## Iain W Manfield

List of Publications by Year in descending order

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Version: 2024-02-01

42 papers

2,621 citations

279487 23 h-index 288905 40 g-index

44 all docs

44 docs citations

44 times ranked

4430 citing authors

#	Article	IF	CITATIONS
1	A Comparative Assessment Study of Known Small-molecule GPVI Modulators. ACS Medicinal Chemistry Letters, 2022, 13, 171-181.	1.3	4
2	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly. Nature Communications, 2022, 13, 1040.	5.8	23
3	Dysregulation of Hepatitis B Virus Nucleocapsid Assembly in vitro by RNA-binding Small Ligands. Journal of Molecular Biology, 2022, 434, 167557.	2.0	6
4	Dataset of high-throughput ligand screening against the RNA Packaging Signals regulating Hepatitis B Virus nucleocapsid formation. Data in Brief, 2022, 42, 108206.	0.5	0
5	Mutations in Spliceosomal Genes PPIL1 and PRP17 Cause Neurodegenerative Pontocerebellar Hypoplasia with Microcephaly. Neuron, 2021, 109, 241-256.e9.	3.8	31
6	GPVI (Glycoprotein VI) Interaction With Fibrinogen Is Mediated by Avidity and the Fibrinogen αC-Region. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1092-1104.	1.1	19
7	A missense variant in specificity protein 6 (SP6) is associated with amelogenesis imperfecta. Human Molecular Genetics, 2020, 29, 1417-1425.	1.4	21
8	Defining the remarkable structural malleability of a bacterial surface protein Rib domain implicated in infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26540-26548.	3.3	15
9	Affimer proteins as a tool to modulate fibrinolysis, stabilize the blood clot, and reduce bleeding complications. Blood, 2019, 133, 1233-1244.	0.6	17
10	TRPA1–FGFR2 binding event is a regulatory oncogenic driver modulated by miRNA-142-3p. Nature Communications, 2017, 8, 947.	5.8	56
11	AtSPX1 affects the AtPHR1–DNA-binding equilibrium by binding monomeric AtPHR1 in solution. Biochemical Journal, 2017, 474, 3675-3687.	1.7	36
12	Application of isothermal titration calorimetry in evaluation of protein–nanoparticle interactions. Journal of Thermal Analysis and Calorimetry, 2017, 127, 605-613.	2.0	25
13	The effects of irradiation on the biological and biomechanical properties of an acellular porcine superflexor tendon graft for cruciate ligament repair. Journal of Biomedical Materials Research - Part B Applied Biomaterials, 2017, 105, 2477-2486.	1.6	26
14	Affimer proteins are versatile and renewable affinity reagents. ELife, 2017, 6, .	2.8	151
15	Direct Evidence for Packaging Signal-Mediated Assembly of Bacteriophage MS2. Journal of Molecular Biology, 2016, 428, 431-448.	2.0	80
16	Bacteriophage MS2 genomic RNA encodes an assembly instruction manual for its capsid. Bacteriophage, 2016, 6, e1157666.	1.9	38
17	Tenascin C upregulates interleukin-6 expression in human cardiac myofibroblasts <i>via</i> toll-like receptor 4. World Journal of Cardiology, 2016, 8, 340.	0.5	31
18	Trivalent Gd-DOTA reagents for modification of proteins. RSC Advances, 2015, 5, 96194-96200.	1.7	9

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19	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. Cell, 2014, 156, 577-589.	13.5	348
20	Epitope detection chromatography: a method to dissect the structural heterogeneity and interâ€connections of plant cellâ€wall matrix glycans. Plant Journal, 2014, 78, 715-722.	2.8	46
21	Mutations of the domain forming the dimeric interface of the <scp>A</scp> rd <scp>A</scp> protein affect dimerization and antimodification activity but not antirestriction activity. FEBS Journal, 2013, 280, 4903-4914.	2.2	5
22	Multiâ€scale spatial heterogeneity of pectic rhamnogalacturonan I ( <scp>RG</scp> –I) structural features in tobacco seed endosperm cell walls. Plant Journal, 2013, 75, 1018-1027.	2.8	32
23	Staphylococcal biofilm-forming protein has a contiguous rod-like structure. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1011-8.	3.3	73
24	From gene expression to gene regulatory networks in Arabidopsis thaliana. BMC Systems Biology, 2009, 3, 85.	3.0	38
25	Mutations involved in Aicardi-Goutià res syndrome implicate SAMHD1 as regulator of the innate immune response. Nature Genetics, 2009, 41, 829-832.	9.4	610
26	Ethylation Interference Footprinting of DNA-Protein Complexes. Methods in Molecular Biology, 2009, 543, 105-120.	0.4	4
27	The <i>S</i> locusâ€linked <i>Primula</i> homeotic mutant <i>sepaloid</i> shows characteristics of a Bâ€function mutant but does not result from mutation in a Bâ€function gene. Plant Journal, 2008, 56, 1-12.	2.8	16
28	Conservation, Convergence, and Divergence of Light-Responsive, Circadian-Regulated, and Tissue-Specific Expression Patterns during Evolution of the Arabidopsis GATA Gene Family. Plant Physiology, 2007, 143, 941-958.	2.3	87
29	Transcript analysis reveals an extended regulon and the importance of protein–protein co-operativity for the Escherichia coli methionine repressor. Biochemical Journal, 2006, 396, 227-234.	1.7	43
30	The Arabidopsis co-expression tool (act): a WWW-based tool and database for microarray-based gene expression analysis. Plant Journal, 2006, 46, 336-348.	2.8	69
31	ArabidopsisPEX19 is a dimeric protein that binds the peroxin PEX10. Molecular Membrane Biology, 2006, 23, 325-336.	2.0	24
32	Arabidopsis Co-expression Tool (ACT): web server tools for microarray-based gene expression analysis. Nucleic Acids Research, 2006, 34, W504-W509.	6.5	145
33	Molecular characterization of DNA sequences from the Primula vulgaris S-locus. Journal of Experimental Botany, 2005, 56, 1177-1188.	2.4	34
34	Re-engineering of the PAM1 phage display monoclonal antibody to produce a soluble, versatile anti-homogalacturonan scFv. Plant Science, 2005, 169, 1090-1095.	1.7	20
35	Novel cell wall architecture of isoxaben-habituated Arabidopsis suspension-cultured cells: global transcript profiling and cellular analysis. Plant Journal, 2004, 40, 260-275.	2.8	144
36	Structural and functional characterisation of the DNA binding domain of the Aspergillus nidulans gene regulatory protein AreA. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1648, 84-89.	1.1	2

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37	A biaryl peptide crosslink in a MetJ peptide model confers cooperative, nonspecific binding to DNA that ablates both repressor binding and In vitro transcription. Bioorganic and Medicinal Chemistry, 2003, 11, 811-816.	1.4	5
38	Structural and Functional Studies of an Intermediate on the Pathway to Operator Binding by Escherichia coli MetJ. Journal of Molecular Biology, 2002, 320, 39-53.	2.0	18
39	Arabidopsis thaliana GATA factors: organisation, expression and DNA-binding characteristics. Plant Molecular Biology, 2002, 50, 43-56.	2.0	101
40	Ethylation Interference., 1994, 30, 125-140.		8
41	Probing met represser–operator recognition in solution. Nature, 1992, 359, 431-433.	13.7	35
42	Cooperative tandem binding of met repressor of Escherichia coli. Nature, 1989, 341, 711-715.	13.7	122