

# Martin A Walsh

## List of Publications by Year in descending order

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83  
papers

4,473  
citations

87888

38  
h-index

110387

64  
g-index

90  
all docs

90  
docs citations

90  
times ranked

6771  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystallographic and electrophilic fragment screening of the SARS-CoV-2 main protease. <i>Nature Communications</i> , 2020, 11, 5047.	12.8	376
2	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. <i>Structure</i> , 2004, 12, 341-353.	3.3	225
3	Structural basis of YAP recognition by TEAD4 in the Hippo pathway. <i>Genes and Development</i> , 2010, 24, 290-300.	5.9	202
4	<i>MxCuBE</i>: a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	2.4	193
5	West Nile Virus Core Protein. <i>Structure</i> , 2004, 12, 1157-1163.	3.3	159
6	Crystal structures of penicillin acylase enzyme-substrate complexes: structural insights into the catalytic mechanism 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2001, 313, 139-150.	4.2	153
7	The Structural Biology Center 19ID undulator beamline: facility specifications and protein crystallographic results. <i>Journal of Synchrotron Radiation</i> , 2006, 13, 30-45.	2.4	143
8	ISPyB: an information management system for synchrotron macromolecular crystallography. <i>Bioinformatics</i> , 2011, 27, 3186-3192.	4.1	135
9	Inhibition of the Hepatitis C Virus NS3/4A Protease. <i>Journal of Biological Chemistry</i> , 2000, 275, 7152-7157.	3.4	116
10	Who checks the checkers? four validation tools applied to eight atomic resolution structures 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 276, 417-436.	4.2	114
11	Crystal Structure and Functional Analysis of the Eukaryotic Class II Release Factor eRF3 from <i>S. pombe</i> . <i>Molecular Cell</i> , 2004, 14, 233-245.	9.7	112
12	Structural basis for translational inhibition by the tumour suppressor Pcd4. <i>EMBO Journal</i> , 2009, 28, 274-285.	7.8	110
13	Taking MAD to the extreme: ultrafast protein structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1168-1173.	2.5	101
14	Refinement of Triclinic Hen Egg-White Lysozyme at Atomic Resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 522-546.	2.5	100
15	Automation of sample mounting for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1251-1259.	2.5	99
16	Sulfur Single-wavelength Anomalous Diffraction Crystal Structure of a Pheromone-Binding Protein from the Honeybee <i>Apis mellifera</i> L. <i>Journal of Biological Chemistry</i> , 2004, 279, 4459-4464.	3.4	98
17	Crystal structure of an <sc>HD</sc> domain cyclic<sc>GMP</sc> phosphodiesterase reveals an enzyme with a novel trinuclear catalytic iron centre. <i>Molecular Microbiology</i> , 2014, 91, 26-38.	2.5	92
18	Elucidation of a sialic acid metabolism pathway in mucus-foraging <i>Ruminococcus gnavus</i> unravels mechanisms of bacterial adaptation to the gut. <i>Nature Microbiology</i> , 2019, 4, 2393-2404.	13.3	83

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19	Structure of RsrI methyltransferase, a member of the N6-adenine beta class of DNA methyltransferases. <i>Nucleic Acids Research</i> , 2000, 28, 3950-3961.	14.5	78
20	Allelic Variation of Bile Salt Hydrolase Genes in <i>Lactobacillus salivarius</i> Does Not Determine Bile Resistance Levels. <i>Journal of Bacteriology</i> , 2009, 191, 5743-5757.	2.2	78
21	Structure of cyanase reveals that a novel dimeric and decameric arrangement of subunits is required for formation of the enzyme active site. <i>Structure</i> , 2000, 8, 505-514.	3.3	75
22	Structural Studies on Flavin Reductase PheA2 Reveal Binding of NAD in an Unusual Folded Conformation and Support Novel Mechanism of Action. <i>Journal of Biological Chemistry</i> , 2004, 279, 12860-12867.	3.4	69
23	Crystal Structure of Human Edc3 and Its Functional Implications. <i>Molecular and Cellular Biology</i> , 2008, 28, 5965-5976.	2.3	69
24	Modulation of the Redox Potentials of FMN in <i>Desulfovibrio vulgaris</i> Flavodoxin: Thermodynamic Properties and Crystal Structures of Glycine-61 Mutants. <i>Biochemistry</i> , 1998, 37, 8405-8416.	2.5	61
25	High-throughput sample handling and data collection at synchrotrons: embedding the ESRF into the high-throughput gene-to-structure pipeline. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1162-1169.	2.5	58
26	Structural and functional studies of <i>Streptococcus pneumoniae</i> neuraminidase B: An intramolecular trans-sialidase. <i>FEBS Letters</i> , 2008, 582, 3348-3352.	2.8	58
27	A novel ADP- and zinc-binding fold from function-directed in vitro evolution. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 382-383.	8.2	55
28	Discovery of SARS-CoV-2 M <sup>pro</sup> peptide inhibitors from modelling substrate and ligand binding. <i>Chemical Science</i> , 2021, 12, 13686-13703.	7.4	54
29	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 152-166.	2.3	54
30	Fucosidases from the human gut symbiont <i>Ruminococcus gnavus</i> . <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 675-693.	5.4	52
31	Crystal Structure of Human Kynurenine Aminotransferase II, a Drug Target for the Treatment of Schizophrenia. <i>Journal of Biological Chemistry</i> , 2008, 283, 3559-3566.	3.4	50
32	Structural Basis for <i>Streptococcus pneumoniae</i> NanA Inhibition by Influenza Antivirals Zanamivir and Oseltamivir Carboxylate. <i>Journal of Molecular Biology</i> , 2011, 409, 496-503.	4.2	50
33	An automatic pipeline for the design of irreversible derivatives identifies a potent SARS-CoV-2 M <sup>pro</sup> inhibitor. <i>Cell Chemical Biology</i> , 2021, 28, 1795-1806.e5.	5.2	50
34	Crystal Structures of Human DcpS in Ligand-free and m <sup>7</sup> GDP-bound forms Suggest a Dynamic Mechanism for Scavenger mRNA Decapping. <i>Journal of Molecular Biology</i> , 2005, 347, 707-718.	4.2	48
35	Interdomain conformational flexibility underpins the activity of UGGT, the eukaryotic glycoprotein secretion checkpoint. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8544-8549.	7.1	48
36	Targeting Cyclic di-GMP Signalling: A Strategy to Control Biofilm Formation?. <i>Current Pharmaceutical Design</i> , 2014, 21, 12-24.	1.9	42

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37	MAD data collection – current trends. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1726-1732.	2.5	40
38	Structural Basis of the Sensor-Synthase Interaction in Autoinduction of the Quorum Sensing Signal DSF Biosynthesis. <i>Structure</i> , 2010, 18, 1199-1209.	3.3	40
39	<i>Streptococcus pneumoniae</i> NanC. <i>Journal of Biological Chemistry</i> , 2015, 290, 27736-27748.	3.4	40
40	Structure of a new crystal form of human Hsp70 ATPase domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1105-1107.	2.5	39
41	Mass spectrometry reveals potential of $\beta$ -lactams as SARS-CoV-2 M <sup>pro</sup> inhibitors. <i>Chemical Communications</i> , 2021, 57, 1430-1433.	4.1	35
42	Crystal structure of MbolIA methyltransferase. <i>Nucleic Acids Research</i> , 2003, 31, 5440-5448.	14.5	33
43	X-ray crystal structure of the <i>Desulfovibrio vulgaris</i> (Hildenborough) apoflavodoxin-riboflavin complex. <i>FEBS Journal</i> , 1998, 258, 362-371.	0.2	32
44	Ultrafast infrared spectroscopy reveals water-mediated coherent dynamics in an enzyme active site. <i>Chemical Science</i> , 2015, 6, 505-516.	7.4	32
45	Crystallographic Investigation of the Role of Aspartate 95 in the Modulation of the Redox Potentials of <i>Desulfovibrio vulgaris</i> Flavodoxin. <i>Biochemistry</i> , 2002, 41, 10950-10962.	2.5	30
46	Lipase-assisted preparation of enantiopure ferrocenyl sulfides possessing planar chirality and their use in the synthesis of chiral sulfoxides. <i>Tetrahedron</i> , 1997, 53, 1361-1368.	1.9	29
47	Measuring protein dynamics with ultrafast two-dimensional infrared spectroscopy. <i>Measurement Science and Technology</i> , 2012, 23, 062001.	2.6	27
48	A complete structural characterization of the desferrioxamine E biosynthetic pathway from the fire blight pathogen <i>Erwinia amylovora</i> . <i>Journal of Structural Biology</i> , 2018, 202, 236-249.	2.8	26
49	The 2-Å... Crystal Structure of 6-Oxo Camphor Hydrolase. <i>Journal of Biological Chemistry</i> , 2003, 278, 1744-1750.	3.4	25
50	<i>ixia</i> <sup>2</sup> . <i>ixia</i> multiplex: a multi-crystal data-analysis pipeline. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 752-769.	2.3	25
51	Bispecific repurposed medicines targeting the viral and immunological arms of COVID-19. <i>Scientific Reports</i> , 2021, 11, 13208.	3.3	24
52	Electron Bio-Imaging Centre (eBIC): the UK national research facility for biological electron microscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 488-495.	2.3	24
53	Penicillin Derivatives Inhibit the SARS-CoV-2 Main Protease by Reaction with Its Nucleophilic Cysteine. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 7682-7696.	6.4	22
54	Crystal Structure of a Human VH: Requirements for Maintaining a Monomeric Fragment. <i>Biochemistry</i> , 2004, 43, 622-628.	2.5	21

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55	Crystal structure of Î-chymotrypsin bound to a peptidyl chloromethyl ketone inhibitor. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 280-286.	2.5	20
56	Unusual Chromophore and Cross-Links in Ranasmurfin: A Blue Protein from the Foam Nests of a Tropical Frog. Angewandte Chemie - International Edition, 2008, 47, 7853-7856.	13.8	20
57	Dimerisation induced formation of the active site and the identification of three metal sites in EAL-phosphodiesterases. Scientific Reports, 2017, 7, 42166.	3.3	20
58	Structural Basis for Regulation and Specificity of Fructooligosaccharide Import in Streptococcus pneumoniae. Structure, 2017, 25, 79-93.	3.3	18
59	Application of In Situ Diffraction in High-Throughput Structure Determination Platforms. Methods in Molecular Biology, 2015, 1261, 233-253.	0.9	18
60	A structural and dynamic investigation of the inhibition of catalase by nitric oxide. Organic and Biomolecular Chemistry, 2013, 11, 7778.	2.8	16
61	A thermophilic mini-chaperonin contains a conserved polypeptide-binding surface: combined crystallographic and NMR studies of the GroEL apical domain with implications for substrate interactions11Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 306, 513-525.	4.2	15
62	Mass Spectrometric Assays Reveal Discrepancies in Inhibition Profiles for the SARS-CoV-2 Papain-Like Protease. ChemMedChem, 2022, 17, .	3.2	14
63	The structure of Erwinia amylovora AvrRpt2 provides insight into protein maturation and induced resistance to fire blight by Malus domestica 5. Journal of Structural Biology, 2019, 206, 233-242.	2.8	12
64	Comparison of the Structure and Activity of Glycosylated and Aglycosylated Human Carboxylesterase 1. PLoS ONE, 2015, 10, e0143919.	2.5	11
65	Lipase catalysed resolution of ferrocene cyanohydrin: access to novel ferrocenyl aminoalcohols and diamines. Tetrahedron: Asymmetry, 1997, 8, 1027-1030.	1.8	9
66	Structure of ribose 5-phosphate isomerase from the probiotic bacterium Lactobacillus salivarius UCC118. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1427-1433.	0.7	8
67	Crystallization of Ranasmurfin, a blue-coloured protein from Polypedates leucomystax. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1124-1126.	0.7	7
68	Structure of the equine arteritis virus nucleocapsid protein reveals a dimer-dimer arrangement. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 581-586.	2.5	7
69	Overcoming the false-minima problem in direct methods: structure determination of the packaging enzyme P4 from bacteriophage Î13. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1238-1244.	2.5	6
70	Structural characterization of the Streptococcus pneumoniae carbohydrate substrate-binding protein SP0092. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 54-61.	0.8	6
71	Diamond Light Source: contributions to SARS-CoV-2 biology and therapeutics. Biochemical and Biophysical Research Communications, 2021, 538, 40-46.	2.1	6
72	Going soft and SAD with manganese. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 108-111.	2.5	5

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73	<i>SynchLink</i> : an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014, 47, 1781-1783.	4.5	5
74	Structural and functional analysis of <i>Erwinia amylovora</i> SrlD. The first crystal structure of a sorbitol-6-phosphate 2-dehydrogenase. <i>Journal of Structural Biology</i> , 2018, 203, 109-119.	2.8	4
75	Expression, purification, crystallization and preliminary crystallographic analysis of the calponin-homology domain of Rng2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1809-1812.	2.5	3
76	Crystallization and preliminary X-ray diffraction analysis of bacteriophage $\phi$ 12 packaging factor P7. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2368-2370.	2.5	3
77	The crystal structure of <i>Erwinia amylovora</i> AmyR, a member of the YbjN protein family, shows similarity to type III secretion chaperones but suggests different cellular functions. <i>PLoS ONE</i> , 2017, 12, e0176049.	2.5	3
78	The structure of nontypeable <i>Haemophilus influenzae</i> SapA in a closed conformation reveals a constricted ligand-binding cavity and a novel RNA binding motif. <i>PLoS ONE</i> , 2021, 16, e0256070.	2.5	3
79	Crystallization and preliminary X-ray crystallographic analysis of the electron-transferring flavoprotein from <i>Megasphaera elsdenii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 461-463.	2.5	2
80	High-resolution structures of <i>Lactobacillus salivarius</i> transketolase in the presence and absence of thiamine pyrophosphate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1327-1334.	0.8	1
81	Crystallization and preliminary crystallographic analysis of an NADH oxidase that functions in peroxide reduction in <i>Thermus aquaticus</i> YT-1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 297-298.	2.5	0
82	Biochemical and Structural Characterization of the Carbohydrate Transport Substrate-binding-protein SP0092. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	0
83	Structure and Regulation of EAL Domain Proteins. , 2020, , 27-48.		0