# Peteris Prusis

List of Publications by Year
in descending order

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| 41 | 2,021 | 236925 | 265206 |
|---|---|---|---|
| papers | citations | 25 h-index | 42 g-index |

| 42 | 42 | 42 | 1483 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | New aspects on the melanocortins and their receptors. Pharmacological Research, 2000, 42, 393-420. | 7.1 | 313 |
| 2 | Discovery of novel melanocortin4 receptor selective MSH analogues. British Journal of Pharmacology, 1998, 124, 75-82. | 5.4 | 129 |
| 3 | Classification of G-protein coupled receptors by alignment-independent extraction of principal chemical properties of primary amino acid sequences. Protein Science, 2002, 11, 795-805. | 7.6 | 124 |
| 4 | Development of proteo-chemometrics: a novel technology for the analysis of drug-receptor interactions. Biochimica Et Biophysica Acta - General Subjects, 2001, 1525, 180-190. | 2.4 | 118 |
| 5 | Polypharmacology modelling using proteochemometrics (PCM): recent methodological developments, applications to target families, and future prospects. MedChemComm, 2015, 6, 24-50. | 3.4 | 109 |
| 6 | Proteochemometrics Modeling of the Interaction of Amine G-Protein Coupled Receptors with a Diverse Set of Ligands. Molecular Pharmacology, 2002, 61, 1465-1475. | 2.3 | 85 |
| 7 | Selectivity of Cyclic [d-Nal7] and [d-Phe7] Substituted MSH Analogues for the Melanocortin Receptor Subtypes. Peptides, 1997, 18, 1009-1013. | 2.4 | 84 |
| 8 | Improved approach for proteochemometrics modeling: application to organic compound–amine G protein-coupled receptor interactions. Bioinformatics, 2005, 21, 4289-4296. | 4.1 | 76 |
| 9 | Long term orexigenic effect of a novel melanocortin 4 receptor selective antagonist. British Journal of Pharmacology, 1999, 126, 27-34. | 5.4 | 70 |
| 10 | Proteochemometric modeling of HIV protease susceptibility. BMC Bioinformatics, 2008, 9, 181. | 2.6 | 70 |
| 11 | Modeling of the three-dimensional structure of the human melanocortin 1 receptor, using an automated method and docking of a rigid cyclic melanocyte-stimulating hormone core peptide. Journal of Molecular Graphics and Modelling, 1997, 15, 307-317. | 2.4 | 64 |
| 12 | Probing the substrate specificity of the dengue virus type 2 NS3 serine protease by using internally quenched fluorescent peptides. Biochemical Journal, 2006, 397, 203-211. | 3.7 | 52 |
| 13 | QSAR and Proteo-chemometric Analysis of the Interaction of a Series of Organic Compounds with Melanocortin Receptor Subtypes. Journal of Medicinal Chemistry, 2003, 46, 2572-2579. | 6.4 | 48 |
| 14 | Binding of cyclic and linear MSH core peptides to the melanocortin receptor subtypes. European Journal of Pharmacology, 1997, 319, 369-373. | 3.5 | 47 |
| 15 | Proteochemometrics analysis of substrate interactions with dengue virus NS3 proteases. Bioorganic and Medicinal Chemistry, 2008, 16, 9369-9377. | 3.0 | 47 |
| 16 | PLS modeling of chimeric MS04/MSH-peptide and MC1/MC3-receptor interactions reveals a novel method for the analysis of ligandâ€“receptor interactions. BBA - Proteins and Proteomics, 2001, 1544, 350-357. | 2.1 | 42 |
| 17 | Proteochemometric Mapping of the Interaction of Organic Compounds with Melanocortin Receptor Subtypes. Molecular Pharmacology, 2005, 67, 50-59. | 2.3 | 38 |
| 18 | Generalized modeling of enzyme-ligand interactions using proteochemometrics and local protein substructures. Proteins: Structure, Function and Bioinformatics, 2006, 65, 568-579. | 2.6 | 38 |

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|---|---|---|---|
| 19 | Prediction of indirect interactions in proteins. BMC Bioinformatics, 2006, 7, 167. | 2.6 | 38 |
| 20 | Design and evaluation of substrate-based octapeptide and non substrate-based tetrapeptide inhibitors of dengue virus NS2Bâ€“NS3 proteases. Biochemical and Biophysical Research Communications, 2013, 434, 767-772. | 2.1 | 34 |
| 21 | Selective properties of C- and N-terminals and core residues of the melanocyte-stimulating hormone on binding to the human melanocortin receptor subtypes. European Journal of Pharmacology, 1998, 349, 359-366. | 3.5 | 32 |
| 22 | Unbiased descriptor and parameter selection confirms the potential of proteochemometric modelling. BMC Bioinformatics, 2005, 6, 50. | 2.6 | 32 |
| 23 | Visually Interpretable Models of Kinase Selectivity Related Features Derived from Field-Based Proteochemometrics. Journal of Chemical Information and Modeling, 2013, 53, 3021-3030. | 5.4 | 30 |
| 24 | Proteo-chemometrics analysis of MSH peptide binding to melanocortin receptors. Protein Engineering, Design and Selection, 2002, 15, 305-311. | 2.1 | 28 |
| 25 | Rough set-based proteochemometrics modeling of G-protein-coupled receptor-ligand interactions. Proteins: Structure, Function and Bioinformatics, 2006, 63, 24-34. | 2.6 | 26 |
| 26 | Characterisation of D117A and H260A mutations in the melanocortin 1 receptor. Molecular and Cellular Endocrinology, 1997, 126, 213-219. | 3.2 | 23 |
| 27 | A Look Inside HIV Resistance through Retroviral Protease Interaction Maps. PLoS Computational Biology, 2007, 3, e48. | 3.2 | 23 |
| 28 | Design of new small cyclic melanocortin receptor-binding peptides using molecular modelling: Role of the His residue in the melanocortin peptide core. European Journal of Medicinal Chemistry, 2001, 36, 137-146. | 5.5 | 22 |
| 29 | Synthesis and Quantitative Structureâ^'Activity Relationship of Hydrazones ofN-Amino-Nâ€˜-hydroxyguanidine as Electron Acceptors for Xanthine Oxidase. Journal of Medicinal Chemistry, 2004, 47, 3105-3110. | 6.4 | 22 |
| 30 | Thyrotropin releasing hormone (TRH) selectively binds and activates the melanocortin 1 receptor. Peptides, 1999, 20, 395-400. | 2.4 | 21 |
| 31 | Evidence Indicating That the TM4, EL2, and TM5 of the Melanocortin 3 Receptor Do Not Participate in Ligand Binding. Biochemical and Biophysical Research Communications, 1996, 229, 687-692. | 2.1 | 18 |
| 32 | Proteochemometric modelling of antibody-antigen interactions using SPOT synthesised peptide arrays. Protein Engineering, Design and Selection, 2007, 20, 301-307. | 2.1 | 17 |
| 33 | Proteochemometric modeling reveals the interaction site for Trp9 modified Î±-MSH peptides in melanocortin receptors. Proteins: Structure, Function and Bioinformatics, 2007, 67, 653-660. | 2.6 | 16 |
| 34 | Proteochemometric analysis of small cyclic peptides' interaction with wild-type and chimeric melanocortin receptors. Proteins: Structure, Function and Bioinformatics, 2007, 69, 83-96. | 2.6 | 15 |
| 35 | Predictive proteochemometric models for kinases derived from 3D protein field-based descriptors. MedChemComm, 2016, 7, 1007-1015. | 3.4 | 12 |
| 36 | 3D proteochemometrics: using three-dimensional information of proteins and ligands to address aspects of the selectivity of serine proteases. MedChemComm, 2017, 8, 1037-1045. | 3.4 | 7 |

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|---|---|---|---|
| 37 | Detection of regions in the MC1 receptor of importance for the selectivity of the MC1 receptor super-selective MS04/MS05 peptides. BBA - Proteins and Proteomics, 2001, 1544, 278-282. | 2.1 | 6 |
| 38 | QSAR of multiple mutated antibodies. Journal of Molecular Recognition, 2007, 20, 97-102. | 2.1 | 6 |
| 39 | Characterization of the enzymatic activity for biphasic competition by guanoxabenz (1-(2,6-dichlorobenzylidene-amino)-3-hydroxyguanidine) at l±2-adrenoceptors. Biochemical Pharmacology, 1998, 56, 1121-1128. | 4.4 | 5 |
| 40 | Conditions for biphasic competition curves in radioligand binding for ligands subjected to metabolic transformation. Biochemical Pharmacology, 1998, 56, 1129-1137. | 4.4 | 3 |
| 41 | Identification of the binding pocket for the TRH peptide in the melanocortin 1 receptor. International Journal of Peptide Research and Therapeutics, 2000, 7, 225-228. | 0.1 | 2 |