

# Raymond J Owens

## List of Publications by Year in descending order

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141  
papers

8,598  
citations

57681

46  
h-index

58552

86  
g-index

152  
all docs

152  
docs citations

152  
times ranked

15283  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural mass spectrometry decodes domain interaction and dynamics of the full-length Human Histone Deacetylase 2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140759.	1.1	0
2	Pathogen-sugar interactions revealed by universal saturation transfer analysis. <i>Science</i> , 2022, 377, .	6.0	24
3	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
4	A COVID-19 vaccine candidate using SpyCatcher multimerization of the SARS-CoV-2 spike protein receptor-binding domain induces potent neutralising antibody responses. <i>Nature Communications</i> , 2021, 12, 542.	5.8	200
5	Transient Transfection and Expression of Eukaryotic Membrane Proteins in Expi293F Cells and Their Screening on a Small Scale: Application for Structural Studies. <i>Methods in Molecular Biology</i> , 2021, 2305, 105-128.	0.4	3
6	Structural basis of antifolate recognition and transport by PCFT. <i>Nature</i> , 2021, 595, 130-134.	13.7	36
7	Cryo-EM structure of PepT2 reveals structural basis for proton-coupled peptide and prodrug transport in mammals. <i>Science Advances</i> , 2021, 7, .	4.7	37
8	Temperature-dependent secretion of Zika virus envelope and non-structural protein 1 in mammalian cells for clinical applications. <i>Journal of Virological Methods</i> , 2021, 294, 114175.	1.0	0
9	The use of nanobodies in a sensitive ELISA test for SARS-CoV-2 Spike 1 protein. <i>Royal Society Open Science</i> , 2021, 8, 211016.	1.1	19
10	A potent SARS-CoV-2 neutralising nanobody shows therapeutic efficacy in the Syrian golden hamster model of COVID-19. <i>Nature Communications</i> , 2021, 12, 5469.	5.8	102
11	Optimized expression and purification of adipose triglyceride lipase improved hydrolytic and transacylation activities in vitro. <i>Journal of Biological Chemistry</i> , 2021, 297, 101206.	1.6	13
12	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.	1.1	3
13	Structural Biology of Nanobodies against the Spike Protein of SARS-CoV-2. <i>Viruses</i> , 2021, 13, 2214.	1.5	16
14	Molecular basis for GTP recognition by light-activated guanylate cyclase RhGC. <i>FEBS Journal</i> , 2020, 287, 2797-2807.	2.2	9
15	Neutralizing nanobodies bind SARS-CoV-2 spike RBD and block interaction with ACE2. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 846-854.	3.6	434
16	The structure-function relationship of oncogenic LMTK3. <i>Science Advances</i> , 2020, 6, .	4.7	18
17	Evaluation of the immunogenicity of prime-boost vaccination with the replication-deficient viral vectored COVID-19 vaccine candidate ChAdOx1 nCoV-19. <i>Npj Vaccines</i> , 2020, 5, 69.	2.9	121
18	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 950-958.	3.6	268

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19	Neutralization of SARS-CoV-2 by Destruction of the Prefusion Spike. <i>Cell Host and Microbe</i> , 2020, 28, 445-454.e6.	5.1	298
20	Optimization of Small-Scale Production of Zika Virus Envelope Glycoprotein by Transient Expression in HEK293 Cells for ELISA. <i>Methods in Molecular Biology</i> , 2020, 2142, 103-112.	0.4	2
21	Overview of a High-Throughput Pipeline for Streamlining the Production of Recombinant Proteins. <i>Methods in Molecular Biology</i> , 2019, 2025, 33-49.	0.4	9
22	Streamlining the production of proteins for structural biology. <i>Biophysical Reviews</i> , 2019, 11, 533-534.	1.5	2
23	Insights from the crystal structure of the chicken CREB3 bZIP suggest that members of the CREB3 subfamily transcription factors may be activated in response to oxidative stress. <i>Protein Science</i> , 2019, 28, 779-787.	3.1	5
24	The role of the light chain in the structure and binding activity of two cattle antibodies that neutralize bovine respiratory syncytial virus. <i>Molecular Immunology</i> , 2019, 112, 123-130.	1.0	11
25	Characterization of a <i>Schistosoma mansoni</i> NDPK expressed in sexual and digestive organs. <i>Molecular and Biochemical Parasitology</i> , 2019, 231, 111-117.	0.5	2
26	Immunogenicity profiling of protein antigens from capsular group B <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , 2019, 9, 6843.	1.6	15
27	Direct imaging of the recruitment and phosphorylation of S6K1 in the mTORC1 pathway in living cells. <i>Scientific Reports</i> , 2019, 9, 3408.	1.6	22
28	In vitro and in vivo characterization of the multiple isoforms of <i>Schistosoma mansoni</i> hypoxanthine-guanine phosphoribosyltransferases. <i>Molecular and Biochemical Parasitology</i> , 2019, 229, 24-34.	0.5	4
29	Crystal structures of VIM $\beta$ 1 complexes explain active site heterogeneity in VIM $\beta$ class metallo $\beta$ -lactamases. <i>FEBS Journal</i> , 2019, 286, 169-183.	2.2	30
30	Highly stable single-strand-specific 3 $\beta$ -nuclease/nucleotidase from <i>Legionella pneumophila</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 114, 776-787.	3.6	5
31	Affimer proteins inhibit immune complex binding to Fc $\gamma$ RIIIa with high specificity through competitive and allosteric modes of action. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E72-E81.	3.3	36
32	Optimization of Zika virus envelope protein production for ELISA and correlation of antibody titers with virus neutralization in Mexican patients from an arbovirus endemic region. <i>Virology Journal</i> , 2018, 15, 193.	1.4	11
33	The molecular structure of <i>Schistosoma mansoni</i> PNP isoform 2 provides insights into the nucleoside selectivity of PNPs. <i>PLoS ONE</i> , 2018, 13, e0203532.	1.1	7
34	Generation and characterisation of recombinant FMDV antibodies: Applications for advancing diagnostic and laboratory assays. <i>PLoS ONE</i> , 2018, 13, e0201853.	1.1	3
35	Structural and kinetic analysis of <i>Schistosoma mansoni</i> Adenylosuccinate Lyase ( Sm ADSL). <i>Molecular and Biochemical Parasitology</i> , 2017, 214, 27-35.	0.5	13
36	CD1a presentation of endogenous antigens by group 2 innate lymphoid cells. <i>Science Immunology</i> , 2017, 2, .	5.6	57

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37	Affimer proteins are versatile and renewable affinity reagents. <i>ELife</i> , 2017, 6, .	2.8	151
38	Expression Screening of Integral Membrane Proteins by Fusion to Fluorescent Reporters. <i>Advances in Experimental Medicine and Biology</i> , 2016, 922, 1-11.	0.8	6
39	Crystal structures of penicillin-binding protein 3 in complexes with azlocillin and cefoperazone in both acylated and deacylated forms. <i>FEBS Letters</i> , 2016, 590, 288-297.	1.3	17
40	Synthesis and characterisation of 5-acyl-6,7-dihydrothieno[3,2-c]pyridine inhibitors of Hedgehog acyltransferase. <i>Data in Brief</i> , 2016, 7, 257-281.	0.5	12
41	Substituted 2-(2-aminopyrimidin-4-yl)pyridine-4-carboxylates as potent inhibitors of JumonjiC domain-containing histone demethylases. <i>Future Medicinal Chemistry</i> , 2016, 8, 1553-1571.	1.1	16
42	Methods in integrated structural biology. <i>Methods</i> , 2016, 95, 1-2.	1.9	0
43	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.	0.4	1
44	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. <i>Scientific Reports</i> , 2015, 5, 14150.	1.6	14
45	Green Fluorescent Protein-based Expression Screening of Membrane Proteins in <i>Escherichia coli</i> . <i>Journal of Visualized Experiments</i> , 2015, , e52357.	0.2	21
46	Comparison of the Structure and Activity of Glycosylated and Aglycosylated Human Carboxylesterase 1. <i>PLoS ONE</i> , 2015, 10, e0143919.	1.1	11
47	Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. <i>Structure</i> , 2015, 23, 1889-1899.	1.6	40
48	Click chemistry armed enzyme-linked immunosorbent assay to measure palmitoylation by hedgehog acyltransferase. <i>Analytical Biochemistry</i> , 2015, 490, 66-72.	1.1	26
49	Structural Proteomics. <i>Methods in Molecular Biology</i> , 2015, 1261, v.	0.4	6
50	Transient Expression in HEK 293 Cells: An Alternative to <i>E. coli</i> for the Production of Secreted and Intracellular Mammalian Proteins. <i>Methods in Molecular Biology</i> , 2015, 1258, 209-222.	0.4	34
51	GFP-Based Expression Screening of Membrane Proteins in Insect Cells Using the Baculovirus System. <i>Methods in Molecular Biology</i> , 2015, 1261, 197-209.	0.4	13
52	Adhiron: a stable and versatile peptide display scaffold for molecular recognition applications. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 145-155.	1.0	136
53	Application of In-Fusion, Cloning for the Parallel Construction of <i>E. coli</i> Expression Vectors. <i>Methods in Molecular Biology</i> , 2014, 1116, 209-234.	0.4	22
54	Assay Platform for Clinically Relevant Metallo- $\beta$ -lactamases. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 6945-6953.	2.9	100

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55	Crystal structure of signal regulatory protein gamma (SIRP <sup>γ3</sup> ) in complex with an antibody Fab fragment. <i>BMC Structural Biology</i> , 2013, 13, 13.	2.3	10
56	Chromophore-Linked Substrate (CLS405): Probing Metallo-β-Lactamase Activity and Inhibition. <i>ChemMedChem</i> , 2013, 8, 1923-1929.	1.6	21
57	A streamlined implementation of the glutamine synthetase-based protein expression system. <i>BMC Biotechnology</i> , 2013, 13, 74.	1.7	8
58	Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity. <i>Journal of Virological Methods</i> , 2013, 187, 406-412.	1.0	51
59	Expression of recombinant glycoproteins in mammalian cells: towards an integrative approach to structural biology. <i>Current Opinion in Structural Biology</i> , 2013, 23, 345-356.	2.6	48
60	Binding of (5 <i>S</i> )-Penicilloic Acid to Penicillin Binding Protein 3. <i>ACS Chemical Biology</i> , 2013, 8, 2112-2116.	1.6	23
61	<i>S</i> -Adenosyl- <i>S</i> -carboxymethyl-L-homocysteine: a novel cofactor found in the putative tRNA-modifying enzyme CmoA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1090-1098.	2.5	20
62	Structure and Assembly of a Trans-Periplasmic Channel for Type IV Pili in <i>Neisseria meningitidis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002923.	2.1	69
63	Structural and Functional Characterization of the Kindlin-1 Pleckstrin Homology Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 43246-43261.	1.6	27
64	Structure of ribose 5-phosphate isomerase from the probiotic bacterium <i>Lactobacillus salivarius</i> UCC118. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1427-1433.	0.7	8
65	Converting Monoclonal Antibodies into Fab Fragments for Transient Expression in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2012, 801, 137-159.	0.4	7
66	<i>In situ</i> macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 592-600.	2.5	113
67	Outrunning free radicals in room-temperature macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 810-818.	2.5	83
68	Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 730-737.	0.7	1
69	Expression of protein complexes using multiple <i>Escherichia coli</i> protein co-expression systems: A benchmarking study. <i>Journal of Structural Biology</i> , 2011, 175, 159-170.	1.3	39
70	xtalPiMS: A PiMS-based web application for the management and monitoring of crystallization trials. <i>Journal of Structural Biology</i> , 2011, 175, 230-235.	1.3	8
71	Crystal Structures of Penicillin-Binding Protein 3 from <i>Pseudomonas aeruginosa</i> : Comparison of Native and Antibiotic-Bound Forms. <i>Journal of Molecular Biology</i> , 2011, 405, 173-184.	2.0	77
72	Methods in structural proteomics. <i>Methods</i> , 2011, 55, 1-2.	1.9	1

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73	Conformational changes in IgE contribute to its uniquely slow dissociation rate from receptor FcεRI. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 571-576.	3.6	105
74	Structure of New Delhi metallo-β-lactamase 1 (NDM-1). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1160-1164.	0.7	76
75	Streamlining Homogeneous Glycoprotein Production for Biophysical and Structural Applications by Targeted Cell Line Development. <i>PLoS ONE</i> , 2011, 6, e27829.	1.1	22
76	Genetic modification of a baculovirus vector for increased expression in insect cells. <i>Cell Biology and Toxicology</i> , 2010, 26, 57-68.	2.4	70
77	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	1.9	289
78	The structure of a reduced form of OxyR from <i>Neisseria meningitidis</i> . <i>BMC Structural Biology</i> , 2010, 10, 10.	2.3	22
79	Novel structural features in two ZHX homeodomains derived from a systematic study of single and multiple domains. <i>BMC Structural Biology</i> , 2010, 10, 13.	2.3	14
80	The crystal structure of NGO0477 from <i>Neisseria gonorrhoeae</i> reveals a novel protein fold incorporating a helix-turn-helix motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1798-1802.	1.5	5
81	Structural and Functional Insights of RANKL-RANK Interaction and Signaling. <i>Journal of Immunology</i> , 2010, 184, 6910-6919.	0.4	103
82	Improved expression of secreted and membrane-targeted proteins in insect cells. <i>Biotechnology and Applied Biochemistry</i> , 2010, 56, 85-93.	1.4	46
83	Recent advances in the production of proteins in insect and mammalian cells for structural biology. <i>Journal of Structural Biology</i> , 2010, 172, 55-65.	1.3	92
84	The structure of CrgA from <i>Neisseria meningitidis</i> reveals a new octameric assembly state for LysR transcriptional regulators. <i>Nucleic Acids Research</i> , 2009, 37, 4545-4558.	6.5	64
85	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. <i>Journal of Virology</i> , 2009, 83, 12895-12906.	1.5	115
86	Structural Plasticity of Eph Receptor A4 Facilitates Cross-Class Ephrin Signaling. <i>Structure</i> , 2009, 17, 1386-1397.	1.6	86
87	Some lessons from the systematic production and structural analysis of soluble $\beta$ 2 T-cell receptors. <i>Journal of Immunological Methods</i> , 2009, 350, 14-21.	0.6	13
88	The structure of NMB1585, a MarR-family regulator from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 204-209.	0.7	9
89	Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 597-600.	0.7	3
90	The Production of Glycoproteins by Transient Expression in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2009, 498, 245-263.	0.4	35

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91	The Tandem Zinc-Finger Region of Human ZHX Adopts a Novel C2H2 Zinc Finger Structure with a C-Terminal Extension. <i>Biochemistry</i> , 2009, 48, 4431-4439.	1.2	12
92	The Precise Engineering of Expression Vectors Using High-Throughput In-Fusion <sup>®</sup> , <sup>®</sup> PCR Cloning. <i>Methods in Molecular Biology</i> , 2009, 498, 75-90.	0.4	46
93	Crystal structure of a 3 $\alpha$ -oxoacyl-(acylcarrier protein) reductase (BA3989) from <i>Bacillus anthracis</i> at 2.4 $\text{Å}$ resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 562-567.	1.5	22
94	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 14-18.	0.7	31
95	Expression, purification and crystallization of a lyssavirus matrix (M) protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 258-262.	0.7	17
96	Structure of the cold-shock domain protein from <i>Neisseria meningitidis</i> reveals a strand-exchanged dimer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 247-251.	0.7	9
97	Structures of an alanine racemase from <i>Bacillus anthracis</i> (BA0252) in the presence and absence of ( <i>R</i> )-1-aminoethylphosphonic acid ( <i>L</i> -Ala-P). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 327-333.	0.7	16
98	Crystallization and preliminary X-ray analysis of CrgA, a LysR-type transcriptional regulator from pathogenic <i>Neisseria meningitidis</i> MC58. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 797-801.	0.7	16
99	Generation of baculovirus vectors for the high-throughput production of proteins in insect cells. <i>Biotechnology and Bioengineering</i> , 2008, 101, 1115-1122.	1.7	52
100	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
101	The Crystal Structure of UMP Kinase from <i>Bacillus anthracis</i> (BA1797) Reveals an Allosteric Nucleotide-Binding Site. <i>Journal of Molecular Biology</i> , 2008, 381, 1098-1105.	2.0	13
102	A pipeline for the production of antibody fragments for structural studies using transient expression in HEK 293T cells. <i>Protein Expression and Purification</i> , 2008, 62, 83-89.	0.6	41
103	Rhabdovirus Matrix Protein Structures Reveal a Novel Mode of Self-Association. <i>PLoS Pathogens</i> , 2008, 4, e1000251.	2.1	71
104	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2-Like Fold but Have Evolved to Inhibit NF- $\kappa$ B rather than Apoptosis. <i>PLoS Pathogens</i> , 2008, 4, e1000128.	2.1	136
105	The Structure and Transcriptional Analysis of a Global Regulator from <i>Neisseria meningitidis</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 14655-14664.	1.6	38
106	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. <i>Journal of General Virology</i> , 2007, 88, 2228-2236.	1.3	52
107	A versatile ligation-independent cloning method suitable for high-throughput expression screening applications. <i>Nucleic Acids Research</i> , 2007, 35, e45-e45.	6.5	499
108	Novel nucleotide triphosphates as potent P2Y2 agonists. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 562-565.	1.0	23

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109	Novel nucleotide triphosphates as potent P2Y2 agonists with enhanced stability over UTP. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 558-561.	1.0	7
110	Analysis of variable N-glycosylation site occupancy in glycoproteins by liquid chromatography electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2007, 361, 149-151.	1.1	12
111	Structure of 5-formyltetrahydrofolate cyclo-ligase from <i>Bacillus anthracis</i> (BA4489). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 168-172.	0.7	11
112	Glycoprotein Structural Genomics: Solving the Glycosylation Problem. <i>Structure</i> , 2007, 15, 267-273.	1.6	273
113	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Å... resolution. <i>Protein Science</i> , 2007, 16, 2294-2300.	3.1	30
114	High-throughput cloning, expression, and purification. , 2007, , 23-44.		0
115	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1103-1113.	2.5	56
116	The impact of protein characterization in structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1125-1136.	2.5	58
117	Application of high-throughput technologies to a structural proteomics-type analysis of <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1267-1275.	2.5	24
118	Structure of the PII signal transduction protein of <i>Neisseria meningitidis</i> at 1.85 Å... resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 494-497.	0.7	12
119	Lysine Methylation as a Routine Rescue Strategy for Protein Crystallization. <i>Structure</i> , 2006, 14, 1617-1622.	1.6	483
120	Benefits of Automated Crystallization Plate Tracking, Imaging, and Analysis. <i>Structure</i> , 2005, 13, 175-182.	1.6	42
121	Sample preparation and mass-spectrometric characterization of crystal-derived protein samples. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 643-645.	2.5	5
122	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 651-657.	2.5	234
123	Crystal structure of nitrogen regulatory protein IIA <sub>Ntr</sub> from <i>Neisseria meningitidis</i> . <i>BMC Structural Biology</i> , 2005, 5, 13.	2.3	23
124	High-resolution structure of the catalytic region of MICAL (molecule interacting with CasL), a multidomain flavoenzyme-signaling molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16836-16841.	3.3	75
125	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. <i>Structure</i> , 2004, 12, 341-353.	1.6	225
126	The crystal structure of IgE Fc reveals an asymmetrically bent conformation. <i>Nature Immunology</i> , 2002, 3, 681-686.	7.0	152



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127	Development of a recombinant cell-based system for the characterisation of phosphodiesterase 4 isoforms and evaluation of inhibitors. <i>Biochemical Pharmacology</i> , 1999, 57, 1375-1382.	2.0	18
128	Human phosphodiesterase 4A: characterization of full-length and truncated enzymes expressed in COS cells. <i>Biochemical Journal</i> , 1997, 326, 53-60.	1.7	32
129	Identification of Contact Residues in the IgE Binding Site of Human Fc $\mu$ RII. <i>Biochemistry</i> , 1997, 36, 15579-15588.	1.2	67
130	Interaction of the Low-Affinity Receptor CD23/Fc $\mu$ RII Lectin Domain with the Fc $\mu$ 3 $\mu$ 4 Fragment of Human Immunoglobulin E. <i>Biochemistry</i> , 1997, 36, 2112-2122.	1.2	62
131	The in vivo and in vitro characterisation of an engineered human antibody to E-selectin. <i>Immunotechnology: an International Journal of Immunological Engineering</i> , 1997, 3, 107-116.	2.4	10
132	Molecular Cloning and Expression of a Human Phosphodiesterase 4C. <i>Cellular Signalling</i> , 1997, 9, 575-585.	1.7	28
133	PDE 4 inhibitors: the use of molecular cloning in the design and development of novel drugs. <i>Drug Discovery Today</i> , 1997, 2, 89-101.	3.2	45
134	Hydrodynamic studies of a complex between the Fc fragment of human IgE and a soluble fragment of the Fc epsilon RI alpha chain.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 1841-1845.	3.3	34
135	Preparation and preclinical evaluation of humanised A33 immunoconjugates for radioimmunotherapy. <i>British Journal of Cancer</i> , 1995, 72, 1364-1372.	2.9	72
136	Secretion of recombinant human IgE-Fc by mammalian cells and biological activity of glycosylation site mutants. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 193-199.	1.0	51
137	The genetic engineering of monoclonal antibodies. <i>Journal of Immunological Methods</i> , 1994, 168, 149-165.	0.6	62
138	New applications for antibodies. <i>Analytical Proceedings</i> , 1990, 27, 2.	0.4	0
139	Site-specific attachment to recombinant antibodies via introduced surface cysteine residues. <i>Protein Engineering, Design and Selection</i> , 1990, 3, 703-708.	1.0	63
140	Localization of the cellular-fibronectin-specific epitope recognized by the monoclonal antibody IST-9 using fusion proteins expressed in <i>E. coli</i> . <i>FEBS Letters</i> , 1987, 215, 269-273.	1.3	92
141	Exon structure of the collagen-binding domain of human fibronectin. <i>FEBS Letters</i> , 1986, 204, 318-322.	1.3	18