Stephen Curry

List of Publications by Year
in descending order

94 papers	11,915 citations	57758 44 h-index	45317 90 g-index
101 all docs	101 docs citations	101 times ranked	10150 citing authors

#	Article	IF	Citations
1	Structural Basis of the Drug-binding Specificity of Human Serum Albumin. Journal of Molecular Biology, 2005, 353, 38-52.	4.2	1,617
2	Crystal structure of human serum albumin complexed with fatty acid reveals an asymmetric distribution of binding sites. Nature Structural Biology, 1998, 5, 827-835.	9.7	1,201
3	The extraordinary ligand binding properties of human serum albumin. IUBMB Life, 2005, 57, 787-796.	3.4	897
4	Crystallographic analysis reveals common modes of binding of medium and long-chain fatty acids to human serum albumin 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 303, 721-732.	4.2	813
5	Crystal Structure Analysis of Warfarin Binding to Human Serum Albumin. Journal of Biological Chemistry, 2001, 276, 22804-22809.	3.4	719
6	Binding of the General Anesthetics Propofol and Halothane to Human Serum Albumin. Journal of Biological Chemistry, 2000, 275, 38731-38738.	3.4	468
7	Crystal structures of human serum albumin complexed with monounsaturated and polyunsaturated fatty acids. Journal of Molecular Biology, 2001, 314, 955-960.	4.2	443
8	Fatty acid binding to human serum albumin: new insights from crystallographic studies. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 1999, 1441, 131-140.	2.4	429
9	Crystal structural analysis of human serum albumin complexed with hemin and fatty acid. BMC Structural Biology, 2003, 3, 6.	2.3	427
10	Structure of a major immunogenic site on foot-and-mouth disease virus. Nature, 1993, 362, 566-568.	27.8	360
11	Location of High and Low Affinity Fatty Acid Binding Sites on Human Serum Albumin Revealed by NMR Drug-competition Analysis. Journal of Molecular Biology, 2006, 361, 336-351.	4.2	301
12	Lessons from the Crystallographic Analysis of Small Molecule Binding to Human Serum Albumin. Drug Metabolism and Pharmacokinetics, 2009, 24, 342-357.	2.2	247
13	Crystallographic Analysis of Human Serum Albumin Complexed with 4Z,15E-Bilirubin-IXÎ±. Journal of Molecular Biology, 2008, 381, 394-406.	4.2	241
14	Molecular Tectonic Model of Virus Structural Transitions: the Putative Cell Entry States of Poliovirus. Journal of Virology, 2000, 74, 1342-1354.	3.4	224
15	Structural basis of albumin-thyroxine interactions and familial dysalbuminemic hyperthyroxinemia. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6440-6445.	7.1	224
16	Structural analysis of cooperative RNA binding by the La motif and central RRM domain of human La protein. Nature Structural and Molecular Biology, 2004, 11, 323-329.	8.2	128
17	Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease. Journal of Biological Chemistry, 2005, 280, 11520-11527.	3.4	126
18	Structural basis of binding of fluorescent, site-specific dansylated amino acids to human serum albumin. Journal of Structural Biology, 2011, 174, 84-91.	2.8	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. Structure, 1996, 4, 135-145.	3.3	100
20	Interactions of very long-chain saturated fatty acids with serum albumin. Journal of Lipid Research, 2002, 43, 1000-1010.	4.2	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. Structure, 2003, 11, 833-843.	3.3	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. Journal of General Virology, 2005, 86, 1909-1920.	2.9	95
23	Beyond Expansion: Structural Studies on the Transport Roles of Human Serum Albumin. Vox Sanguinis, 2002, 83, 315-319.	1.5	92
24	A peptide motif in Raver1 mediates splicing repression by interaction with the PTB RRM2 domain. Nature Structural and Molecular Biology, 2006, 13, 839-848.	8.2	92
25	Structural insights into the transcriptional and translational roles of Ebp1. EMBO Journal, 2007, 26, 3936-3944.	7.8	88
26	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. Structure, 2004, 12, 1631-1643.	3.3	87
27	Structural and Mutagenic Analysis of Foot-and-Mouth Disease Virus 3C Protease Reveals the Role of the Î²-Ribbon in Proteolysis. Journal of Virology, 2007, 81, 115-124.	3.4	81
28	Polypyrimidine Tract Binding Protein Stabilizes the Encephalomyocarditis Virus IRES Structure via Binding Multiple Sites in a Unique Orientation. Molecular Cell, 2009, 34, 556-568.	9.7	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. Journal of Biological Chemistry, 2011, 286, 14427-14434.	3.4	78
30	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. Structure, 1995, 3, 571-580.	3.3	77
31	Photosensitized Reduction of Water to Hydrogen Using Human Serum Albumin Complexed with Zincâ^'Protoporphyrin IX. Journal of the American Chemical Society, 2006, 128, 16297-16301.	13.7	77
32	Defining the roles and interactions of PTB. Biochemical Society Transactions, 2012, 40, 815-820.	3.4	76
33	Structural Analysis Reveals Conformational Plasticity in the Recognition of RNA 3â€² Ends by the Human La Protein. Structure, 2008, 16, 852-862.	3.3	71
34	Role of RNA Structure and RNA Binding Activity of Foot-and-Mouth Disease Virus 3C Protein in VPg Uridylylation and Virus Replication. Journal of Virology, 2006, 80, 9865-9875.	3.4	65
35	Insights into Cleavage Specificity from the Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease Complexed with a Peptide Substrate. Journal of Molecular Biology, 2010, 395, 375-389.	4.2	63
36	Conformation of Polypyrimidine Tract Binding Protein in Solution. Structure, 2006, 14, 1021-1027.	3.3	60

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37	O2and CO Binding Properties of Artificial Hemoproteins Formed by Complexing Iron Protoporphyrin IX with Human Serum Albumin Mutants. Journal of the American Chemical Society, 2005, 127, 15933-15942.	13.7	59
38	Foot-and-mouth disease virus 3C protease: Recent structural and functional insights into an antiviral target. International Journal of Biochemistry and Cell Biology, 2007, 39, 1-6.	2.8	58
39	Titration calculations of foot-and-mouth disease virus capsids and their stabilities as a function of pH 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 275, 295-308.	4.2	57
40	Foot-and-Mouth Disease Virus 2C Is a Hexameric AAA+ Protein with a Coordinated ATP Hydrolysis Mechanism. Journal of Biological Chemistry, 2010, 285, 24347-24359.	3.4	57
41	Norovirus Translation Requires an Interaction between the C Terminus of the Genome-linked Viral Protein VPg and Eukaryotic Translation Initiation Factor 4G. Journal of Biological Chemistry, 2014, 289, 21738-21750.	3.4	53
42	Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity. Journal of Virological Methods, 2013, 187, 406-412.	2.1	51
43	Analysis of the interaction with the hepatitis C virus mRNA reveals an alternative mode of RNA recognition by the human La protein. Nucleic Acids Research, 2012, 40, 1381-1394.	14.5	47
44	Structural studies of poliovirus mutants that overcome receptor defects. Nature Structural Biology, 1997, 4, 666-674.	9.7	44
45	Probing the structure of the warfarin-binding site on human serum albumin using site-directed mutagenesis. Proteins: Structure, Function and Bioinformatics, 2002, 47, 116-125.	2.6	44
46	Evolutionary analysis of serotype A foot-and-mouth disease viruses circulating in Pakistan and Afghanistan during 2002â€“2009. Journal of General Virology, 2011, 92, 2849-2864.	2.9	44
47	Structures of the Compact Helical Core Domains of Feline Calicivirus and Murine Norovirus VPg Proteins. Journal of Virology, 2013, 87, 5318-5330.	3.4	44
48	Dioxygenation of Human Serum Albumin Having a Prosthetic Heme Group in a Tailor-Made Heme Pocket. Journal of the American Chemical Society, 2004, 126, 14304-14305.	13.7	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. PLoS Pathogens, 2016, 12, e1005379.	4.7	40
50	Detailed insights from microarray and crystallographic studies into carbohydrate recognition by microneme protein 1 (MIC1) of Toxoplasma gondii. Protein Science, 2009, 18, 1935-1947.	7.6	37
51	Crystallographic Analysis of Polypyrimidine Tract-Binding Protein-Raver1 Interactions Involved in Regulation of Alternative Splicing. Structure, 2011, 19, 1816-1825.	3.3	37
52	The polypyrimidine tract binding protein is a monomer. Rna, 2005, 11, 1803-1808.	3.5	35
53	Foot-and-Mouth Disease Virus 3C Protease Induces Fragmentation of the Golgi Compartment and Blocks Intra-Golgi Transport. Journal of Virology, 2013, 87, 11721-11729.	3.4	35
54	Crystallization of foot-and-mouth disease virus 3C protease: surface mutagenesis and a novel crystal-optimization strategy. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 646-650.	2.5	34

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55	Genetic Engineering of the Heme Pocket in Human Serum Albumin:â€‰ Modulation of O₂ Binding of Iron Protoporphyrin IX by Variation of Distal Amino Acids. Journal of the American Chemical Society, 2007, 129, 11286-11295.	13.7	34
56	Activation of picornaviral IRESs by PTB shows differential dependence on each PTB RNA-binding domain. Rna, 2011, 17, 1120-1131.	3.5	33
57	Crystallographic analysis reveals the structural basis of the high-affinity binding of iophenoxic acid to human serum albumin. BMC Structural Biology, 2011, 11, 18.	2.3	31
58	Changing how we evaluate research is difficult, but not impossible. ELife, 2020, 9, .	6.0	30
59	Human Norovirus NS3 Has RNA Helicase and Chaperoning Activities. Journal of Virology, 2018, 92, .	3.4	28
60	Chemical shift mapping of RNA interactions with the polypyrimidine tract binding protein. Nucleic Acids Research, 2002, 30, 456-462.	14.5	25
61	Structural Biology: A Century-long Journey into an Unseen World. Interdisciplinary Science Reviews, 2015, 40, 308-328.	1.4	25
62	Solution Structure and RNA Interactions of the RNA Recognition Motif from Eukaryotic Translation Initiation Factor 4Bâ€. Biochemistry, 2003, 42, 8966-8975.	2.5	24
63	Structure of a Murine Norovirus NS6 Protease-Product Complex Revealed by Adventitious Crystallisation. PLoS ONE, 2012, 7, e38723.	2.5	24
64	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. Journal of Molecular Biology, 1992, 228, 1263-1268.	4.2	23
65	Plasma albumin as a fatty acid carrier. Advances in Molecular and Cell Biology, 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. Journal of Virology, 2018, 92, .	3.4	23
67	Inhibition of viral suppressor of RNAi proteins by designer peptides protects from enteroviral infection inÂvivo. Immunity, 2021, 54, 2231-2244.e6.	14.3	23
68	Getting to the end of RNA: Structural analysis of protein recognition of 5â€² and 3â€² termini. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2009, 1789, 653-666.	1.9	21
69	Resonance assignment and secondary structure of an N-terminal fragment of the human La protein. Journal of Biomolecular NMR, 2003, 27, 93-94.	2.8	16
70	A continuous assay for foot-and-mouth disease virus 3C protease activity. Analytical Biochemistry, 2007, 368, 130-137.	2.4	16
71	The organization of RNA contacts by PTB for regulation ofFASsplicing. Nucleic Acids Research, 2014, 42, 8605-8620.	14.5	16
72	A terminal affair: 3â€²-end recognition by the human La protein. Trends in Biochemical Sciences, 2006, 31, 303-305.	7.5	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 O2 and CO binding to iron protoporphyrin IX. Organic and Biomolecular Chemistry, 2009, 7, 3836.	2.8	15
74	NMR assignment of the N-terminal region of human La free and in complex with RNA. Biomolecular NMR Assignments, 2008, 2, 107-109.	0.8	10
75	Creating SPACE to evolve academic assessment. ELife, 2021, 10, .	6.0	10
76	Solution and crystal structures of a C-terminal fragment of the neuronal isoform of the polypyrimidine tract binding protein (nPTB). PeerJ, 2014, 2, e305.	2.0	9
77	Structure determination of Murine Norovirus NS6 proteases with C-terminal extensions designed to probe proteaseâ€"substrate interactions. PeerJ, 2015, 3, e798.	2.0	9
78	The RNA Helicase eIF4A Is Required for Sapovirus Translation. Journal of Virology, 2016, 90, 5200-5204.	3.4	8
79	Design and synthesis of irreversible inhibitors of foot-and-mouth disease virus 3C protease. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 490-494.	2.2	7
80	Crystal structure of the 3C protease from Southern African Territories type 2 foot-and-mouth disease virus. PeerJ, 2016, 4, e1964.	2.0	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). Journal of Biomolecular NMR, 2002, 22, 387-388.	2.8	5
82	Letter to the Editor: Resonance Assignment and Secondary Structure of the La Motif. Journal of Biomolecular NMR, 2004, 29, 449-450.	2.8	5
83	Widen the channels of communication with society. Nature, 2009, 458, 702-702.	27.8	5
84	Effect of foot-and-mouth disease virus capsid precursor protein and 3C protease expression on bovine herpesvirus 1 replication. Archives of Virology, 2010, 155, 723-731.	2.1	5
85	Resonance assignment and topology of the 2H, 13C, 15N labelled 29 kDa N-terminal fragment of the polypyrimidine tract binding protein (PTB). Journal of Biomolecular NMR, 2002, 24, 79-80.	2.8	3
86	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 383-384.	2.8	2
87	Open access - reasons to be cheerful: a reply to Agrawal. Trends in Plant Science, 2014, 19, 196-197.	8.8	2
88	What is the meaning of Brexit?. EMBO Reports, 2016, 17, 1239-1240.	4.5	2
89	Guest Editorial: Open Access: Principles, Practice, and Potential. ACS Omega, 2017, 2, 2803-2804.	3.5	2
90	O2 Binding Properties of Human Serum Albumin Quadruple Mutant Complexed Iron Protoporphyrin IX with Axial His-186 Coordination. Chemistry Letters, 2009, 38, 776-777.	1.3	1

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91	By the people, for the people. New Scientist, 2012, 214, 26-27.	0.0	0
92	UK research reform: protest now. Nature, 2016, 539, 357-357.	27.8	0
93	Open access: brave new world requires bravery. Insights: the UKSG Journal, 2013, 26, 22-27.	0.4	0
94	Brexit: scientific responses have to be personal and political. Matters, 0, , .	1.0	0