## Johanna Hakanpää

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. Science, 2021, 372, 642-646.	12.6	240
2	Structure and function of the N-terminal domain of the yeast telomerase reverse transcriptase. Nucleic Acids Research, 2018, 46, 1525-1540.	14.5	19
3	Structural and functional insights into the unique CBS–CP12 fusion protein family in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7141-7146.	7.1	20
4	Novel non-β-lactam inhibitor of β-lactamase TEM-171 based on acylated phenoxyaniline. Biochimie, 2017, 132, 45-53.	2.6	26
5	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring forÂhigh- and low-energy phasing with variable beam focusing. Journal of Synchrotron Radiation, 2017, 24, 323-332.	2.4	155
6	Amphiphilic nanotubes in the crystal structure of a biosurfactant protein hydrophobin HFBII. Chemical Communications, 2011, 47, 9843.	4.1	6
7	Crystal structures of Trichoderma reesei β-galactosidase reveal conformational changes in the active site. Journal of Structural Biology, 2011, 174, 156-163.	2.8	47
8	Polysaccharides as Precipitants in Protein Crystallization for X-Ray Diffraction Studies. Crystal Growth and Design, 2011, 11, 1152-1158.	3.0	2
9	The Contribution of Polystyrene Nanospheres towards the Crystallization of Proteins. PLoS ONE, 2009, 4, e4198.	2.5	24
10	Crystallization and preliminary diffraction analysis of a β-galactosidase fromTrichoderma reesei. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 767-769.	0.7	3
11	Characterization and crystallization of a recombinant IgE Fab fragment in complex with the bovine β-lactoglobulin allergen. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 25-28.	0.7	13
12	Crystal Structures of Hydrophobin HFBII in the Presence of Detergent Implicate the Formation of Fibrils and Monolayer Films. Journal of Biological Chemistry, 2007, 282, 28733-28739.	3.4	50
13	Molecular Interactions between a Recombinant IgE Antibody and the Î <sup>2</sup> -Lactoglobulin Allergen. Structure, 2007, 15, 1413-1421.	3.3	125
14	Hydrophobin HFBII in detail: ultrahigh-resolution structure at 0.75â€Ã Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 356-367.	2.5	71
15	Two crystal structures of Trichoderma reesei hydrophobin HFBIThe structure of a protein amphiphile with and without detergent interaction. Protein Science, 2006, 15, 2129-2140.	7.6	158
16	Determination of thioxylo-oligosaccharide binding to family 11 xylanases using electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry and X-ray crystallography. FEBS Journal, 2005, 272, 2317-2333.	4.7	28
17	Crystallization and preliminary X-ray characterization ofTrichoderma reeseihydrophobin HFBII. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 163-165.	2.5	16
18	Atomic Resolution Structure of the HFBII Hydrophobin, a Self-assembling Amphiphile. Journal of Biological Chemistry, 2004, 279, 534-539.	3.4	205