Richard B Sessions

List of Publications by Year
in descending order

81 papers	4,253 citations	172207 29 h-index	123241 61 g-index
92 all docs	92 docs citations	92 times ranked	7973 citing authors

#	Article	IF	Citations
1	Neuropilin-1 is a host factor for SARS-CoV-2 infection. Science, 2020, 370, 861-865.	6.0	1,015
2	Self-Assembling Cages from Coiled-Coil Peptide Modules. Science, 2013, 340, 595-599.	6.0	451
3	Computational design of water-soluble Î±-helical barrels. Science, 2014, 346, 485-488.	6.0	306
4	Retriever is a multiprotein complex for retromer-independent endosomal cargo recycling. Nature Cell Biology, 2017, 19, 1214-1225.	4.6	243
5	A unique PDZ domain and arrestin-like fold interaction reveals mechanistic details of endocytic recycling by SNX27-retromer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3604-13.	3.3	151
6	CCBuilder: an interactive web-based tool for building, designing and assessing coiled-coil protein assemblies. Bioinformatics, 2014, 30, 3029-3035.	1.8	103
7	A monodisperse transmembrane Î±-helical peptide barrel. Nature Chemistry, 2017, 9, 411-419.	6.6	97
8	A Designed System for Assessing How Sequence Affects Î± to Î² Conformational Transitions in Proteins. Journal of Biological Chemistry, 2002, 277, 10150-10155.	1.6	94
9	On the Calculation of Acyl Chain Order Parameters from Lipid Simulations. Journal of Chemical Theory and Computation, 2017, 13, 5683-5696.	2.3	92
10	Construction and in vivo assembly of a catalytically proficient and hyperthermostable de novo enzyme. Nature Communications, 2017, 8, 358.	5.8	91
11	High performance in silico virtual drug screening on many-core processors. International Journal of High Performance Computing Applications, 2015, 29, 119-134.	2.4	86
12	Protochlorophyllide oxidoreductase: A homology model examined by site-directed mutagenesis. Proteins: Structure, Function and Bioinformatics, 2001, 44, 329-335.	1.5	78
13	Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein**. Angewandte Chemie - International Edition, 2021, 60, 7098-7110.	7.2	77
14	Local and macroscopic electrostatic interactions in single Î±-helices. Nature Chemical Biology, 2015, 11, 221-228.	3.9	72
15	Antiproliferative and Antimigratory Effects of a Novel YAPâ€“TEAD Interaction Inhibitor Identified Using in Silico Molecular Docking. Journal of Medicinal Chemistry, 2019, 62, 1291-1305.	2.9	66
16	Cryo-EM of multiple cage architectures reveals a universal mode of clathrin self-assembly. Nature Structural and Molecular Biology, 2019, 26, 890-898.	3.6	56
17	Decorating Self-Assembled Peptide Cages with Proteins. ACS Nano, 2017, 11, 7901-7914.	7.3	55
18	Predicting and Experimentally Validating Hot-Spot Residues at Proteinâ€“Protein Interfaces. ACS Chemical Biology, 2019, 14, 2252-2263.	1.6	54

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19	Discovery of SARS-CoV-2 M^{pro} peptide inhibitors from modelling substrate and ligand binding. Chemical Science, 2021, 12, 13686-13703.	3.7	54
20	ISAMBARD: an open-source computational environment for biomolecular analysis, modelling and design. Bioinformatics, 2017, 33, 3043-3050.	1.8	48
21	Ab initio protein structure prediction using physicochemical potentials and a simplified off-lattice model. Proteins: Structure, Function and Bioinformatics, 2001, 43, 186-202.	1.5	46
22	A potential interaction between the SARS-CoV-2 spike protein and nicotinic acetylcholine receptors. Biophysical Journal, 2021, 120, 983-993.	0.2	43
23	Thermodynamic Properties of Transient Intermediates and Transition States in the Folding of Two Contrasting Protein Structuresâ€. Biochemistry, 1998, 37, 2538-2545.	1.2	41
24	BAlaS: fast, interactive and accessible computational alanine-scanning using BudeAlaScan. Bioinformatics, 2020, 36, 2917-2919.	1.8	39
25	Effects of Mutations on the Thermodynamics of a Protein Folding Reaction:Â Implications for the Mechanism of Formation of the Intermediate and Transition Statesâ€. Biochemistry, 2000, 39, 3480-3485.	1.2	37
26	Structural and Functional Analysis of Cell Wall-anchored Polypeptide Adhesin BspA in Streptococcus agalactiae. Journal of Biological Chemistry, 2016, 291, 15985-16000.	1.6	36
27	Beyond icosahedral symmetry in packings of proteins in spherical shells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9014-9019.	3.3	36
28	New sequence data enable modelling of the fungal alternative oxidase and explain an absence of regulation by pyruvate. FEBS Letters, 2000, 481, 141-146.	1.3	35
29	Identification of key binding site residues of MCT1 for AR-C155858 reveals the molecular basis of its isoform selectivity. Biochemical Journal, 2015, 466, 177-188.	1.7	35
30	A Rare Mutation in SMAD9 Associated With High Bone Mass Identifies the SMADâ€Ðependent BMP Signaling Pathway as a Potential Anabolic Target for Osteoporosis. Journal of Bone and Mineral Research, 2020, 35, 92-105.	3.1	34
31	Unlocking Nicotinic Selectivity via Direct Câ€'H Functionalization of (â^')-Cytisine. CheM, 2018, 4, 1710-1725.	5.8	31
32	A tetrapeptide class of biased analgesics from an Australian fungus targets the Âμ-opioid receptor. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22353-22358.	3.3	31
33	Water as a Conformational Editor in Protein Folding. Journal of Molecular Biology, 2004, 343, 1125-1133.	2.0	29
34	Structural characterization of a methionine-rich, emulsifying protein from sunflower seed. Proteins: Structure, Function and Bioinformatics, 2000, 38, 341-349.	1.5	26
35	Drug Binding Poses Relate Structure with Efficacy in the Î¼ Opioid Receptor. Journal of Molecular Biology, 2017, 429, 1840-1851.	2.0	26
36	A General Mechanism for Signal Propagation in the Nicotinic Acetylcholine Receptor Family. Journal of the American Chemical Society, 2019, 141, 19953-19958.	6.6	25

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37	Identification of the Initial Steps in Signal Transduction in the Î±4Î²2 Nicotinic Receptor: Insights from Equilibrium and Nonequilibrium Simulations. Structure, 2019, 27, 1171-1183.e3.	1.6	24
38	Novel Anti-Inflammatory Peptides Based on Chemokineâ€“Glycosaminoglycan Interactions Reduce Leukocyte Migration and Disease Severity in a Model of Rheumatoid Arthritis. Journal of Immunology, 2018, 200, 3201-3217.	0.4	23
39	The type 2 diabetes gene product STARD10 is a phosphoinositide-binding protein that controls insulin secretory granule biogenesis. Molecular Metabolism, 2020, 40, 101015.	3.0	22
40	Steps for Shigella Gatekeeper Protein MxiC Function in Hierarchical Type III Secretion Regulation. Journal of Biological Chemistry, 2017, 292, 1705-1723.	1.6	22
41	Human Mutation within Per-Arnt-Sim (PAS) Domain-containing Protein Kinase (PASK) Causes Basal Insulin Hypersecretion*. Journal of Biological Chemistry, 2011, 286, 44005-44014.	1.6	21
42	A suite of de novo c -type cytochromes for functional oxidoreductase engineering. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 493-502.	0.5	20
43	Protease-Activated Receptor 4 Variant p.Tyr157Cys Reduces Platelet Functional Responses and Alters Receptor Trafficking. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 952-960.	1.1	18
44	Molecular modelling and site-directed mutagenesis of the inositol 1,3,4,5-tetrakisphosphate-binding pleckstrin homology domain from the Ras GTPase-activating protein GAP1IP4BP. Biochemical Journal, 2000, 349, 333-342.	1.7	17
45	The de novo design of a biocompatible and functional integral membrane protein using minimal sequence complexity. Scientific Reports, 2018, 8, 14564.	1.6	16
46	Stapled Peptides as HIFâ€1Î±/p300 Inhibitors: Helicity Enhancement in the Bound State Increases Inhibitory Potency. Chemistry - A European Journal, 2020, 26, 7638-7646.	1.7	16
47	Insight into the molecular mechanism behind PEG-mediated stabilization of biofluid lipases. Scientific Reports, 2018, 8, 12293.	1.6	15
48	FKBP12.6 Activates RyR1: Investigating the Amino Acid Residues Critical for Channel Modulation. Biophysical Journal, 2014, 106, 824-833.	0.2	14
49	Site Saturation Mutagenesis Applications onCandida methylicaFormate Dehydrogenase. Scientifica, 2016, 2016, 1-7.	0.6	13
50	A general method of domain closure is applied to phosphoglycerate kinase and the result compared with the crystal structure of a closed conformation of the enzyme. Proteins: Structure, Function and Bioinformatics, 1998, 30, 372-380.	1.5	12
51	In Silico-Guided Rational Drug Design and Semi-synthesis of C(2)-Functionalized Huperzine A Derivatives as Acetylcholinesterase Inhibitors. ACS Omega, 2021, 6, 19924-19939.	1.6	11
52	Identification and Therapeutic Potential of a Vitronectin Binding Region of Meningococcal Msf. PLoS ONE, 2015, 10, e0124133.	1.1	10
53	Brazilin Removes Toxic Alpha-Synuclein and Seeding Competent Assemblies from Parkinson Brain by Altering Conformational Equilibrium. Journal of Molecular Biology, 2021, 433, 166878.	2.0	10
54	Multiâ€modal adaptorâ€clathrin contacts drive coated vesicle assembly. EMBO Journal, 2021, 40, e108795.	3.5	8

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55	Interaction With the Lipid Membrane Influences Fentanyl Pharmacology. Advances in Drug and Alcohol Research, 0, 2, .	2.5	8
56	Frontispiz: Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein. Angewandte Chemie, 2021, 133, .	1.6	7
57	Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein**. Angewandte Chemie, 2021, 133, 7174-7186.	1.6	6
58	A conserved arginine with nonâ€conserved function is a key determinant of agonist selectivity in Î±7 nicotinic ACh receptors. British Journal of Pharmacology, 2021, 178, 1651-1668.	2.7	6
59	Identification and validation of novel microtubule suppressors with an imidazopyridine scaffold through structure-based virtual screening and docking. RSC Medicinal Chemistry, 2022, 13, 929-943.	1.7	6
60	Correlation of the enzyme activities ofBacillus stearothermophilus lactate dehydrogenase on three substrates with the results of molecular dynamics/energy minimization conformational searching. , 1997, 29, 228-239.		5
61	Bioinformatic analysis of meningococcal Msf and Opc to inform vaccine antigen design. PLoS ONE, 2018, 13, e0193940.	1.1	5
62	The dynamical interplay between a megadalton peptide nanocage and solutes probed by microsecond atomistic MD; implications for design. Physical Chemistry Chemical Physics, 2019, 21, 137-147.	1.3	5
63	Small-residue packing motifs modulate the structure and function of a minimal de novo membrane protein. Scientific Reports, 2020, 10, 15203.	1.6	5
64	Query-guided proteinâ€“protein interaction inhibitor discovery. Chemical Science, 2021, 12, 4753-4762.	3.7	5
65	Towards optimizing peptide-based inhibitors of proteinâ€“protein interactions: predictive saturation variation scanning (PreSaVS). RSC Chemical Biology, 2021, 2, 1474-1478.	2.0	5
66	The structural basis for high affinity binding of Î±1-acid glycoprotein to the potent antitumor compound UCN-01. Journal of Biological Chemistry, 2021, 297, 101392.	1.6	5
67	The bar-hinge motor: a synthetic protein design exploiting conformational switching to achieve directional motility. New Journal of Physics, 2019, 21, 013002.	1.2	4
68	Voltage Sensor Gating Charge Transfer in a hERG Potassium ChannelÂModel. Biophysical Journal, 2014, 107, L25-L28.	0.2	3
69	Internal (His)6-tagging delivers a fully functional hetero-oligomeric class II chaperonin in high yield. Scientific Reports, 2016, 6, 20696.	1.6	3
70	The Aminotriazole Antagonist Cmpdâ€1 Stabilises a Distinct Inactive State of the Adenosine 2A Receptor. Angewandte Chemie - International Edition, 2019, 58, 9399-9403.	7.2	3
71	Identification of Î²-strand mediated proteinâ€“protein interaction inhibitors using ligand-directed fragment ligation. Chemical Science, 2021, 12, 2286-2293.	3.7	3
72	The Lysozyme Inhibitor Thionine Acetate Is Also an Inhibitor of the Soluble Lytic Transglycosylase Slt35 from Escherichia coli. Molecules, 2021, 26, 4189.	1.7	3

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73	Investigating the Conformational Preferences of Transforming Growth Factor-Î² Isoforms using Targeted Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2009, 5, 482-490.	2.3	2
74	Perhydrohelicenes and other diamond-lattice based hydrocarbons: the choreography of inversion. Chemical Science, 2017, 8, 6389-6399.	3.7	2
75	Biophysical characterization of the ETV6 PNT domain polymerization interfaces. Journal of Biological Chemistry, 2021, 296, 100284.	1.6	2
76	A Multipronged Screening Approach Targeting Inhibition of ETV6 PNT Domain Polymerization. SLAS Discovery, 2021, 26, 698-711.	1.4	2
77	Understanding p300-transcription factor interactions using sequence variation and hybridization. RSC Chemical Biology, 2022, 3, 592-603.	2.0	2
78	Intraring allostery controls the function and assembly of a heteroâ€oligomeric class II chaperonin. FASEB Journal, 2018, 32, 2223-2234.	0.2	1
79	The Aminotriazole Antagonist Cmpdâ€1 Stabilises a Distinct Inactive State of the Adenosine 2A Receptor. Angewandte Chemie, 2019, 131, 9499-9503.	1.6	1
80	Tetherin/BST2, a physiologically and therapeutically relevant regulator of platelet receptor signalling. Blood Advances, 2021, 5, 1884-1898.	2.5	1
81	Frontispiece: Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein. Angewandte Chemie - International Edition, 2021, 60, .	7.2	0