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	Creating SPACE to evolve academic assessment. ELife, 2021, 10, .	2.8	10
2	Inhibition of viral suppressor of RNAi proteins by designer peptides protects from enteroviral infection inÂvivo. Immunity, 2021, 54, 2231-2244.e6.	6.6	23
3	Changing how we evaluate research is difficult, but not impossible. ELife, 2020, 9, .	2.8	30
4	Human Norovirus NS3 Has RNA Helicase and Chaperoning Activities. Journal of Virology, 2018, 92, .	1.5	28
5	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, .	1.5	23
6	Guest Editorial: Open Access: Principles, Practice, and Potential. ACS Omega, 2017, 2, 2803-2804.	1.6	2
7	UK research reform: protest now. Nature, 2016, 539, 357-357.	13.7	0
8	What is the meaning of Brexit?. EMBO Reports, 2016, 17, 1239-1240.	2.0	2
9	The RNA Helicase eIF4A Is Required for Sapovirus Translation. Journal of Virology, 2016, 90, 5200-5204.	1.5	8
10	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.	2.1	40
11	Crystal structure of the 3C protease from Southern African Territories type 2 foot-and-mouth disease virus. PeerJ, 2016, 4, e1964.	0.9	6
12	Structural Biology: A Century-long Journey into an Unseen World. Interdisciplinary Science Reviews, 2015, 40, 308-328.	1.0	25
13	Structure determination of Murine Norovirus NS6 proteases with C-terminal extensions designed to probe proteaseâ€“substrate interactions. PeerJ, 2015, 3, e798.	0.9	9
14	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.	1.6	53
15	The organization of RNA contacts by PTB for regulation of<i>FAS</i>splicing. Nucleic Acids Research, 2014, 42, 8605-8620.	6.5	16
16	Design and synthesis of irreversible inhibitors of foot-and-mouth disease virus 3C protease. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 490-494.	1.0	7
17	Open access - reasons to be cheerful: a reply to Agrawal. Trends in Plant Science, 2014, 19, 196-197.	4.3	2
18	Solution and crystal structures of a C-terminal fragment of the neuronal isoform of the polypyrimidine tract binding protein (nPTB). PeerJ, 2014, 2, e305.	0.9	9

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19	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.	1.0	51
20	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.	1.5	35
21	Structures of the Compact Helical Core Domains of Feline Calicivirus and Murine Norovirus VPg Proteins. Journal of Virology, 2013, 87, 5318-5330.	1.5	44
22	Open access: brave new world requires bravery. Insights: the UKSG Journal, 2013, 26, 22-27.	0.1	0
23	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.	6.5	47
24	By the people, for the people. New Scientist, 2012, 214, 26-27.	0.0	0
25	Defining the roles and interactions of PTB. Biochemical Society Transactions, 2012, 40, 815-820.	1.6	76
26	Structure of a Murine Norovirus NS6 Protease-Product Complex Revealed by Adventitious Crystallisation. PLoS ONE, 2012, 7, e38723.	1.1	24
27	Structural basis of binding of fluorescent, site-specific dansylated amino acids to human serum albumin. Journal of Structural Biology, 2011, 174, 84-91.	1.3	121
28	Crystallographic Analysis of Polypyrimidine Tract-Binding Protein-Raver1 Interactions Involved in Regulation of Alternative Splicing. Structure, 2011, 19, 1816-1825.	1.6	37
29	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
30	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.	1.3	44
31	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.	1.6	78
32	Activation of picornaviral IRESs by PTB shows differential dependence on each PTB RNA-binding domain. Rna, 2011, 17, 1120-1131.	1.6	33
33	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.	0.9	5
34	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.	1.6	57
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.	2.0	63
36	Lessons from the Crystallographic Analysis of Small Molecule Binding to Human Serum Albumin. Drug Metabolism and Pharmacokinetics, 2009, 24, 342-357.	1.1	247

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37	Detailed insights from microarray and crystallographic studies into carbohydrate recognition by microneme protein 1 (MIC1) of <i>Toxoplasma gondii</i>. Protein Science, 2009, 18, 1935-1947.	3.1	37
38	Widen the channels of communication with society. Nature, 2009, 458, 702-702.	13.7	5
39	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.	0.9	21
40	Polypyrimidine Tract Binding Protein Stabilizes the Encephalomyocarditis Virus IRES Structure via Binding Multiple Sites in a Unique Orientation. Molecular Cell, 2009, 34, 556-568.	4.5	81
41	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.	1.5	15
42	O2 Binding Properties of Human Serum Albumin Quadruple Mutant Complexed Iron Protoporphyrin IX with Axial His-186 Coordination. Chemistry Letters, 2009, 38, 776-777.	0.7	1
43	NMR assignment of the N-terminal region of human La free and in complex with RNA. Biomolecular NMR Assignments, 2008, 2, 107-109.	0.4	10
44	Structural Analysis Reveals Conformational Plasticity in the Recognition of RNA 3â€² Ends by the Human La Protein. Structure, 2008, 16, 852-862.	1.6	71
45	Crystallographic Analysis of Human Serum Albumin Complexed with 4Z,15E-Bilirubin-IXÎ±. Journal of Molecular Biology, 2008, 381, 394-406.	2.0	241
46	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.	1.5	81
47	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.	1.2	58
48	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.	6.6	34
49	A continuous assay for foot-and-mouth disease virus 3C protease activity. Analytical Biochemistry, 2007, 368, 130-137.	1.1	16
50	Structural insights into the transcriptional and translational roles of Ebp1. EMBO Journal, 2007, 26, 3936-3944.	3.5	88
51	Photosensitized Reduction of Water to Hydrogen Using Human Serum Albumin Complexed with Zincâˆ’Protoporphyrin IX. Journal of the American Chemical Society, 2006, 128, 16297-16301.	6.6	77
52	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.	2.0	301
53	A peptide motif in Raver1 mediates splicing repression by interaction with the PTB RRM2 domain. Nature Structural and Molecular Biology, 2006, 13, 839-848.	3.6	92
54	Conformation of Polypyrimidine Tract Binding Protein in Solution. Structure, 2006, 14, 1021-1027.	1.6	60

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55	A terminal affair: 3â€²-end recognition by the human La protein. Trends in Biochemical Sciences, 2006, 31, 303-305.	3.7	15
56	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.	1.5	65
57	The extraordinary ligand binding properties of human serum albumin. IUBMB Life, 2005, 57, 787-796.	1.5	897
58	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
59	The polypyrimidine tract binding protein is a monomer. Rna, 2005, 11, 1803-1808.	1.6	35
60	Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease. Journal of Biological Chemistry, 2005, 280, 11520-11527.	1.6	126
61	Structural Basis of the Drug-binding Specificity of Human Serum Albumin. Journal of Molecular Biology, 2005, 353, 38-52.	2.0	1,617
62	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.	1.3	95
63	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.	6.6	59
64	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.	3.6	128
65	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. Structure, 2004, 12, 1631-1643.	1.6	87
66	Letter to the Editor: Resonance Assignment and Secondary Structure of the La Motif. Journal of Biomolecular NMR, 2004, 29, 449-450.	1.6	5
67	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.	6.6	40
68	Resonance assignment and secondary structure of an N-terminal fragment of the human La protein. Journal of Biomolecular NMR, 2003, 27, 93-94.	1.6	16
69	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.	1.6	96
70	Crystal structural analysis of human serum albumin complexed with hemin and fatty acid. BMC Structural Biology, 2003, 3, 6.	2.3	427
71	Solution Structure and RNA Interactions of the RNA Recognition Motif from Eukaryotic Translation Initiation Factor 4Bâ€. Biochemistry, 2003, 42, 8966-8975.	1.2	24
72	Plasma albumin as a fatty acid carrier. Advances in Molecular and Cell Biology, 2003, , 29-46.	0.1	23

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73	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.	3.3	224
74	Chemical shift mapping of RNA interactions with the polypyrimidine tract binding protein. Nucleic Acids Research, 2002, 30, 456-462.	6.5	25
75	Interactions of very long-chain saturated fatty acids with serum albumin. Journal of Lipid Research, 2002, 43, 1000-1010.	2.0	99
76	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.	1.5	44
77	Beyond Expansion: Structural Studies on the Transport Roles of Human Serum Albumin. Vox Sanguinis, 2002, 83, 315-319.	0.7	92
78	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.	1.6	5
79	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.	1.6	3
80	Crystal structures of human serum albumin complexed with monounsaturated and polyunsaturated fatty acids. Journal of Molecular Biology, 2001, 314, 955-960.	2.0	443
81	Crystal Structure Analysis of Warfarin Binding to Human Serum Albumin. Journal of Biological Chemistry, 2001, 276, 22804-22809.	1.6	719
82	Binding of the General Anesthetics Propofol and Halothane to Human Serum Albumin. Journal of Biological Chemistry, 2000, 275, 38731-38738.	1.6	468
83	Molecular Tectonic Model of Virus Structural Transitions: the Putative Cell Entry States of Poliovirus. Journal of Virology, 2000, 74, 1342-1354.	1.5	224
84	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.	2.0	813
85	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 383-384.	1.6	2
86	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.	1.2	429
87	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
88	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.	2.0	57
89	Structural studies of poliovirus mutants that overcome receptor defects. Nature Structural Biology, 1997, 4, 666-674.	9.7	44
90	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.	1.6	100

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91	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. Structure, 1995, 3, 571-580.	1.6	77
92	Structure of a major immunogenic site on foot-and-mouth disease virus. Nature, 1993, 362, 566-568.	13.7	360
93	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. Journal of Molecular Biology, 1992, 228, 1263-1268.	2.0	23
94	Brexit: scientific responses have to be personal and political. Matters, 0, , .	1.0	0