Christian X Weichenberger

List of Publications by Year
in descending order

31 papers	**1,305** citations	623734 **14** h-index	454955 **30** g-index
33 all docs	**33** docs citations	**33** times ranked	**4166** citing authors

#	Article	IF	Citations
1	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. Pathogens and Global Health, 2022, 116, 128-136.	2.3	4
2	Transcriptomic and genomic studies classify NKL54 as a histone deacetylase inhibitor with indirect influence on MEF2-dependent transcription. Nucleic Acids Research, 2022, 50, 2566-2586.	14.5	12
3	Prevalence and determinants of serum antibodies to SARS-CoV-2 in the general population of the Gardena valley. Epidemiology and Infection, 2021, 149, e194.	2.1	8
4	Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. Biomolecules, 2021, 11, 1663.	4.0	5
5	Familial Aggregation of Endemic Congenital Hypothyroidism Syndrome in Congo (DR): Historical Data. Nutrients, 2020, 12, 3021.	4.1	1
6	ensembldb: an R package to create and use Ensembl-based annotation resources. Bioinformatics, 2019, 35, 3151-3153.	4.1	90
7	Comparative assessment of different familial aggregation methods in the context of large and unstructured pedigrees. Bioinformatics, 2019, 35, 69-76.	4.1	3
8	Detect, correct, retract: How to manage incorrect structural models. FEBS Journal, 2018, 285, 444-466.	4.7	49
9	HDAC Inhibition Improves the Sarcoendoplasmic Reticulum Ca2+-ATPase Activity in Cardiac Myocytes. International Journal of Molecular Sciences, 2018, 19, 419.	4.1	21
10	Inclusion of biological knowledge in a Bayesian shrinkage model for joint estimation of SNP effects. Genetic Epidemiology, 2017, 41, 320-331.	1.3	5
11	<i>Twilight</i>reloaded: the peptide experience. Acta Crystallographica Section D: Structural Biology, 2017, 73, 211-222.	2.3	9
12	Exploring Approaches for Detecting Protein Functional Similarity within an Orthology-based Framework. Scientific Reports, 2017, 7, 381.	3.3	6
13	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
14	FamAgg: an R package to evaluate familial aggregation of traits in large pedigrees. Bioinformatics, 2016, 32, 1583-1585.	4.1	17
15	Dintor: functional annotation of genomic and proteomic data. BMC Genomics, 2015, 16, 1081.	2.8	10
16	The solvent component of macromolecular crystals. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1023-1038.	2.5	47
17	FlyOde - a platform for community curation and interactive visualization of dynamic gene regulatory networks in Drosophila eye development. F1000Research, 2015, 4, 1484.	1.6	4
18	Ten years of probabilistic estimates of biocrystal solvent content: new insights<i>via</i>nonparametric kernel density estimate. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1579-1588.	2.5	57

#	Article	IF	Citations
19	SNP Prioritization Using a Bayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13
20	Importance of Different Types of Prior Knowledge in Selecting Genome‐Wide Findings for Follow‐Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14
21	Techniques, tools and best practices for ligand electron-density analysis and results from their application to deposited crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 150-167.	2.5	94
22	Visualizing ligand molecules in twilight electron density. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 195-200.	0.7	63
23	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	2.5	38
24	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
25	Structure of a Novel Winged-Helix Like Domain from Human NFRKB Protein. PLoS ONE, 2012, 7, e43761.	2.5	5
26	CARD8 and NLRP1 Undergo Autoproteolytic Processing through a ZU5-Like Domain. PLoS ONE, 2011, 6, e27396.	2.5	168
27	Detection of unrealistic molecular environments in protein structures based on expected electron densities. Journal of Biomolecular NMR, 2010, 47, 33-40.	2.8	7
28	Visualization of unfavorable interactions in protein folds. Bioinformatics, 2008, 24, 1206-1207.	4.1	8
29	NQ-Flipper: recognition and correction of erroneous asparagine and glutamine side-chain rotamers in protein structures. Nucleic Acids Research, 2007, 35, W403-W406.	14.5	57
30	Self-Consistent Assignment of Asparagine and Glutamine Amide Rotamers in Protein Crystal Structures. Structure, 2006, 14, 967-972.	3.3	25
31	NQ-Flipper: validation and correction of asparagine/glutamine amide rotamers in protein crystal structures. Bioinformatics, 2006, 22, 1397-1398.	4.1	30