

Gregory B Gloor

List of Publications by Year in descending order

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113
papers

11,692
citations

71102

41
h-index

32842

100
g-index

120
all docs

120
docs citations

120
times ranked

15593
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome Datasets Are Compositional: And This Is Not Optional. <i>Frontiers in Microbiology</i> , 2017, 8, 2224.	3.5	1,794
2	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	27.8	901
3	Unifying the analysis of high-throughput sequencing datasets: characterizing RNA-seq, 16S rRNA gene sequencing and selective growth experiments by compositional data analysis. <i>Microbiome</i> , 2014, 2, 15.	11.1	816
4	Stool substitute transplant therapy for the eradication of <i>Clostridium difficile</i> infection: "RePOOPulating" the gut. <i>Microbiome</i> , 2013, 1, 3.	11.1	621
5	ANOVA-Like Differential Expression (ALDEx) Analysis for Mixed Population RNA-Seq. <i>PLoS ONE</i> , 2013, 8, e67019.	2.5	560
6	Microbiota restoration: natural and supplemented recovery of human microbial communities. <i>Nature Reviews Microbiology</i> , 2011, 9, 27-38.	28.6	461
7	The Microbiota of Breast Tissue and Its Association with Breast Cancer. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5039-5048.	3.1	397
8	Microbiota of Human Breast Tissue. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3007-3014.	3.1	376
9	Human milk microbiota profiles in relation to birthing method, gestation and infant gender. <i>Microbiome</i> , 2016, 4, 1.	11.1	315
10	Compositional analysis: a valid approach to analyze microbiome high-throughput sequencing data. <i>Canadian Journal of Microbiology</i> , 2016, 62, 692-703.	1.7	294
11	Microbiome Profiling by Illumina Sequencing of Combinatorial Sequence-Tagged PCR Products. <i>PLoS ONE</i> , 2010, 5, e15406.	2.5	259
12	Comparative meta-RNA-seq of the vaginal microbiota and differential expression by <i>Lactobacillus iners</i> in health and dysbiosis. <i>Microbiome</i> , 2013, 1, 12.	11.1	238
13	Probiotic Administration Attenuates Myocardial Hypertrophy and Heart Failure After Myocardial Infarction in the Rat. <i>Circulation: Heart Failure</i> , 2014, 7, 491-499.	3.9	231
14	Deep Sequencing of the Vaginal Microbiota of Women with HIV. <i>PLoS ONE</i> , 2010, 5, e12078.	2.5	230
15	Mutual Information in Protein Multiple Sequence Alignments Reveals Two Classes of Coevolving Positions. <i>Biochemistry</i> , 2005, 44, 7156-7165.	2.5	227
16	It's all relative: analyzing microbiome data as compositions. <i>Annals of Epidemiology</i> , 2016, 26, 322-329.	1.9	216
17	High throughput sequencing methods and analysis for microbiome research. <i>Journal of Microbiological Methods</i> , 2013, 95, 401-414.	1.6	210
18	At the crossroads of vaginal health and disease, the genome sequence of <i>Lactobacillus iners</i> AB-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4688-4695.	7.1	201

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19	A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019, 8, .	6.4	187
20	Randomized Open-Label Pilot Study of the Influence of Probiotics and the Gut Microbiome on Toxic Metal Levels in Tanzanian Pregnant Women and School Children. <i>MBio</i> , 2014, 5, e01580-14.	4.1	163
21	Vaginal Microbiome and Epithelial Gene Array in Post-Menopausal Women with Moderate to Severe Dryness. <i>PLoS ONE</i> , 2011, 6, e26602.	2.5	154
22	The Gut Microbiota of Healthy Aged Chinese Is Similar to That of the Healthy Young. <i>MSphere</i> , 2017, 2, .	2.9	141
23	A multi-platform metabolomics approach identifies highly specific biomarkers of bacterial diversity in the vagina of pregnant and non-pregnant women. <i>Scientific Reports</i> , 2015, 5, 14174.	3.3	113
24	Metabolic products of the intestinal microbiome and extremes of atherosclerosis. <i>Atherosclerosis</i> , 2018, 273, 91-97.	0.8	104
25	Tapping natural reservoirs of homing endonucleases for targeted gene modification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13077-13082.	7.1	90
26	Displaying Variation in Large Datasets: Plotting a Visual Summary of Effect Sizes. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 971-979.	1.7	87
27	Microbiota at Multiple Body Sites during Pregnancy in a Rural Tanzanian Population and Effects of Moringa-Supplemented Probiotic Yogurt. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4965-4975.	3.1	85
28	Placental microRNAs in pregnancies with early onset intrauterine growth restriction and preeclampsia: potential impact on gene expression and pathophysiology. <i>BMC Medical Genomics</i> , 2019, 12, 91.	1.5	82
29	Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. <i>Microbiome</i> , 2014, 2, 24.	11.1	81
30	Efficient inter-species conjugative transfer of a CRISPR nuclease for targeted bacterial killing. <i>Nature Communications</i> , 2019, 10, 4544.	12.8	78
31	Regulation of cell proliferation and survival: Convergence of protein kinases and caspases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 505-510.	2.3	75
32	Changes in vaginal microbiota following antimicrobial and probiotic therapy. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 27799.	3.5	71
33	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. <i>Journal of Proteomics</i> , 2015, 118, 49-62.	2.4	64
34	Persistence of the Oral Probiotic <i>Streptococcus salivarius</i> M18 Is Dose Dependent and Megaplasmid Transfer Can Augment Their Bacteriocin Production and Adhesion Characteristics. <i>PLoS ONE</i> , 2013, 8, e65991.	2.5	61
35	A Canadian Working Group Report on Fecal Microbial Therapy: Microbial Ecosystems Therapeutics. <i>Canadian Journal of Gastroenterology & Hepatology</i> , 2012, 26, 457-462.	1.7	59
36	A Multiplex Human Syndrome Implicates a Key Role for Intestinal Cell Kinase in Development of Central Nervous, Skeletal, and Endocrine Systems. <i>American Journal of Human Genetics</i> , 2009, 84, 134-147.	6.2	58

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37	Expanding the UniFrac Toolbox. PLoS ONE, 2016, 11, e0161196.	2.5	58
38	Analysis of neonatal brain lacking ATRX or MeCP2 reveals changes in nucleosome density, CTCF binding and chromatin looping. Nucleic Acids Research, 2014, 42, 8356-8368.	14.5	55
39	A Systems Biology Approach Investigating the Effect of Probiotics on the Vaginal Microbiome and Host Responses in a Double Blind, Placebo-Controlled Clinical Trial of Post-Menopausal Women. PLoS ONE, 2014, 9, e104511.	2.5	55
40	Subinhibitory Antibiotic Therapy Alters Recurrent Urinary Tract Infection Pathogenesis through Modulation of Bacterial Virulence and Host Immunity. MBio, 2015, 6, .	4.1	52
41	Genome Sequence of Lactobacillus pentosus KCA1: Vaginal Isolate from a Healthy Premenopausal Woman. PLoS ONE, 2013, 8, e59239.	2.5	50
42	A truncated form of the bacteriophage Mu B protein promotes conservative integration, but not replicative Transposition, of Mu DNA. Cell, 1985, 41, 857-865.	28.9	47
43	Linear Association in Compositional Data Analysis. Austrian Journal of Statistics, 2018, 47, 3-31.	0.6	44
44	New Primers for Discovering Fungal Diversity Using Nuclear Large Ribosomal DNA. PLoS ONE, 2016, 11, e0159043.	2.5	43
45	Comparative Genomic and Phenotypic Analysis of the Vaginal Probiotic Lactobacillus rhamnosus GR-1. Frontiers in Microbiology, 2018, 9, 1278.	3.5	42
46	Moderate Renal Impairment and Toxic Metabolites Produced by the Intestinal Microbiome: Dietary Implications. , 2019, 29, 55-64.		42
47	Distinct <i>P</i> -Element Excision Products in Somatic and Germline Cells of <i>Drosophila melanogaster</i> . Genetics, 2000, 155, 1821-1830.	2.9	41
48	Biasing genome-editing events toward precise length deletions with an RNA-guided TevCas9 dual nuclease. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14988-14993.	7.1	39
49	Effect of Oral Probiotic Lactobacillus rhamnosus GR-1 and Lactobacillus reuteri RC-14 on the Vaginal Microbiota, Cytokines and Chemokines in Pregnant Women. Nutrients, 2020, 12, 368.	4.1	39
50	Administration of defined microbiota is protective in a murine Salmonella infection model. Scientific Reports, 2015, 5, 16094.	3.3	38
51	The lectin-like protein 1 in Lactobacillus rhamnosus GR-1 mediates tissue-specific adherence to vaginal epithelium and inhibits urogenital pathogens. Scientific Reports, 2016, 6, 37437.	3.3	38
52	Influence of the Vaginal Microbiota on Toxic Shock Syndrome Toxin 1 Production by Staphylococcus aureus. Applied and Environmental Microbiology, 2013, 79, 1835-1842.	3.1	35
53	A Novel Transmembrane Protein Recruits Numb to the Plasma Membrane during Asymmetric Cell Division. Journal of Biological Chemistry, 2004, 279, 11304-11312.	3.4	34
54	Mediterranean Diet Score: Associations with Metabolic Products of the Intestinal Microbiome, Carotid Plaque Burden, and Renal Function. Nutrients, 2018, 10, 779.	4.1	32

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55	Homology Requirements for Targeting Heterologous Sequences During <i>P</i> -Induced Gap Repair in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1997, 147, 689-699.	2.9	32
56	Control of catalytic efficiency by a coevolving network of catalytic and noncatalytic residues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2376-83.	7.1	31
57	Solution NMR Structure and X-ray Absorption Analysis of the C-Terminal Zinc-Binding Domain of the SecA ATPase. <i>Biochemistry</i> , 2004, 43, 9361-9371.	2.5	30
58	Is There a Role for Probiotics in the Prevention of Preterm Birth?. <i>Frontiers in Immunology</i> , 2015, 6, 62.	4.8	29
59	Evaluation of sampling and storage procedures on preserving the community structure of stool microbiota: A simple at-home toilet-paper collection method. <i>Journal of Microbiological Methods</i> , 2018, 144, 117-121.	1.6	29
60	Mutational analysis of the C-terminal FATC domain of <i>Saccharomyces cerevisiae</i> Tra1. <i>Current Genetics</i> , 2010, 56, 447-465.	1.7	28
61	Exploring a Road Map to Counter Misconceptions About the Cervicovaginal Microbiome and Disease. <i>Reproductive Sciences</i> , 2012, 19, 1154-1162.	2.5	28
62	Gene conversion in mitotically dividing cells: a view from <i>Drosophila</i> . <i>Trends in Genetics</i> , 1998, 14, 43-46.	6.7	26
63	Mutual information is critically dependent on prior assumptions: would the <i>correct</i> estimate of mutual information please identify itself?. <i>Bioinformatics</i> , 2010, 26, 1135-1139.	4.1	23
64	Identifying and Seeing beyond Multiple Sequence Alignment Errors Using Intra-Molecular Protein Covariation. <i>PLoS ONE</i> , 2010, 5, e11082.	2.5	23
65	Functionally Compensating Coevolving Positions Are Neither Homoplastic Nor Conserved in Clades. <i>Molecular Biology and Evolution</i> , 2010, 27, 1181-1191.	8.9	22
66	Genetic Evidence Links the ASTRA Protein Chaperone Component Tti2 to the SAGA Transcription Factor Tra1. <i>Genetics</i> , 2012, 191, 765-780.	2.9	22
67	The distribution and functional properties of Pelizaeus's Merzbacher-like disease-linked Cx47 mutations on Cx47/Cx47 homotypic and Cx47/Cx43 heterotypic gap junctions. <i>Biochemical Journal</i> , 2013, 452, 249-258.	3.7	22
68	Microbial composition analysis of <i>Clostridium difficile</i> infections in an ulcerative colitis patient treated with multiple fecal microbiota transplantations. <i>Journal of Crohn's and Colitis</i> , 2014, 8, 1133-1137.	1.3	21
69	Bacterial metatranscriptome analysis of a probiotic yogurt using an RNA-Seq approach. <i>International Dairy Journal</i> , 2014, 39, 284-292.	3.0	20
70	Harnessing microbiome and probiotic research in sub-Saharan Africa: recommendations from an African workshop. <i>Microbiome</i> , 2014, 2, 12.	11.1	20
71	Metabolic derangements identified through untargeted metabolomics in a cross-sectional study of Nigerian children with severe acute malnutrition. <i>Metabolomics</i> , 2017, 13, 1.	3.0	20
72	Impact of Technical Sources of Variation on the Hand Microbiome Dynamics of Healthcare Workers. <i>PLoS ONE</i> , 2014, 9, e88999.	2.5	20

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73	The oral microbiome of patients with axial spondyloarthritis compared to healthy individuals. PeerJ, 2016, 4, e2095.	2.0	19
74	Pilot assessment of probiotics for pregnant women in Rwanda. PLoS ONE, 2018, 13, e0195081.	2.5	19
75	Targeted sequencing reveals expanded genetic diversity of human transfer RNAs. RNA Biology, 2019, 16, 1574-1585.	3.1	19
76	A unified genetic, computational and experimental framework identifies functionally relevant residues of the homing endonuclease I-Bmol. Nucleic Acids Research, 2010, 38, 2411-2427.	14.5	17
77	Ureteral Stent Microbiota Is Associated with Patient Comorbidities but Not Antibiotic Exposure. Cell Reports Medicine, 2020, 1, 100094.	6.5	16
78	ATP(GTP)-dependent conversion of MVM parvovirus single-stranded DNA to its replicative form by a purified 10 S species of mouse DNA polymerase I±. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1984, 781, 216-224.	2.4	14
79	Expression of Single Chain Antibodies (ScFvs) for c-myc Oncoprotein in Recombinant Escherichia coli Membranes by Using the Ice-Nucleation Protein of Pseudomonas syringae. Biotechnology Progress, 2000, 16, 557-563.	2.6	14
80	Protein Sequence Alignment Analysis by Local Covariation: Coevolution Statistics Detect Benchmark Alignment Errors. PLoS ONE, 2012, 7, e37645.	2.5	13
81	Telomere-to-telomere genome assembly of <i>Phaeodactylum tricornutum</i> . PeerJ, 0, 10, e13607.	2.0	13
82	Population Differences at MHC Do Not Explain Enhanced Resistance of Song Sparrows to Local Parasites. Journal of Heredity, 2017, 108, esw082.	2.4	12
83	A Haemophilus sp. dominates the microbiota of sputum from UK adults with non-severe community acquired pneumonia and chronic lung disease. Scientific Reports, 2019, 9, 2388.	3.3	12
84	Sequence of bacteriophage MuNandPgenes. Nucleic Acids Research, 1988, 16, 5211-5212.	14.5	11
85	Acceptor Stem Differences Contribute to Species-Specific Use of Yeast and Human tRNAs ^{er} . Genes, 2018, 9, 612.	2.4	11
86	Lactobacillus rhamnosus GR-1 Attenuates Induction of Hypertrophy in Cardiomyocytes but Not through Secreted Protein MSP-1 (p75). PLoS ONE, 2017, 12, e0168622.	2.5	11
87	Impact of birth weight and postnatal diet on the gut microbiota of young adult guinea pigs. PeerJ, 2017, 5, e2840.	2.0	11
88	Gene-targeting in Drosophila validated. Trends in Genetics, 2001, 17, 549-551.	6.7	10
89	Mutations in the extra sex combs and Enhancer of Polycomb Genes Increase Homologous Recombination in Somatic Cells of Drosophila melanogaster. Genetics, 2006, 172, 2367-2377.	2.9	10
90	Editorial: Compositional data analysis and related methods applied to genomics—a first special issue from NAR Genomics and Bioinformatics. NAR Genomics and Bioinformatics, 2020, 2, lqaa103.	3.2	10

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91	Phosphate-regulated expression of the SARS-CoV-2 receptor-binding domain in the diatom <i>Phaeodactylum tricornutum</i> for pandemic diagnostics. <i>Scientific Reports</i> , 2022, 12, 7010.	3.3	10
92	Active site residue identity regulates cleavage preference of LAGLIDADG homing endonucleases. <i>Nucleic Acids Research</i> , 2018, 46, 11990-12007.	14.5	9
93	From RNA-seq to Biological Inference: Using Compositional Data Analysis in Meta-Transcriptomics. <i>Methods in Molecular Biology</i> , 2018, 1849, 193-213.	0.9	9
94	A mutation in the serine protease TMPRSS4 in a novel pediatric neurodegenerative disorder. <i>Orphanet Journal of Rare Diseases</i> , 2013, 8, 126.	2.7	8
95	Preen gland microbiota of songbirds differ across populations but not sexes. <i>Journal of Animal Ecology</i> , 2021, 90, 2202-2212.	2.8	8
96	How to Compute with DNA. <i>Lecture Notes in Computer Science</i> , 1999, , 269-282.	1.3	8
97	Modifying a covarying proteinâ€“DNA interaction changes substrate preference of a site-specific endonuclease. <i>Nucleic Acids Research</i> , 2019, 47, 10830-10841.	14.5	7
98	Different and diverse anaerobic microbiota were seen in women living with <sc>HIV</sc> with unsuppressed <sc>HIV</sc> viral load and in women with recurrent bacterial vaginosis: a cohort study. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020, 127, 250-259.	2.3	7
99	The C-terminal Residues of <i>Saccharomyces cerevisiae</i> Mec1 Are Required for Its Localization, Stability, and Function. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1661-1674.	1.8	6
100	The Effect of Heterologous Insertions on Gene Conversion in Mitotically Dividing Cells in <i>Drosophila melanogaster</i>. <i>Genetics</i> , 2002, 161, 249-258.	2.9	6
101	4 The role of sequence homology in the repair of DNA double-strand breaks in <i>Drosophila</i> . <i>Advances in Genetics</i> , 2002, 46, 91-117.	1.8	5
102	Gene Targeting in <i>Drosophila</i>. , 2004, 260, 097-114.		4
103	A Multiplex Human Syndrome Implicates a Key Role for Intestinal Cell Kinase in Development of Central Nervous, Skeletal, and Endocrine Systems. <i>American Journal of Human Genetics</i> , 2009, 84, 822.	6.2	3
104	Cloning of <i>Thalassiosira pseudonana</i> â€™s Mitochondrial Genome in <i>Saccharomyces cerevisiae</i> and <i>Escherichia coli</i> . <i>Biology</i> , 2020, 9, 358.	2.8	3
105	Bioinformatics Identification of Coevolving Residues. <i>Methods in Molecular Biology</i> , 2014, 1123, 223-243.	0.9	3
106	Research Priorities in the Field of Posttraumatic Pain and Disability: Results of a Transdisciplinary Consensus-Generating Workshop. <i>Pain Research and Management</i> , 2016, 2016, 1-8.	1.8	2
107	Unaccounted risk of cardiovascular disease: the role of the microbiome in lipid metabolism. <i>Current Opinion in Lipidology</i> , 2019, 30, 125-133.	2.7	2
108	Finding the Centre: Compositional Asymmetry in High-Throughput Sequencing Datasets. , 2021, , 329-346.		2

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109	TOWARDS A DNA SOLUTION TO THE SHORTEST COMMON SUPERSTRING PROBLEM. International Journal on Artificial Intelligence Tools, 1999, 08, 385-399.	1.0	1
110	Estimating the evidence of selection and the reliability of inference in unigenic evolution. Algorithms for Molecular Biology, 2010, 5, 35.	1.2	1
111	Loss of nonsense mediated decay suppresses mutations in <i>Saccharomyces cerevisiae</i> TRA1. BMC Genetics, 2012, 13, 19.	2.7	1
112	Data on the gut and saliva microbiota from a cohort of atherosclerosis patients determined by 16S rRNA gene sequencing. Data in Brief, 2018, 19, 481-485.	1.0	1
113	omicplotR: visualizing omic datasets as compositions. BMC Bioinformatics, 2019, 20, 580.	2.6	0