

Stephen Curry

List of Publications by Year in descending order

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94
papers

11,915
citations

66250

44
h-index

51423

90
g-index

101
all docs

101
docs citations

101
times ranked

11310
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis of the Drug-binding Specificity of Human Serum Albumin. <i>Journal of Molecular Biology</i> , 2005, 353, 38-52.	2.0	1,617
2	Crystal structure of human serum albumin complexed with fatty acid reveals an asymmetric distribution of binding sites. <i>Nature Structural Biology</i> , 1998, 5, 827-835.	9.7	1,201
3	The extraordinary ligand binding properties of human serum albumin. <i>IUBMB Life</i> , 2005, 57, 787-796.	1.5	897
4	Crystallographic analysis reveals common modes of binding of medium and long-chain fatty acids to human serum albumin 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 303, 721-732.	2.0	813
5	Crystal Structure Analysis of Warfarin Binding to Human Serum Albumin. <i>Journal of Biological Chemistry</i> , 2001, 276, 22804-22809.	1.6	719
6	Binding of the General Anesthetics Propofol and Halothane to Human Serum Albumin. <i>Journal of Biological Chemistry</i> , 2000, 275, 38731-38738.	1.6	468
7	Crystal structures of human serum albumin complexed with monounsaturated and polyunsaturated fatty acids. <i>Journal of Molecular Biology</i> , 2001, 314, 955-960.	2.0	443
8	Fatty acid binding to human serum albumin: new insights from crystallographic studies. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 131-140.	1.2	429
9	Crystal structural analysis of human serum albumin complexed with hemin and fatty acid. <i>BMC Structural Biology</i> , 2003, 3, 6.	2.3	427
10	Structure of a major immunogenic site on foot-and-mouth disease virus. <i>Nature</i> , 1993, 362, 566-568.	13.7	360
11	Location of High and Low Affinity Fatty Acid Binding Sites on Human Serum Albumin Revealed by NMR Drug-competition Analysis. <i>Journal of Molecular Biology</i> , 2006, 361, 336-351.	2.0	301
12	Lessons from the Crystallographic Analysis of Small Molecule Binding to Human Serum Albumin. <i>Drug Metabolism and Pharmacokinetics</i> , 2009, 24, 342-357.	1.1	247
13	Crystallographic Analysis of Human Serum Albumin Complexed with 4Z,15E-Bilirubin-IX β . <i>Journal of Molecular Biology</i> , 2008, 381, 394-406.	2.0	241
14	Molecular Tectonic Model of Virus Structural Transitions: the Putative Cell Entry States of Poliovirus. <i>Journal of Virology</i> , 2000, 74, 1342-1354.	1.5	224
15	Structural basis of albumin-thyroxine interactions and familial dysalbuminemic hyperthyroxinemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6440-6445.	3.3	224
16	Structural analysis of cooperative RNA binding by the La motif and central RRM domain of human La protein. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 323-329.	3.6	128
17	Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease. <i>Journal of Biological Chemistry</i> , 2005, 280, 11520-11527.	1.6	126
18	Structural basis of binding of fluorescent, site-specific dansylated amino acids to human serum albumin. <i>Journal of Structural Biology</i> , 2011, 174, 84-91.	1.3	121

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19	Perturbations in the surface structure of A22 Iraq foot-and-mouth disease virus accompanying coupled changes in host cell specificity and antigenicity. <i>Structure</i> , 1996, 4, 135-145.	1.6	100
20	Interactions of very long-chain saturated fatty acids with serum albumin. <i>Journal of Lipid Research</i> , 2002, 43, 1000-1010.	2.0	99
21	Structure of the C-Terminal Domain of Human La Protein Reveals a Novel RNA Recognition Motif Coupled to a Helical Nuclear Retention Element. <i>Structure</i> , 2003, 11, 833-843.	1.6	96
22	Structure of Foot-and-mouth disease virus serotype A1061 alone and complexed with oligosaccharide receptor: receptor conservation in the face of antigenic variation. <i>Journal of General Virology</i> , 2005, 86, 1909-1920.	1.3	95
23	Beyond Expansion: Structural Studies on the Transport Roles of Human Serum Albumin. <i>Vox Sanguinis</i> , 2002, 83, 315-319.	0.7	92
24	A peptide motif in Raver1 mediates splicing repression by interaction with the PTB RRM2 domain. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 839-848.	3.6	92
25	Structural insights into the transcriptional and translational roles of Ebp1. <i>EMBO Journal</i> , 2007, 26, 3936-3944.	3.5	88
26	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. <i>Structure</i> , 2004, 12, 1631-1643.	1.6	87
27	Structural and Mutagenic Analysis of Foot-and-Mouth Disease Virus 3C Protease Reveals the Role of the Î²-Ribbon in Proteolysis. <i>Journal of Virology</i> , 2007, 81, 115-124.	1.5	81
28	Polypyrimidine Tract Binding Protein Stabilizes the Encephalomyocarditis Virus IRES Structure via Binding Multiple Sites in a Unique Orientation. <i>Molecular Cell</i> , 2009, 34, 556-568.	4.5	81
29	Structural Insights into Differences in Drug-binding Selectivity between Two Forms of Human Î±1-Acid Glycoprotein Genetic Variants, the A and F1*S Forms. <i>Journal of Biological Chemistry</i> , 2011, 286, 14427-14434.	1.6	78
30	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. <i>Structure</i> , 1995, 3, 571-580.	1.6	77
31	Photosensitized Reduction of Water to Hydrogen Using Human Serum Albumin Complexed with Zincâˆ²-Protoporphylin IX. <i>Journal of the American Chemical Society</i> , 2006, 128, 16297-16301.	6.6	77
32	Defining the roles and interactions of PTB. <i>Biochemical Society Transactions</i> , 2012, 40, 815-820.	1.6	76
33	Structural Analysis Reveals Conformational Plasticity in the Recognition of RNA 3' Ends by the Human La Protein. <i>Structure</i> , 2008, 16, 852-862.	1.6	71
34	Role of RNA Structure and RNA Binding Activity of Foot-and-Mouth Disease Virus 3C Protein in VPg Uridylolation and Virus Replication. <i>Journal of Virology</i> , 2006, 80, 9865-9875.	1.5	65
35	Insights into Cleavage Specificity from the Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease Complexed with a Peptide Substrate. <i>Journal of Molecular Biology</i> , 2010, 395, 375-389.	2.0	63
36	Conformation of Polypyrimidine Tract Binding Protein in Solution. <i>Structure</i> , 2006, 14, 1021-1027.	1.6	60

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37	O ₂ and CO Binding Properties of Artificial Hemoproteins Formed by Complexing Iron Protoporphyrin IX with Human Serum Albumin Mutants. <i>Journal of the American Chemical Society</i> , 2005, 127, 15933-15942.	6.6	59
38	Foot-and-mouth disease virus 3C protease: Recent structural and functional insights into an antiviral target. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 1-6.	1.2	58
39	Titration calculations of foot-and-mouth disease virus capsids and their stabilities as a function of pH 1. Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1998, 275, 295-308.	2.0	57
40	Foot-and-Mouth Disease Virus 2C Is a Hexameric AAA+ Protein with a Coordinated ATP Hydrolysis Mechanism. <i>Journal of Biological Chemistry</i> , 2010, 285, 24347-24359.	1.6	57
41	Norovirus Translation Requires an Interaction between the C Terminus of the Genome-linked Viral Protein VPg and Eukaryotic Translation Initiation Factor 4G. <i>Journal of Biological Chemistry</i> , 2014, 289, 21738-21750.	1.6	53
42	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
43	Analysis of the interaction with the hepatitis C virus mRNA reveals an alternative mode of RNA recognition by the human La protein. <i>Nucleic Acids Research</i> , 2012, 40, 1381-1394.	6.5	47
44	Structural studies of poliovirus mutants that overcome receptor defects. <i>Nature Structural Biology</i> , 1997, 4, 666-674.	9.7	44
45	Probing the structure of the warfarin-binding site on human serum albumin using site-directed mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 116-125.	1.5	44
46	Evolutionary analysis of serotype A foot-and-mouth disease viruses circulating in Pakistan and Afghanistan during 2002-2009. <i>Journal of General Virology</i> , 2011, 92, 2849-2864.	1.3	44
47	Structures of the Compact Helical Core Domains of Feline Calicivirus and Murine Norovirus VPg Proteins. <i>Journal of Virology</i> , 2013, 87, 5318-5330.	1.5	44
48	Dioxygenation of Human Serum Albumin Having a Prosthetic Heme Group in a Tailor-Made Heme Pocket. <i>Journal of the American Chemical Society</i> , 2004, 126, 14304-14305.	6.6	40
49	A Conserved Interaction between a C-Terminal Motif in Norovirus VPg and the HEAT-1 Domain of eIF4G Is Essential for Translation Initiation. <i>PLoS Pathogens</i> , 2016, 12, e1005379.	2.1	40
50	Detailed insights from microarray and crystallographic studies into carbohydrate recognition by microneme protein 1 (MIC1) of <i>Toxoplasma gondii</i> . <i>Protein Science</i> , 2009, 18, 1935-1947.	3.1	37
51	Crystallographic Analysis of Polypyrimidine Tract-Binding Protein-Raver1 Interactions Involved in Regulation of Alternative Splicing. <i>Structure</i> , 2011, 19, 1816-1825.	1.6	37
52	The polypyrimidine tract binding protein is a monomer. <i>Rna</i> , 2005, 11, 1803-1808.	1.6	35
53	Foot-and-Mouth Disease Virus 3C Protease Induces Fragmentation of the Golgi Compartment and Blocks Intra-Golgi Transport. <i>Journal of Virology</i> , 2013, 87, 11721-11729.	1.5	35
54	Crystallization of foot-and-mouth disease virus 3C protease: surface mutagenesis and a novel crystal-optimization strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 646-650.	2.5	34

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55	Genetic Engineering of the Heme Pocket in Human Serum Albumin: Modulation of O_2 Binding of Iron Protoporphyrin IX by Variation of Distal Amino Acids. <i>Journal of the American Chemical Society</i> , 2007, 129, 11286-11295.	6.6	34
56	Activation of picornaviral IRESs by PTB shows differential dependence on each PTB RNA-binding domain. <i>Rna</i> , 2011, 17, 1120-1131.	1.6	33
57	Crystallographic analysis reveals the structural basis of the high-affinity binding of iophenoxic acid to human serum albumin. <i>BMC Structural Biology</i> , 2011, 11, 18.	2.3	31
58	Changing how we evaluate research is difficult, but not impossible. <i>ELife</i> , 2020, 9, .	2.8	30
59	Human Norovirus NS3 Has RNA Helicase and Chaperoning Activities. <i>Journal of Virology</i> , 2018, 92, .	1.5	28
60	Chemical shift mapping of RNA interactions with the polypyrimidine tract binding protein. <i>Nucleic Acids Research</i> , 2002, 30, 456-462.	6.5	25
61	Structural Biology: A Century-long Journey into an Unseen World. <i>Interdisciplinary Science Reviews</i> , 2015, 40, 308-328.	1.0	25
62	Solution Structure and RNA Interactions of the RNA Recognition Motif from Eukaryotic Translation Initiation Factor 4B. <i>Biochemistry</i> , 2003, 42, 8966-8975.	1.2	24
63	Structure of a Murine Norovirus NS6 Protease-Product Complex Revealed by Adventitious Crystallisation. <i>PLoS ONE</i> , 2012, 7, e38723.	1.1	24
64	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1992, 228, 1263-1268.	2.0	23
65	Plasma albumin as a fatty acid carrier. <i>Advances in Molecular and Cell Biology</i> , 2003, , 29-46.	0.1	23
66	The Cellular Chaperone Heat Shock Protein 90 Is Required for Foot-and-Mouth Disease Virus Capsid Precursor Processing and Assembly of Capsid Pentamers. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
67	Inhibition of viral suppressor of RNAi proteins by designer peptides protects from enteroviral infection in vivo. <i>Immunity</i> , 2021, 54, 2231-2244.e6.	6.6	23
68	Getting to the end of RNA: Structural analysis of protein recognition of 5' and 3' termini. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 653-666.	0.9	21
69	Resonance assignment and secondary structure of an N-terminal fragment of the human La protein. <i>Journal of Biomolecular NMR</i> , 2003, 27, 93-94.	1.6	16
70	A continuous assay for foot-and-mouth disease virus 3C protease activity. <i>Analytical Biochemistry</i> , 2007, 368, 130-137.	1.1	16
71	The organization of RNA contacts by PTB for regulation of FAS splicing. <i>Nucleic Acids Research</i> , 2014, 42, 8605-8620.	6.5	16
72	A terminal affair: 3'-end recognition by the human La protein. <i>Trends in Biochemical Sciences</i> , 2006, 31, 303-305.	3.7	15

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73	The role of an amino acid triad at the entrance of the heme pocket in human serum albumin for O ₂ and CO binding to iron protoporphyrin IX. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 3836.	1.5	15
74	NMR assignment of the N-terminal region of human La free and in complex with RNA. <i>Biomolecular NMR Assignments</i> , 2008, 2, 107-109.	0.4	10
75	Creating SPACE to evolve academic assessment. <i>ELife</i> , 2021, 10, .	2.8	10
76	Solution and crystal structures of a C-terminal fragment of the neuronal isoform of the polypyrimidine tract binding protein (nPTB). <i>PeerJ</i> , 2014, 2, e305.	0.9	9
77	Structure determination of Murine Norovirus NS6 proteases with C-terminal extensions designed to probe protease-substrate interactions. <i>PeerJ</i> , 2015, 3, e798.	0.9	9
78	The RNA Helicase eIF4A Is Required for Sapovirus Translation. <i>Journal of Virology</i> , 2016, 90, 5200-5204.	1.5	8
79	Design and synthesis of irreversible inhibitors of foot-and-mouth disease virus 3C protease. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 490-494.	1.0	7
80	Crystal structure of the 3C protease from Southern African Territories type 2 foot-and-mouth disease virus. <i>PeerJ</i> , 2016, 4, e1964.	0.9	6
81	Resonance assignment and secondary structure determination of a C-terminal fragment of the lupus autoantigen (La) protein containing a putative RNA recognition motif (RRM). <i>Journal of Biomolecular NMR</i> , 2002, 22, 387-388.	1.6	5
82	Letter to the Editor: Resonance Assignment and Secondary Structure of the La Motif. <i>Journal of Biomolecular NMR</i> , 2004, 29, 449-450.	1.6	5
83	Widen the channels of communication with society. <i>Nature</i> , 2009, 458, 702-702.	13.7	5
84	Effect of foot-and-mouth disease virus capsid precursor protein and 3C protease expression on bovine herpesvirus 1 replication. <i>Archives of Virology</i> , 2010, 155, 723-731.	0.9	5
85	Resonance assignment and topology of the 2H, 13C, 15N labelled 29 kDa N-terminal fragment of the polypyrimidine tract binding protein (PTB). <i>Journal of Biomolecular NMR</i> , 2002, 24, 79-80.	1.6	3
86	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1999, 14, 383-384.	1.6	2
87	Open access - reasons to be cheerful: a reply to Agrawal. <i>Trends in Plant Science</i> , 2014, 19, 196-197.	4.3	2
88	What is the meaning of Brexit?. <i>EMBO Reports</i> , 2016, 17, 1239-1240.	2.0	2
89	Guest Editorial: Open Access: Principles, Practice, and Potential. <i>ACS Omega</i> , 2017, 2, 2803-2804.	1.6	2
90	O ₂ Binding Properties of Human Serum Albumin Quadruple Mutant Complexed Iron Protoporphyrin IX with Axial His-186 Coordination. <i>Chemistry Letters</i> , 2009, 38, 776-777.	0.7	1

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91	By the people, for the people. <i>New Scientist</i> , 2012, 214, 26-27.	0.0	0
92	UK research reform: protest now. <i>Nature</i> , 2016, 539, 357-357.	13.7	0
93	Open access: brave new world requires bravery. <i>Insights: the UKSC Journal</i> , 2013, 26, 22-27.	0.1	0
94	Brexit: scientific responses have to be personal and political. <i>Matters</i> , 0, , .	1.0	0