

# Leila Lo Leggio

## List of Publications by Year in descending order

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108  
papers

6,942  
citations

126907

33  
h-index

60623

81  
g-index

109  
all docs

109  
docs citations

109  
times ranked

6967  
citing authors

#	ARTICLE	IF	CITATIONS
1	Flexible linker modulates the binding affinity of the TP901-1 CI phage repressor to DNA. <i>FEBS Journal</i> , 2022, 289, 1135-1148.	4.7	3
2	Protonation State of an Important Histidine from High Resolution Structures of Lytic Polysaccharide Monoxygenases. <i>Biomolecules</i> , 2022, 12, 194.	4.0	12
3	Mechanism and biomass association of glucuronoyl esterase: an $\hat{\pm}/\hat{l}^2$ hydrolase with potential in biomass conversion. <i>Nature Communications</i> , 2022, 13, 1449.	12.8	15
4	Identification of the molecular determinants driving the substrate specificity of fungal lytic polysaccharide monoxygenases (LPMOs). <i>Journal of Biological Chemistry</i> , 2021, 296, 100086.	3.4	19
5	Estimating the accuracy of calculated electron paramagnetic resonance hyperfine couplings for a lytic polysaccharide monoxygenase. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 555-567.	4.1	11
6	Calmodulin complexes with brain and muscle creatine kinase peptides. <i>Current Research in Structural Biology</i> , 2021, 3, 121-132.	2.2	5
7	Lytic polysaccharide monoxygenases and other histidine-brace copper proteins: structure, oxygen activation and biotechnological applications. <i>Biochemical Society Transactions</i> , 2021, 49, 531-540.	3.4	35
8	Guest-protein incorporation into solvent channels of a protein host crystal (hostal). <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 471-485.	2.3	1
9	Probing the determinants of the transglycosylation/hydrolysis partition in a retaining $\hat{\pm}$ -l-arabinofuranosidase. <i>New Biotechnology</i> , 2021, 62, 68-78.	4.4	12
10	Copper binding and reactivity at the histidine brace motif: insights from mutational analysis of the <i>Pseudomonas fluorescens</i> copper chaperone CopC. <i>FEBS Letters</i> , 2021, 595, 1708-1720.	2.8	9
11	Structural and Functional Analysis of a Multimodular Hyperthermostable Xylanase-Glucuronoyl Esterase from <i>Caldicellulosiruptor kristjansonii</i> . <i>Biochemistry</i> , 2021, 60, 2206-2220.	2.5	7
12	Crystal structures of Val58Ile tryptophan repressor in a domain-swapped array in the presence and absence of L-tryptophan. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 215-225.	0.8	0
13	Inhibition of lytic polysaccharide monoxygenase by natural plant extracts. <i>New Phytologist</i> , 2021, 232, 1337-1349.	7.3	12
14	Engineering the substrate binding site of the hyperthermostable archaeal endo- $\hat{2}$ -1,4-galactanase from <i>Ignisphaera aggregans</i> . <i>Biotechnology for Biofuels</i> , 2021, 14, 183.	6.2	6
15	Characterization of the genetic switch from phage $\hat{13}$ important for <i>Staphylococcus aureus</i> colonization in humans. <i>MicrobiologyOpen</i> , 2021, 10, e1245.	3.0	2
16	Scission of Glucosidic Bonds by a <i>Lentinus similis</i> Lytic Polysaccharide Monoxygenases Is Strictly Dependent on H <sub>2</sub> O while the Oxidation of Saccharide Products Depends on O <sub>2</sub> . <i>ACS Catalysis</i> , 2021, 11, 13848-13859.	11.2	17
17	A fungal family of lytic polysaccharide monoxygenase-like copper proteins. <i>Nature Chemical Biology</i> , 2020, 16, 345-350.	8.0	63
18	Biochemical evidence of both copper chelation and oxygenase activity at the histidine brace. <i>Scientific Reports</i> , 2020, 10, 16369.	3.3	27

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19	Repression of the lysogenic PR promoter in bacteriophage TP901-1 through binding of a CI-MOR complex to a composite OM-OR operator. <i>Scientific Reports</i> , 2020, 10, 8659.	3.3	6
20	Revealing the mechanism of repressor inactivation during switching of a temperate bacteriophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20576-20585.	7.1	6
21	Oligosaccharide Binding and Thermostability of Two Related AA9 Lytic Polysaccharide Monoxygenases. <i>Biochemistry</i> , 2020, 59, 3347-3358.	2.5	17
22	A lytic polysaccharide monoxygenase-like protein functions in fungal copper import and meningitis. <i>Nature Chemical Biology</i> , 2020, 16, 337-344.	8.0	61
23	An 1,4- $\alpha$ -Glucosyltransferase Defines a New Maltodextrin Catabolism Scheme in <i>Lactobacillus acidophilus</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	8
24	Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis. <i>Science Advances</i> , 2019, 5, eaaw7696.	10.3	120
25	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monoxygenases. <i>Journal of Biological Chemistry</i> , 2019, 294, 17117-17130.	3.4	30
26	Structure of <i>Aspergillus aculeatus</i> $\beta$ -1,4-galactanase in complex with galactobiose. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 399-404.	0.8	6
27	Substrate preference of an ABC importer corresponds to selective growth on $\beta$ -(1,6)-galactosides in <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 11701-11711.	3.4	21
28	Structure-function analyses reveal that a glucuronoyl esterase from <i>Teredinibacter turnerae</i> interacts with carbohydrates and aromatic compounds. <i>Journal of Biological Chemistry</i> , 2019, 294, 6635-6644.	3.4	21
29	Further structural studies of the lytic polysaccharide monoxygenase <i>Ao</i> AA13 belonging to the starch-active AA13 family. <i>Amylase</i> , 2019, 3, 41-54.	1.6	4
30	Structural and biochemical studies of the glucuronoyl esterase OtCE15A illuminate its interaction with lignocellulosic components. <i>Journal of Biological Chemistry</i> , 2019, 294, 19978-19987.	3.4	17
31	Structure and Dynamics of a Promiscuous Xanthan Lyase from <i>Paenibacillus nanensis</i> and the Design of Variants with Increased Stability and Activity. <i>Cell Chemical Biology</i> , 2019, 26, 191-202.e6.	5.2	13
32	Structure of a hyperthermostable carbonic anhydrase identified from an active hydrothermal vent chimney. <i>Enzyme and Microbial Technology</i> , 2018, 114, 48-54.	3.2	14
33	Structural basis of the bacteriophage <i>TP</i> $\lambda$ CI repressor dimerization and interaction with <i>DNA</i> . <i>FEBS Letters</i> , 2018, 592, 1738-1750.	2.8	5
34	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
35	Recent insights into lytic polysaccharide monoxygenases (LPMOs). <i>Biochemical Society Transactions</i> , 2018, 46, 1431-1447.	3.4	82
36	Structure of a lytic polysaccharide monoxygenase from <i>Aspergillus fumigatus</i> and an engineered thermostable variant. <i>Carbohydrate Research</i> , 2018, 469, 55-59.	2.3	35

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37	Biochemical and structural features of diverse bacterial glucuronoyl esterases facilitating recalcitrant biomass conversion. <i>Biotechnology for Biofuels</i> , 2018, 11, 213.	6.2	35
38	NCAM2 Fibronectin type-III domains form a rigid structure that binds and activates the Fibroblast Growth Factor Receptor. <i>Scientific Reports</i> , 2018, 8, 8957.	3.3	16
39	Learning from oligosaccharide soaks of crystals of an AA13 lytic polysaccharide monooxygenase: crystal packing, ligand binding and active-site disorder. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 64-76.	2.3	16
40	Unliganded and substrate bound structures of the cellooligosaccharide active lytic polysaccharide monooxygenase LsAA9A at low pH. <i>Carbohydrate Research</i> , 2017, 448, 187-190.	2.3	25
41	Discovery of $\beta$ -l-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. <i>Journal of Biological Chemistry</i> , 2017, 292, 21092-21101.	3.4	8
42	Structural and electronic determinants of lytic polysaccharide monooxygenase reactivity on polysaccharide substrates. <i>Nature Communications</i> , 2017, 8, 1064.	12.8	134
43	Expression, refolding and spectroscopic characterization of fibronectin type III (FnIII)-homology domains derived from human fibronectin leucine rich transmembrane protein (FLRT)-1, -2, and -3. <i>PeerJ</i> , 2017, 5, e3550.	2.0	3
44	Structural characterization of the thermostable <i>Bradyrhizobium japonicum</i> sorbitol dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 846-852.	0.8	7
45	Structural and dynamics studies of a truncated variant of CI repressor from bacteriophage TP901-1. <i>Scientific Reports</i> , 2016, 6, 29574.	3.3	13
46	Lytic polysaccharide monooxygenases: a crystallographer's view on a new class of biomass-degrading enzymes. <i>IUCr</i> , 2016, 3, 448-467.	2.2	84
47	The molecular basis of polysaccharide cleavage by lytic polysaccharide monooxygenases. <i>Nature Chemical Biology</i> , 2016, 12, 298-303.	8.0	264
48	NAC Transcription Factors: From Structure to Function in Stress-Associated Networks. , 2016, , 199-212.		13
49	Structure of dimeric, recombinant <i>Sulfolobus solfataricus</i> phosphoribosyl diphosphate synthase: a bent dimer defining the adenine specificity of the substrate ATP. <i>Extremophiles</i> , 2015, 19, 407-415.	2.3	3
50	Structure and boosting activity of a starch-degrading lytic polysaccharide monooxygenase. <i>Nature Communications</i> , 2015, 6, 5961.	12.8	254
51	Effect of mutations on the thermostability of <i>Aspergillus aculeatus</i> $\beta$ -1,4-galactanase. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 256-264.	4.1	14
52	A $\beta$ -galactosidase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B-04 gives insight into substrate specificities of $\beta$ -galactoside catabolism within <i>Bifidobacterium</i> . <i>Molecular Microbiology</i> , 2014, 94, 1024-1040.	2.5	35
53	Purification, crystal structure determination and functional characterization of type III antifreeze proteins from the European eelpout <i>Zoarces viviparus</i> . <i>Cryobiology</i> , 2014, 69, 163-168.	0.7	15
54	An l-glucitol oxidizing dehydrogenase from <i>Bradyrhizobium japonicum</i> USDA 110 for production of d-sorbose with enzymatic or electrochemical cofactor regeneration. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3023-3032.	3.6	9

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55	Binding of the N-Terminal Domain of the Lactococcal Bacteriophage TP901-1 CI Repressor to Its Target DNA: A Crystallography, Small Angle Scattering, and Nuclear Magnetic Resonance Study. <i>Biochemistry</i> , 2013, 52, 6892-6904.	2.5	12
56	Recent insight into oligosaccharide uptake and metabolism in probiotic bacteria. <i>Biocatalysis and Biotransformation</i> , 2013, 31, 226-235.	2.0	23
57	Crystallization and preliminary crystallographic analysis of an <i>Escherichia coli</i> -selected mutant of the nuclease domain of the metallo-nuclease colicin E7. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 551-554.	0.7	2
58	A Snapshot into the Metabolism of Isomalto-oligosaccharides in Probiotic Bacteria. <i>Journal of Applied Glycoscience</i> (1999), 2013, 60, 95-100.	0.7	5
59	DNA binding by the plant-specific NAC transcription factors in crystal and solution: a firm link to WRKY and GCM transcription factors. <i>Biochemical Journal</i> , 2012, 444, 395-404.	3.7	77
60	Enzymology and Structure of the GH13_31 Glucan 1,6- $\alpha$ -Glucosidase That Confers Isomaltooligosaccharide Utilization in the Probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Bacteriology</i> , 2012, 194, 4249-4259.	2.2	69
61	A STRUCTURAL OVERVIEW OF GH61 PROTEINS – FUNGAL CELLULOSE DEGRADING POLYSACCHARIDE MONOOXYGENASES. <i>Computational and Structural Biotechnology Journal</i> , 2012, 2, e201209019.	4.1	37
62	Raffinose family oligosaccharide utilisation by probiotic bacteria: insight into substrate recognition, molecular architecture and diversity of GH36 $\beta$ -galactosidases. <i>Biocatalysis and Biotransformation</i> , 2012, 30, 316-325.	2.0	15
63	Structure-based engineering of glucose specificity in a family 10 xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>Process Biochemistry</i> , 2012, 47, 358-365.	3.7	12
64	S3-5 The utilization routes of iso maltooligosaccharides by probiotics : an enzymatic and genetic overview. <i>Bulletin of Applied Glycoscience</i> , 2012, 2, B59.	0.0	0
65	Insights into the oxidative degradation of cellulose by a copper metalloenzyme that exploits biomass components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15079-15084.	7.1	861
66	Crystal Structure of $\beta$ -Galactosidase from <i>Lactobacillus acidophilus</i> NCFM: Insight into Tetramer Formation and Substrate Binding. <i>Journal of Molecular Biology</i> , 2011, 412, 466-480.	4.2	63
67	Structure of a dimeric fungal $\beta$ -type carbonic anhydrase. <i>FEBS Letters</i> , 2011, 585, 1042-1048.	2.8	35
68	Activity of three $\beta$ -1,4-galactanases on small chromogenic substrates. <i>Carbohydrate Research</i> , 2011, 346, 2028-2033.	2.3	14
69	Rational Engineering of Mannosyl Binding in the Distal Glycone Subsites of <i>Cellulomonas fimi</i> Endo- $\beta$ -1,4-mannanase: Mannosyl Binding Promoted at Subsite $\beta$ 2 and Demoted at Subsite $\beta$ 3. <i>Biochemistry</i> , 2010, 49, 4884-4896.	2.5	34
70	Structural and Biochemical Studies Elucidate the Mechanism of Rhamnogalacturonan Lyase from <i>Aspergillus aculeatus</i> . <i>Journal of Molecular Biology</i> , 2010, 404, 100-111.	4.2	26
71	Stimulation of Lignocellulosic Biomass Hydrolysis by Proteins of Glycoside Hydrolase Family 61: Structure and Function of a Large, Enigmatic Family. <i>Biochemistry</i> , 2010, 49, 3305-3316.	2.5	679
72	Investigating the binding of $\beta$ -1,4-galactan to <i>Bacillus licheniformis</i> $\beta$ -1,4-galactanase by crystallography and computational modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 977-989.	2.6	17

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73	Crystal Structures of <i>A. acidocaldarius</i> Endoglucanase Cel9A in Complex with Cello-Oligosaccharides: Strong $\alpha$ 1 and $\alpha$ 2 Subsites Mimic Cellobiohydrolase Activity. <i>Journal of Molecular Biology</i> , 2009, 394, 61-70.	4.2	26
74	Short strong hydrogen bonds in proteins: a case study of rhamnogalacturonan acetyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 851-863.	2.5	46
75	Identification of Quaternary Structure and Functional Domains of the CI Repressor from Bacteriophage TP901-1. <i>Journal of Molecular Biology</i> , 2008, 376, 983-996.	4.2	19
76	Kinetics and stereochemistry of the <i>Cellulomonas fimi</i> $\alpha$ -mannanase studied using $^1\text{H-NMR}$ . <i>Biocatalysis and Biotransformation</i> , 2008, 26, 86-95.	2.0	10
77	$\alpha$ -Amylase from mung beans ( <i>Vigna radiata</i> ) – Correlation of biochemical properties and tertiary structure by homology modelling. <i>Phytochemistry</i> , 2007, 68, 1623-1631.	2.9	39
78	Structure of the <i>Sulfolobus solfataricus</i> $\alpha$ -Glucosidase: Implications for Domain Conservation and Substrate Recognition in GH31. <i>Journal of Molecular Biology</i> , 2006, 358, 1106-1124.	4.2	126
79	Mapping of an Internal Protease Cleavage Site in the Ssy5p Component of the Amino Acid Sensor of <i>Saccharomyces cerevisiae</i> and Functional Characterization of the Resulting Pro- and Protease Domains by Gain-of-Function Genetics. <i>Eukaryotic Cell</i> , 2006, 5, 601-608.	3.4	24
80	Characterization of different crystal forms of the $\alpha$ -glucosidase MalA from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1039-1042.	0.7	6
81	DNA-binding specificity and molecular functions of NAC transcription factors. <i>Plant Science</i> , 2005, 169, 785-797.	3.6	171
82	NAC transcription factors: structurally distinct, functionally diverse. <i>Trends in Plant Science</i> , 2005, 10, 79-87.	8.8	1,214
83	The Structure and Characterization of a Modular Endo- $\alpha$ -1,4-mannanase from <i>Cellulomonas fimi</i> . <i>Biochemistry</i> , 2005, 44, 12700-12708.	2.5	63
84	Structure of the conserved domain of ANAC, a member of the NAC family of transcription factors. <i>EMBO Reports</i> , 2004, 5, 297-303.	4.5	388
85	Preliminary crystallographic analysis of the NAC domain of ANAC, a member of the plant-specific NAC transcription factor family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 112-115.	2.5	28
86	The Structure of Endo- $\alpha$ -1,4-galactanase from <i>Bacillus licheniformis</i> in Complex with Two Oligosaccharide Products. <i>Journal of Molecular Biology</i> , 2004, 341, 107-117.	4.2	28
87	Crystallization and preliminary X-ray analysis of <i>Alicyclobacillus acidocaldarius</i> endoglucanase CelA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 139-141.	2.5	9
88	The Structure and Specificity of <i>Escherichia coli</i> Maltose Acetyltransferase Give New Insight into the LacA Family of Acyltransferases. <i>Biochemistry</i> , 2003, 42, 5225-5235.	2.5	33
89	Structure of two fungal $\alpha$ -1,4-galactanases: Searching for the basis for temperature and pH optimum. <i>Protein Science</i> , 2003, 12, 1195-1204.	7.6	41
90	<i>Lactococcus lactis</i> Dihydroorotate Dehydrogenase A Mutants Reveal Important Facets of the Enzymatic Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 28812-28822.	3.4	28

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91	Aspergillus aculeatus $\beta$ -1,4-Galactanase: Substrate Recognition and Relations to Other Glycoside Hydrolases in Clan GH-A. Biochemistry, 2002, 41, 15135-15143.	2.5	37
92	The 1.62 Å... structure ofThermoascus aurantiacusendoglucanase: completing the structural picture of subfamilies in glycoside hydrolase family 5. FEBS Letters, 2002, 523, 103-108.	2.8	73
93	Gene cloning, sequencing, and characterization of a family 9 endoglucanase (CelA) with an unusual pattern of activity from the thermoacidophile Alicyclobacillus acidocaldarius ATCC27009. Applied Microbiology and Biotechnology, 2002, 60, 428-436.	3.6	63
94	Crystallization and preliminary X-ray characterization of a thermostable pectate lyase fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 709-711.	2.5	4
95	Substrate specificity and subsite mobility inT. aurantiacusxylanase 10A. FEBS Letters, 2001, 509, 303-308.	2.8	51
96	Anisotropic refinement of the structure ofThermoascus aurantiacusxylanase I. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 385-392.	2.5	5
97	Crystallization and preliminary X-ray analysis of maltose O-acetyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1915-1918.	2.5	4
98	X-ray crystallographic study of xylopentaose binding toPseudomonas fluorescens xylanase A. Proteins: Structure, Function and Bioinformatics, 2000, 41, 362-373.	2.6	28
99	Characterization and crystallization of an active N-terminally truncated form of the Escherichia coli glycogen branching enzyme. FEBS Journal, 2000, 267, 2150-2155.	0.2	26
100	Xylanase-oligosaccharide interactions studied by a competitive enzyme assay. Enzyme and Microbial Technology, 1999, 25, 701-709.	3.2	18
101	High resolution structure and sequence ofT. aurantiacus Xylanase I: Implications for the evolution of thermostability in family 10 xylanases and enzymes with $\beta$ -barrel architecture. Proteins: Structure, Function and Bioinformatics, 1999, 36, 295-306.	2.6	75
102	High resolution structure and sequence of T. aurantiacus xylanase I: implications for the evolution of thermostability in family 10 xylanases and enzymes with (beta)alpha-barrel architecture. Proteins: Structure, Function and Bioinformatics, 1999, 36, 295-306.	2.6	24
103	Superfamilies: the 4/7 superfamily of $\beta$ -barrel glycosidases and the right-handed parallel $\beta$ -helix superfamily. Biochemical Society Transactions, 1998, 26, 190-197.	3.4	12
104	Crystallization and preliminary X-ray analysis of the major endoglucanase fromThermoascus aurantiacus. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 599-604.	2.5	11
105	Inhibition of sperm-zona binding by suramin, a potential lead compound for design of new anti-fertility agents. Molecular Human Reproduction, 1996, 2, 597-605.	2.8	25
106	$\beta$ -Glucosidase, $\beta$ -galactosidase, family A cellulases, family F xylanases and two barley glycanases form a superfamily of enzymes with 8-fold $\beta$ architecture and with two conserved glutamates near the carboxy-terminal ends of $\beta$ -strands four and seven. FEBS Letters, 1995, 362, 281-285.	2.8	245
107	Structure of the catalytic core of the family F xylanase from Pseudomonas fluorescens and identification of the xylopentaose-binding sites. Structure, 1994, 2, 1107-1116.	3.3	148
108	Insulin-stimulated GLUT4 glucose transporter recycling. A problem in membrane protein subcellular trafficking through multiple pools. Journal of Biological Chemistry, 1994, 269, 17516-24.	3.4	132