Peter M Colman

List of Publications by Year
in descending order

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93 papers	15,115 citations	41258 49 h-index	43802 91 g-index
129 all docs	129 docs citations	129 times ranked	13573 citing authors

#	Article	IF	Citations
1	Ion currents through Kir potassium channels are gated by anionic lipids. Nature Communications, 2022, 13, 490.	5.8	9
2	The Bak core dimer focuses triacylglycerides in the membrane. Biophysical Journal, 2022, 121, 347-360.	0.2	1
3	Structure of the BAK-activating antibody 7D10 bound to BAK reveals an unexpected role for the Î±1-Î±2 loop in BAK activation. Cell Death and Differentiation, 2022, 29, 1757-1768.	5.0	4
4	Optimization of Benzothiazole and Thiazole Hydrazones as Inhibitors of Schistosome BCL-2. ACS Infectious Diseases, 2021, 7, 1143-1163.	1.8	3
5	Structure-Guided Development of Potent Benzoylurea Inhibitors of BCL-X_L and BCL-2. Journal of Medicinal Chemistry, 2021, 64, 5447-5469.	2.9	5
6	Structure of detergent-activated BAK dimers derived from the inert monomer. Molecular Cell, 2021, 81, 2123-2134.e5.	4.5	26
7	EBV BCL-2 homologue BHRF1 drives chemoresistance and lymphomagenesis by inhibiting multiple cellular pro-apoptotic proteins. Cell Death and Differentiation, 2020, 27, 1554-1568.	5.0	35
8	BAK core dimers bind lipids and can be bridged by them. Nature Structural and Molecular Biology, 2020, 27, 1024-1031.	3.6	49
9	A small molecule interacts with VDAC2 to block mouse BAK-driven apoptosis. Nature Chemical Biology, 2019, 15, 1057-1066.	3.9	30
10	Structures of BCL-2 in complex with venetoclax reveal the molecular basis of resistance mutations. Nature Communications, 2019, 10, 2385.	5.8	139
11	Insights into pituitary tumorigenesis: from Sanger sequencing to next-generation sequencing and beyond. Expert Review of Endocrinology and Metabolism, 2019, 14, 399-418.	1.2	8
12	Ensemble Properties of Bax Determine Its Function. Structure, 2018, 26, 1346-1359.e5.	1.6	34
13	Colin Wesley Ward 1943â€“2017. Historical Records of Australian Science, 2018, 29, 191.	0.3	0
14	Dysglycemia and Index60 as Prediagnostic End Points for Type 1 Diabetes Prevention Trials. Diabetes Care, 2017, 40, 1494-1499.	4.3	28
15	Conversion of Bim-BH3 from Activator to Inhibitor of Bak through Structure-Based Design. Molecular Cell, 2017, 68, 659-672.e9.	4.5	57
16	Vale Colin Wardâ€”A Leader in Receptor Structural Biology. Frontiers in Endocrinology, 2017, 8, 95.	1.5	0
17	Physiological restraint of Bak by Bcl-x_L is essential for cell survival. Genes and Development, 2016, 30, 1240-1250.	2.7	40
18	Targeting BCL-2-like Proteins to Kill Cancer Cells. Trends in Cancer, 2016, 2, 443-460.	3.8	114

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19	Intense focal pituitary FDG uptake due to intravascular large Bâ€cell lymphoma in pyrexia of unknown origin. American Journal of Hematology, 2016, 91, 1167-1168.	2.0	2
20	The Functional Differences between Pro-survival and Pro-apoptotic B Cell Lymphoma 2 (Bcl-2) Proteins Depend on Structural Differences in Their Bcl-2 Homology 3 (BH3) Domains. Journal of Biological Chemistry, 2014, 289, 36001-36017.	1.6	33
21	Crystallography and New Medicines: Examples from Influenza and Cell Death. Australian Journal of Chemistry, 2014, 67, 1720.	0.5	2
22	NMR studies of interactions between Bax and BH3 domain-containing peptides in the absence and presence of CHAPS. Archives of Biochemistry and Biophysics, 2014, 545, 33-43.	1.4	11
23	Structural Insight into BH3 Domain Binding of Vaccinia Virus Antiapoptotic F1L. Journal of Virology, 2014, 88, 8667-8677.	1.5	37
24	De-Novo Designed Library of Benzoylureas as Inhibitors of BCL-X_L: Synthesis, Structural and Biochemical Characterization. Journal of Medicinal Chemistry, 2014, 57, 1323-1343.	2.9	33
25	Structure-Guided Rescaffolding of Selective Antagonists of BCL-X_L. ACS Medicinal Chemistry Letters, 2014, 5, 662-667.	1.3	37
26	Bak Core and Latch Domains Separate during Activation, and Freed Core Domains Form Symmetric Homodimers. Molecular Cell, 2014, 55, 938-946.	4.5	140
27	Discovery of a Potent and Selective BCL-X_L Inhibitor with in Vivo Activity. ACS Medicinal Chemistry Letters, 2014, 5, 1088-1093.	1.3	242
28	Early days in drug discovery by crystallography â€“ personal recollections. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 60-62.	0.3	3
29	Bax Crystal Structures Reveal How BH3 Domains Activate Bax and Nucleate Its Oligomerization to Induce Apoptosis. Cell, 2013, 152, 519-531.	13.5	491
30	Structure-guided design of a selective BCL-XL inhibitor. Nature Chemical Biology, 2013, 9, 390-397.	3.9	324
31	Discovery of Potent and Selective Benzothiazole Hydrazone Inhibitors of Bcl-X_L. Journal of Medicinal Chemistry, 2013, 56, 5514-5540.	2.9	60
32	Sheeppox Virus SPPV14 Encodes a Bcl-2-Like Cell Death Inhibitor That Counters a Distinct Set of Mammalian Proapoptotic Proteins. Journal of Virology, 2012, 86, 11501-11511.	1.5	41
33	The Dendritic Cell Receptor Clec9A Binds Damaged Cells via Exposed Actin Filaments. Immunity, 2012, 36, 646-657.	6.6	272
34	Evaluation of Diverse Î±/Î²-Backbone Patterns for Functional Î±-Helix Mimicry: Analogues of the Bim BH3 Domain. Journal of the American Chemical Society, 2012, 134, 315-323.	6.6	144
35	Crystal Structure of a BCL-W Domain-Swapped Dimer: Implications for the Function of BCL-2 Family Proteins. Structure, 2011, 19, 1467-1476.	1.6	25
36	Structural Basis of Bclâ€x_L Recognition by a BH3â€Mimetic Î±/Î²â€Peptide Generated by Sequenceâ€Based Design. ChemBioChem, 2011, 12, 2025-2032.	1.3	56

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37	Mutation to Bax beyond the BH3 Domain Disrupts Interactions with Pro-survival Proteins and Promotes Apoptosis. Journal of Biological Chemistry, 2011, 286, 7123-7131.	1.6	96
38	Discovery and molecular characterization of a Bcl-2â€“regulated cell death pathway in schistosomes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6999-7003.	3.3	53
39	Vaccinia Virus F1L Interacts with Bak Using Highly Divergent Bcl-2 Homology Domains and Replaces the Function of Mcl-1. Journal of Biological Chemistry, 2010, 285, 4695-4708.	1.6	26
40	Structural Basis for Apoptosis Inhibition by Epstein-Barr Virus BHRF1. PLoS Pathogens, 2010, 6, e1001236.	2.1	99
41	Novel Bcl-2 Homology-3 Domain-like Sequences Identified from Screening Randomized Peptide Libraries for Inhibitors of the Pro-survival Bcl-2 Proteins. Journal of Biological Chemistry, 2009, 284, 31315-31326.	1.6	29
42	Conformational Changes in Bcl-2 Pro-survival Proteins Determine Their Capacity to Bind Ligands. Journal of Biological Chemistry, 2009, 284, 30508-30517.	1.6	79
43	Highâ€Resolution Structural Characterization of a Helical Î±/Î²â€Peptide Foldamer Bound to the Antiâ€Apoptotic Protein Bclâ€x_L. Angewandte Chemie - International Edition, 2009, 48, 4318-4322.	7.2	143
44	Structural Insights into the Protease-like Antigen Plasmodium falciparum SERA5 and Its Noncanonical Active-Site Serine. Journal of Molecular Biology, 2009, 392, 154-165.	2.0	35
45	New Antivirals and Drug Resistance. Annual Review of Biochemistry, 2009, 78, 95-118.	5.0	65
46	BCL-2 family antagonists for cancer therapy. Nature Reviews Drug Discovery, 2008, 7, 989-1000.	21.5	549
47	To Trigger Apoptosis, Bak Exposes Its BH3 Domain and Homodimerizes via BH3:Groove Interactions. Molecular Cell, 2008, 30, 369-380.	4.5	296
48	A novel BH3 ligand that selectively targets Mcl-1 reveals that apoptosis can proceed without Mcl-1 degradation. Journal of Cell Biology, 2008, 180, 341-355.	2.3	157
49	Structural insights into the degradation of Mcl-1 induced by BH3 domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6217-6222.	3.3	397
50	A Structural Viral Mimic of Prosurvival Bcl-2:ÂAÂPivotal Role for Sequestering ProapoptoticÂBax and Bak. Molecular Cell, 2007, 25, 933-942.	4.5	125
51	Structure of Leishmania mexicana Phosphomannomutase Highlights Similarities with Human Isoforms. Journal of Molecular Biology, 2006, 363, 215-227.	2.0	38
52	Structure of glyceraldehyde-3-phosphate dehydrogenase fromPlasmodium falciparum. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1213-1221.	2.5	28
53	Differential Targeting of Prosurvival Bcl-2 Proteins by Their BH3-Only Ligands Allows Complementary Apoptotic Function. Molecular Cell, 2005, 17, 393-403.	4.5	1,639
54	Zanamivir: an influenza virus neuraminidase inhibitor. Expert Review of Anti-Infective Therapy, 2005, 3, 191-199.	2.0	24

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55	Structure of the Haemagglutinin-neuraminidase from Human Parainfluenza Virus Type III. Journal of Molecular Biology, 2004, 335, 1343-1357.	2.0	200
56	Tethered Neuraminidase Inhibitors That Bind an Influenza Virus: A First Step Towards a Diagnostic Method for Influenza. Angewandte Chemie - International Edition, 2003, 42, 3118-3121.	7.2	22
57	The structural biology of type I viral membrane fusion. Nature Reviews Molecular Cell Biology, 2003, 4, 309-319.	16.1	408
58	Specificity and Promiscuity in Protein - Ligand and Protein - Protein Interactions. Australian Journal of Chemistry, 2003, 56, 763.	0.5	3
59	Modelling the structure of the fusion protein from human respiratory syncytial virus. Protein Engineering, Design and Selection, 2002, 15, 365-371.	1.0	28
60	Structural Studies of the Resistance of Influenza Virus Neuramindase to Inhibitors. Journal of Medicinal Chemistry, 2002, 45, 2207-2212.	2.9	125
61	The Trypanosomal Trans-Sialidase. Structure, 2002, 10, 1466-1468.	1.6	10
62	Sialidase inhibitors related to zanamivir. Further SAR studies of 4-amino-4H-pyran-2-carboxylic acid-6-propylamides. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 669-673.	1.0	46
63	Cloning, Expression, and Crystallization of the Fusion Protein of Newcastle Disease Virus. Virology, 2001, 290, 290-299.	1.1	31
64	Analysis of inhibitor binding in influenza virus neuraminidase. Protein Science, 2001, 10, 689-696.	3.1	97
65	The Structure of the Fusion Glycoprotein of Newcastle Disease Virus Suggests a Novel Paradigm for the Molecular Mechanism of Membrane Fusion. Structure, 2001, 9, 255-266.	1.6	201
66	Dihydropyrancarboxamides Related to Zanamivir:Â A New Series of Inhibitors of Influenza Virus Sialidases. 2. Crystallographic and Molecular Modeling Study of Complexes of 4-Amino-4H-pyran-6-carboxamides and Sialidase from Influenza Virus Types A and B. Journal of Medicinal Chemistry, 1998, 41, 798-807.	2.9	197
67	Drug design against a shifting target: a structural basis for resistance to inhibitors in a variant of influenza virus neuraminidase. Structure, 1998, 6, 735-746.	1.6	210
68	Three-dimensional structures of single-chain Fv-neuraminidase complexes. Journal of Molecular Biology, 1998, 279, 901-910.	2.0	32
69	Mutations in a Conserved Residue in the Influenza Virus Neuraminidase Active Site Decreases Sensitivity to Neu5Ac2en-Derived Inhibitors. Journal of Virology, 1998, 72, 2456-2462.	1.5	175
70	Electrostatic complementarity at protein/protein interfaces 1 1Edited by B. Honig. Journal of Molecular Biology, 1997, 268, 570-584.	2.0	255
71	Novel inhibitors of influenza sialidases related to GG167 structure-activity, crystallographic and Molecular dynamics studies with 4H-pyran-2-carboxylic acid 6-carboxamides. Bioorganic and Medicinal Chemistry Letters, 1996, 6, 2931-2936.	1.0	58
72	Threeâ€dimensional structure of the complex of 4â€guanidinoâ€Neu5Ac2en and influenza virus neuraminidase. Protein Science, 1995, 4, 1081-1087.	3.1	176

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73	Generation and Characterization of an Influenza Virus Neuraminidase Variant with Decreased Sensitivity to the Neuraminidase-Specific Inhibitor 4-Guanidino-Neu5Ac2en. Virology, 1995, 214, 475-484.	1.1	155
74	The Function of the Hypothalamicâ€“Pituitaryâ€“Adrenal Axis in Alzheimer's Disease. British Journal of Psychiatry, 1994, 165, 650-657.	1.7	18
75	The three-dimensional structure of N -acetylneuraminate lyase from Escherichia coli. Structure, 1994, 2, 361-369.	1.6	123
76	The structure of a complex between the NC10 antibody and influenza virus neuraminidase and comparison with the overlapping binding site of the NC41 antibody. Structure, 1994, 2, 733-746.	1.6	157
77	Recombinant anti-sialidase single-chain variable fragment antibody. Characterization, formation of dimer and higher-molecular-mass multimers and the solution of the crystal structure of the single-chain variable fragment/sialidase complex. FEBS Journal, 1994, 221, 151-157.	0.2	115
78	Recombinant antineuraminidase single chain antibody: Expression, characterization, and crystallization in complex with antigen. Proteins: Structure, Function and Bioinformatics, 1993, 16, 57-63.	1.5	58
79	Rational design of potent sialidase-based inhibitors of influenza virus replication. Nature, 1993, 363, 418-423.	13.7	1,823
80	Shape Complementarity at Protein/Protein Interfaces. Journal of Molecular Biology, 1993, 234, 946-950.	2.0	1,231
81	The structure of the complex between influenza virus neuraminidase and sialic acid, the viral receptor. Proteins: Structure, Function and Bioinformatics, 1992, 14, 327-332.	1.5	399
82	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	13.7	1,199
83	The disulphide bonds of an Asian influenza virus neuraminidase. FEBS Letters, 1983, 153, 29-33.	1.3	12
84	The Structure of Cucurbitin: Subunit Symmetry and Organization in situ. FEBS Journal, 1980, 103, 585-588.	0.2	30
85	Crystal structure of the human Fab fragment Kol and its comparison with the intact Kol molecule. Journal of Molecular Biology, 1978, 121, 441-459.	2.0	62
86	Preliminary crystallographic data for a copper-containing protein, plastocyanin. Journal of Molecular Biology, 1977, 110, 187-189.	2.0	23
87	Preliminary crystallographic data for a basic copper-containing protein from cucumber seedlings. Journal of Molecular Biology, 1977, 112, 649-650.	2.0	30
88	Structure of the human antibody molecule kol (immunoglobulin G1): An electron density map at 5 Ã... resolution. Journal of Molecular Biology, 1976, 100, 257-278.	2.0	160
89	The use of rotation and translation functions in the interpretation of low resolution electron density maps. Journal of Molecular Biology, 1976, 100, 278-282.	2.0	13
90	Crystallographic Structural Studies of a Human Fc-Fragment. I. An Electron-Density Map at 4 Ã... Resolution and a Partial Model. Hoppe-Seyler's Zeitschrift FÃ¼r Physiologische Chemie, 1976, 357, 435-446.	1.7	56

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91	Crystallographic structure studies of an IgG molecule and an Fc fragment. Nature, 1976, 264, 415-420.	13.7	423
92	Crystallographic Structural Studies of a Human Fc Fragment. II. A Complete Model Based on a Fourier Map at 3.5 Å... Resolution. Hoppe-Seyler's Zeitschrift FÃ¼r Physiologische Chemie, 1976, 357, 1421-1434.	1.7	120
93	Crystal and Molecular Structure of a Dimer Composed of the Variable Portions of the Bence-Jones Protein REI. FEBS Journal, 1974, 45, 513-524.	0.2	220