

Paul S Freemont

List of Publications by Year in descending order

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Version: 2024-02-01

202
papers

18,706
citations

12597

71
h-index

15253

130
g-index

226
all docs

226
docs citations

226
times ranked

19200
citing authors

#	ARTICLE	IF	CITATIONS
1	Community transmission and viral load kinetics of the SARS-CoV-2 delta (B.1.617.2) variant in vaccinated and unvaccinated individuals in the UK: a prospective, longitudinal, cohort study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 183-195.	4.6	585
2	Transmissibility of SARS-CoV-2 among fully vaccinated individuals – Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 18-19.	4.6	3
3	Pandemic preparedness: synthetic biology and publicly funded biofoundries can rapidly accelerate response time. <i>Nature Communications</i> , 2022, 13, 453.	5.8	7
4	Multiplexed immunosensors for point-of-care diagnostic applications. <i>Biosensors and Bioelectronics</i> , 2022, 203, 114050.	5.3	69
5	Reconstituting the complete biosynthesis of D-lysergic acid in yeast. <i>Nature Communications</i> , 2022, 13, 712.	5.8	14
6	A global forum on synthetic biology: the need for international engagement. <i>Nature Communications</i> , 2022, 13, .	5.8	9
7	Combinatorial metabolic pathway assembly approaches and toolkits for modular assembly. <i>Metabolic Engineering</i> , 2021, 63, 81-101.	3.6	34
8	Refactoring of a synthetic raspberry ketone pathway with EcoFlex. <i>Microbial Cell Factories</i> , 2021, 20, 116.	1.9	12
9	Biofoundries are a nucleating hub for industrial translation. <i>Synthetic Biology</i> , 2021, 6, ysab013.	1.2	13
10	AL-PHA beads: Bioplastic-based protease biosensors for global health applications. <i>Materials Today</i> , 2021, 47, 25-37.	8.3	11
11	Cell-free gene expression. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	71
12	High-yield one-pot™ biosynthesis of raspberry ketone, a high-value fine chemical. <i>Synthetic Biology</i> , 2021, 6, ysab021.	1.2	3
13	Optimized protocol for a quantitative SARS-CoV-2 duplex RT-qPCR assay with internal human sample sufficiency control. <i>Journal of Virological Methods</i> , 2021, 294, 114174.	1.0	16
14	A High-Yield &Streptomyces Transcription-Translation Toolkit for Synthetic Biology and Natural Product Applications. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	3
15	<i>Bacillus subtilis</i> YngB contributes to wall teichoic acid glucosylation and glycolipid formation during anaerobic growth. <i>Journal of Biological Chemistry</i> , 2021, 296, 100384.	1.6	10
16	A <i>Streptomyces venezuelae</i> Cell-Free Toolkit for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2021, 10, 402-411.	1.9	26
17	Structural basis for the inhibition of the <i>Bacillus subtilis</i> c-di-AMP cyclase CdaA by the phosphoglucomutase GlmM. <i>Journal of Biological Chemistry</i> , 2021, 297, 101317.	1.6	10
18	Rapid design and implementation of an adaptive pooling workflow for SARS-CoV-2 testing in an NHS diagnostic laboratory: a proof-of-concept study. <i>Wellcome Open Research</i> , 2021, 6, 268.	0.9	4

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19	GenoChemetic Strategy for Derivatization of the Violacein Natural Product Scaffold. <i>ACS Chemical Biology</i> , 2021, 16, 2116-2123.	1.6	12
20	A high-throughput pipeline for scalable kit-free RNA extraction. <i>Scientific Reports</i> , 2021, 11, 23260.	1.6	3
21	Crystal structure of the catalytic D2 domain of the AAA+ ATPase p97 reveals a putative helical splitâ€washerâ€™type mechanism for substrate unfolding. <i>FEBS Letters</i> , 2020, 594, 933-943.	1.3	6
22	Bacteriophage MS2 displays unreported capsid variability assembling <i>T<i>T</i>=A4</i> and mixed capsids. <i>Molecular Microbiology</i> , 2020, 113, 143-152.	1.2	24
23	Cell-Free Protein Synthesis as a Prototyping Platform for Mammalian Synthetic Biology. <i>ACS Synthetic Biology</i> , 2020, 9, 144-156.	1.9	31
24	A role for Biofoundries in rapid development and validation of automated SARS-CoV-2 clinical diagnostics. <i>Nature Communications</i> , 2020, 11, 4464.	5.8	52
25	A Biosynthetic Platform for Antimalarial Drug Discovery. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	12
26	Biological Materials: The Next Frontier for Cell-Free Synthetic Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 399.	2.0	40
27	The long journey towards standards for engineering biosystems. <i>EMBO Reports</i> , 2020, 21, e50521.	2.0	46
28	Synthetic Biology and the United Nations. <i>Trends in Biotechnology</i> , 2019, 37, 1146-1151.	4.9	16
29	The <i>Pseudomonas aeruginosa</i> T6SS Delivers a Periplasmic Toxin that Disrupts Bacterial Cell Morphology. <i>Cell Reports</i> , 2019, 29, 187-201.e7.	2.9	82
30	Inhibition of the <i>Staphylococcus aureus</i> c-di-AMP cyclase DacA by direct interaction with the phosphoglucosamine mutase GlmM. <i>PLoS Pathogens</i> , 2019, 15, e1007537.	2.1	35
31	Utilising datasheets for the informed automated design and build of a synthetic metabolic pathway. <i>Journal of Biological Engineering</i> , 2019, 13, 8.	2.0	24
32	Building a global alliance of biofoundries. <i>Nature Communications</i> , 2019, 10, 2040.	5.8	167
33	Miniaturisation of high-throughput plasmid DNA library preparation for next-generation sequencing using multifactorial optimisation. <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 57-66.	1.8	15
34	Whole-Cell Biosensor with Tunable Limit of Detection Enables Low-Cost Agglutination Assays for Medical Diagnostic Applications. <i>ACS Sensors</i> , 2019, 4, 370-378.	4.0	57
35	Synthetic biology industry: data-driven design is creating new opportunities in biotechnology. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 651-657.	1.1	35
36	Rapid acquisition and model-based analysis of cell-free transcriptionâ€™translation reactions from nonmodel bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4340-E4349.	3.3	162

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37	Atomic Structure of Type VI Contractile Sheath from <i>Pseudomonas aeruginosa</i> . <i>Structure</i> , 2018, 26, 329-336.e3.	1.6	29
38	Cell-free prototyping strategies for enhancing the sustainable production of polyhydroxyalkanoates bioplastics. <i>Synthetic Biology</i> , 2018, 3, ysy016.	1.2	39
39	Structural basis for recognition and repair of the 3'-phosphate by NExo, a base excision DNA repair nuclease from <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2018, 46, 11980-11989.	6.5	4
40	EcoFlex: A Multifunctional MoClo Kit for <i>E. coli</i> Synthetic Biology. <i>Methods in Molecular Biology</i> , 2018, 1772, 429-444.	0.4	9
41	Whole-cell <i>Escherichia coli</i> lactate biosensor for monitoring mammalian cell cultures during biopharmaceutical production. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1290-1300.	1.7	42
42	<i>Streptomyces venezuelae</i> as a next generation cell-free synthetic biology tool. <i>Biotechnology Journal</i> , 2017, 12, 1600678.	1.8	73
43	Inhibitor Selectivity for Cyclin-Dependent Kinase-7: A Structural, Thermodynamic, and Modelling Study. <i>ChemMedChem</i> , 2017, 12, 372-380.	1.6	29
44	With all due respect to Maholo, lab automation isn't anthropomorphic. <i>Nature Biotechnology</i> , 2017, 35, 312-314.	9.4	14
45	Cell-free synthetic biology for in vitro prototype engineering. <i>Biochemical Society Transactions</i> , 2017, 45, 785-791.	1.6	37
46	Current and future therapies for <i>Pseudomonas aeruginosa</i> infection in patients with cystic fibrosis. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	85
47	Opportunities for applying whole-cell bioreporters towards parasite detection. <i>Microbial Biotechnology</i> , 2017, 10, 244-249.	2.0	7
48	A Cell-Free Biosensor for Detecting Quorum Sensing Molecules in <i>P. aeruginosa</i> -Infected Respiratory Samples. <i>ACS Synthetic Biology</i> , 2017, 6, 2293-2301.	1.9	130
49	The AAA+ ATPase p97, a cellular multitool. <i>Biochemical Journal</i> , 2017, 474, 2953-2976.	1.7	111
50	Engineering biology: a key driver of the bioeconomy. <i>Engineering Biology</i> , 2017, 1, 3-6.	0.8	2
51	Genome sequence and plasmid transformation of the model high-yield bacterial cellulose producer <i>Gluconacetobacter hansenii</i> ATCC 53582. <i>Scientific Reports</i> , 2016, 6, 23635.	1.6	61
52	Delineation of metabolic gene clusters in plant genomes by chromatin signatures. <i>Nucleic Acids Research</i> , 2016, 44, 2255-2265.	6.5	66
53	EcoFlex: A Multifunctional MoClo Kit for <i>E. coli</i> Synthetic Biology. <i>ACS Synthetic Biology</i> , 2016, 5, 1059-1069.	1.9	149
54	<i>Pseudomonas aeruginosa</i> infection in cystic fibrosis: pathophysiological mechanisms and therapeutic approaches. <i>Expert Review of Respiratory Medicine</i> , 2016, 10, 685-697.	1.0	114

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55	The Foundry: the DNA synthesis and construction Foundry at Imperial College. <i>Biochemical Society Transactions</i> , 2016, 44, 687-688.	1.6	19
56	Development of a <i>Bacillus subtilis</i> cell-free transcription-translation system for prototyping regulatory elements. <i>Metabolic Engineering</i> , 2016, 38, 370-381.	3.6	112
57	Synthetic beta-solenoid proteins with the fragment-free computational design of a beta-hairpin extension. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10346-10351.	3.3	28
58	The second messenger c-di-AMP inhibits the osmolyte uptake system OpuC in <i>Staphylococcus aureus</i> . <i>Science Signaling</i> , 2016, 9, ra81.	1.6	87
59	Computational protein design with backbone plasticity. <i>Biochemical Society Transactions</i> , 2016, 44, 1523-1529.	1.6	16
60	Structural biology: Baseplates in contractile machines. <i>Nature Microbiology</i> , 2016, 1, 16104.	5.9	8
61	TssA forms a gp6-like ring attached to the type VI secretion sheath. <i>EMBO Journal</i> , 2016, 35, 1613-1627.	3.5	84
62	Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3431-40.	3.3	173
63	Protocol for the Standardisation of Transcriptional Measurements. <i>Springer Protocols</i> , 2015, , 9-26.	0.1	3
64	Complex Structure and Biochemical Characterization of the <i>Staphylococcus aureus</i> Cyclic Diadenylate Monophosphate (c-di-AMP)-binding Protein PstA, the Founding Member of a New Signal Transduction Protein Family. <i>Journal of Biological Chemistry</i> , 2015, 290, 2888-2901.	1.6	47
65	The N-terminal Region of the Ubiquitin Regulatory X (UBX) Domain-containing Protein 1 (UBXD1) Modulates Interdomain Communication within the Valosin-containing Protein p97. <i>Journal of Biological Chemistry</i> , 2015, 290, 29414-29427.	1.6	26
66	A Forward-Design Approach to Increase the Production of Poly-3-Hydroxybutyrate in Genetically Engineered <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0117202.	1.1	11
67	New quantitative approaches reveal the spatial preference of nuclear compartments in mammalian fibroblasts. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140894.	1.5	0
68	Multilevel Regulation and Translational Switches in Synthetic Biology. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2015, 9, 485-496.	2.7	12
69	Developments in the Tools and Methodologies of Synthetic Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 60.	2.0	78
70	Structural and Mechanistic Insight into the <i>Listeria monocytogenes</i> Two-enzyme Lipoteichoic Acid Synthesis System. <i>Journal of Biological Chemistry</i> , 2014, 289, 28054-28069.	1.6	25
71	Coevolution of the ATPase ClpV, the Sheath Proteins TssB and TssC, and the Accessory Protein TagJ/HsiE1 Distinguishes Type VI Secretion Classes. <i>Journal of Biological Chemistry</i> , 2014, 289, 33032-33043.	1.6	50
72	The p97-FAF1 Protein Complex Reveals a Common Mode of p97 Adaptor Binding. <i>Journal of Biological Chemistry</i> , 2014, 289, 12077-12084.	1.6	24

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73	One-pot DNA construction for synthetic biology: the Modular Overlap-Directed Assembly with Linkers (MODAL) strategy. <i>Nucleic Acids Research</i> , 2014, 42, e7-e7.	6.5	99
74	How Synthetic Biology Will Reconsider Natural Bioluminescence and Its Applications. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2014, 145, 3-30.	0.6	9
75	Co-culture systems and technologies: taking synthetic biology to the next level. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140065.	1.5	428
76	R2oDNA Designer: Computational Design of Biologically Neutral Synthetic DNA Sequences. <i>ACS Synthetic Biology</i> , 2014, 3, 525-528.	1.9	63
77	Inter-ring rotations of AAA ATPase p97 revealed by electron cryomicroscopy. <i>Open Biology</i> , 2014, 4, 130142.	1.5	23
78	In Vivo and In Vitro Characterization of 70 Constitutive Promoters by Real-Time PCR and Fluorescent Measurements. <i>Methods in Molecular Biology</i> , 2013, 1073, 61-74.	0.4	3
79	Engineering Microbial Biosensors. <i>Methods in Microbiology</i> , 2013, 40, 119-156.	0.4	21
80	Validation of an entirely in vitro approach for rapid prototyping of DNA regulatory elements for synthetic biology. <i>Nucleic Acids Research</i> , 2013, 41, 3471-3481.	6.5	161
81	The HsiB1C1 (TssB-TssC) Complex of the <i>Pseudomonas aeruginosa</i> Type VI Secretion System Forms a Bacteriophage Tail Sheathlike Structure. <i>Journal of Biological Chemistry</i> , 2013, 288, 7536-7548.	1.6	77
82	Validating a Coarse-Grained Potential Energy Function through Protein Loop Modelling. <i>PLoS ONE</i> , 2013, 8, e65770.	1.1	14
83	Design of a prototype flow microreactor for synthetic biology in vitro. <i>Lab on A Chip</i> , 2013, 13, 3426.	3.1	29
84	The Role of the N-Domain in the ATPase Activity of the Mammalian AAA ATPase p97/VCP. <i>Journal of Biological Chemistry</i> , 2012, 287, 8561-8570.	1.6	104
85	Distinct conformations of the protein complex p97-Ufd1-Npl4 revealed by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1098-1103.	3.3	41
86	Specialization of an Exonuclease III family enzyme in the repair of 3' DNA lesions during base excision repair in the human pathogen <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 2065-2075.	6.5	10
87	The archetype <i>Pseudomonas aeruginosa</i> proteins TssB and TagJ form a novel subcomplex in the bacterial type VI secretion system. <i>Molecular Microbiology</i> , 2012, 86, 437-456.	1.2	22
88	The <i>Salmonella</i> Kinase SteC Targets the MAP Kinase MEK to Regulate the Host Actin Cytoskeleton. <i>Cell Host and Microbe</i> , 2012, 12, 657-668.	5.1	71
89	Structural basis for the recognition and cleavage of abasic DNA in <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16852-16857.	3.3	19
90	Analysis of Spatial Point Patterns in Nuclear Biology. <i>PLoS ONE</i> , 2012, 7, e36841.	1.1	5

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91	A network of enzymes involved in repair of oxidative DNA damage in <i>Neisseria meningitidis</i> . <i>Molecular Microbiology</i> , 2012, 83, 1064-1079.	1.2	20
92	Synthetic biology – the state of play. <i>FEBS Letters</i> , 2012, 586, 2029-2036.	1.3	68
93	Regulation of p97 in the ubiquitin–proteasome system by the UBX protein-family. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 125-129.	1.9	61
94	PML Nuclear Bodies and Other Trim-Defined Subcellular Compartments. <i>Advances in Experimental Medicine and Biology</i> , 2012, 770, 39-58.	0.8	11
95	Computational design approaches and tools for synthetic biology. <i>Integrative Biology (United Kingdom)</i> , 2011, 1, 107-114.	0.6	74
96	Interaction between Nucleosome Assembly Protein 1-like Family Members. <i>Journal of Molecular Biology</i> , 2011, 407, 647-660.	2.0	35
97	Structure–function analysis of HsiF, a gp25-like component of the type VI secretion system, in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 3292-3305.	0.7	52
98	Methodology for Quantitative Analysis of 3-D Nuclear Architecture. , 2011, , 173-187.		2
99	A Novel Pyrazolo[1,5- <i>a</i>]pyrimidine Is a Potent Inhibitor of Cyclin-Dependent Protein Kinases 1, 2, and 9, Which Demonstrates Antitumor Effects in Human Tumor Xenografts Following Oral Administration. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 8508-8522.	2.9	84
100	Structural and functional implications of phosphorylation and acetylation in the regulation of the AAA+ protein p97. This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 41-48.	0.9	35
101	PML nuclear bodies and their spatial relationships in the mammalian cell nucleus. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 1182.	3.0	16
102	Opportunities for microfluidic technologies in synthetic biology. <i>Journal of the Royal Society Interface</i> , 2009, 6, S493-506.	1.5	64
103	Structure-based mechanism of lipoteichoic acid synthesis by <i>Staphylococcus aureus</i> LtaS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1584-1589.	3.3	93
104	Automated Assignment in Selectively Methyl-Labeled Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 9480-9481.	6.6	30
105	Segmentation of Fluorescence Microscopy Images for Quantitative Analysis of Cell Nuclear Architecture. <i>Biophysical Journal</i> , 2009, 96, 3379-3389.	0.2	29
106	Analysis of Nucleotide Binding to P97 Reveals the Properties of a Tandem AAA Hexameric ATPase. <i>Journal of Biological Chemistry</i> , 2008, 283, 13745-13752.	1.6	72
107	Insights into adaptor binding to the AAA protein p97. <i>Biochemical Society Transactions</i> , 2008, 36, 62-67.	1.6	120
108	Detailed Structural Insights into the p97-Npl4-Ufd1 Interface. <i>Journal of Biological Chemistry</i> , 2007, 282, 21361-21369.	1.6	60

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109	SseL, a Salmonella deubiquitinase required for macrophage killing and virulence. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3502-3507.	3.3	208
110	Quantitative Analysis of Cell Nucleus Organisation. PLoS Computational Biology, 2007, 3, e138.	1.5	21
111	Different Quaternary Structures of Human RECQ1 Are Associated with Its Dual Enzymatic Activity. PLoS Biology, 2007, 5, e20.	2.6	59
112	Structural insights into the p97-Ufd1-Npl4 complex. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 467-472.	3.3	87
113	A New Labeling Method for Methyl Transverse Relaxation-Optimized Spectroscopy NMR Spectra of Alanine Residues. Journal of the American Chemical Society, 2007, 129, 15428-15429.	6.6	108
114	Breast cancer associated transcriptional repressor PLU-1/JARID1B interacts directly with histone deacetylases. International Journal of Cancer, 2007, 121, 265-275.	2.3	87
115	AP endonuclease paralogues with distinct activities in DNA repair and bacterial pathogenesis. EMBO Journal, 2007, 26, 1363-1372.	3.5	47
116	SteC is a Salmonella kinase required for SPI-2-dependent F-actin remodelling. Cellular Microbiology, 2007, 10, 070720190331003-???.	1.1	79
117	Cd36, a class B scavenger receptor, functions as a monomer to bind acetylated and oxidized low-density lipoproteins. Protein Science, 2007, 16, 2531-2541.	3.1	29
118	p37 Is a p97 Adaptor Required for Golgi and ER Biogenesis in Interphase and at the End of Mitosis. Developmental Cell, 2006, 11, 803-816.	3.1	95
119	Going through the motions: The ATPase cycle of p97. Journal of Structural Biology, 2006, 156, 12-28.	1.3	90
120	Conformational changes in the AAA ATPase p97/p47 adaptor complex. EMBO Journal, 2006, 25, 1967-1976.	3.5	95
121	The Transcriptional Regulator CBP Has Defined Spatial Associations within Interphase Nuclei. PLoS Computational Biology, 2006, 2, e139.	1.5	24
122	The ProMiscuously (PML) exciting nuclear protein has another partner. Blood, 2005, 105, 3393-3394.	0.6	0
123	Structural basis of the interaction between the AAA ATPase p97/VCP and its adaptor protein p47. EMBO Journal, 2004, 23, 1030-1039.	3.5	172
124	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. EMBO Journal, 2004, 23, 1463-1473.	3.5	65
125	Letter to the Editor: Complete Backbone Resonance Assignments of p47: The 41kDa Adaptor Protein of the AAA ATPase p97. Journal of Biomolecular NMR, 2004, 28, 309-310.	1.6	4
126	Promyelocytic leukemia nuclear bodies associate with transcriptionally active genomic regions. Journal of Cell Biology, 2004, 164, 515-526.	2.3	206

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127	SUMO. <i>Current Biology</i> , 2003, 13, R258-R259.	1.8	8
128	Mutations in a Sar1 GTPase of COPII vesicles are associated with lipid absorption disorders. <i>Nature Genetics</i> , 2003, 34, 29-31.	9.4	359
129	The crystal structure of murine p97/VCP at 3.6Å.... <i>Journal of Structural Biology</i> , 2003, 144, 337-348.	1.3	166
130	Motions and Negative Cooperativity Between p97 Domains Revealed by Cryo-electron Microscopy and Quantised Elastic Deformational Model. <i>Journal of Molecular Biology</i> , 2003, 327, 619-629.	2.0	97
131	Human PLU-1 Has Transcriptional Repression Properties and Interacts with the Developmental Transcription Factors BF-1 and PAX9. <i>Journal of Biological Chemistry</i> , 2003, 278, 20507-20513.	1.6	80
132	Two Nonconsensus Sites in the Epstein-Barr Virus Oncoprotein EBNA3A Cooperate to Bind the Co-repressor Carboxyl-terminal-binding Protein (CtBP). <i>Journal of Biological Chemistry</i> , 2002, 277, 47197-47204.	1.6	79
133	VCIP135, a novel essential factor for p97/p47-mediated membrane fusion, is required for Golgi and ER assembly in vivo. <i>Journal of Cell Biology</i> , 2002, 159, 855-866.	2.3	188
134	Characterisation and developmental expression of mouse Plu-1, a homologue of a human nuclear protein (PLU-1) which is specifically up-regulated in breast cancer. <i>Mechanisms of Development</i> , 2002, 119, S239-S246.	1.7	23
135	Machinery of protein folding and unfolding. <i>Current Opinion in Structural Biology</i> , 2002, 12, 231-238.	2.6	48
136	Solution structure and interaction surface of the C-terminal domain from p47: A major p97-cofactor involved in SNARE disassembly. <i>Journal of Molecular Biology</i> , 2001, 311, 255-263.	2.0	80
137	High resolution crystal structures of T4 phage Î²-glucosyltransferase: induced fit and effect of substrate and metal binding 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 311, 569-577.	2.0	66
138	BRCT Domain Interactions in the Heterodimeric DNA Repair Protein XRCC1âˆ“DNA Ligase III. <i>Biochemistry</i> , 2001, 40, 5906-5913.	1.2	59
139	PML protein isoforms and the RBCC/TRIM motif. <i>Oncogene</i> , 2001, 20, 7223-7233.	2.6	410
140	Role of Promyelocytic Leukemia (Pml) Sumolation in Nuclear Body Formation, 11s Proteasome Recruitment, and as2O3-Induced Pml or Pml/Retinoic Acid Receptor Î± Degradation. <i>Journal of Experimental Medicine</i> , 2001, 193, 1361-1372.	4.2	462
141	PML bodies associate specifically with the MHC gene cluster in interphase nuclei. <i>Journal of Cell Science</i> , 2001, 114, 3705-3716.	1.2	109
142	Ubiquitination: RING for destruction?. <i>Current Biology</i> , 2000, 10, R84-R87.	1.8	464
143	Role of SUMO-1âˆ“modified PML in nuclear body formation. <i>Blood</i> , 2000, 95, 2748-2752.	0.6	493
144	HPC3 Is a New Human Polycomb Orthologue That Interacts and Associates with RING1 and Bmi1 and Has Transcriptional Repression Properties. <i>Journal of Biological Chemistry</i> , 2000, 275, 28785-28792.	1.6	65

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145	Substitution of Asp-210 in HAP1 (APE/Ref-1) eliminates endonuclease activity but stabilises substrate binding. <i>Nucleic Acids Research</i> , 2000, 28, 2207-2213.	6.5	53
146	Biochemical analyses of the AF10 protein: the extended LAP/PHD-finger mediates oligomerisation 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2000, 299, 369-378.	2.0	62
147	The BRCA1 C-terminal domain: structure and function. <i>Mutation Research DNA Repair</i> , 2000, 460, 319-332.	3.8	128
148	Structure of the AAA ATPase p97. <i>Molecular Cell</i> , 2000, 6, 1473-1484.	4.5	394
149	Fold recognition study of alpha3-galactosyltransferase and molecular modeling of the nucleotide sugar-binding domain. <i>Glycobiology</i> , 1999, 9, 713-722.	1.3	19
150	A Novel Gene (PLU-1) Containing Highly Conserved Putative DNA/Chromatin Binding Motifs Is Specifically Up-regulated in Breast Cancer. <i>Journal of Biological Chemistry</i> , 1999, 274, 15633-15645.	1.6	203
151	An NSF function distinct from ATPase-dependent SNARE disassembly is essential for Golgi membrane fusion. <i>Nature Cell Biology</i> , 1999, 1, 335-340.	4.6	58
152	SSX and the synovial-sarcoma-specific chimaeric protein SYT-SSX co-localize with the human Polycomb group complex. <i>Oncogene</i> , 1999, 18, 2739-2746.	2.6	103
153	Oligomeric ring structure of the Bloom's syndrome helicase. <i>Current Biology</i> , 1999, 9, 597-600.	1.8	129
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