# Quentin K Kaas

List of Publications by Year
in descending order

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|---|---|---|---|
| 101<br>papers | 6,604<br>citations | 61857<br>43<br>h-index | 66788<br>78<br>g-index |
| 107<br>all docs | 107<br>docs citations | 107<br>times ranked | 6042<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Mutagenesis of bracelet cyclotide hyen D reveals functionally and structurally critical residues for membrane binding and cytotoxicity. Journal of Biological Chemistry, 2022, 298, 101822. | 1.6 | 4 |
| 2 | Mutagenesis of cyclotide Cter 27 exemplifies a robust folding strategy for bracelet cyclotides. Peptide Science, 2022, 114, . | 1.0 | 3 |
| 3 | Development of novel frog‑skin peptide scaffolds with selectivity towards melanocortin receptor subtypes. Peptide Science, 2021, 113, e24209. | 1.0 | 1 |
| 4 | Computational and Functional Mapping of Human and Rat α6β4 Nicotinic Acetylcholine Receptors Reveals Species-Specific Ligand-Binding Motifs. Journal of Medicinal Chemistry, 2021, 64, 1685-1700. | 2.9 | 11 |
| 5 | Designed β-Hairpins Inhibit LDH5 Oligomerization and Enzymatic Activity. Journal of Medicinal Chemistry, 2021, 64, 3767-3779. | 2.9 | 12 |
| 6 | Engineered Conotoxin Differentially Blocks and Discriminates Rat and Human α7 Nicotinic Acetylcholine Receptors. Journal of Medicinal Chemistry, 2021, 64, 5620-5631. | 2.9 | 7 |
| 7 | Melanocortin 1 Receptor Agonists Based on a Bivalent, Bicyclic Peptide Framework. Journal of Medicinal Chemistry, 2021, 64, 9906-9915. | 2.9 | 6 |
| 8 | Interactions of Globular and Ribbon [γ4E]GID with α4β2 Neuronal Nicotinic Acetylcholine Receptor. Marine Drugs, 2021, 19, 482. | 2.2 | 2 |
| 9 | Hormone-like conopeptides – new tools for pharmaceutical design. RSC Medicinal Chemistry, 2020, 11, 1235-1251. | 1.7 | 11 |
| 10 | Discovery and mechanistic studies of cytotoxic cyclotides from the medicinal herb Hybanthus enneaspermus. Journal of Biological Chemistry, 2020, 295, 10911-10925. | 1.6 | 22 |
| 11 | 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. | 3.3 | 59 |
| 12 | Exploring the Sequence Diversity of Cyclotides from Vietnamese *Viola* Species. Journal of Natural Products, 2020, 83, 1817-1828. | 1.5 | 12 |
| 13 | A bifunctional asparaginyl endopeptidase efficiently catalyzes both cleavage and cyclization of cyclic trypsin inhibitors. Nature Communications, 2020, 11, 1575. | 5.8 | 61 |
| 14 | Neuropeptide signalling systems – An underexplored target for venom drug discovery. Biochemical Pharmacology, 2020, 181, 114129. | 2.0 | 17 |
| 15 | 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. | 2.5 | 16 |
| 16 | Structure and Activity Studies of Disulfide-Deficient Analogues of α0-Conotoxin GeXIVA. Journal of Medicinal Chemistry, 2020, 63, 1564-1575. | 2.9 | 13 |
| 17 | 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. | 2.9 | 20 |
| 18 | A suite of kinetically superior AEP ligases can cyclise an intrinsically disordered protein. Scientific Reports, 2019, 9, 10820. | 1.6 | 47 |

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|---|---------|-----|-----------|
| 19 | Conotoxins: Chemistry and Biology. Chemical Reviews, 2019, 119, 11510-11549. | 23.0 | 174 |
| 20 | In Silico Design of MDM2â€Targeting Peptides from a Naturally Occurring Constrained Peptide. ChemMedChem, 2019, 14, 1710-1716. | 1.6 | 1 |
| 21 | 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. | 1.6 | 8 |
| 22 | Insecticidal spider toxins are high affinity positive allosteric modulators of the nicotinic acetylcholine receptor. FEBS Letters, 2019, 593, 1336-1350. | 1.3 | 23 |
| 23 | Molecular dynamics simulations of dihydroâ€Î²â€erythroidine bound to the human Î±4Î²2 nicotinic acetylcholine receptor. British Journal of Pharmacology, 2019, 176, 2750-2763. | 2.7 | 11 |
| 24 | Conformational Flexibility Is a Determinant of Permeability for Cyclosporin. Journal of Physical Chemistry B, 2018, 122, 2261-2276. | 1.2 | 104 |
| 25 | 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. | 2.9 | 29 |
| 26 | ArachnoServer 3.0: an online resource for automated discovery, analysis and annotation of spider toxins. Bioinformatics, 2018, 34, 1074-1076. | 1.8 | 86 |
| 27 | 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. | 2.7 | 36 |
| 28 | 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. | 2.9 | 19 |
| 29 | Molecular basis for the production of cyclic peptides by plant asparaginyl endopeptidases. Nature Communications, 2018, 9, 2411. | 5.8 | 99 |
| 30 | Prediction of disulfide dihedral angles using chemical shifts. Chemical Science, 2018, 9, 6548-6556. | 3.7 | 30 |
| 31 | Bioactive Compounds Isolated from Neglected Predatory Marine Gastropods. Marine Drugs, 2018, 16, 118. | 2.2 | 17 |
| 32 | Computational Studies of Snake Venom Toxins. Toxins, 2018, 10, 8. | 1.5 | 22 |
| 33 | Stoichiometry dependent inhibition of rat Î±3Î²4 nicotinic acetylcholine receptor by the ribbon isomer of Î±-conotoxin AuIB. Biochemical Pharmacology, 2018, 155, 288-297. | 2.0 | 14 |
| 34 | 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. | 1.6 | 13 |
| 35 | 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. | 2.0 | 29 |
| 36 | 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. | 1.3 | 11 |

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|---|---------|----|-----------|
| 37 | α-Conotoxin [S9A]TxID Potently Discriminates between α3β4 and α6/α3β4 Nicotinic Acetylcholine Receptors. Journal of Medicinal Chemistry, 2017, 60, 5826-5833. | 2.9 | 30 |
| 38 | Role of CysI–CysIIIDisulfide Bond on the Structure and Activity of α-Conotoxins at Human Neuronal Nicotinic Acetylcholine Receptors. ACS Omega, 2017, 2, 4621-4631. | 1.6 | 12 |
| 39 | Backbone cyclization of analgesic conotoxin GeXIVA facilitates direct folding of the ribbon isomer. Journal of Biological Chemistry, 2017, 292, 17101-17112. | 1.6 | 15 |
| 40 | Modelling the interactions between animal venom peptides and membrane proteins. Neuropharmacology, 2017, 127, 20-31. | 2.0 | 14 |
| 41 | Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335. | 13.7 | 327 |
| 42 | Front Cover: Cyclisation of Disulfide-Rich Conotoxins in Drug Design Applications (Eur. J. Org. Chem.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 1.2 | 0 |
| 43 | Cyclisation of Disulfide–Rich Conotoxins in Drug Design Applications. European Journal of Organic Chemistry, 2016, 2016, 3462-3472. | 1.2 | 13 |
| 44 | Efficient enzymatic cyclization of an inhibitory cystine knot–containing peptide. Biotechnology and Bioengineering, 2016, 113, 2202-2212. | 1.7 | 22 |
| 45 | Less is More: Design of a Highly Stable Disulfide-Deleted Mutant of Analgesic Cyclic α-Conotoxin Vc1.1. Scientific Reports, 2015, 5, 13264. | 1.6 | 42 |
| 46 | 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. | 1.4 | 8 |
| 47 | Bioinformatics-Aided Venomics. Toxins, 2015, 7, 2159-2187. | 1.5 | 38 |
| 48 | Efficient backbone cyclization of linear peptides by a recombinant asparaginyl endopeptidase. Nature Communications, 2015, 6, 10199. | 5.8 | 186 |
| 49 | Cloning, synthesis, and characterization of αO-conotoxin GeXIVA, a potent α9α10 nicotinic acetylcholine receptor antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4026-35. | 3.3 | 91 |
| 50 | Key Residues in the Nicotinic Acetylcholine Receptor β2 Subunit Contribute to α-Conotoxin LvIA Binding. Journal of Biological Chemistry, 2015, 290, 9855-9862. | 1.6 | 18 |
| 51 | Design of substrate-based BCR-ABL kinase inhibitors using the cyclotide scaffold. Scientific Reports, 2015, 5, 12974. | 1.6 | 58 |
| 52 | Lysine-rich Cyclotides: A New Subclass of Circular Knotted Proteins from Violaceae. ACS Chemical Biology, 2015, 10, 2491-2500. | 1.6 | 34 |
| 53 | The Evolution of *Momordica* Cyclic Peptides. Molecular Biology and Evolution, 2015, 32, 392-405. | 3.5 | 26 |
| 54 | Characterisation of the subunit genes of pyrophosphate-dependent phosphofructokinase from loquat (Eriobotrya japonica Lindl.). Tree Genetics and Genomes, 2014, 10, 1465-1476. | 0.6 | 3 |

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| 55 | Prediction and characterization of cyclic proteins from sequences in three domains of life. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 181-190. | 1.1 | 19 |
| 56 | Discovery, Synthesis, and Structure–Activity Relationships of Conotoxins. Chemical Reviews, 2014, 114, 5815-5847. | 23.0 | 258 |
| 57 | A novel α4/7–conotoxin LvIA from Conus lividus that selectively blocks α3β2 vs. α6/α3β2β3 nicotinic acetylcholine receptors. FASEB Journal, 2014, 28, 1842-1853. | 0.2 | 64 |
| 58 | A systematic approach to document cyclotide distribution in plant species from genomic, transcriptomic, and peptidomic analysis. Biopolymers, 2013, 100, 433-437. | 1.2 | 26 |
| 59 | High-affinity Cyclic Peptide Matriptase Inhibitors. Journal of Biological Chemistry, 2013, 288, 13885-13896. | 1.6 | 122 |
| 60 | Isolation and Characterization of A Cytosolic Pyruvate Kinase cDNA From Loquat (Eriobotrya japonica) Tj ETQq0 0 0 rgBT /Overlock 10 T | 1.0 | 17 |
| 61 | NMR of plant proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2013, 71, 1-34. | 3.9 | 5 |
| 62 | Determination of the α-Conotoxin Vc1.1 Binding Site on the α9α10 Nicotinic Acetylcholine Receptor. Journal of Medicinal Chemistry, 2013, 56, 3557-3567. | 2.9 | 84 |
| 63 | Precursor De13.1 from Conus delessertii defines the novel G gene superfamily. Peptides, 2013, 41, 17-20. | 1.2 | 14 |
| 64 | Transcriptomic Messiness in the Venom Duct of Conus miles Contributes to Conotoxin Diversity. Molecular and Cellular Proteomics, 2013, 12, 3824-3833. | 2.5 | 70 |
| 65 | Deep Venomics Reveals the Mechanism for Expanded Peptide Diversity in Cone Snail Venom. Molecular and Cellular Proteomics, 2013, 12, 312-329. | 2.5 | 180 |
| 66 | Elucidation of relaxin-3 binding interactions in the extracellular loops of RXFP3. Frontiers in Endocrinology, 2013, 4, 13. | 1.5 | 48 |
| 67 | ConoServer: updated content, knowledge, and discovery tools in the conopeptide database. Nucleic Acids Research, 2012, 40, D325-D330. | 6.5 | 298 |
| 68 | Delineation of the Unbinding Pathway of α-Conotoxin ImI from the α7 Nicotinic Acetylcholine Receptor. Journal of Physical Chemistry B, 2012, 116, 6097-6105. | 1.2 | 31 |
| 69 | 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. | 2.8 | 21 |
| 70 | Cyclization of conotoxins to improve their biopharmaceutical properties. Toxicon, 2012, 59, 446-455. | 0.8 | 68 |
| 71 | ArachnoServer 2.0, an updated online resource for spider toxin sequences and structures. Nucleic Acids Research, 2011, 39, D653-D657. | 6.5 | 159 |
| 72 | Engineering of Conotoxins for the Treatment of Pain. Current Pharmaceutical Design, 2011, 17, 4242-4253. | 0.9 | 47 |

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| 73 | Blockade of Neuronal Î±7-nAChR by Î±-Conotoxin ImI Explained by Computational Scanning and Energy Calculations. PLoS Computational Biology, 2011, 7, e1002011. | 1.5 | 77 |
| 74 | Identification of candidates for cyclotide biosynthesis and cyclisation by expressed sequence tag analysis of Oldenlandia affinis. BMC Genomics, 2010, 11, 111. | 1.2 | 30 |
| 75 | A new â€œeraâ€•for cyclotide sequencing. Biopolymers, 2010, 94, 592-601. | 1.2 | 45 |
| 76 | Analysis and classification of circular proteins in CyBase. Biopolymers, 2010, 94, 584-591. | 1.2 | 67 |
| 77 | 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. | 3.3 | 63 |
| 78 | Conopeptide characterization and classifications: An analysis using ConoServer. Toxicon, 2010, 55, 1491-1509. | 0.8 | 198 |
| 79 | 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. | 6.5 | 232 |
| 80 | Antimicrobial peptides in plants.. , 2010, , 40-71. | | 7 |
| 81 | ArachnoServer: a database of protein toxins from spiders. BMC Genomics, 2009, 10, 375. | 1.2 | 58 |
| 82 | Despite a Conserved Cystine Knot Motif, Different Cyclotides Have Different Membrane Binding Modes. Biophysical Journal, 2009, 97, 1471-1481. | 0.2 | 74 |
| 83 | IMGT-Kaleidoscope, the formal IMGT-ONTOLOGY paradigm. Biochimie, 2008, 90, 570-583. | 1.3 | 107 |
| 84 | 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 |
| 85 | ConoServer, a database for conopeptide sequences and structures. Bioinformatics, 2008, 24, 445-446. | 1.8 | 193 |
| 86 | IMGT Standardization for Molecular Characterization of the T-cell Receptor/Peptide/MHC Complexes. , 2008, , 19-49. | | 17 |
| 87 | IMGT Colliers de Perles: Standardized Sequence-Structure Representations of the IgSF and MhcSF Superfamily Domains. Current Bioinformatics, 2007, 2, 21-30. | 0.7 | 46 |
| 88 | KNOTTIN: the knottin or inhibitor cystine knot scaffold in 2007. Nucleic Acids Research, 2007, 36, D314-D319. | 6.5 | 140 |
| 89 | CyBase: a database of cyclic protein sequences and structures, with applications in protein discovery and engineering. Nucleic Acids Research, 2007, 36, D206-D210. | 6.5 | 242 |
| 90 | Structureâ€"function relationships of the variable domains of monoclonal antibodies approved for cancer treatment. Critical Reviews in Oncology/Hematology, 2007, 64, 210-225. | 2.0 | 69 |

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| 91 | 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. | 1.0 | 454 |
| 92 | IMGT unique numbering for MHC groove G-DOMAIN and MHC superfamily (MhcSF) G-LIKE-DOMAIN. Developmental and Comparative Immunology, 2005, 29, 917-938. | 1.0 | 104 |
| 93 | IMGT-Choreography for immunogenetics and immunoinformatics. In Silico Biology, 2005, 5, 45-60. | 0.4 | 102 |
| 94 | T cell receptor/peptide/MHC molecular characterization and standardized pMHC contact sites in IMGT/3Dstructure-DB. In Silico Biology, 2005, 5, 505-28. | 0.4 | 38 |
| 95 | 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. | 6.5 | 145 |
| 96 | The KNOTTIN website and database: a new information system dedicated to the knottin scaffold. Nucleic Acids Research, 2004, 32, 156D-159. | 6.5 | 102 |
| 97 | IMGT, the international ImMunoGeneTics information system(R). Nucleic Acids Research, 2004, 33, D593-D597. | 6.5 | 251 |
| 98 | 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. | 1.2 | 7 |
| 99 | IMGT-ONTOLOGY for immunogenetics and immunoinformatics. In Silico Biology, 2004, 4, 17-29. | 0.4 | 119 |
| 100 | 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. | 1.2 | 4 |
| 101 | SCORE: predicting the core of protein models. Bioinformatics, 2001, 17, 541-550. | 1.8 | 17 |