

# Scott W Lovell

## List of Publications by Year in descending order

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34  
papers

1,132  
citations

567281  
15  
h-index

414414  
32  
g-index

36  
all docs

36  
docs citations

36  
times ranked

1903  
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad-Spectrum Antivirals against 3C or 3C-Like Proteases of Picornaviruses, Noroviruses, and Coronaviruses. <i>Journal of Virology</i> , 2012, 86, 11754-11762.	3.4	277
2	3C-like protease inhibitors block coronavirus replication in vitro and improve survival in MERS-CoV-infected mice. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	187
3	Structure-guided design of potent and permeable inhibitors of MERS coronavirus 3CL protease that utilize a piperidine moiety as a novel design element. <i>European Journal of Medicinal Chemistry</i> , 2018, 150, 334-346.	5.5	96
4	Postinfection treatment with a protease inhibitor increases survival of mice with a fatal SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	61
5	Structure-Guided Design and Optimization of Dipeptidyl Inhibitors of Norovirus 3CL Protease. Structure-Activity Relationships and Biochemical, X-ray Crystallographic, Cell-Based, and In Vivo Studies. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 3144-3155.	6.4	51
6	Structure/Function Relationships of Adipose Phospholipase A2 Containing a Cys-His-His Catalytic Triad. <i>Journal of Biological Chemistry</i> , 2012, 287, 35260-35274.	3.4	45
7	Macrocyclic peptides delineate locked-open inhibition mechanism for microorganism phosphoglycerate mutases. <i>Nature Communications</i> , 2017, 8, 14932.	12.8	41
8	Structure-Guided Design of Conformationally Constrained Cyclohexane Inhibitors of Severe Acute Respiratory Syndrome Coronavirus-2 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10047-10058.	6.4	38
9	A potential regulatory loop between Lin28B:miR-212 in androgen-independent prostate cancer. <i>International Journal of Oncology</i> , 2014, 45, 2421-2429.	3.3	34
10	Characterization of the Bacterioferritin/Bacterioferritin Associated Ferredoxin Protein-Protein Interaction in Solution and Determination of Binding Energy Hot Spots. <i>Biochemistry</i> , 2015, 54, 6162-6175.	2.5	28
11	Structural and Biochemical Characterization of Chlamydia trachomatis Hypothetical Protein CT263 Supports That Menaquinone Synthesis Occurs through the Futasolone Pathway. <i>Journal of Biological Chemistry</i> , 2014, 289, 32214-32229.	3.4	23
12	Hypothetical protein CT398 (CdsZ) interacts with If <sup>54</sup> (RpoN)-holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2015, 24, 1617-1632.	7.6	23
13	Structure-Guided Design of Potent Inhibitors of SARS-CoV-2 3CL Protease: Structural, Biochemical, and Cell-Based Studies. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 17846-17865.	6.4	22
14	Structural characterization of the Man5 glycoform of human IgG3 Fc. <i>Molecular Immunology</i> , 2017, 92, 28-37.	2.2	21
15	Structure-based exploration and exploitation of the S4 subsite of norovirus 3CL protease in the design of potent and permeable inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2017, 126, 502-516.	5.5	20
16	Structure-Guided Design of Potent Spirocyclic Inhibitors of Severe Acute Respiratory Syndrome Coronavirus-2 3C-like Protease. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 7818-7832.	6.4	20
17	Single-domain antibodies pinpoint potential targets within Shigella invasion plasmid antigen D of the needle tip complex for inhibition of type III secretion. <i>Journal of Biological Chemistry</i> , 2017, 292, 16677-16687.	3.4	16
18	The Structures of SctK and SctD from Pseudomonas aeruginosa Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform. <i>Journal of Molecular Biology</i> , 2020, 432, 166693.	4.2	14

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19	Using disruptive insertional mutagenesis to identify the <i>in situ</i> structure–function landscape of the <i>Shigella</i> translocator protein IpaB. <i>Protein Science</i> , 2018, 27, 1392-1406.	7.6	13
20	1.65 Å resolution structure of the AraC-family transcriptional activator ToxT from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 726-731.	0.8	13
21	Replacing Arginine 33 for Alanine in the Hemophore HasA from <i>Pseudomonas aeruginosa</i> Causes Closure of the H32 Loop in the Apo-Protein. <i>Biochemistry</i> , 2016, 55, 2622-2631.	2.5	12
22	Structural and ligand binding analyses of the periplasmic sensor domain of RsbU in <i>Chlamydia trachomatis</i> support a role in TCA cycle regulation. <i>Molecular Microbiology</i> , 2020, 113, 68-88.	2.5	11
23	Structural insight into the novel iron coordination and domain interactions of transferrin from a model insect, <i>Manduca sexta</i> . <i>Protein Science</i> , 2021, 30, 408-422.	7.6	9
24	Bfd, a New Class of [2Fe-2S] Protein That Functions in Bacterial Iron Homeostasis, Requires a Structural Anion Binding Site. <i>Biochemistry</i> , 2018, 57, 5533-5543.	2.5	8
25	Structure of the Diphtheria Toxin at Acidic pH: Implications for the Conformational Switching of the Translocation Domain. <i>Toxins</i> , 2020, 12, 704.	3.4	8
26	1.15 Å resolution structure of the proteasome-assembly chaperone Nas2 PDZ domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 418-423.	0.8	7
27	Structural and Inhibitory Effects of Hinge Loop Mutagenesis in Serpin-2 from the Malaria Vector <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 2946-2956.	3.4	7
28	High-resolution crystal structures of two crystal forms of human cyclophilin D in complex with PEG 400 molecules. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 717-722.	0.8	5
29	Crystal Structure of VapBC-1 from Nontypeable <i>Haemophilus influenzae</i> and the Effect of PIN Domain Mutations on Survival during Infection. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	5
30	Crystal structure of histone-like protein from <i>Streptococcus mutans</i> refined to 1.9 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 257-262.	0.8	4
31	1.45 Å resolution structure of SRPN18 from the malaria vector <i>Anopheles gambiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 853-862.	0.8	3
32	<i>PHIP</i> gene variants with protein modeling, interactions, and clinical phenotypes. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 579-589.	1.2	3
33	Structure–activity relationship of ipglyceride binding to phosphoglycerate mutases. <i>Journal of Biological Chemistry</i> , 2021, 296, 100628.	3.4	2
34	Potent Protease Inhibitors of Highly Pathogenic Lagoviruses: Rabbit Hemorrhagic Disease Virus and European Brown Hare Syndrome Virus. <i>Microbiology Spectrum</i> , 0, , .	3.0	1