Thomas R Caulfield

List of Publications by Year
in descending order

79 papers	5,219 citations	159585 30 h-index	91884 69 g-index
82 all docs	82 docs citations	82 times ranked	9480 citing authors

#	Article	IF	Citations
1	Clinical description & molecular modeling of novel MAX pathogenic variant causing pheochromocytoma in family, supports paternal parent-of-origin effect. Cancer Genetics, 2021, 252-253, 107-110.	0.4	2
2	Attacking COVID-19 Progression Using Multi-Drug Therapy for Synergetic Target Engagement. Biomolecules, 2021, 11, 787.	4.0	14
3	Structural And Computational Perspectives of Selectively Targeting Mutant Proteins. Current Drug Discovery Technologies, 2021, 18, 365-378.	1.2	4
4	Platforms for Personalized Polytherapeutics Discovery in COVID-19. Journal of Molecular Biology, 2021, 433, 166945.	4.2	4
5	Endotheliitis, endothelin, and endothelin receptor blockers in COVID-19. Medical Hypotheses, 2021, 150, 110564.	1.5	11
6	A novel, germline, deactivating CBL variant p.L493F alters domain orientation and is associated with multiple childhood cancers. Cancer Genetics, 2021, 254-255, 18-24.	0.4	2
7	Role of PLEXIND1/TGFÎ² Signaling Axis in Pancreatic Ductal Adenocarcinoma Progression Correlates with the Mutational Status of KRAS. Cancers, 2021, 13, 4048.	3.7	4
8	APOE3 -Jacksonville (V236E) variant reduces self-aggregation and risk of dementia. Science Translational Medicine, 2021, 13, eabc9375.	12.4	37
9	A Virtual Screening Platform Identifies Chloroethylagelastatin A as a Potential Ribosomal Inhibitor. Biomolecules, 2020, 10, 1407.	4.0	1
10	Genomics combined with a protein informatics platform to assess a novel pathogenic variant c.1024 A>G (p.K342E) in OPA1 in a patient with autosomal dominant optic atrophy. Ophthalmic Genetics, 2020, 41, 563-569.	1.2	1
11	An activating germline IDH1 variant associated with a tumor entity characterized by unilateral and bilateral chondrosarcoma of the mastoid. Human Genetics and Genomics Advances, 2020, 1, 100006.	1.7	3
12	ACEI/ARB therapy in COVID-19: the double-edged sword of ACE2 and SARS-CoV-2 viral docking. Critical Care, 2020, 24, 475.	5.8	27
13	Structural Models for the Dynamic Effects of Loss-of-Function Variants in the Human SIM1 Protein Transcriptional Activation Domain. Biomolecules, 2020, 10, 1314.	4.0	3
14	FAM111A protects replication forks from protein obstacles via its trypsin-like domain. Nature Communications, 2020, 11, 1318.	12.8	67
15	Examination of Molecular Effects of MYLK Deletion in a Patient with Extensive Aortic, Carotid, and Abdominal Dissections That Underlie the Genetic Dysfunction. Case Reports in Medicine, 2020, 2020, 1-7.	0.7	2
16	Characterization of a Pathogenic Variant in the ABCD1 Gene Through Protein Molecular Modeling. Case Reports in Genetics, 2020, 2020, 1-7.	0.2	2
17	Functional Analysis of the SIM1 Variant p.G715V in 2 Patients With Obesity. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 355-361.	3.6	11
18	Molecular Inhibitor of QSOX1 Suppresses Tumor Growth In Vivo. Molecular Cancer Therapeutics, 2020, 19, 112-122.	4.1	17

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19	Three-tier stratification for CNS COVID-19 to help decide which patients should undergo lumbar puncture with CSF analysis: A case report and literature review. Romanian Journal of Internal Medicine = Revue Roumaine De Medecine Interne, 2020, 59, 88-92.	0.6	4
20	Apolipoprotein E and Alzheimer disease: pathobiology and targeting strategies. Nature Reviews Neurology, 2019, 15, 501-518.	10.1	734
21	Design and Evaluation of PEGylated Liposomal Formulation of a Novel Multikinase Inhibitor for Enhanced Chemosensitivity and Inhibition of Metastatic Pancreatic Ductal Adenocarcinoma. Bioconjugate Chemistry, 2019, 30, 2703-2713.	3.6	12
22	Integrative data fusion for comprehensive assessment of a novel CHEK2 variant using combined genomics, imaging, and functionalâ€“structural assessments via protein informatics. Molecular Omics, 2019, 15, 59-66.	2.8	9
23	Genomic Observations of a Rare/Pathogenic SMAD3 Variant in Loeysâ€“Dietz Syndrome 3 Confirmed by Protein Informatics and Structural Investigations. Medicina (Lithuania), 2019, 55, 137.	2.0	4
24	Disulfide engineering of human Kunitz-type serine protease inhibitors enhances proteolytic stability and target affinity toward mesotrypsin. Journal of Biological Chemistry, 2019, 294, 5105-5120.	3.4	20
25	Protein informatics combined with multiple data sources enriches the clinical characterization of novel <scp>TRPV</scp>4 variant causing an intermediate skeletal dysplasia. Molecular Genetics & Genomic Medicine, 2019, 7, e566.	1.2	8
26	Development of multi-drug loaded PEGylated nanodiamonds to inhibit tumor growth and metastasis in genetically engineered mouse models of pancreatic cancer. Nanoscale, 2019, 11, 22006-22018.	5.6	40
27	Molecular Dynamics Simulations Suggest a Non-Doublet Decoding Model of â€“1 Frameshifting by tRNASer3. Biomolecules, 2019, 9, 745.	4.0	11
28	Structural Basis for Improved Proteolytic Stability and Target Affinity of Disulfide engineered Human Kunitzâ€type Serine Protease Inhibitors. FASEB Journal, 2019, 33, 472.1.	0.5	0
29	Protein molecular modeling techniques investigating novel <scp>TAB</scp>2 variant R347X causing cardiomyopathy and congenital heart defects in multigenerational family. Molecular Genetics & Genomic Medicine, 2018, 6, 666-672.	1.2	19
30	TRIO gene segregation in a family with cerebellar ataxia. Neurologia I Neurochirurgia Polska, 2018, 52, 743-749.	1.2	5
31	Protein modeling and clinical description of a novel inâ€frame <scp>GLB</scp>1 deletion causing <scp>GM</scp>1 gangliosidosis type <scp>II</scp>. Molecular Genetics & Genomic Medicine, 2018, 6, 1229-1235.	1.2	6
32	The PINK1 p.I368N Mutation Affects Protein Stability and Kinase Activity with Its Structural Change. Juntendo Medical Journal, 2018, 64, 17-30.	0.1	0
33	Whole Exome Sequencing and Molecular Modeling of a Missense Variant in TNFAIP3 That Segregates with Disease in a Family with Chronic Urticaria and Angioedema. Case Reports in Genetics, 2018, 2018, 1-6.	0.2	5
34	Protein molecular modeling shows residue T599 is critical to wild-type function of POLG and description of a novel variant associated with the SANDO phenotype. Human Genome Variation, 2018, 5, 18016.	0.7	6
35	Personalized molecular modeling for pinpointing associations of protein dysfunction and variants associated with hereditary cancer syndromes. Molecular Genetics & Genomic Medicine, 2018, 6, 805-810.	1.2	4
36	Molecular Dissection of FUS Points at Synergistic Effect of Low-Complexity Domains in Toxicity. Cell Reports, 2018, 24, 529-537.e4.	6.4	74

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37	Accelerated bottom-up drug design platform enables the discovery of novel stearoyl-CoA desaturase 1 inhibitors for cancer therapy. Oncotarget, 2018, 9, 3-20.	1.8	35
38	Parkin. , 2018, , 3786-3794.		0
39	The PINK1 p.I368N mutation affects protein stability and ubiquitin kinase activity. Molecular Neurodegeneration, 2017, 12, 32.	10.8	62
40	Reply: Heterozygous PINK1 p.G411S in rapid eye movement sleep behaviour disorder. Brain, 2017, 140, e33-e33.	7.6	2
41	Multifaceted peptide assisted one-pot synthesis of gold nanoparticles for plectin-1 targeted gemcitabine delivery in pancreatic cancer. Nanoscale, 2017, 9, 15622-15634.	5.6	46
42	A novel splice site variant in <scp>CYP</scp>11A1 in trans with the p.E314K variant in a male patient with congenital adrenal insufficiency. Molecular Genetics & Genomic Medicine, 2017, 5, 781-787.	1.2	14
43	Heterozygous PINK1 p.G411S increases risk of Parkinsonâ€™s disease via a dominant-negative mechanism. Brain, 2017, 140, 98-117.	7.6	116
44	PINK1, Parkin, and Mitochondrial Quality Control: What can we Learn about Parkinsonâ€™s Disease Pathobiology?. Journal of Parkinson's Disease, 2017, 7, 13-29.	2.8	175
45	Small molecule inhibitors of mesotrypsin from a structure-based docking screen. PLoS ONE, 2017, 12, e0176694.	2.5	16
46	Parkin. , 2017, , 1-9.		0
47	An Acrobatic Substrate Metamorphosis Reveals a Requirement for Substrate Conformational Dynamics in Trypsin Proteolysis. Journal of Biological Chemistry, 2016, 291, 26304-26319.	3.4	22
48	Parkin. , 2016, , 1-9.		0
49	Activation of the E3 ubiquitin ligase Parkin. Biochemical Society Transactions, 2015, 43, 269-274.	3.4	45
50	(Pathoâ€)physiological relevance of <scp>PINK</scp> 1â€dependent ubiquitin phosphorylation. EMBO Reports, 2015, 16, 1114-1130.	4.5	147
51	Structural and Functional Impact of Parkinson Disease-Associated Mutations in the E3 Ubiquitin Ligase Parkin. Human Mutation, 2015, 36, 774-786.	2.5	69
52	Synthesis and Evaluation of Derivatives of the Proteasome Deubiquitinase Inhibitor bâ€<scp>AP</scp>15. Chemical Biology and Drug Design, 2015, 86, 1036-1048.	3.2	83
53	Selective Targeting of Extracellular Insulin-Degrading Enzyme by Quasi-Irreversible Thiol-Modifying Inhibitors. ACS Chemical Biology, 2015, 10, 2716-2724.	3.4	22
54	Targeted inhibition of the deubiquitinating enzymes, <scp>USP</scp>14 and <scp>UCHL</scp>5, induces proteotoxic stress and apoptosis in <scp>W</scp>aldenstrÃ¶m macroglobulinaemia tumour cells. British Journal of Haematology, 2015, 169, 377-390.	2.5	55

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55	Phosphorylation by PINK1 Releases the UBL Domain and Initializes the Conformational Opening of the E3 Ubiquitin Ligase Parkin. PLoS Computational Biology, 2014, 10, e1003935.	3.2	95
56	Aggregation-prone c9FTD/ALS poly(GA) RAN-translated proteins cause neurotoxicity by inducing ER stress. Acta Neuropathologica, 2014, 128, 505-524.	7.7	284
57	Targeted manipulation of the sortilinâ€“progranulin axis rescues progranulin haploinsufficiency. Human Molecular Genetics, 2014, 23, 1467-1478.	2.9	96
58	An integrated approach to the discovery of potent agelastatin A analogues for brain tumors: chemical synthesis and biological, physicochemical and CNS pharmacokinetic analyses. MedChemComm, 2013, 4, 1093.	3.4	19
59	Unconventional Translation of C9ORF72 GGGGCC Expansion Generates Insoluble Polypeptides Specific to c9FTD/ALS. Neuron, 2013, 77, 639-646.	8.1	962
60	Optimization of Peptide Hydroxamate Inhibitors of Insulin-Degrading Enzyme Reveals Marked Substrate-Selectivity. Journal of Medicinal Chemistry, 2013, 56, 2246-2255.	6.4	51
61	Antisense transcripts of the expanded C9ORF72 hexanucleotide repeat form nuclear RNA foci and undergo repeat-associated non-ATG translation in c9FTD/ALS. Acta Neuropathologica, 2013, 126, 829-844.	7.7	506
62	Long-range Electrostatic Complementarity Governs Substrate Recognition by Human Chymotrypsin C, a Key Regulator of Digestive Enzyme Activation. Journal of Biological Chemistry, 2013, 288, 9848-9859.	3.4	32
63	Stearoyl-CoA Desaturase 1 Is a Novel Molecular Therapeutic Target for Clear Cell Renal Cell Carcinoma. Clinical Cancer Research, 2013, 19, 2368-2380.	7.0	214
64	The dual functions of the extreme N-terminus of TDP-43 in regulating its biological activity and inclusion formation. Human Molecular Genetics, 2013, 22, 3112-3122.	2.9	156
65	Inhibition of Prohormone Convertases PC1/3 and PC2 by 2,5-Dideoxystreptamine Derivatives. Molecular Pharmacology, 2012, 81, 440-454.	2.3	24
66	Pharmacokinetics of Agelastatin A in the central nervous system. MedChemComm, 2012, 3, 233-237.	3.4	15
67	Pharmacokinetics of bendamustine in the central nervous system: chemoinformatic screening followed by validation in a murine model. MedChemComm, 2012, 3, 1526.	3.4	8
68	An Induced-Fit Docking Method for Refining Drug-Receptor Interactions Derived from Maxwellian-Assessor Nanoprobes (Quantum Mechanics-Based Criterion Assessment) Placed Over Adaptive Intervals of Molecular Dynamics Sampling. Biophysical Journal, 2012, 102, 171a-172a.	0.5	3
69	Motion of transfer RNA from the A/T state into the Aâ€site using docking and simulations. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2489-2500.	2.6	52
70	Inhibition of PC1/3 and PC2 by 2,5â€dideoxystreptamine derivatives. FASEB Journal, 2012, 26, 557.2.	0.5	0
71	Molecular dynamics simulations of human DNA methyltransferase 3B with selective inhibitor nanaomycin A. Journal of Structural Biology, 2011, 176, 185-191.	2.8	77
72	Integrating Virtual Screening and Combinatorial Chemistry for Accelerated Drug Discovery. Combinatorial Chemistry and High Throughput Screening, 2011, 14, 475-487.	1.1	122

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73	Advances in the computational development of DNA methyltransferase inhibitors. Drug Discovery Today, 2011, 16, 418-425.	6.4	80
74	Comparative molecular field analysis (CoMFA) and comparative molecular similarity indices analysis (CoMSIA) of some benzimidazole derivatives with trichomonicidal activity. European Journal of Medicinal Chemistry, 2011, 46, 3499-3508.	5.5	23
75	Inter-ring rotation of apolipoprotein A-I protein monomers for the double-belt model using biased molecular dynamics. Journal of Molecular Graphics and Modelling, 2011, 29, 1006-1014.	2.4	38
76	Examinations of tRNA Range of Motion Using Simulations of Cryo-EM Microscopy and X-Ray Data. Journal of Biophysics, 2011, 2011, 1-11.	0.8	40
77	Nanaomycin A Selectively Inhibits DNMT3B and Reactivates Silenced Tumor Suppressor Genes in Human Cancer Cells. Molecular Cancer Therapeutics, 2010, 9, 3015-3023.	4.1	154
78	A Structural Model for the Large Subunit of the Mammalian Mitochondrial Ribosome. Journal of Molecular Biology, 2006, 358, 193-212.	4.2	85
79	Molecular Modeling and Phenotypic Description of a Patient with a Novel Exonic Deletion of <i>GALNS</i> with Resultant Morquio Syndrome with Two Successful Pregnancies. Molecular Syndromology, 0, , 1-8.	0.8	0