

Gerd Schluckebier

List of Publications by Year in descending order

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27
papers

1,444
citations

430754

18
h-index

526166

27
g-index

27
all docs

27
docs citations

27
times ranked

1566
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Investigations of Full-Length Insulin Receptor Dynamics and Signalling. <i>Journal of Molecular Biology</i> , 2022, 434, 167458.	2.0	34
2	Exploring the complex map of insulin polymorphism: a novel crystalline form in the presence of <i>m</i> -cresol. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 366-374.	1.1	2
3	Cross-species reactive monoclonal antibodies against the extracellular domains of the insulin receptor and IGF1 receptor. <i>Journal of Immunological Methods</i> , 2019, 465, 20-26.	0.6	5
4	Structures of insect Imp-L2 suggest an alternative strategy for regulating the bioavailability of insulin-like hormones. <i>Nature Communications</i> , 2018, 9, 3860.	5.8	22
5	Structural insight into antibody-mediated antagonism of the Glucagon-like peptide-1 Receptor. <i>Scientific Reports</i> , 2016, 6, 26236.	1.6	24
6	Human insulin polymorphism upon ligand binding and pH variation: the case of 4-ethylresorcinol. <i>IUCr</i> , 2015, 2, 534-544.	1.0	19
7	Novel crystalline phase and first-order phase transitions of human insulin complexed with two distinct phenol derivatives. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 819-828.	2.5	17
8	SAXS-Guided Metadynamics. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 3491-3498.	2.3	37
9	The challenge of improved secretory production of active pharmaceutical ingredients in <i>Saccharomyces cerevisiae</i> : A case study on human insulin analogs. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2764-2774.	1.7	5
10	Ligand-Controlled Assembly of Hexamers, Dihexamers, and Linear Multihexamer Structures by the Engineered Acylated Insulin Degludec. <i>Biochemistry</i> , 2013, 52, 295-309.	1.2	72
11	High-resolution powder X-ray data reveal the T_6 hexameric form of bovine insulin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 978-990.	2.5	20
12	Structural studies of human insulin cocrystallized with phenol or resorcinol via powder diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1632-1641.	2.5	22
13	Structural and Biological Properties of the <i>Drosophila</i> Insulin-like Peptide 5 Show Evolutionary Conservation. <i>Journal of Biological Chemistry</i> , 2011, 286, 661-673.	1.6	61
14	Kinetic Evidence for the Sequential Association of Insulin Binding Sites 1 and 2 to the Insulin Receptor and the Influence of Receptor Isoform,. <i>Biochemistry</i> , 2010, 49, 6234-6246.	1.2	14
15	Crystal structure of Ultralente [®] A microcrystalline insulin suspension. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 1018-1027.	1.5	22
16	Successful cryocooling of protein microcrystalline samples for powder diffraction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s320-s321.	0.3	1
17	Binding mode of Thioflavin T in insulin amyloid fibrils. <i>Journal of Structural Biology</i> , 2007, 159, 483-497.	1.3	193
18	Crystallographic characterization of two novel crystal forms of human insulin induced by chaotropic agents and a shift in pH. <i>BMC Structural Biology</i> , 2007, 7, 83.	2.3	22

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19	Structural characterization of insulin NPH formulations. <i>European Journal of Pharmaceutical Sciences</i> , 2007, 30, 414-423.	1.9	37
20	Characterization of insulin microcrystals using powder diffraction and multivariate data analysis. <i>Journal of Applied Crystallography</i> , 2006, 39, 391-400.	1.9	37
21	The 2.2 Å... structure of the rRNA methyltransferase ErmC ² and its complexes with cofactor and cofactor analogs: implications for the reaction mechanism. <i>Journal of Molecular Biology</i> , 1999, 289, 277-291.	2.0	94
22	Crystal Structure of ErmC ¹ , an rRNA Methyltransferase Which Mediates Antibiotic Resistance in Bacteria ¹ . <i>Biochemistry</i> , 1998, 37, 7103-7112.	1.2	101
23	Differential binding of S-adenosylmethionine S-adenosylhomocysteine and Sinefungin to the adenine-specific DNA methyltransferase M. Taq I 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 1997, 265, 56-67.	2.0	113
24	A model for DNA binding and enzyme action derived from crystallographic studies of the TaqI N6-adenine-methyltransferase. <i>Gene</i> , 1995, 157, 131-134.	1.0	37
25	Universal Catalytic Domain Structure of AdoMet-dependent Methyltransferases. <i>Journal of Molecular Biology</i> , 1995, 247, 16-20.	2.0	246
26	X-ray crystallographic and calorimetric studies of the effects of the mutation Trp59 Tyr in ribonuclease T1. <i>FEBS Journal</i> , 1994, 220, 527-534.	0.2	14
27	Three-dimensional structure of the adenine-specific DNA methyltransferase M.Taq I in complex with the cofactor S-adenosylmethionine.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10957-10961.	3.3	173