

# Anu Koivula

## List of Publications by Year in descending order

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83  
papers

4,583  
citations

87888

38  
h-index

98798

67  
g-index

83  
all docs

83  
docs citations

83  
times ranked

4253  
citing authors

#	ARTICLE	IF	CITATIONS
1	Traffic Jams Reduce Hydrolytic Efficiency of Cellulase on Cellulose Surface. <i>Science</i> , 2011, 333, 1279-1282.	12.6	501
2	High Speed Atomic Force Microscopy Visualizes Processive Movement of <i>Trichoderma reesei</i> Cellobiohydrolase I on Crystalline Cellulose. <i>Journal of Biological Chemistry</i> , 2009, 284, 36186-36190.	3.4	259
3	Lignocellulosic ethanol: From science to industry. <i>Biomass and Bioenergy</i> , 2012, 46, 13-24.	5.7	213
4	Crystallographic evidence for substrate ring distortion and protein conformational changes during catalysis in cellobiohydrolase Cel16A from <i>Trichoderma reesei</i> . <i>Structure</i> , 1999, 7, 1035-1045.	3.3	164
5	Activity Studies and Crystal Structures of Catalytically Deficient Mutants of Cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Molecular Biology</i> , 1996, 264, 337-349.	4.2	162
6	Engineering the Exo-loop of <i>Trichoderma reesei</i> Cellobiohydrolase, Cel7A. A comparison with <i>Phanerochaete chrysosporium</i> Cel7D. <i>Journal of Molecular Biology</i> , 2003, 333, 817-829.	4.2	152
7	Crystal structure of a laccase from <i>Melanocarpus albomyces</i> with an intact trinuclear copper site. <i>Nature Structural Biology</i> , 2002, 9, 601-5.	9.7	151
8	High level secretion of cellobiohydrolases by <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2011, 4, 30.	6.2	140
9	The Active Site of Cellobiohydrolase Cel6A from <i>Trichoderma reesei</i> : The Roles of Aspartic Acids D221 and D175. <i>Journal of the American Chemical Society</i> , 2002, 124, 10015-10024.	13.7	133
10	Characterization of <i>Trichoderma reesei</i> cellobiohydrolase Cel7A secreted from <i>Pichia pastoris</i> using two different promoters. <i>Biotechnology and Bioengineering</i> , 2000, 69, 486-494.	3.3	123
11	Expression of <i>Talaromyces emersonii</i> cellobiohydrolase Cel7A in <i>Saccharomyces cerevisiae</i> and rational mutagenesis to improve its thermostability and activity. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 69-79.	2.1	118
12	Tryptophan 272: an essential determinant of crystalline cellulose degradation by <i>Trichoderma reesei</i> cellobiohydrolase Cel6A. <i>FEBS Letters</i> , 1998, 429, 341-346.	2.8	115
13	Cloning, expression, and characterization of novel thermostable family 7 cellobiohydrolases. <i>Biotechnology and Bioengineering</i> , 2008, 101, 515-528.	3.3	115
14	Kinetic and biochemical properties of high and low redox potential laccases from fungal and plant origin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 899-908.	2.3	101
15	Structure-Function Studies of a <i>Melanocarpus albomyces</i> Laccase Suggest a Pathway for Oxidation of Phenolic Compounds. <i>Journal of Molecular Biology</i> , 2009, 392, 895-909.	4.2	99
16	Production and applications of carbohydrate-derived sugar acids as generic biobased chemicals. <i>Critical Reviews in Biotechnology</i> , 2016, 36, 904-916.	9.0	84
17	Random mutagenesis used to probe the structure and function of <i>Bacillus stearothermophilus</i> alpha-amylase. <i>Protein Engineering, Design and Selection</i> , 1990, 3, 181-191.	2.1	79
18	The Tryptophan Residue at the Active Site Tunnel Entrance of <i>Trichoderma reesei</i> Cellobiohydrolase Cel7A Is Important for Initiation of Degradation of Crystalline Cellulose. <i>Journal of Biological Chemistry</i> , 2013, 288, 13503-13510.	3.4	77

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19	The active site of <i>Trichoderma reesei</i> cellobiohydrolase II: the role of tyrosine 169. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 691-699.	2.1	75
20	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for bioconversion of d-xylose to d-xylonate. <i>Metabolic Engineering</i> , 2012, 14, 427-436.	7.0	74
21	Essential role of the C-terminus in <i>Melanocarpus albomyces</i> laccase for enzyme production, catalytic properties and structure. <i>FEBS Journal</i> , 2009, 276, 6285-6300.	4.7	73
22	A Glucose/Oxygen Enzymatic Fuel Cell based on Gold Nanoparticles modified Graphene Screen-Printed Electrode. Proof-of-Concept in Human Saliva. <i>Sensors and Actuators B: Chemical</i> , 2018, 256, 921-930.	7.8	72
23	Crystal structure of an ascomycete fungal laccase from <i>Thielavia arenaria</i> – common structural features of ascomycete laccases. <i>FEBS Journal</i> , 2011, 278, 2283-2295.	4.7	71
24	Development of a printable laccase-based biocathode for fuel cell applications. <i>Enzyme and Microbial Technology</i> , 2008, 43, 93-102.	3.2	68
25	Improving the thermostability and activity of <i>Melanocarpus albomyces</i> cellobiohydrolase Cel7B. <i>Applied Microbiology and Biotechnology</i> , 2009, 83, 261-272.	3.6	61
26	The relationship between thermal stability and pH optimum studied with wild-type and mutant <i>Trichoderma reesei</i> cellobiohydrolase Cel7A. <i>FEBS Journal</i> , 2003, 270, 841-848.	0.2	60
27	Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19-30.	3.7	59
28	Cello-Oligosaccharide Hydrolysis by Cellobiohydrolase II from <i>Trichoderma reesei</i> . Association and Rate Constants Derived from an Analysis of Progress Curves. <i>FEBS Journal</i> , 1996, 240, 584-591.	0.2	58
29	Single-molecule Imaging Analysis of Elementary Reaction Steps of <i>Trichoderma reesei</i> Cellobiohydrolase I (Cel7A) Hydrolyzing Crystalline Cellulose II <sub>±</sub> and III. <i>Journal of Biological Chemistry</i> , 2014, 289, 14056-14065.	3.4	50
30	A crystallographic and spectroscopic study on the effect of X-ray radiation on the crystal structure of <i>Melanocarpus albomyces</i> laccase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 929-934.	2.1	49
31	Crystal structures of <i>Melanocarpus albomyces</i> cellobiohydrolase Cel7B in complex with cellooligomers show high flexibility in the substrate binding. <i>Protein Science</i> , 2008, 17, 1383-1394.	7.6	49
32	Engineering chitinases for the synthesis of chitin oligosaccharides: Catalytic amino acid mutations convert the GH-18 family glycoside hydrolases into transglycosylases. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2012, 74, 89-96.	1.8	46
33	Effect of temperature on lignin-derived inhibition studied with three structurally different cellobiohydrolases. <i>Bioresource Technology</i> , 2013, 146, 118-125.	9.6	46
34	Identification in <i>Agrobacterium tumefaciens</i> of the d-galacturonic acid dehydrogenase gene. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 901-909.	3.6	42
35	Heterologous expression of <i>Melanocarpus albomyces</i> cellobiohydrolase Cel7B, and random mutagenesis to improve its thermostability. <i>Enzyme and Microbial Technology</i> , 2007, 41, 234-243.	3.2	41
36	Electrochemical evaluation of electron transfer kinetics of high and low redox potential laccases on gold electrode surface. <i>Electrochimica Acta</i> , 2010, 56, 817-827.	5.2	41

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37	Probing pH-Dependent Functional Elements in Proteins: A Modification of Carboxylic Acid Pairs in <i>Trichoderma reesei</i> Cellobiohydrolase Cel6A. <i>Biochemistry</i> , 2003, 42, 10095-10103.	2.5	40
38	A new method for random mutagenesis of complete genes: enzymatic generation of mutant libraries in vitro. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 63-68.	2.1	39
39	A comparative study of two retaining enzymes of <i>Trichoderma reesei</i> : transglycosylation of oligosaccharides catalysed by the cellobiohydrolase I, Cel7A, and the $\beta$ -mannanase, Man5A. <i>FEBS Letters</i> , 1999, 443, 149-153.	2.8	38
40	Engineering chimeric thermostable GH7 cellobiohydrolases in <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2991-3001.	3.6	35
41	Toward understanding of carbohydrate binding and substrate specificity of a glycosyl hydrolase 18 family (GH-18) chitinase from <i>Trichoderma harzianum</i> . <i>Glycobiology</i> , 2009, 19, 1116-1126.	2.5	33
42	Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19.	3.7	29
43	Characterization of a novel <i>Agrobacterium tumefaciens</i> Galactarolactone Cycloisomerase Enzyme for Direct Conversion of d-Galactarolactone to 3-Deoxy-2-keto-l-threo-hexarate. <i>Journal of Biological Chemistry</i> , 2012, 287, 17662-17671.	3.4	28
44	Characterization and mutagenesis of two novel iron-sulphur cluster pentonate dehydratases. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7549-7563.	3.6	27
45	Differential recognition of animal type 4-galactosylated and 3-fucosylated chito-oligosaccharides by two family 18 chitinases from <i>Trichoderma harzianum</i> . <i>Glycobiology</i> , 2004, 14, 1303-1313.	2.5	26
46	The catalytic amino-acid residues in the active site of cellobiohydrolase 1 are involved in chiral recognition. <i>Journal of Biotechnology</i> , 1997, 57, 115-125.	3.8	25
47	Crystal Structure of Uronate Dehydrogenase from <i>Agrobacterium tumefaciens</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 27294-27300.	3.4	25
48	The Crystal Structure of a Bacterial l-Arabinonate Dehydratase Contains a [2Fe-2S] Cluster. <i>ACS Chemical Biology</i> , 2017, 12, 1919-1927.	3.4	25
49	Characterization of the wheat germ agglutinin binding to self-assembled monolayers of neoglycoconjugates by AFM and SPR. <i>Glycobiology</i> , 2009, 19, 633-643.	2.5	24
50	Visualization of Cellobiohydrolase I from <i>Trichoderma reesei</i> Moving on Crystalline Cellulose Using High-Speed Atomic Force Microscopy. <i>Methods in Enzymology</i> , 2012, 510, 169-182.	1.0	24
51	Expression of Two Novel $\beta$ -Glucosidases from <i>Chaetomium atrobrunneum</i> in <i>Trichoderma reesei</i> and Characterization of the Heterologous Protein Products. <i>Molecular Biotechnology</i> , 2016, 58, 821-831.	2.4	24
52	Heterologous expression and site-directed mutagenesis studies of two <i>Trichoderma harzianum</i> chitinases, Chit33 and Chit42, in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2007, 51, 216-226.	1.3	21
53	The crystal structure of D-xylonate dehydratase reveals functional features of enzymes from the llv/ED dehydratase family. <i>Scientific Reports</i> , 2018, 8, 865.	3.3	21
54	Substrate specificity of 2-deoxy-D-ribose 5-phosphate aldolase (DERA) assessed by different protein engineering and machine learning methods. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 10515-10529.	3.6	21

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55	Progress-Curve Analysis Shows that Glucose Inhibits the Cellotriose Hydrolysis Catalysed by Cellobiohydrolase II from <i>Trichoderma reesei</i> . <i>FEBS Journal</i> , 1995, 231, 250-258.	0.2	19
56	Cloning of novel bacterial xylanases from lignocellulose-enriched compost metagenomic libraries. <i>AMB Express</i> , 2019, 9, 124.	3.0	18
57	Hydrolyses of $\beta$ - and $\beta$ -cellobiosyl fluorides by Cel6A (cellobiohydrolase II) of <i>Trichoderma reesei</i> and <i>Humicola insolens</i> . <i>Biochemical Journal</i> , 2000, 345, 315-319.	3.7	17
58	Crystal Structures of an Enantioselective Fab-fragment in Free and Complex Forms. <i>Journal of Molecular Biology</i> , 2006, 357, 471-480.	4.2	17
59	A novel aldose-aldose oxidoreductase for co-production of D-xylonate and xylitol from D-xylose with <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9439-9447.	3.6	17
60	Immunoaffinity Chromatographic Purification of Cellobiohydrolase II Mutants from Recombinant <i>Trichoderma reesei</i> Strains Devoid of Major Endoglucanase Genes. <i>Protein Expression and Purification</i> , 1996, 8, 391-400.	1.3	16
61	Effect of oxidation on cellulose and water structure: a molecular dynamics simulation study. <i>Cellulose</i> , 2021, 28, 3917-3933.	4.9	16
62	l-Arabinose/d-galactose 1-dehydrogenase of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> characterised and applied for bioconversion of l-arabinose to l-arabonate with <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9653-9665.	3.6	15
63	In vitro reconstitution and characterisation of the oxidative d-xylose pathway for production of organic acids and alcohols. <i>AMB Express</i> , 2019, 9, 48.	3.0	15
64	Structure and function of <i>Caulobacter crescentus</i> aldose-aldose oxidoreductase. <i>Biochemical Journal</i> , 2015, 472, 297-307.	3.7	10
65	Development of a High-Throughput Format for Solid-Phase Extraction of Enantiomers Using an Immunosorbent in 384-Well Plates. <i>Analytical Chemistry</i> , 2005, 77, 3038-3044.	6.5	9
66	Structure and Function of a Decarboxylating <i>Agrobacterium tumefaciens</i> Keto-deoxy- <i>d</i> -galactarate Dehydratase. <i>Biochemistry</i> , 2014, 53, 8052-8060.	2.5	9
67	Hydrolyses of $\beta$ - and $\beta$ -cellobiosyl fluorides by Cel6A (cellobiohydrolase II) of <i>Trichoderma reesei</i> and <i>Humicola insolens</i> . <i>Biochemical Journal</i> , 2000, 345, 315.	3.7	8
68	Modes of action of two <i>Trichoderma reesei</i> cellobiohydrolases. <i>Progress in Biotechnology</i> , 1995, 10, 211-224.	0.2	7
69	Current state of and need for enzyme engineering of 2-deoxy-D-ribose 5-phosphate aldolases and its impact. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 6215-6228.	3.6	7
70	Oxidative modification of cellulosic fibres by lytic polysaccharide monooxygenase AA9A from <i>Trichoderma reesei</i> . <i>Cellulose</i> , 2022, 29, 6021-6038.	4.9	7
71	Bioconjugation with Aminoalkylhydrazine for Efficient Mass Spectrometry-Based Detection of Small Carbonyl Compounds. <i>ACS Omega</i> , 2019, 4, 13447-13453.	3.5	6
72	Preliminary X-ray analysis of cellobiohydrolase Cel7B from <i>Melanocarpus albomyces</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 754-757.	0.7	5

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73	Mutation of fungal endoglucanases into glycosynthases and characterization of their acceptor substrate specificity. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2007, 44, 106-116.	1.8	5
74	Performance of a Printable Enzymatic Fuel Cell: Study on Mediated ThL Laccase Cathode. <i>ECS Transactions</i> , 2009, 25, 1-10.	0.5	5
75	Purification, crystallization and preliminary X-ray diffraction analysis of a novel keto-deoxy-D-galactarate (KDG) dehydratase from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 49-52.	0.8	4
76	Characterization of a unique <i>Caulobacter crescentus</i> aldose-aldose oxidoreductase having dual activities. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 673-685.	3.6	4
77	Xylonolactonase from <i>Caulobacter crescentus</i> Is a Mononuclear Nonheme Iron Hydrolase. <i>Biochemistry</i> , 2021, 60, 3046-3049.	2.5	4
78	Three-dimensional structure of xylonolactonase from <i>Caulobacter crescentus</i> : A mononuclear iron enzyme of the 6-bladed propeller hydrolase family. <i>Protein Science</i> , 2022, 31, 371-383.	7.6	4
79	Inhibitory effect of lignin on the hydrolysis of xylan by thermophilic and thermolabile GH11 xylanases. , 2022, 15, 49.		4
80	Progress-Curve Analysis Shows that Glucose Inhibits the Cellotriose Hydrolysis Catalysed by Cellobiohydrolase II from <i>Trichoderma Reesei</i> . <i>FEBS Journal</i> , 1995, 231, 250-258.	0.2	3
81	Crystallization and X-ray diffraction analysis of an L-arabinonate dehydratase from <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> and a D-xylonate dehydratase from <i>Caulobacter crescentus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> . 2016, 72, 604-608.	0.8	3
82	Role of Tryptophan 38 in Loading Substrate Chain into the Active-site Tunnel of Cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Applied Glycoscience</i> (1999), 2021, 68, 19-29.	0.7	2
83	Polysaccharide-Acting Enzymes and Their Applications. , 2012, , 375-392.		1