2.3	104
20	Conformational Flexibility Is a Determinant of Permeability for Cyclosporin. Journal of Physical Chemistry B, 2018, 122, 2261-2276.	2.6	104
21	The KNOTTIN website and database: a new information system dedicated to the knottin scaffold. Nucleic Acids Research, 2004, 32, 156D-159.	14.5	102
22	IMGT-Choreography for immunogenetics and immunoinformatics. In Silico Biology, 2005, 5, 45-60.	0.9	102
23	Molecular basis for the production of cyclic peptides by plant asparaginyl endopeptidases. Nature Communications, 2018, 9, 2411.	12.8	99
24	Cloning, synthesis, and characterization of Î±O-conotoxin GeXIVA, a potent Î±9Î±10 nicotinic acetylcholine receptor antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4026-35.	7.1	91
25	ArachnoServer 3.0: an online resource for automated discovery, analysis and annotation of spider toxins. Bioinformatics, 2018, 34, 1074-1076.	4.1	86
26	Determination of the Î±-Conotoxin Vc1.1 Binding Site on the Î±9Î±10 Nicotinic Acetylcholine Receptor. Journal of Medicinal Chemistry, 2013, 56, 3557-3567.	6.4	84
27	Blockade of Neuronal Î±7-nAChR by Î±-Conotoxin ImI Explained by Computational Scanning and Energy Calculations. PLoS Computational Biology, 2011, 7, e1002011.	3.2	77
28	Despite a Conserved Cystine Knot Motif, Different Cyclotides Have Different Membrane Binding Modes. Biophysical Journal, 2009, 97, 1471-1481.	0.5	74
29	IG, TR and IgSF, MHC and MhcSF: what do we learn from the IMGT Colliers de Perles?. Briefings in Functional Genomics & Proteomics, 2008, 6, 253-264.	3.8	71
30	Transcriptomic Messiness in the Venom Duct of Conus miles Contributes to Conotoxin Diversity. Molecular and Cellular Proteomics, 2013, 12, 3824-3833.	3.8	70
31	Structureâ€"function relationships of the variable domains of monoclonal antibodies approved for cancer treatment. Critical Reviews in Oncology/Hematology, 2007, 64, 210-225.	4.4	69
32	Cyclization of conotoxins to improve their biopharmaceutical properties. Toxicon, 2012, 59, 446-455.	1.6	68
33	Analysis and classification of circular proteins in CyBase. Biopolymers, 2010, 94, 584-591.	2.4	67
34	A novel Î±4/7â€conotoxin LvIA from Conus lividus that selectively blocks Î±3Î²2 vs. Î±6/Î±3Î²2Î²3 nicotinic acetylcholine receptors. FASEB Journal, 2014, 28, 1842-1853.	0.5	64
35	Molecular basis for the resistance of an insect chymotrypsin to a potato type II proteinase inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15016-15021.	7.1	63
36	A bifunctional asparaginyl endopeptidase efficiently catalyzes both cleavage and cyclization of cyclic trypsin inhibitors. Nature Communications, 2020, 11, 1575.	12.8	61

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37	Structural venomics reveals evolution of a complex venom by duplication and diversification of an ancient peptide-encoding gene. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11399-11408.	7.1	59
38	ArachnoServer: a database of protein toxins from spiders. BMC Genomics, 2009, 10, 375.	2.8	58
39	Design of substrate-based BCR-ABL kinase inhibitors using the cyclotide scaffold. Scientific Reports, 2015, 5, 12974.	3.3	58
40	Elucidation of relaxin-3 binding interactions in the extracellular loops of RXFP3. Frontiers in Endocrinology, 2013, 4, 13.	3.5	48
41	Engineering of Conotoxins for the Treatment of Pain. Current Pharmaceutical Design, 2011, 17, 4242-4253.	1.9	47
42	A suite of kinetically superior AEP ligases can cyclise an intrinsically disordered protein. Scientific Reports, 2019, 9, 10820.	3.3	47
43	IMGT Colliers de Perles: Standardized Sequence-Structure Representations of the IgSF and MhcSF Superfamily Domains. Current Bioinformatics, 2007, 2, 21-30.	1.5	46
44	A new â€œeraâ€• for cyclotide sequencing. Biopolymers, 2010, 94, 592-601.	2.4	45
45	Less is More: Design of a Highly Stable Disulfide-Deleted Mutant of Analgesic Cyclic Î±-Conotoxin Vc1.1. Scientific Reports, 2015, 5, 13264.	3.3	42
46	Bioinformatics-Aided Venomics. Toxins, 2015, 7, 2159-2187.	3.4	38
47	T cell receptor/peptide/MHC molecular characterization and standardized pMHC contact sites in IMGT/3Dstructure-DB. In Silico Biology, 2005, 5, 505-28.	0.9	38
48	Cyclic analogues of Î±â€conotoxin Vc1.1 inhibit colonic nociceptors and provide analgesia in a mouse model of chronic abdominal pain. British Journal of Pharmacology, 2018, 175, 2384-2398.	5.4	36
49	Lysine-rich Cyclotides: A New Subclass of Circular Knotted Proteins from Violaceae. ACS Chemical Biology, 2015, 10, 2491-2500.	3.4	34
50	Delineation of the Unbinding Pathway of Î±-Conotoxin ImI from the Î±7 Nicotinic Acetylcholine Receptor. Journal of Physical Chemistry B, 2012, 116, 6097-6105.	2.6	31
51	Identification of candidates for cyclotide biosynthesis and cyclisation by expressed sequence tag analysis of Oldenlandia affinis. BMC Genomics, 2010, 11, 111.	2.8	30
52	Î±-Conotoxin [S9A]TxID Potently Discriminates between Î±3Î²4 and Î±6/Î±3Î²4 Nicotinic Acetylcholine Receptors. Journal of Medicinal Chemistry, 2017, 60, 5826-5833.	6.4	30
53	Prediction of disulfide dihedral angles using chemical shifts. Chemical Science, 2018, 9, 6548-6556.	7.4	30
54	Î±O-Conotoxin GeXIVA disulfide bond isomers exhibit differential sensitivity for various nicotinic acetylcholine receptors but retain potency and selectivity for the human Î±9Î±10 subtype. Neuropharmacology, 2017, 127, 243-252.	4.1	29

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55	Development of Novel Melanocortin Receptor Agonists Based on the Cyclic Peptide Framework of Sunflower Trypsin Inhibitor-1. Journal of Medicinal Chemistry, 2018, 61, 3674-3684.	6.4	29
56	A systematic approach to document cyclotide distribution in plant species from genomic, transcriptomic, and peptidomic analysis. Biopolymers, 2013, 100, 433-437.	2.4	26
57	The Evolution of<i>Momordica</i>Cyclic Peptides. Molecular Biology and Evolution, 2015, 32, 392-405.	8.9	26
58	Insecticidal spider toxins are high affinity positive allosteric modulators of the nicotinic acetylcholine receptor. FEBS Letters, 2019, 593, 1336-1350.	2.8	23
59	Efficient enzymatic cyclization of an inhibitory cystine knotâ€containing peptide. Biotechnology and Bioengineering, 2016, 113, 2202-2212.	3.3	22
60	Computational Studies of Snake Venom Toxins. Toxins, 2018, 10, 8.	3.4	22
61	Discovery and mechanistic studies of cytotoxic cyclotides from the medicinal herb Hybanthus enneaspermus. Journal of Biological Chemistry, 2020, 295, 10911-10925.	3.4	22
62	The Cold Awakening of Doritaenopsis â€˜Tinny Tenderâ€™ Orchid Flowers: The Role of Leaves in Cold-induced Bud Dormancy Release. Journal of Plant Growth Regulation, 2012, 31, 139-155.	5.1	21
63	Enhanced Activity against Multidrug-Resistant Bacteria through Coapplication of an Analogue of Tachyplesin I and an Inhibitor of the QseC/B Signaling Pathway. Journal of Medicinal Chemistry, 2020, 63, 3475-3484.	6.4	20
64	Prediction and characterization of cyclic proteins from sequences in three domains of life. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 181-190.	2.3	19
65	Single Amino Acid Substitution in Î±-Conotoxin TxID Reveals a Specific Î±3Î²4 Nicotinic Acetylcholine Receptor Antagonist. Journal of Medicinal Chemistry, 2018, 61, 9256-9265.	6.4	19
66	Key Residues in the Nicotinic Acetylcholine Receptor Î²2 Subunit Contribute to Î±-Conotoxin LvIA Binding. Journal of Biological Chemistry, 2015, 290, 9855-9862.	3.4	18
67	SCORE: predicting the core of protein models. Bioinformatics, 2001, 17, 541-550.	4.1	17
68	Isolation and Characterization of A Cytosolic Pyruvate Kinase cDNA From Loquat (Eriobotrya japonica) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	17
69	Bioactive Compounds Isolated from Neglected Predatory Marine Gastropods. Marine Drugs, 2018, 16, 118.	4.6	17
70	Neuropeptide signalling systems â€" An underexplored target for venom drug discovery. Biochemical Pharmacology, 2020, 181, 114129.	4.4	17
71	IMGT Standardization for Molecular Characterization of the T-cell Receptor/Peptide/MHC Complexes. , 2008, , 19-49.		17
72	Mapping the Molecular Surface of the Analgesic NaV1.7-Selective Peptide Pn3a Reveals Residues Essential for Membrane and Channel Interactions. ACS Pharmacology and Translational Science, 2020, 3, 535-546.	4.9	16

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73	Backbone cyclization of analgesic conotoxin GeXIVA facilitates direct folding of the ribbon isomer. Journal of Biological Chemistry, 2017, 292, 17101-17112.	3.4	15
74	Precursor De13.1 from Conus delessertii defines the novel G gene superfamily. Peptides, 2013, 41, 17-20.	2.4	14
75	Modelling the interactions between animal venom peptides and membrane proteins. Neuropharmacology, 2017, 127, 20-31.	4.1	14
76	Stoichiometry dependent inhibition of rat Î±3Î²4 nicotinic acetylcholine receptor by the ribbon isomer of Î±-conotoxin AuIB. Biochemical Pharmacology, 2018, 155, 288-297.	4.4	14
77	Cyclisation of Disulfideâ€Rich Conotoxins in Drug Design Applications. European Journal of Organic Chemistry, 2016, 2016, 3462-3472.	2.4	13
78	Distinct but overlapping binding sites of agonist and antagonist at the relaxin family peptide 3 (RXFP3) receptor. Journal of Biological Chemistry, 2018, 293, 15777-15789.	3.4	13
79	Structure and Activity Studies of Disulfide-Deficient Analogues of Î±O-Conotoxin GeXIVA. Journal of Medicinal Chemistry, 2020, 63, 1564-1575.	6.4	13
80	Role of CysIâ€"CysIIIDisulfide Bond on the Structure and Activity of Î±-Conotoxins at Human Neuronal Nicotinic Acetylcholine Receptors. ACS Omega, 2017, 2, 4621-4631.	3.5	12
81	Exploring the Sequence Diversity of Cyclotides from Vietnamese <i>Viola</i> Species. Journal of Natural Products, 2020, 83, 1817-1828.	3.0	12
82	Designed Î²-Hairpins Inhibit LDH5 Oligomerization and Enzymatic Activity. Journal of Medicinal Chemistry, 2021, 64, 3767-3779.	6.4	12
83	Development of efficient docking strategies and structure-activity relationship study of the c-Met type II inhibitors. Journal of Molecular Graphics and Modelling, 2017, 75, 241-249.	2.4	11
84	Molecular dynamics simulations of dihydroâ€Î²â€erythroidine bound to the human Î±4Î²2 nicotinic acetylcholine receptor. British Journal of Pharmacology, 2019, 176, 2750-2763.	5.4	11
85	Hormone-like conopeptides â€" new tools for pharmaceutical design. RSC Medicinal Chemistry, 2020, 11, 1235-1251.	3.9	11
86	Computational and Functional Mapping of Human and Rat Î±6Î²4 Nicotinic Acetylcholine Receptors Reveals Species-Specific Ligand-Binding Motifs. Journal of Medicinal Chemistry, 2021, 64, 1685-1700.	6.4	11
87	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	3.0	8
88	Periplasmic Expression of 4/7 Î±-Conotoxin TxIA Analogs in E. coli Favors Ribbon Isomer Formation â€" Suggestion of a Binding Mode at the Î±7 nAChR. Frontiers in Pharmacology, 2019, 10, 577.	3.5	8
89	High-Resolution X-ray Structure of the Unexpectedly Stable Dimer of the [Lys(-2)-Arg(-1)-des(17â^'21)]Endothelin-1 Peptideâ€¡. Biochemistry, 2004, 43, 15154-15168.	2.5	7
90	Engineered Conotoxin Differentially Blocks and Discriminates Rat and Human Î±7 Nicotinic Acetylcholine Receptors. Journal of Medicinal Chemistry, 2021, 64, 5620-5631.	6.4	7

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91	Antimicrobial peptides in plants.. , 2010, , 40-71.		7
92	Melanocortin 1 Receptor Agonists Based on a Bivalent, Bicyclic Peptide Framework. Journal of Medicinal Chemistry, 2021, 64, 9906-9915.	6.4	6
93	NMR of plant proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2013, 71, 1-34.	7.5	5
94	The [Lys-2-Arg-1-des(17â^'21)]-Endothelin-1 Peptide Retains the Specific Arg-1â^'Asp8 Salt Bridge but Reveals Discrepancies between NMR Data and Molecular Dynamics Simulations. Biochemistry, 2002, 41, 11099-11108.	2.5	4
95	Mutagenesis of bracelet cyclotide hyen D reveals functionally and structurally critical residues for membrane binding and cytotoxicity. Journal of Biological Chemistry, 2022, 298, 101822.	3.4	4
96	Characterisation of the subunit genes of pyrophosphate-dependent phosphofructokinase from loquat (Eriobotrya japonica Lindl.). Tree Genetics and Genomes, 2014, 10, 1465-1476.	1.6	3
97	Mutagenesis of cyclotide Cter 27 exemplifies a robust folding strategy for bracelet cyclotides. Peptide Science, 2022, 114, .	1.8	3
98	Interactions of Globular and Ribbon [Î³4E]GID with Î±4Î²2 Neuronal Nicotinic Acetylcholine Receptor. Marine Drugs, 2021, 19, 482.	4.6	2
99	In Silico Design of MDM2â€Targeting Peptides from a Naturally Occurring Constrained Peptide. ChemMedChem, 2019, 14, 1710-1716.	3.2	1
100	Development of novel frogâ€skin peptide scaffolds with selectivity towards melanocortin receptor subtypes. Peptide Science, 2021, 113, e24209.	1.8	1
101	Front Cover: Cyclisation of Disulfide-Rich Conotoxins in Drug Design Applications (Eur. J. Org. Chem.) Tj ETQq1 1 0.784314 rgBT /Overlo	2.4	0