Michael T Zimmermann

List of Publications by Year
in descending order

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132 papers	3,444 citations	201385 27 h-index	174990 52 g-index
142 all docs	142 docs citations	142 times ranked	6905 citing authors

#	Article	IF	Citations
1	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
2	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. Nature, 2010, 467, 484-488.	13.7	223
3	Crystal structure of the CusBA heavy-metal efflux complex of Escherichia coli. Nature, 2011, 470, 558-562.	13.7	201
4	Mitochondrial Metabolic Reprogramming by CD36 Signaling Drives Macrophage Inflammatory Responses. Circulation Research, 2019, 125, 1087-1102.	2.0	114
5	ICGA-PSO-ELM Approach for Accurate Multiclass Cancer Classification Resulting in Reduced Gene Sets in Which Genes Encoding Secreted Proteins Are Highly Represented. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 452-463.	1.9	93
6	MACE: model based analysis of ChIP-exo. Nucleic Acids Research, 2014, 42, e156-e156.	6.5	84
7	Understanding Proteinâ€“Nanoparticle Interaction: A New Gateway to Disease Therapeutics. Bioconjugate Chemistry, 2014, 25, 1078-1090.	1.8	76
8	Recessive MYH6 Mutations in Hypoplastic Left Heart With Reduced Ejection Fraction. Circulation: Cardiovascular Genetics, 2015, 8, 564-571.	5.1	72
9	Genome-wide associations of CD46 and IFI44L genetic variants with neutralizing antibody response to measles vaccine. Human Genetics, 2017, 136, 421-435.	1.8	59
10	Novel Type of Renal Amyloidosis Derived from Apolipoprotein-CII. Journal of the American Society of Nephrology: JASN, 2017, 28, 439-445.	3.0	57
11	Computational and experimental characterization of RNA cubic nanoscaffolds. Methods, 2014, 67, 256-265.	1.9	55
12	Recurrent MSCE116K mutations in ALK-negative anaplastic large cell lymphoma. Blood, 2019, 133, 2776-2789.	0.6	55
13	Whole-exome analysis reveals novel somatic genomic alterations associated with outcome in immunochemotherapy-treated diffuse large B-cell lymphoma. Blood Cancer Journal, 2015, 5, e346-e346.	2.8	54
14	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. PLoS ONE, 2016, 11, e0152034.	1.1	53
15	Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9443-9448.	3.3	47
16	Pathogenic SPTBN1 variants cause an autosomal dominant neurodevelopmental syndrome. Nature Genetics, 2021, 53, 1006-1021.	9.4	44
17	TNNI3K mutation in familial syndrome of conduction system disease, atrial tachyarrhythmia and dilated cardiomyopathy. Human Molecular Genetics, 2014, 23, 5793-5804.	1.4	41
18	Clinical Proteome Informatics Workbench Detects Pathogenic Mutations in Hereditary Amyloidoses. Journal of Proteome Research, 2014, 13, 2352-2358.	1.8	40

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19	Immunosenescence-Related Transcriptomic and Immunologic Changes in Older Individuals Following Influenza Vaccination. Frontiers in Immunology, 2016, 7, 450.	2.2	40
20	Transcriptional signatures of influenza A/H1N1-specific IgG memory-like B cell response in older individuals. Vaccine, 2016, 34, 3993-4002.	1.7	39
21	MAVENs: Motion analysis and visualization of elastic networks and structural ensembles. BMC Bioinformatics, 2011, 12, 264.	1.2	37
22	Predict drug sensitivity of cancer cells with pathway activity inference. BMC Medical Genomics, 2019, 12, 15.	0.7	36
23	Transcriptomic signatures of cellular and humoral immune responses in older adults after seasonal influenza vaccination identified by data-driven clustering. Scientific Reports, 2018, 8, 739.	1.6	34
24	Revealing Rotational Modes of Functionalized Gold Nanorods on Live Cell Membranes. Small, 2013, 9, 785-792.	5.2	33
25	Elastic network models capture the motions apparent within ensembles of RNA structures. Rna, 2014, 20, 792-804.	1.6	33
26	Novel NR2F1 variants likely disrupt DNA binding: molecular modeling in two cases, review of published cases, genotypeâ€“phenotype correlation, and phenotypic expansion of the Boschâ€“Boonstraâ€“Schaaf optic atrophy syndrome. Journal of Physical Education and Sports Management, 2017, 3, a002162.	0.5	33
27	Clinical and Biochemical Phenotypes in a Family With ENPP1 Mutations. Journal of Bone and Mineral Research, 2020, 35, 662-670.	3.1	33
28	Integration of Immune Cell Populations, mRNA-Seq, and CpG Methylation to Better Predict Humoral Immunity to Influenza Vaccination: Dependence of mRNA-Seq/CpG Methylation on Immune Cell Populations. Frontiers in Immunology, 2017, 8, 445.	2.2	29
29	De novo RRAGC mutation activates mTORC1 signaling in syndromic fetal dilated cardiomyopathy. Human Genetics, 2016, 135, 909-917.	1.8	28
30	SASH3variants cause a novel form of X-linked combined immunodeficiency with immune dysregulation. Blood, 2021, 138, 1019-1033.	0.6	28
31	The importance of slow motions for protein functional loops. Physical Biology, 2012, 9, 014001.	0.8	27
32	Hereditary Lysozyme Amyloidosis Variant p.Leu102Ser Associates with Unique Phenotype. Journal of the American Society of Nephrology: JASN, 2017, 28, 431-438.	3.0	27
33	Gene signatures associated with adaptive humoral immunity following seasonal influenza A/H1N1 vaccination. Genes and Immunity, 2016, 17, 371-379.	2.2	26
34	RNA Sequencing Reveals Cancerâ€Associated Changes in Laryngeal Cells Exposed to Nonâ€Acid Pepsin. Laryngoscope, 2021, 131, 121-129.	1.1	26
35	Somatic PIK3R1 variation as a cause of vascular malformations and overgrowth. Genetics in Medicine, 2021, 23, 1882-1888.	1.1	26
36	Gene signatures related to HAI response following influenza A/H1N1 vaccine in older individuals. Heliyon, 2016, 2, e00098.	1.4	25

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37	Combining Statistical Potentials with Dynamics-Based Entropies Improves Selection from Protein Decoys and Docking Poses. Journal of Physical Chemistry B, 2012, 116, 6725-6731.	1.2	24
38	Ribosome Mechanics Informs about Mechanism. Journal of Molecular Biology, 2016, 428, 802-810.	2.0	24
39	Impairment of the mitochondrial one-carbon metabolism enzyme SHMT2 causes a novel brain and heart developmental syndrome. Acta Neuropathologica, 2020, 140, 971-975.	3.9	24
40	Impact of integrated translational research on clinical exome sequencing. Genetics in Medicine, 2021, 23, 498-507.	1.1	24
41	A Computational Investigation on the Connection between Dynamics Properties of Ribosomal Proteins and Ribosome Assembly. PLoS Computational Biology, 2012, 8, e1002530.	1.5	22
42	Novel de novo variant in EBF3 is likely to impact DNA binding in a patient with a neurodevelopmental disorder and expanded phenotypes: patient report, in silico functional assessment, and review of published cases. Journal of Physical Education and Sports Management, 2017, 3, a001743.	0.5	22
43	Apolipoprotein CII Amyloidosis Associated With p.Lys41Thr Mutation. Kidney International Reports, 2018, 3, 1193-1201.	0.4	21
44	Genetic variations in human papillomavirus and cervical cancer outcomes. International Journal of Cancer, 2019, 144, 2206-2214.	2.3	21
45	Whole Transcriptome Profiling Identifies CD93 and Other Plasma Cell Survival Factor Genes Associated with Measles-Specific Antibody Response after Vaccination. PLoS ONE, 2016, 11, e0160970.	1.1	20
46	Molecular modeling and molecular dynamic simulation of the effects of variants in the TGFBR2 kinase domain as a paradigm for interpretation of variants obtained by next generation sequencing. PLoS ONE, 2017, 12, e0170822.	1.1	19
47	A Novel Kleefstra Syndrome-associated Variant That Affects the Conserved TPLX Motif within the Ankyrin Repeat of EHMT1 Leads to Abnormal Protein Folding. Journal of Biological Chemistry, 2017, 292, 3866-3876.	1.6	18
48	A Patient With Hereditary ATTR and a Novel AGel p.Ala578Pro Amyloidosis. Mayo Clinic Proceedings, 2018, 93, 1678-1682.	1.4	18
49	RITAN: rapid integration of term annotation and network resources. PeerJ, 2019, 7, e6994.	0.9	17
50	The gut microbiome in solid organ transplantation. Pediatric Transplantation, 2020, 24, e13866.	0.5	17
51	Free energies for coarse-grained proteins by integrating multibody statistical contact potentials with entropies from elastic network models. Journal of Structural and Functional Genomics, 2011, 12, 137-147.	1.2	16
52	Polymorphisms in STING Affect Human Innate Immune Responses to Poxviruses. Frontiers in Immunology, 2020, 11, 567348.	2.2	15
53	Structural Origins of Misfolding Propensity in the Platelet Adhesive Von Willebrand Factor A1 Domain. Biophysical Journal, 2015, 109, 398-406.	0.2	14
54	A novel ANO3 variant identified in a 53-year-old woman presenting with hyperkinetic dysarthria, blepharospasm, hyperkinesias, and complex motorÂtics. BMC Medical Genetics, 2016, 17, 93.	2.1	14

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55	Novel BRAF alteration in desmoplastic infantile ganglioglioma with response to targeted therapy. Acta Neuropathologica Communications, 2018, 6, 118.	2.4	14
56	Factors correlating with significant differences between X-ray structures of myoglobin. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 481-491.	2.5	13
57	Molecular characterization of known and novel ACVR1 variants in phenotypes of aberrant ossification. American Journal of Medical Genetics, Part A, 2019, 179, 1764-1777.	0.7	13
58	Motor Neuron Generation from iPSCs from Identical Twins Discordant for Amyotrophic Lateral Sclerosis. Cells, 2020, 9, 571.	1.8	13
59	De novo coding variants in the AGO1 gene cause a neurodevelopmental disorder with intellectual disability. Journal of Medical Genetics, 2022, 59, 965-975.	1.5	13
60	Recursive Indirect-Paths Modularity (RIP-M) for Detecting Community Structure in RNA-Seq Co-expression Networks. Frontiers in Genetics, 2016, 7, 80.	1.1	12
61	Assessing Human Genetic Variations in Glucose Transporter SLC2A10 and Their Role in Altering Structural and Functional Properties. Frontiers in Genetics, 2018, 9, 276.	1.1	12
62	Novel KLHL26 variant associated with a familial case of Ebsteinâ€™s anomaly and left ventricular noncompaction. Molecular Genetics & Genomic Medicine, 2020, 8, e1152.	0.6	11
63	Molecular mechanics and dynamic simulations of well-known Kabuki syndrome-associated KDM6A variants reveal putative mechanisms of dysfunction. Orphanet Journal of Rare Diseases, 2021, 16, 66.	1.2	11
64	Protein Loop Dynamics Are Complex and Depend on the Motions of the Whole Protein. Entropy, 2012, 14, 687-700.	1.1	10
65	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. Journal of Biomedical Semantics, 2016, 7, 24.	0.9	10
66	A case of Coffinâ€“Siris syndrome with severe congenital heart disease and a novel SMARCA4 variant. Journal of Physical Education and Sports Management, 2019, 5, a003962.	0.5	10
67	Molecular modeling of LDLR aids interpretation of genomic variants. Journal of Molecular Medicine, 2019, 97, 533-540.	1.7	10
68	POLD1 Deficiency Reveals a Role for POLD1 in DNA Repair and T and B Cell Development. Journal of Clinical Immunology, 2021, 41, 270-273.	2.0	10
69	<scp>RNA</scp> Sequencing and Pathways Analyses of Middle Ear Epithelia From Patients With Otitis Media. Laryngoscope, 2021, 131, 2590-2597.	1.1	10
70	The development of non-coding RNA ontology. International Journal of Data Mining and Bioinformatics, 2016, 15, 214.	0.1	9
71	Microglia Influence Neurofilament Deposition in ALS iPSC-Derived Motor Neurons. Genes, 2022, 13, 241.	1.0	9
72	Functional validation reveals the novel missense V419L variant in TGFBR2 associated with Loeysâ€“Dietz syndrome (LDS) impairs canonical TGF-Î² signaling. Journal of Physical Education and Sports Management, 2017, 3, a001727.	0.5	7

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73	The Importance of Biologic Knowledge and Gene Expression Context for Genomic Data Interpretation. Frontiers in Genetics, 2018, 9, 670.	1.1	7
74	Aurora kinase B-phosphorylated HP1Î± functions in chromosomal instability. Cell Cycle, 2019, 18, 1407-1421.	1.3	7
75	Novel destabilizing Dynactin variant (DCTN1 p.Tyr78His) in patient with Perry syndrome. Parkinsonism and Related Disorders, 2020, 77, 110-113.	1.1	7
76	Interaction between Mas1 and AT1RA contributes to enhancement of skeletal muscle angiogenesis by angiotensin-(1-7) in Dahl salt-sensitive rats. PLoS ONE, 2020, 15, e0232067.	1.1	7
77	Protein modeling and clinical description of a novel inâ€frame <i>‹scp›GLB‹/scp›1‹/i› deletion causing ‹scp›GM‹/scp›1 gangliosidosis type ‹scp›II‹/scp›. Molecular Genetics & Genomic Medicine, 2018, 6, 1229-1235.	0.6	6
78	X-Linked Lymphoproliferative Syndrome Presenting as Adult-Onset Multi-Infarct Dementia. Journal of Neuropathology and Experimental Neurology, 2019, 78, 460-466.	0.9	6
79	Genetic variants in DGAT1 cause diverse clinical presentations of malnutrition through a specific molecular mechanism. European Journal of Medical Genetics, 2020, 63, 103817.	0.7	6
80	Structural bioinformatics enhances mechanistic interpretation of genomic variation, demonstrated through the analyses of 935 distinct RAS family mutations. Bioinformatics, 2021, 37, 1367-1375.	1.8	6
81	KrasG12D induces changes in chromatin territories that differentially impact early nuclear reprogramming in pancreatic cells. Genome Biology, 2021, 22, 289.	3.8	6
82	Gain and loss of TASK3 channel function and its regulation by novel variation cause KCNK9 imprinting syndrome. Genome Medicine, 2022, 14, .	3.6	6
83	Even pore-localizing missense variants at highly conserved sites in KCNQ1 -encoded K v 7.1 channels may have wild-type function and not cause type 1 long QT syndrome: Do not rely solely on the genetic test company's interpretation. HeartRhythm Case Reports, 2018, 4, 37-44.	0.2	5
84	Modeling postâ€translational modifications and cancerâ€associated mutations that impact the heterochromatin protein 1Î±â€importin Î± heterodimers. Proteins: Structure, Function and Bioinformatics, 2019, 87, 904-916.	1.5	5
85	Novel biallelic variants in MSTO1 associated with mitochondrial myopathy. Journal of Physical Education and Sports Management, 2019, 5, a004309.	0.5	5
86	Inactivation of the Euchromatic Histone-Lysine N-Methyltransferase 2 Pathway in Pancreatic Epithelial Cells Antagonizes Cancer Initiation and Pancreatitis-Associated Promotion by Altering Growth and Immune Gene Expression Networks. Frontiers in Cell and Developmental Biology, 2021, 9, 681153.	1.8	5
87	Immunoglobulin Structure Exhibits Control over CDR Motion. Immunome Research, 2011, 7, .	0.1	5
88	â€œThe moleculeâ€™s the thing:â€•the promise of molecular modeling and dynamic simulations in aiding the prioritization and interpretation of genomic testing results. F1000Research, 2016, 5, 766.	0.8	5
89	Structural bioinformatics enhances the interpretation of somatic mutations in KDM6A found in human cancers. Computational and Structural Biotechnology Journal, 2022, 20, 2200-2211.	1.9	5
90	Novel Pathogenic Variant in TGFBR2 Confirmed by Molecular Modeling Is a Rare Cause of Loeys-Dietz Syndrome. Case Reports in Genetics, 2017, 2017, 1-4.	0.1	4

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91	Discovery, expression, cellular localization, and molecular properties of a novel, alternative spliced HP1Î³ isoform, lacking the chromoshadow domain. PLoS ONE, 2020, 15, e0217452.	1.1	4
92	Defining the genotypic and phenotypic spectrum of X-linked MSL3-related disorder. Genetics in Medicine, 2021, 23, 384-395.	1.1	4
93	Interpreting Sequence Variation in PDAC-Predisposing Genes Using a Multi-Tier Annotation Approach Performed at the Gene, Patient, and Cohort Level. Frontiers in Oncology, 2021, 11, 606820.	1.3	4
94	Mutations Targeting the ErbB Pathway and MSC in Peripheral T-Cell Lymphoma. Blood, 2015, 126, 2681-2681.	0.6	4
95	â€œThe moleculeâ€™s the thing:â€•the promise of molecular modeling and dynamic simulations in aiding the prioritization and interpretation of genomic testing results. F1000Research, 2016, 5, 766.	0.8	4
96	Enhanced interpretation of 935 hotspot and non-hotspot RAS variants using evidence-based structural bioinformatics. Computational and Structural Biotechnology Journal, 2022, 20, 117-127.	1.9	4
97	NADPH oxidase 4 contributes to TRPV4-mediated endothelium-dependent vasodilation in human arterioles by regulating protein phosphorylation of TRPV4 channels. Basic Research in Cardiology, 2022, 117, 24.	2.5	4
98	Short paths in protein structure space originate in graph structure. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, E137; author reply E138.	3.3	3
99	Functional characterization of a <scp>GFAP</scp> variant of uncertain significance in an Alexander disease case within the setting of an individualized medicine clinic. Clinical Case Reports (discontinued), 2016, 4, 885-895.	0.2	3
100	The impact of pharmacokinetic gene profiles across human cancers. BMC Cancer, 2018, 18, 577.	1.1	3
101	A homozygous missense variant in UBE2T is associated with a mild Fanconi anemia phenotype. Haematologica, 2021, 106, 1188-1192.	1.7	3
102	Computational modeling reveals key molecular properties and dynamic behavior of disruptor of telomeric silencing 1â€like (DOT1L) and partnering complexes involved in leukemogenesis. Proteins: Structure, Function and Bioinformatics, 2022, 90, 282-298.	1.5	3
103	Prognostic effect of specific RAS/BRAF mutations in patients (pts) with metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2020, 38, 4050-4050.	0.8	3
104	PANDA: pathway and annotation explorer for visualizing and interpreting gene-centric data. PeerJ, 2015, 3, e970.	0.9	3
105	Adverse Drug Event-based Stratification of Tumor Mutations: A Case Study of Breast Cancer Patients Receiving Aromatase Inhibitors. AMIA ... Annual Symposium proceedings, 2014, 2014, 1160-9.	0.2	3
106	Functional validation of TERT and TERC variants of uncertain significance in patients with short telomere syndromes. Blood Cancer Journal, 2020, 10, 120.	2.8	2
107	â€œThe moleculeâ€™s the thing:â€•the promise of molecular modeling and dynamic simulations in aiding the prioritization and interpretation of genomic testing results. F1000Research, 0, 5, 766.	0.8	2
108	New Methods to Improve Protein Structure Prediction and Refinement. Biophysical Journal, 2013, 104, 229a.	0.2	1

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109	Biallelic variants in PROZ as a cause of hypercoagulability and livedo racemosa. Thrombosis Research, 2020, 195, 187-189.	0.8	1
110	P2T2: Protein Panoramic annoTation Tool for the interpretation of protein coding genetic variants. JAMIA Open, 2021, 4, ooab065.	1.0	1
111	Drug Normalization for Cancer Therapeutic and Druggable Genome Target Discovery. AMIA Summits on Translational Science Proceedings, 2015, 2015, 72-6.	0.4	1
112	Single-sample expression-based chemo-sensitivity score improves survival associations independently from genomic mutations for ovarian cancer Patients. AMIA Summits on Translational Science Proceedings, 2016, 2016, 94-100.	0.4	1
113	Integrative Modeling, Molecular Mechanics, and Molecular Dynamics Evaluation of Genomics Variants in KMT2C (MLL3), a Gene Involved in Kleefstra Syndrome Type 2. FASEB Journal, 2022, 36, .	0.2	1
114	Immunoglobulin functional motions and their effects on the complementarity determining regions. , 2010, , .		0
115	Computing Entropies for Binding and Refinement of Protein Structures. Biophysical Journal, 2012, 102, 25a.	0.2	0
116	Coarse-Grained Computational Characterization of RNA Nanocube Flexibility Correlates with Experiments. Biophysical Journal, 2013, 104, 16a.	0.2	0
117	A domain ontology for the Non-Coding RNA field. , 2015, , .		0
118	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. Lecture Notes in Computer Science, 2019, , 356-369.	1.0	0
119	Impact of KRAS alterations in localized pancreatic cancer (PC).. Journal of Clinical Oncology, 2021, 39, 431-431.	0.8	0
120	Germline evaluation of patients undergoing tumor genomic profiling: An academic cancer centerâ€™s experience with implementing a germline review protocol. Journal of Genetic Counseling, 2021, 30, 900-910.	0.9	0
121	Adverse Drug Events-based Tumor Stratification for Ovarian Cancer Patients Receiving Platinum Therapy. AMIA Summits on Translational Science Proceedings, 2015, 2015, 51-5.	0.4	0
122	A Semantic Web-based System for Mining Genetic Mutations in Cancer Clinical Trials. AMIA Summits on Translational Science Proceedings, 2015, 2015, 142-6.	0.4	0
123	Molecular Modeling is an Enabling Approach to Complement and Enhance Channelopathy Research. , 2022, 12, 3141-3166.		0
124	Abstract 4163: Genomic variation in PDAC-predisposing genes identified using the MCW germline exome panel. , 2019, , .		0
125	Title is missing!. , 2020, 15, e0232067.		0
126	Title is missing!. , 2020, 15, e0232067.		0

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127	Title is missing!. , 2020, 15, e0232067.		0
128	Title is missing!. , 2020, 15, e0232067.		0
129	Defining the Mutational Landscape That Affects the Histone Demethylase KDM6A/UTX in Human Cancer. FASEB Journal, 2022, 36, .	0.2	0
130	Epigenomic mechanisms used by KrasG12D to regulate inflammatory gene clusters in epithelial pancreatic cancer cells, which are critical for reprogramming the tumor microenvironment. FASEB Journal, 2022, 36, .	0.2	0
131	Transcriptional Landscape Established by the Euchromatic Histoneâ€lysine Nâ€methyltransferase Pathway During Pancreas Ontogenesis and Pancreatitis. FASEB Journal, 2022, 36, .	0.2	0
132	To ChIP, or to CUT, that is the question: Comparative Evaluation of NextGen Methodologies for Studying the genomeâ€wide distribution of Histone H3 Lysine 9 diâ€methyl mark in pancreatic cells. FASEB Journal, 2022, 36, .	0.2	0