Neil Q Mcdonald

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7648328/publications.pdf

Version: 2024-02-01

83 papers	13,615 citations	53794 45 h-index	58581 82 g-index
90 all docs	90 docs citations	90 times ranked	22587 citing authors

#	Article	IF	Citations
1	Discovery of N-Trisubstituted Pyrimidine Derivatives as Type I RET and RET Gatekeeper Mutant Inhibitors with a Novel Kinase Binding Pose. Journal of Medicinal Chemistry, 2022, 65, 1536-1551.	6.4	4
2	Bimodal regulation of axonal transport by the GDNF-RET signalling axis in healthy and diseased motor neurons. Cell Death and Disease, 2022, 13, .	6.3	9
3	Equivocal, explicit and emergent actions of PKC isoforms in cancer. Nature Reviews Cancer, 2021, 21, 51-63.	28.4	37
4	A two-site flexible clamp mechanism for RET-GDNF-GFRÎ±1 assembly reveals both conformational adaptation and strict geometric spacing. Structure, 2021, 29, 694-708.e7.	3.3	6
5	Co-ordinated control of the Aurora B abscission checkpoint by PKCÎµ complex assembly, midbody recruitment and retention. Biochemical Journal, 2021, 478, 2247-2263.	3.7	3
6	A genetically-encoded crosslinker screen identifies SERBP1 as a PKCÎµ substrate influencing translation and cell division. Nature Communications, 2021, 12, 6934.	12.8	7
7	Activation of the receptor tyrosine kinase RET improves long-term hematopoietic stem cell outgrowth and potency. Blood, 2020, 136, 2535-2547.	1.4	21
8	Cryo-EM structures of the XPF-ERCC1 endonuclease reveal how DNA-junction engagement disrupts an auto-inhibited conformation. Nature Communications, 2020, 11, 1120.	12.8	24
9	Bioisosteric Discovery of NPA101.3, a Second-Generation RET/VEGFR2 Inhibitor Optimized for Single-Agent Polypharmacology. Journal of Medicinal Chemistry, 2020, 63, 4506-4516.	6.4	20
10	Optimised oligonucleotide substrates to assay XPF-ERCC1 nuclease activity for the discovery of DNA repair inhibitors. Chemical Communications, 2019, 55, 11671-11674.	4.1	2
11	RPEL-family rhoGAPs link Rac/Cdc42 GTP loading to G-actin availability. Nature Cell Biology, 2019, 21, 845-855.	10.3	24
12	Competitive Inhibition of aPKC by Par-3/Bazooka and Other Substrates. Developmental Cell, 2019, 49, 680.	7.0	2
13	The Rho-family GEF FARP2 is activated by aPKCÎ¹ to control polarity and tight junction formation. Journal of Cell Science, 2019, 132, .	2.0	15
14	Activation of the Receptor Tyrosine Kinase (RET) By GDNF/GFRÎ±1 Improves Cord Blood-Derived HSC in Vitro expansion and In Vivo engraftment. Blood, 2019, 134, 1924-1924.	1.4	0
15	A secondary RET mutation in the activation loop conferring resistance to vandetanib. Nature Communications, 2018, 9, 625.	12.8	75
16	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. Science Translational Medicine, 2017, 9, .	12.4	55
17	RET Functions as a Dual-Specificity Kinase that Requires Allosteric Inputs from Juxtamembrane Elements. Cell Reports, 2016, 17, 3319-3332.	6.4	28
18	Exon Skipping in the RET Gene Encodes Novel Isoforms That Differentially Regulate RET Protein Signal Transduction. Journal of Biological Chemistry, 2016, 291, 16249-16262.	3.4	10

#	Article	IF	Citations
19	aPKC Inhibition by Par3 CR3 Flanking Regions Controls Substrate Access and Underpins Apical-Junctional Polarization. Developmental Cell, 2016, 38, 384-398.	7.0	56
20	The discovery of 2-substituted phenol quinazolines as potent RET kinase inhibitors with improved KDR selectivity. European Journal of Medicinal Chemistry, 2016, 112, 20-32.	5.5	32
21	Structures of the human Pals1 PDZ domain with and without ligand suggest gated access of Crb to the PDZ peptide-binding groove. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 555-564.	2.5	24
22	Functional implications of assigned, assumed and assembled PKC structures. Biochemical Society Transactions, 2014, 42, 35-41.	3.4	4
23	RET Recognition of GDNF-GFRÎ±1 Ligand by a Composite Binding Site Promotes Membrane-Proximal Self-Association. Cell Reports, 2014, 8, 1894-1904.	6.4	51
24	Oncogenic RET Kinase Domain Mutations Perturb the Autophosphorylation Trajectory by Enhancing Substrate Presentation In trans. Molecular Cell, 2014, 53, 738-751.	9.7	55
25	Architecture and DNA Recognition Elements of the Fanconi Anemia FANCM-FAAP24 Complex. Structure, 2013, 21, 1648-1658.	3.3	26
26	14-3-3 Proteins Interact with a Hybrid Prenyl-Phosphorylation Motif to Inhibit G Proteins. Cell, 2013, 153, 640-653.	28.9	93
27	Adenosine-binding motif mimicry and cellular effects of a thieno[2,3-d]pyrimidine-based chemical inhibitor of atypical protein kinase C isoenzymes. Biochemical Journal, 2013, 451, 329-342.	3.7	51
28	A Cancer-Associated Mutation in Atypical Protein Kinase CÎ¹ Occurs in a Substrate-Specific Recruitment Motif. Science Signaling, 2013, 6, ra82.	3.6	25
29	A winged helix domain in human MUS81 binds DNA and modulates the endonuclease activity of MUS81 complexes. Nucleic Acids Research, 2013, 41, 9741-9752.	14.5	14
30	G-actin regulates the shuttling and PP1 binding of the RPEL protein Phactr1 to control actomyosin assembly. Journal of Cell Science, 2012, 125, 5860-5872.	2.0	54
31	Fluorescence-based incision assay for human XPFâ€“ERCC1 activity identifies important elements of DNA junction recognition. Nucleic Acids Research, 2012, 40, e101-e101.	14.5	24
32	Structures of the Phactr1 RPEL Domain and RPEL Motif Complexes with G-Actin Reveal the Molecular Basis for Actin Binding Cooperativity. Structure, 2012, 20, 1960-1970.	3.3	32
33	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892.	27.0	6,769
34	Focal Adhesion Kinase (FAK) Binds RET Kinase via Its FERM Domain, Priming a Direct and Reciprocal RET-FAK Transactivation Mechanism. Journal of Biological Chemistry, 2011, 286, 17292-17302.	3.4	50
35	Structure of a Pentavalent G-Actinâ€¢MRTF-A Complex Reveals How G-Actin Controls Nucleocytoplasmic Shuttling of a Transcriptional Coactivator. Science Signaling, 2011, 4, ra40.	3.6	90
36	Molecular Recognition of the Tes LIM2â€“3 Domains by the Actin-related Protein Arp7A. Journal of Biological Chemistry, 2011, 286, 11543-11554.	3.4	36

#	Article	IF	Citations
37	Synthesis, structureâ€“activity relationship and crystallographic studies of 3-substituted indolin-2-one RET inhibitors. Bioorganic and Medicinal Chemistry, 2010, 18, 1482-1496.	3.0	64
38	Mammal-restricted elements predispose human RET to folding impairment by HSCR mutations. Nature Structural and Molecular Biology, 2010, 17, 726-731.	8.2	47
39	Identification of tyrosine 806 as a molecular determinant of RET kinase sensitivity to ZD6474. Endocrine-Related Cancer, 2009, 16, 233-241.	3.1	37
40	Protein kinase C interventionâ€”the state of play. Current Opinion in Cell Biology, 2009, 21, 268-279.	5.4	88
41	Recognition of an intraâ€chain tandem 14â€3â€3 binding site within PKCÎµ. EMBO Reports, 2009, 10, 983-989.	4.5	86
42	Molecular basis for G-actin binding to RPEL motifs from the serum response factor coactivator MAL. EMBO Journal, 2008, 27, 3198-3208.	7.8	92
43	Structure of a Conserved Dimerization Domain within the F-box Protein Fbxo7 and the PI31 Proteasome Inhibitor. Journal of Biological Chemistry, 2008, 283, 22325-22335.	3.4	83
44	Structural and Functional Relationships of the XPF/MUS81 Family of Proteins. Annual Review of Biochemistry, 2008, 77, 259-287.	11.1	244
45	Identification of FAAP24, a Fanconi Anemia Core Complex Protein that Interacts with FANCM. Molecular Cell, 2007, 25, 331-343.	9.7	264
46	Tes, a Specific Mena Interacting Partner, Breaks the Rules for EVH1 Binding. Molecular Cell, 2007, 28, 1071-1082.	9.7	66
47	The mitochondrial protease HtrA2 is regulated by Parkinson's disease-associated kinase PINK1. Nature Cell Biology, 2007, 9, 1243-1252.	10.3	441
48	Disruption of methylarginine metabolism impairs vascular homeostasis. Nature Medicine, 2007, 13, 198-203.	30.7	370
49	A Small-Molecule Inhibitor for Phosphatase and Tensin Homologue Deleted on Chromosome 10 (PTEN). ACS Chemical Biology, 2006, 1, 780-790.	3.4	131
50	A heterozygous effect for PINK1 mutations in Parkinson's disease?. Annals of Neurology, 2006, 60, 414-419.	5.3	149
51	Structure and Chemical Inhibition of the RET Tyrosine Kinase Domain. Journal of Biological Chemistry, 2006, 281, 33577-33587.	3.4	237
52	Structure of an XPF endonuclease with and without DNA suggests a model for substrate recognition. EMBO Journal, 2005, 24, 895-905.	7.8	105
53	Transforming activity of Fbxo7 is mediated specifically through regulation of cyclin D/cdk6. EMBO Journal, 2005, 24, 3104-3116.	7.8	80
54	The solution structure of the Josephin domain of ataxin-3: Structural determinants for molecular recognition. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10493-10498.	7.1	176

#	Article	IF	Citations
55	Phosphorylation of a Distinct Structural Form of Phosphatidylinositol Transfer Protein Î± at Ser166 by Protein Kinase C Disrupts Receptor-mediated Phospholipase C Signaling by Inhibiting Delivery of Phosphatidylinositol to Membranes. Journal of Biological Chemistry, 2004, 279, 47159-47171.	3.4	21
56	Molecular interactions of fission yeast Skp1 and its role in the DNA damage checkpoint. Genes To Cells, 2004, 9, 367-382.	1.2	34
57	Structure-Function Analysis of Phosphatidylinositol Transfer Protein Alpha Bound to Human Phosphatidylinositol. Structure, 2004, 12, 317-326.	3.3	90
58	Crystallization of the xeroderma pigmentosum group F endonuclease fromAeropyrum pernix. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1658-1661.	2.5	2
59	The Mycobacterium tuberculosis ino1 gene is essential for growth and virulence. Molecular Microbiology, 2004, 51, 1003-1014.	2.5	85
60	S -nitrosylation of dimethylarginine dimethylaminohydrolase regulates enzyme activity: Further interactions between nitric oxide synthase and dimethylarginine dimethylaminohydrolase. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13527-13532.	7.1	278
61	The Dual Mechanism of Separase Regulation by Securin. Current Biology, 2002, 12, 973-982.	3.9	131
62	Crystal Structure of Inositol 1-Phosphate Synthase from Mycobacterium tuberculosis, a Key Enzyme in Phosphatidylinositol Synthesis. Structure, 2002, 10, 393-402.	3.3	62
63	Structure-activity relationship of the p55 TNF receptor death domain and its lymphoproliferation mutants. FEBS Journal, 2001, 268, 1382-1391.	0.2	5
64	Structural insights into the hydrolysis of cellular nitric oxide synthase inhibitors by dimethylarginine dimethylaminohydrolase. Nature Structural Biology, 2001, 8, 679-683.	9.7	200
65	SAC1 Encodes a Regulated Lipid Phosphoinositide Phosphatase, Defects in Which Can Be Suppressed by the Homologous Inp52p and Inp53p Phosphatases. Journal of Biological Chemistry, 2000, 275, 801-808.	3.4	108
66	The three-dimensional solution structure and dynamic properties of the human FADD death domain 1 1Edited by A. Fersht. Journal of Molecular Biology, 2000, 302, 171-188.	4.2	89
67	Crystal structure of the MAPK phosphatase Pyst1 catalytic domain and implications for regulated activation. Nature Structural Biology, 1999, 6, 174-181.	9.7	141
68	Functional evaluation of tumour-specific variants of p16INK4a/CDKN2A: correlation with protein structure information. Oncogene, 1999, 18, 5423-5434.	5.9	69
69	Overcoming inhibitions: subversion of CKI function by viral cyclins. Trends in Biochemical Sciences, 1999, 24, 116-120.	7.5	24
70	Ankyrin for clues about the function 0fp16INK4a. Nature Structural Biology, 1998, 5, 85-88.	9.7	11
71	Preliminary X-ray analysis of a C2-like domain from protein kinase C-Î´. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 693-696.	2.5	4
72	Structure of mouse 7S NGF: a complex of nerve growth factor with four binding proteins. Structure, 1997, 5, 1275-1285.	3.3	68

#	Article	IF	Citations
73	Structure of Î²2-bungarotoxin: potassium channel binding by Kunitz modules and targeted phospholipase action. Structure, 1995, 3, 1109-1119.	3.3	107
74	Structural Determinants of Neurotrophin Action. Journal of Biological Chemistry, 1995, 270, 19669-19672.	3.4	65
75	Localization of Functional Receptor Epitopes on the Structure of Ciliary Neurotrophic Factor Indicates a Conserved, Function-related Epitope Topography among Helical Cytokines. Journal of Biological Chemistry, 1995, 270, 14007-14014.	3.4	58
76	Nerve growth factor: Structure/function relationships. Protein Science, 1994, 3, 1901-1913.	7.6	69
77	Topological similarities in TGF-Î²2, PDGF-BB and NGF define a superfamily of polypeptide growth factors. Structure, 1993, 1, 153-159.	3.3	152
78	Does Noggin head a new class of Kunitz domain?. Trends in Biochemical Sciences, 1993, 18, 208-209.	7.5	13
79	Nerve growth factor revisited. Trends in Biochemical Sciences, 1993, 18, 48-52.	7.5	94
80	McDonald and colleagues reply. Trends in Biochemical Sciences, 1993, 18, 425-426.	7.5	1
81	A structural superfamily of growth factors containing a cystine knot motif. Cell, 1993, 73, 421-424.	28.9	525
82	New protein fold revealed by a 2.3-Ã... resolution crystal structure of nerve growth factor. Nature, 1991, 354, 411-414.	27.8	500
83	Structure-function relationships of growth factors and their receptors. British Medical Bulletin, 1989, 45, 554-569.	6.9	19