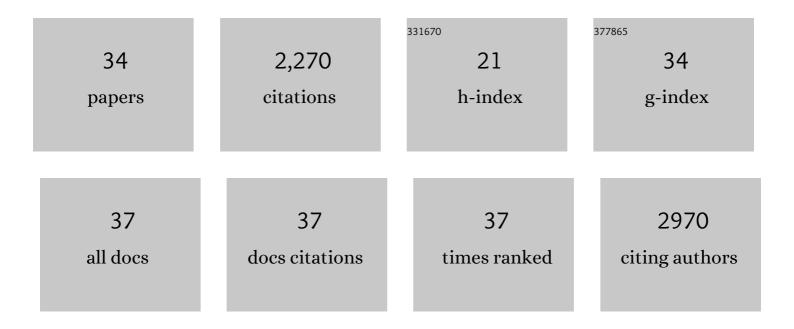
## Erik Martinez-Hackert

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5354747/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Fortilin interacts with TGF-β1 and prevents TGF-β receptor activation. Communications Biology, 2022, 5, 157.	4.4	5
2	Type II BMP and activin receptors BMPR2 and ACVR2A share a conserved mode of growth factor recognition. Journal of Biological Chemistry, 2022, 298, 102076.	3.4	4
3	Receptor binding competition: A paradigm for regulating TGF-β family action. Cytokine and Growth Factor Reviews, 2021, 57, 39-54.	7.2	49
4	Smad2/3 Activation Regulates Smad1/5/8 Signaling via a Negative Feedback Loop to Inhibit 3T3-L1 Adipogenesis. International Journal of Molecular Sciences, 2021, 22, 8472.	4.1	9
5	BMP-4 Extraction from Extracellular Matrix and Analysis of Heparin-Binding Properties. Molecular Biotechnology, 2021, , 1.	2.4	2
6	Activins as Dual Specificity TGF-β Family Molecules: SMAD-Activation via Activin- and BMP-Type 1 Receptors. Biomolecules, 2020, 10, 519.	4.0	29
7	Activin A forms a non-signaling complex with ACVR1 and type II Activin/BMP receptors via its finger 2 tip loop. ELife, 2020, 9, .	6.0	45
8	Transcriptomic profiling of the myeloma bone-lining niche reveals BMP signalling inhibition to improve bone disease. Nature Communications, 2019, 10, 4533.	12.8	46
9	High-Throughput, Biosensor-Based Approach to Examine Bone Morphogenetic Protein (BMP)–Receptor Interactions. Methods in Molecular Biology, 2019, 1891, 37-49.	0.9	4
10	Biochemical and Cellular Analysis Reveals Ligand Binding Specificities, a Molecular Basis for Ligand Recognition, and Membrane Association-dependent Activities of Cripto-1 and Cryptic. Journal of Biological Chemistry, 2017, 292, 4138-4151.	3.4	12
11	Structural basis for potency differences between GDF8 and GDF11. BMC Biology, 2017, 15, 19.	3.8	90
12	Bulk cell density and Wnt/TGFbeta signalling regulate mesendodermal patterning of human pluripotent stem cells. Nature Communications, 2016, 7, 13602.	12.8	105
13	Determination of half-maximal inhibitory concentration using biosensor-based protein interaction analysis. Analytical Biochemistry, 2016, 508, 97-103.	2.4	105
14	Transforming Growth Factor-β Family Ligands Can Function as Antagonists by Competing for Type II Receptor Binding. Journal of Biological Chemistry, 2016, 291, 10792-10804.	3.4	96
15	New Ligand Binding Function of Human Cerberus and Role of Proteolytic Processing in Regulating Ligand–Receptor Interactions and Antagonist Activity. Journal of Molecular Biology, 2016, 428, 590-602.	4.2	22
16	Human Cerberus Prevents Nodal-Receptor Binding, Inhibits Nodal Signaling, and Suppresses Nodal-Mediated Phenotypes. PLoS ONE, 2015, 10, e0114954.	2.5	28
17	Structural determinants of host specificity of complement Factor H recruitment by <i>Streptococcus pneumoniae</i> . Biochemical Journal, 2015, 465, 325-335.	3.7	15
18	Specificity and Structure of a High Affinity Activin Receptor-like Kinase 1 (ALK1) Signaling Complex. Journal of Biological Chemistry, 2012, 287, 27313-27325.	3.4	148

Erik Martinez-Hackert

#	Article	IF	CITATIONS
19	Structural Analysis of Protein Folding by the Long-Chain Archaeal Chaperone FKBP26. Journal of Molecular Biology, 2011, 407, 450-464.	4.2	9
20	Crystal structure of a potassium ion transporter, TrkH. Nature, 2011, 471, 336-340.	27.8	120
21	Characterization of the Ligand Binding Functionality of the Extracellular Domain of Activin Receptor Type IIB. Journal of Biological Chemistry, 2010, 285, 21037-21048.	3.4	123
22	Promiscuous Substrate Recognition in Folding and Assembly Activities of the Trigger Factor Chaperone. Cell, 2009, 138, 923-934.	28.9	140
23	How a T Cell Receptor-like Antibody Recognizes Major Histocompatibility Complex-bound Peptide. Journal of Biological Chemistry, 2008, 283, 29053-29059.	3.4	41
24	Structures of and interactions between domains of trigger factor fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 536-547.	2.5	18
25	Structural Basis for Degenerate Recognition of Natural HIV Peptide Variants by Cytotoxic Lymphocytes*. Journal of Biological Chemistry, 2006, 281, 20205-20212.	3.4	22
26	Crystal Structure of the Moloney Murine Leukemia Virus RNase H Domain. Journal of Virology, 2006, 80, 8379-8389.	3.4	56
27	Distinct Molecular Mechanisms Account for the Specificity of Two Different T-Cell Receptorsâ€. Biochemistry, 2003, 42, 4709-4716.	2.5	52
28	Orientation of OmpR monomers within an OmpR:DNA complex determined by DNA affinity cleaving 1 1Edited by K. Yamamoto. Journal of Molecular Biology, 1999, 285, 555-566.	4.2	49
29	Structural relationships in the OmpR family of winged-helix transcription factors 1 1Edited by M. Gottesman. Journal of Molecular Biology, 1997, 269, 301-312.	4.2	260
30	The DNA-binding domain of OmpR: crystal structures of a winged helix transcription factor. Structure, 1997, 5, 109-124.	3.3	237
31	Crystallization, Xâ€ray studies, and siteâ€directed cysteine mutagenesis of the DNAâ€binding domain of OmpR. Protein Science, 1996, 5, 1429-1433.	7.6	15
32	Purification, crystallization, and preliminary X-ray diffraction analyses of the bacterial chemotaxis receptor modifying enzymes. Proteins: Structure, Function and Bioinformatics, 1995, 21, 345-350.	2.6	11
33	Crystal Structure of the Catalytic Domain of the Chemotaxis Receptor Methylesterase, CheB. Journal of Molecular Biology, 1995, 250, 276-290.	4.2	70
34	Structure of the magnesium-bound form of CheY and mechanism of phosphoryl transfer in bacterial chemotaxis. Biochemistry, 1993, 32, 13375-13380.	2.5	229