Marko HyvÃ¶nen

List of Publications by Year
in descending order

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75 papers	3,769 citations	172457 29 h-index	138484 58 g-index
88 all docs	88 docs citations	88 times ranked	4936 citing authors

#	Article	IF	Citations
1	Structure of the WW domain of a kinase-associated protein complexed with a proline-rich peptide. Nature, 1996, 382, 646-649.	27.8	426
2	PH domain: the first anniversary. Trends in Biochemical Sciences, 1994, 19, 349-353.	7.5	332
3	T7 Vectors with a Modified T7lacPromoter for Expression of Proteins inEscherichia coli. Analytical Biochemistry, 1996, 236, 371-373.	2.4	273
4	Ultrahigh-throughput discovery of promiscuous enzymes by picodroplet functional metagenomics. Nature Communications, 2015, 6, 10008.	12.8	225
5	Structure of the PH domain from Bruton's tyrosine kinase in complex with inositol 1,3,4,5-tetrakisphosphate. Structure, 1999, 7, 449-460.	3.3	197
6	Functionalised staple linkages for modulating the cellular activity of stapled peptides. Chemical Science, 2014, 5, 1804-1809.	7.4	165
7	Structural basis for the inhibition of activin signalling by follistatin. EMBO Journal, 2006, 25, 1035-1045.	7.8	141
8	Using a Fragmentâ€Based Approach To Target Proteinâ€“Protein Interactions. ChemBioChem, 2013, 14, 332-342.	2.6	115
9	Double Strainâ€Promoted Macrocyclization for the Rapid Selection of Cellâ€Active Stapled Peptides. Angewandte Chemie - International Edition, 2015, 54, 15410-15413.	13.8	101
10	An efficient, multiply promiscuous hydrolase in the alkaline phosphatase superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2740-2745.	7.1	87
11	A general approach for the site-selective modification of native proteins, enabling the generation of stable and functional antibodyâ€“drug conjugates. Chemical Science, 2019, 10, 694-700.	7.4	85
12	Alternative modulation of proteinâ€“protein interactions by small molecules. Current Opinion in Biotechnology, 2015, 35, 78-85.	6.6	80
13	Structure and activation of pro-activin A. Nature Communications, 2016, 7, 12052.	12.8	74
14	Allosteric modulation of AURKA kinase activity by a small-molecule inhibitor of its protein-protein interaction with TPX2. Scientific Reports, 2016, 6, 28528.	3.3	66
15	A New Member of the Alkaline Phosphatase Superfamily with a Formylglycine Nucleophile: Structural and Kinetic Characterisation of a Phosphonate Monoester Hydrolase/Phosphodiesterase from Rhizobium leguminosarum. Journal of Molecular Biology, 2008, 384, 120-136.	4.2	65
16	Structure of the human myostatin precursor and determinants of growth factor latency. EMBO Journal, 2018, 37, 367-383.	7.8	58
17	From Crystal Packing to Molecular Recognition: Prediction and Discovery of a Binding Site on the Surface of Poloâ€Like Kinase 1. Angewandte Chemie - International Edition, 2011, 50, 4003-4006.	13.8	57
18	Specific inhibition of CK2Î± from an anchor outside the active site. Chemical Science, 2016, 7, 6839-6845.	7.4	55

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19	Macrocyclized Extended Peptides: Inhibiting the Substrate-Recognition Domain of Tankyrase. Journal of the American Chemical Society, 2017, 139, 2245-2256.	13.7	55
20	Structure of Gremlin-1 and analysis of its interaction with BMP-2. Biochemical Journal, 2016, 473, 1593-1604.	3.7	52
21	A fragment-based approach leading to the discovery of a novel binding site and the selective CK2 inhibitor CAM4066. Bioorganic and Medicinal Chemistry, 2017, 25, 3471-3482.	3.0	48
22	Crystal Structures of the Heparan Sulfate-binding Domain of Follistatin. Journal of Biological Chemistry, 2003, 278, 39969-39977.	3.4	45
23	Organoid culture media formulated with growth factors of defined cellular activity. Scientific Reports, 2019, 9, 6193.	3.3	42
24	Human BDNF/TrkB variants impair hippocampal synaptogenesis and associate with neurobehavioural abnormalities. Scientific Reports, 2020, 10, 9028.	3.3	40
25	A new â€˜totalâ€™ activin B enzymeâ€linked immunosorbent assay (ELISA): development and validation for human samples. Clinical Endocrinology, 2009, 71, 867-873.	2.4	38
26	Smallâ€Molecule Inhibitors That Target Proteinâ€“Protein Interactions in the RAD51 Family of Recombinases. ChemMedChem, 2015, 10, 296-303.	3.2	36
27	Selective small molecule inhibitor of the Mycobacterium tuberculosis fumarate hydratase reveals an allosteric regulatory site. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7503-7508.	7.1	36
28	Novel non-ATP competitive small molecules targeting the CK2 Î±/Î² interface. Bioorganic and Medicinal Chemistry, 2018, 26, 3016-3020.	3.0	35
29	Balancing Specificity and Promiscuity in Enzyme Evolution: Multidimensional Activity Transitions in the Alkaline Phosphatase Superfamily. Journal of the American Chemical Society, 2019, 141, 370-387.	13.7	35
30	Evolutionary repurposing of a sulfatase: A new Michaelis complex leads to efficient transition state charge offset. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7293-E7302.	7.1	34
31	Twoâ€Component Stapling of Biologically Active and Conformationally Constrained Peptides: Past, Present, and Future. Advanced Therapeutics, 2018, 1, 1800052.	3.2	33
32	Adhesion of Endothelial Cells to NOV Is Mediated by the Integrins Î±vÎ²3 and Î±5Î²1. Journal of Vascular Research, 2003, 40, 234-243.	1.4	32
33	Second-generation CK2Î± inhibitors targeting the Î±D pocket. Chemical Science, 2018, 9, 3041-3049.	7.4	32
34	From a metagenomic source to a high-resolution structure of a novel alkaline esterase. Applied Microbiology and Biotechnology, 2017, 101, 4935-4949.	3.6	31
35	Molecular characterization of latent GDF8 reveals mechanisms of activation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E866-E875.	7.1	30
36	Quantitative Affinity Determination by Fluorescence Anisotropy Measurements of Individual Nanoliter Droplets. Analytical Chemistry, 2017, 89, 1092-1101.	6.5	27

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37	Efficient development of stable and highly functionalised peptides targeting the CK2Î±/CK2Î² proteinâ€“protein interaction. Chemical Science, 2019, 10, 5056-5063.	7.4	27
38	A small-molecule inhibitor of the BRCA2-RAD51 interaction modulates RAD51 assembly and potentiates DNA damage-induced cell death. Cell Chemical Biology, 2021, 28, 835-847.e5.	5.2	27
39	Structural analyses of von Willebrand factor C domains of collagen 2A and CCN3 reveal an alternative mode of binding to bone morphogenetic protein-2. Journal of Biological Chemistry, 2017, 292, 12516-12527.	3.4	25
40	Pathogenic ACVR1^{R206H} activation by Activin Aâ€induced receptor clustering and autophosphorylation. EMBO Journal, 2021, 40, e106317.	7.8	24
41	Structureâ€activity relationship of the peptide bindingâ€motif mediating the BRCA2:RAD51 proteinâ€“protein interaction. FEBS Letters, 2016, 590, 1094-1102.	2.8	20
42	Rab5-mediated endocytosis of activin is not required for gene activation or long-range signalling inXenopus. Development (Cambridge), 2009, 136, 2803-2813.	2.5	19
43	Chemical probes targeting the kinase CK2: a journey outside the catalytic box. Organic and Biomolecular Chemistry, 2021, 19, 4380-4396.	2.8	19
44	CHRD, a novel domain in the BMP inhibitor chordin, is also found in microbial proteins. Trends in Biochemical Sciences, 2003, 28, 470-473.	7.5	18
45	Development of a new antibody to the human inhibin/activin Î²B subunit and its application to improved inhibin B ELISAs. Journal of Immunological Methods, 2008, 329, 102-111.	1.4	18
46	Structural and Mechanistic Analysis of the Choline Sulfatase from Sinorhizobium melliloti: A Class I Sulfatase Specific for an Alkyl Sulfate Ester. Journal of Molecular Biology, 2018, 430, 1004-1023.	4.2	18
47	A cryptic hydrophobic pocket in the polo-box domain of the polo-like kinase PLK1 regulates substrate recognition and mitotic chromosome segregation. Scientific Reports, 2019, 9, 15930.	3.3	17
48	Secreted BMP antagonists and their role in cancer and bone metastases. Bone, 2020, 137, 115455.	2.9	16
49	Downfalls of Chemical Probes Acting at the Kinase ATP-Site: CK2 as a Case Study. Molecules, 2021, 26, 1977.	3.8	16
50	Functional metagenomic screening identifies an unexpected Î²-glucuronidase. Nature Chemical Biology, 2022, 18, 1096-1103.	8.0	16
51	Computationally-guided optimization of small-molecule inhibitors of the Aurora A kinaseâ€“TPX2 proteinâ€“protein interaction. Chemical Communications, 2017, 53, 9372-9375.	4.1	15
52	Water-soluble, stable and azide-reactive strained dialkynes for biocompatible double strain-promoted click chemistry. Organic and Biomolecular Chemistry, 2019, 17, 8014-8018.	2.8	14
53	Diarylethene moiety as an enthalpy-entropy switch: photoisomerizable stapled peptides for modulating p53/MDM2 interaction. Organic and Biomolecular Chemistry, 2020, 18, 5359-5369.	2.8	14
54	Engineering Archeal Surrogate Systems for the Development of Proteinâ€“Protein Interaction Inhibitors against Human RAD51. Journal of Molecular Biology, 2016, 428, 4589-4607.	4.2	13

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55	Development of a multipurpose scaffold for the display of peptide loops. Protein Engineering, Design and Selection, 2017, 30, 419-430.	2.1	12
56	Proposed Allosteric Inhibitors Bind to the ATP Site of CK2Î±. Journal of Medicinal Chemistry, 2020, 63, 12786-12798.	6.4	12
57	Improved RAD51 binders through motif shuffling based on the modularity of BRC repeats. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	12
58	Demonstration of the utility of DOS-derived fragment libraries for rapid hit derivatisation in a multidirectional fashion. Chemical Science, 2020, 11, 10792-10801.	7.4	11
59	Poxviruses and paramyxoviruses use a conserved mechanism of STAT1 antagonism to inhibit interferon signaling. Cell Host and Microbe, 2022, 30, 357-372.e11.	11.0	9
60	Anthraquinone derivatives as ADP-competitive inhibitors of liver pyruvate kinase. European Journal of Medicinal Chemistry, 2022, 234, 114270.	5.5	8
61	Genomic structure and transcript analysis of the Rapid Alkalinization Factor (RALF) gene family during host-pathogen crosstalk in Fragaria vesca and Fragaria x ananassa strawberry. PLoS ONE, 2020, 15, e0226448.	2.5	7
62	Unraveling the Mechanics of a Repeat-Protein Nanospring: From Folding of Individual Repeats to Fluctuations of the Superhelix. ACS Nano, 2022, 16, 3895-3905.	14.6	6
63	ATP halfâ€sites in RadA and RAD51 recombinases bind nucleotides. FEBS Open Bio, 2016, 6, 372-385.	2.3	5
64	The thrombospondin module 1 domain of the matricellular protein CCN3 shows an atypical disulfide pattern and incomplete CWR layers. Acta Crystallographica Section D: Structural Biology, 2020, 76, 124-134.	2.3	5
65	Embryonic stem cells are devoid of macropinocytosis, a trafficking pathway for activin A in differentiated cells. Journal of Cell Science, 2021, 134, .	2.0	4
66	Combined transcriptomic and phosphoproteomic analysis of BMP4 signaling in human embryonic stem cells. Stem Cell Research, 2021, 50, 102133.	0.7	3
67	The role of pro-domains in human growth factors and cytokines. Biochemical Society Transactions, 2021, 49, 1963-1973.	3.4	2
68	Divergent binding mode for a protozoan BRC repeat to RAD51. Biochemical Journal, 2022, 479, 1031-1043.	3.7	2
69	Supporting data on combined transcriptomic and phosphoproteomic analysis of BMP4 signaling in human embryonic stem cells. Data in Brief, 2021, 35, 106844.	1.0	1
70	Development of small cyclic peptides targeting the CK2Î±/Î² interface. Chemical Communications, 2022, , .	4.1	1
71	Comparing the Solution Conformation and Activinâ€binding of Follistatin Isoforms. FASEB Journal, 2018, 32, 659.5.	0.5	0
72	Title is missing!. , 2020, 15, e0226448.		0

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73	Title is missing!. , 2020, 15, e0226448.		0
74	Title is missing!. , 2020, 15, e0226448.		0
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