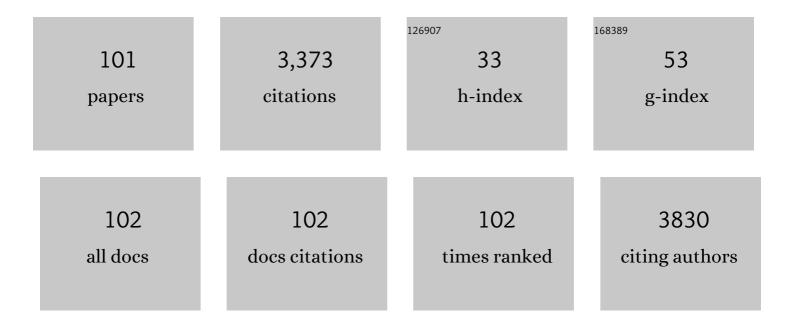
Olli T Pentikäinen

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Selective Binding of Collagen Subtypes by Integrin α1I, α2I, and α10I Domains. Journal of Biological Chemistry, 2001, 276, 48206-48212.	3.4	221
2	MMGBSA As a Tool To Understand the Binding Affinities of Filamin–Peptide Interactions. Journal of Chemical Information and Modeling, 2013, 53, 2626-2633.	5.4	205
3	BODIL: a molecular modeling environment for structure-function analysis and drug design. Journal of Computer-Aided Molecular Design, 2004, 18, 401-419.	2.9	200
4	α11β1 Integrin Recognizes the GFOGER Sequence in Interstitial Collagens. Journal of Biological Chemistry, 2003, 278, 7270-7277.	3.4	143
5	Structure of three tandem filamin domains reveals auto-inhibition of ligand binding. EMBO Journal, 2007, 26, 3993-4004.	7.8	134
6	A Peptide Inhibiting the Collagen Binding Function of Integrin α2I Domain. Journal of Biological Chemistry, 1999, 274, 3513-3521.	3.4	81
7	Rocker: Open source, easy-to-use tool for AUC and enrichment calculations and ROC visualization. Journal of Cheminformatics, 2016, 8, 45.	6.1	80
8	Synthesis and Pharmacological Characterization of N3-Substituted Willardiine Derivatives:Â Role of the Substituent at the 5-Position of the Uracil Ring in the Development of Highly Potent and Selective GLUK5Kainate Receptor Antagonists. Journal of Medicinal Chemistry, 2007, 50, 1558-1570.	6.4	70
9	Integrin α2I Domain Recognizes Type I and Type IV Collagens by Different Mechanisms. Journal of Biological Chemistry, 2000, 275, 3348-3354.	3.4	65
10	Molecular Basis of Filamin A-FilGAP Interaction and Its Impairment in Congenital Disorders Associated with Filamin A Mutations. PLoS ONE, 2009, 4, e4928.	2.5	65
11	Modeling of interactions between xenobiotics and cytochrome P450 (CYP) enzymes. Frontiers in Pharmacology, 2015, 6, 123.	3.5	65
12	AMPA receptors and bacterial periplasmic amino acid-binding proteins share the ionic mechanism of ligand recognition. EMBO Journal, 1998, 17, 4704-4711.	7.8	61
13	Vascular amine oxidases are needed for leukocyte extravasation into inflamed joints in vivo. Arthritis and Rheumatism, 2006, 54, 2852-2862.	6.7	54
14	Full Domain Closure of the Ligand-binding Core of the Ionotropic Glutamate Receptor iGluR5 Induced by the High Affinity Agonist Dysiherbaine and the Functional Antagonist 8,9-Dideoxyneodysiherbaine. Journal of Biological Chemistry, 2009, 284, 14219-14229.	3.4	53
15	Divergent Pharmacological Activity of Novel Marine-Derived Excitatory Amino Acids on Glutamate Receptors. Journal of Pharmacology and Experimental Therapeutics, 2005, 314, 1068-1078.	2.5	52
16	New inhibitors of 17β-hydroxysteroid dehydrogenase type 1. Molecular and Cellular Endocrinology, 2006, 248, 192-198.	3.2	51
17	Case-specific performance of MM-PBSA, MM-GBSA, and SIE in virtual screening. Journal of Molecular Graphics and Modelling, 2015, 62, 303-318.	2.4	49
18	Characterization of Bile Salt/Cyclodextrin Interactions Using Isothermal Titration Calorimetry. Langmuir, 2001, 17, 7107-7111.	3.5	48

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19	Chicken avidin-related proteins show altered biotin-binding and physico-chemical properties as compared with avidin. Biochemical Journal, 2002, 363, 609-617.	3.7	47
20	Construction of Hevein (Hev b 6.02) with Reduced Allergenicity for Immunotherapy of Latex Allergy by Comutation of Six Amino Acid Residues on the Conformational IgE Epitopes. Journal of Immunology, 2004, 172, 2621-2628.	0.8	47
21	Pro-prion Binds Filamin A, Facilitating Its Interaction with Integrin β1, and Contributes to Melanomagenesis. Journal of Biological Chemistry, 2010, 285, 30328-30339.	3.4	46
22	Mammary-derived growth inhibitor (MDGI) interacts with integrin α-subunits and suppresses integrin activity and invasion. Oncogene, 2010, 29, 6452-6463.	5.9	45
23	Chicken Avidin-related Protein 4/5 Shows Superior Thermal Stability when Compared with Avidin while Retaining High Affinity to Biotin. Journal of Biological Chemistry, 2004, 279, 9337-9343.	3.4	44
24	2NH and 3OH are crucial structural requirements in sphingomyelin for sticholysin II binding and pore formation in bilayer membranes. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 1390-1395.	2.6	44
25	A small-molecule inhibitor of integrin α2β1 introduces a new strategy for antithrombotic therapy. Thrombosis and Haemostasis, 2010, 103, 387-397.	3.4	40
26	Suitability of <scp>MMGBSA</scp> for the selection of correct ligand binding modes from docking results. Chemical Biology and Drug Design, 2019, 93, 522-538.	3.2	38
27	The Major Conformational IgE-binding Epitopes of Hevein (Hev b6.02) Are Identified by a Novel Chimera-based Allergen Epitope Mapping Strategy. Journal of Biological Chemistry, 2002, 277, 22656-22661.	3.4	37
28	Chicken avidin-related proteins show altered biotin-binding and physico-chemical properties as compared with avidin. Biochemical Journal, 2002, 363, 609.	3.7	37
29	Novel α2β1 Integrin Inhibitors Reveal That Integrin Binding to Collagen under Shear Stress Conditions Does Not Require Receptor Preactivation. Journal of Biological Chemistry, 2012, 287, 44694-44702.	3.4	37
30	Molecular and ecological signs of mitochondrial adaptation: consequences for introgression?. Heredity, 2014, 113, 277-286.	2.6	37
31	The Influence of Hydrogen Bonding on Sphingomyelin/Colipid Interactions in Bilayer Membranes. Biophysical Journal, 2016, 110, 431-440.	0.5	37
32	Binding Properties of HABA-Type Azo Derivatives to Avidin and Avidin-Related Protein 4. Chemistry and Biology, 2006, 13, 1029-1039.	6.0	36
33	Structure-Activity Relationship Analysis of 3-Phenylcoumarin-Based Monoamine Oxidase B Inhibitors. Frontiers in Chemistry, 2018, 6, 41.	3.6	36
34	Jararhagin-derived RKKH Peptides Induce Structural Changes in α11 Domain of Human Integrin α1β1. Journal of Biological Chemistry, 2004, 279, 7962-7970.	3.4	35
35	Ultrafast protein structure-based virtual screening with Panther. Journal of Computer-Aided Molecular Design, 2015, 29, 989-1006.	2.9	34
36	"RKKH―Peptides from the Snake Venom Metalloproteinase ofBothrops jararaca Bind Near the Metal Ion-dependent Adhesion Site of the Human Integrin α2 I-domain. Journal of Biological Chemistry, 1999, 274, 31493-31505.	3.4	33

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37	Novel Analogs and Stereoisomers of the Marine Toxin Neodysiherbaine with Specificity for Kainate Receptors. Journal of Pharmacology and Experimental Therapeutics, 2008, 324, 484-496.	2.5	33
38	Cystic Fibrosis Transmembrane Conductance Regulator Interacts with Multiple Immunoglobulin Domains of Filamin A. Journal of Biological Chemistry, 2010, 285, 17156-17165.	3.4	31
39	Determination of Binding Site Residues Responsible for the Subunit Selectivity of Novel Marine-Derived Compounds on Kainate Receptors. Molecular Pharmacology, 2006, 69, 1849-1860.	2.3	30
40	Ligand-binding Domain Determines Endoplasmic Reticulum Exit of AMPA Receptors. Journal of Biological Chemistry, 2010, 285, 36032-36039.	3.4	29
41	Identification of estrogen receptor α ligands with virtual screening techniques. Journal of Molecular Graphics and Modelling, 2016, 64, 30-39.	2.4	29
42	A holistic view on c-Kit in cancer: Structure, signaling, pathophysiology and its inhibitors. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188631.	7.4	29
43	Comparison of Virtual High-Throughput Screening Methods for the Identification of Phosphodiesterase-5 Inhibitors. Journal of Chemical Information and Modeling, 2011, 51, 1353-1363.	5.4	28
44	Selective agonist binding of (S)-2-amino-3-(3-hydroxy-5-methyl-4-isoxazolyl)propionic acid (AMPA) and 2S-(2α,3β,4β)-2-carboxy-4-(1-methylethenyl)-3-pyrrolidineacetic acid (kainate) receptors: a molecular modeling study. Biochemical Pharmacology, 2003, 66, 2413-2425.	4.4	26
45	Cooperative symmetric to asymmetric conformational transition of the <i>apo</i> â€form of scavenger decapping enzyme revealed by simulations. Proteins: Structure, Function and Bioinformatics, 2008, 70, 498-508.	2.6	26
46	Synthesis, in Vitro Activity, and Three-Dimensional Quantitative Structureâ^'Activity Relationship of Novel Hydrazine Inhibitors of Human Vascular Adhesion Protein-1. Journal of Medicinal Chemistry, 2010, 53, 6301-6315.	6.4	26
47	Full and Partial Agonism of Ionotropic Glutamate Receptors Indicated by Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2011, 51, 1037-1047.	5.4	26
48	Coumarin-Based Profluorescent and Fluorescent Substrates for Determining Xenobiotic-Metabolizing Enzyme Activities In Vitro. International Journal of Molecular Sciences, 2020, 21, 4708.	4.1	26
49	The core domain of retrotransposon integrase in Hordeum: predicted structure and evolution. Molecular Biology and Evolution, 1998, 15, 1135-1144.	8.9	25
50	Identification of the Privileged Position in the Imidazo[1,2- <i>a</i>]pyridine Ring of Phosphonocarboxylates for Development of Rab Geranylgeranyl Transferase (RGGT) Inhibitors. Journal of Medicinal Chemistry, 2017, 60, 8781-8800.	6.4	25
51	Blocking oestradiol synthesis pathways with potent and selective coumarin derivatives. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 743-754.	5.2	25
52	A dimeric ternary complex of FGFR1, heparin and FGF-1 leads to an â€~electrostatic sandwich' model for heparin binding. Structure, 1999, 7, 699-709.	3.3	24
53	Small Molecule Designed to Target Metal Binding Site in the α2I Domain Inhibits Integrin Function. Journal of Medicinal Chemistry, 2007, 50, 2742-2746.	6.4	24
54	Novel Hydrazine Molecules as Tools To Understand the Flexibility of Vascular Adhesion Protein-1 Ligand-Binding Site: Toward More Selective Inhibitors. Journal of Medicinal Chemistry, 2011, 54, 2143-2154.	6.4	24

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55	Temperatureâ€dependent mutational robustness can explain faster molecular evolution at warm temperatures, affecting speciation rate and global patterns of species diversity. Ecography, 2016, 39, 1025-1033.	4.5	23
56	Exploring kainate receptor pharmacology using molecular dynamics simulations. Neuropharmacology, 2010, 58, 515-527.	4.1	22
57	Getting Docking into Shape Using Negative Image-Based Rescoring. Journal of Chemical Information and Modeling, 2019, 59, 3584-3599.	5.4	22
58	Cyanidinâ€3â€glucoside binds to talin and modulates colon cancer cell adhesions and 3D growth. FASEB Journal, 2020, 34, 2227-2237.	0.5	21
59	Subtype selectivity and flexibility of ionotropic glutamate receptors upon antagonist ligand binding. Organic and Biomolecular Chemistry, 2006, 4, 1058.	2.8	20
60	Efficient Virtual Screening Using Multiple Protein Conformations Described as Negative Images of the Ligand-Binding Site. Journal of Chemical Information and Modeling, 2010, 50, 1005-1011.	5.4	20
61	Improving Docking Performance Using Negative Image-Based Rescoring. Frontiers in Pharmacology, 2018, 9, 260.	3.5	20
62	A Novel Structural Unit in the N-terminal Region of Filamins. Journal of Biological Chemistry, 2014, 289, 8588-8598.	3.4	18
63	Molecular Docking-Based Design and Development of a Highly Selective Probe Substrate for UDP-glucuronosyltransferase 1A10. Molecular Pharmaceutics, 2018, 15, 923-933.	4.6	16
64	Development of new Coumarin-based profluorescent substrates for human cytochrome P450 enzymes. Xenobiotica, 2019, 49, 1015-1024.	1.1	16
65	Structural Mechanism of N-Methyl-D-Aspartate Receptor Type 1 Partial Agonism. PLoS ONE, 2012, 7, e47604.	2.5	16
66	Pharmacological activity of C10-substituted analogs of the high-affinity kainate receptor agonist dysiherbaine. Neuropharmacology, 2010, 58, 640-649.	4.1	15
67	Fluorescent Small Molecule Probe to Modulate and Explore α2β1 Integrin Function. Journal of the American Chemical Society, 2011, 133, 14558-14561.	13.7	15
68	l-Arabinose/d-galactose 1-dehydrogenase of Rhizobium leguminosarum bv. trifolii characterised and applied for bioconversion of l-arabinose to l-arabonate with Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2014, 98, 9653-9665.	3.6	15
69	Molecular mechanism of T-cell protein tyrosine phosphatase (TCPTP) activation by mitoxantrone. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1988-1997.	2.3	14
70	Inhibitory effects and oxidation of 6-methylcoumarin, 7-methylcoumarin and 7-formylcoumarin <i>via</i> human CYP2A6 and its mouse and pig orthologous enzymes. Xenobiotica, 2016, 46, 14-24.	1.1	14
71	Screening of Natural Products Targeting SARS-CoV-2–ACE2 Receptor Interface – A MixMD Based HTVS Pipeline. Frontiers in Chemistry, 2020, 8, 589769.	3.6	14
72	Skeletal Dysplasia Mutations Effect on Human Filamins' Structure and Mechanosensing. Scientific Reports, 2017, 7, 4218.	3.3	13

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73	Inhibition of human CYP1 enzymes by a classical inhibitor αâ€naphthoflavone and a novel inhibitor <i>N</i> â€(3, 5â€dichlorophenyl)cyclopropanecarboxamide: An in vitro and in silico study. Chemical Biology and Drug Design, 2020, 95, 520-533.	3.2	13
74	Fragment―and negative imageâ€based screening of phosphodiesterase 10A inhibitors. Chemical Biology and Drug Design, 2019, 94, 1799-1812.	3.2	11
75	Discrimination between Agonists and Antagonists by the α-Amino-3-hydroxy-5-methyl-4-isoxazole Propionic Acid-selective Glutamate Receptor. Journal of Biological Chemistry, 2002, 277, 41940-41947.	3.4	10
76	Model structures of the N-methyl-d-aspartate receptor subunit NR1 explain the molecular recognition of agonist and antagonist ligands. Journal of Structural Biology, 2004, 145, 205-215.	2.8	10
77	Discovery of Retinoic Acid-Related Orphan Receptor γt Inverse Agonists via Docking and Negative Image-Based Screening. ACS Omega, 2018, 3, 6259-6266.	3.5	10
78	Reliability of Virtual Screening Methods in Prediction of PDE4Binhibitor Activity. Current Drug Discovery Technologies, 2015, 12, 117-126.	1.2	10
79	Antiferritin VL homodimer binds human spleen ferritin with high specificity. Journal of Structural Biology, 2002, 138, 171-186.	2.8	9
80	Functional Display of an α2 Integrin-Specific Motif (RKK) on the Surface of Baculovirus Particles. Technology in Cancer Research and Treatment, 2005, 4, 437-445.	1.9	9
81	A Practical Perspective: The Effect of Ligand Conformers on the Negative Image-Based Screening. International Journal of Molecular Sciences, 2019, 20, 2779.	4.1	9
82	Determinants of antagonist binding at the α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor subunit, GluR-D. FEBS Journal, 2002, 269, 6261-6270.	0.2	8
83	Substrate Selectivity of Coumarin Derivatives by Human CYP1 Enzymes: In Vitro Enzyme Kinetics and In Silico Modeling. ACS Omega, 2021, 6, 11286-11296.	3.5	8
84	Structure–activity relationship of sphingomyelin analogs with sphingomyelinase from Bacillus cereus. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 474-480.	2.6	7
85	Inhibition of Pneumolysin Cytotoxicity by Hydrolysable Tannins. Antibiotics, 2020, 9, 930.	3.7	7
86	Blockage of collagen binding to integrin α2β1: structure–activity relationship of protein–protein interaction inhibitors. MedChemComm, 2011, 2, 764.	3.4	6
87	Molecular docking and oxidation kinetics of 3-phenyl coumarin derivatives by human CYP2A13. Xenobiotica, 2021, 51, 1207-1216.	1.1	6
88	Coumarins as Tool Compounds to Aid the Discovery of Selective Function Modulators of Steroid Hormone Binding Proteins. Molecules, 2021, 26, 5142.	3.8	6
89	Computational Study on the Inhibitory Effect of Natural Compounds against the SARS-CoV-2 Proteins. Bioinorganic Chemistry and Applications, 2022, 2022, 1-19.	4.1	6
90	Effects of cold acclimation and dsRNA injections on Gs1l gene splicing in Drosophila montana. Scientific Reports, 2018, 8, 7577.	3.3	4

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91	In vitro glucuronidation of 7-hydroxycoumarin derivatives in intestine and liver microsomes of Beagle dogs. European Journal of Pharmaceutical Sciences, 2020, 141, 105118.	4.0	3
92	Detection of Binding Sites on SARS-CoV-2 Spike Protein Receptor-Binding Domain by Molecular Dynamics Simulations in Mixed Solvents. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1281-1289.	3.0	3
93	Sdfconf: A Novel, Flexible, and Robust Molecular Data Management Tool. Journal of Chemical Information and Modeling, 2022, 62, 9-15.	5.4	3
94	Optimization of Cavity-Based Negative Images to Boost Docking Enrichment in Virtual Screening. Journal of Chemical Information and Modeling, 2022, , .	5.4	2
95	Rational design, optimization, and biological evaluation of novel α-Phosphonopropionic acids as covalent inhibitors of Rab geranylgeranyl transferase. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 940-951.	5.2	2
96	<i>In vitro</i> sulfonation of 7-hydroxycoumarin derivatives in liver cytosol of human and six animal species. Xenobiotica, 2020, 50, 885-893.	1.1	1
97	Negative Image-Based Screening: Rigid Docking Using Cavity Information. Methods in Molecular Biology, 2021, 2266, 125-140.	0.9	1
98	Ligand-Enhanced Negative Images Optimized for Docking Rescoring. International Journal of Molecular Sciences, 2022, 23, 7871.	4.1	1
99	A dimeric ternary complex of FGFR1, heparin and FGF-1 leads to an â€~electrostatic sandwich' model for heparin binding. Structure, 1999, 7, R198.	3.3	0
100	Negative Image-Based Rescoring: Using Cavity Information to Improve Docking Screening. Methods in Molecular Biology, 2021, 2266, 141-154.	0.9	0
101	Coumarins as Tool Compounds to Aid the Discovery of Selective Function Modulators of Steroid Hormone Binding Proteins. Molecules, 2021, 26, .	3.8	0