

# Steven J Johnson

## List of Publications by Year in descending order

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93  
papers

5,458  
citations

76196

40  
h-index

88477

70  
g-index

118  
all docs

118  
docs citations

118  
times ranked

6666  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and function of a family of tick-derived complement inhibitors targeting properdin. <i>Nature Communications</i> , 2022, 13, 317.	5.8	8
2	Structure and mechanism of the proton-driven motor that powers type 9 secretion and gliding motility. <i>Nature Microbiology</i> , 2021, 6, 221-233.	5.9	47
3	Molecular structure of the intact bacterial flagellar basal body. <i>Nature Microbiology</i> , 2021, 6, 712-721.	5.9	61
4	Molecular Basis for <i>Bordetella pertussis</i> Interference with Complement, Coagulation, Fibrinolytic, and Contact Activation Systems: the Cryo-EM Structure of the Vag8-C1 Inhibitor Complex. <i>MBio</i> , 2021, 12, .	1.8	4
5	Nonameric structures of the cytoplasmic domain of FlhA and SctV in the context of the full-length protein. <i>PLoS ONE</i> , 2021, 16, e0252800.	1.1	21
6	The conserved C2 phospholipid-binding domain in Delta contributes to robust Notch signalling. <i>EMBO Reports</i> , 2021, 22, e52729.	2.0	3
7	An inhibitor of complement C5 provides structural insights into activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 362-370.	3.3	27
8	Structures of the stator complex that drives rotation of the bacterial flagellum. <i>Nature Microbiology</i> , 2020, 5, 1553-1564.	5.9	131
9	SIMPLE 3.0. Stream single-particle cryo-EM analysis in real time. <i>Journal of Structural Biology: X</i> , 2020, 4, 100040.	0.7	23
10	The substrate specificity switch FlhB assembles onto the export gate to regulate type three secretion. <i>Nature Communications</i> , 2020, 11, 1296.	5.8	52
11	Symmetry mismatch in the MS-ring of the bacterial flagellar rotor explains the structural coordination of secretion and rotation. <i>Nature Microbiology</i> , 2020, 5, 966-975.	5.9	62
12	Structures of SALSA/DMBT1 SRCR domains reveal the conserved ligand-binding mechanism of the ancient SRCR fold. <i>Life Science Alliance</i> , 2020, 3, e201900502.	1.3	16
13	The Structure of an Injectisome Export Gate Demonstrates Conservation of Architecture in the Core Export Gate between Flagellar and Virulence Type III Secretion Systems. <i>MBio</i> , 2019, 10, .	1.8	48
14	Structure-based design of chimeric antigens for multivalent protein vaccines. <i>Nature Communications</i> , 2018, 9, 1051.	5.8	26
15	Structure of the core of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 583-590.	3.6	153
16	Virulence Associated Gene 8 of <i>Bordetella pertussis</i> Enhances Contact System Activity by Inhibiting the Regulatory Function of Complement Regulator C1 Inhibitor. <i>Frontiers in Immunology</i> , 2018, 9, 1172.	2.2	10
17	A key centriole assembly interaction interface between human Plk4 and STIL appears to not be conserved in flies. <i>Biology Open</i> , 2017, 6, 381-389.	0.6	14
18	Structural Basis for Mitotic Centrosome Assembly in Flies. <i>Cell</i> , 2017, 169, 1078-1089.e13.	13.5	99

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19	“To Cross-Seed or Not To Cross-Seed”: A Pilot Study Using Metallo- $\beta$ -lactamases. <i>Crystal Growth and Design</i> , 2017, 17, 913-924.	1.4	8
20	Structural basis of cholesterol binding by a novel clade of dendritic cell modulators from ticks. <i>Scientific Reports</i> , 2017, 7, 16057.	1.6	14
21	SALSA “ Step by step. <i>Molecular Immunology</i> , 2017, 89, 197.	1.0	0
22	Functional Prioritization and Hydrogel Regulation Phenomena Created by a Combinatorial Pearl-Associated Two-Protein Biomineralization Model System. <i>Biochemistry</i> , 2017, 56, 3607-3618.	1.2	15
23	Validation of Reef-Scale Thermal Stress Satellite Products for Coral Bleaching Monitoring. <i>Remote Sensing</i> , 2016, 8, 59.	1.8	76
24	Characterisation of <i>Shigella</i> ...Spa33 and <i>Thermotoga</i> ...FlIM/N reveals a new model for C $\alpha$ ring assembly in T3SS. <i>Molecular Microbiology</i> , 2016, 99, 749-766.	1.2	62
25	Structural and functional insights into properdin of the complement alternative pathway. <i>Immunobiology</i> , 2016, 221, 1225.	0.8	0
26	Structural basis for therapeutic inhibition of complement C5. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 378-386.	3.6	94
27	509. <i>Critical Care Medicine</i> , 2015, 43, 129.	0.4	0
28	The Micronesia Challenge: Assessing the Relative Contribution of Stressors on Coral Reefs to Facilitate Science-to-Management Feedback. <i>PLoS ONE</i> , 2015, 10, e0130823.	1.1	56
29	Mechanism of Thiosulfate Oxidation in the SoxA Family of Cysteine-ligated Cytochromes. <i>Journal of Biological Chemistry</i> , 2015, 290, 9209-9221.	1.6	19
30	Structural basis for specificity and promiscuity in a carrier protein/enzyme system from the sulfur cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E7166-75.	3.3	24
31	Structures of CD6 and Its Ligand CD166 Give Insight into Their Interaction. <i>Structure</i> , 2015, 23, 1426-1436.	1.6	53
32	The homo-oligomerisation of both Sas-6 and Ana2 is required for efficient centriole assembly in flies. <i>ELife</i> , 2015, 4, e07236.	2.8	49
33	Polymorphisms in the Human Inhibitory Signal-regulatory Protein $\beta$ Do Not Affect Binding to Its Ligand CD47. <i>Journal of Biological Chemistry</i> , 2014, 289, 10024-10028.	1.6	39
34	Crystal Structure of the <i>Bacillus subtilis</i> Phosphodiesterase PhoD Reveals an Iron and Calcium-containing Active Site. <i>Journal of Biological Chemistry</i> , 2014, 289, 30889-30899.	1.6	96
35	Nonfunctional Variant 3 Factor H Binding Proteins as Meningococcal Vaccine Candidates. <i>Infection and Immunity</i> , 2014, 82, 1157-1163.	1.0	23
36	Dry roasting enhances peanut-induced allergic sensitization across mucosal and cutaneous routes in mice. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 1453-1456.	1.5	41

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37	The Centrosome-Specific Phosphorylation of Cnn by Polo/Plk1 Drives Cnn Scaffold Assembly and Centrosome Maturation. <i>Developmental Cell</i> , 2014, 28, 659-669.	3.1	166
38	Outcomes by Sex Following Treatment Initiation With Atazanavir Plus Ritonavir or Efavirenz With Abacavir/Lamivudine or Tenofovir/Emtricitabine. <i>Clinical Infectious Diseases</i> , 2014, 58, 555-563.	2.9	30
39	Building a secreting nanomachine: a structural overview of the T3SS. <i>Current Opinion in Structural Biology</i> , 2014, 25, 111-117.	2.6	50
40	Architecture of the major component of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 99-104.	3.6	200
41	Structures of CD200/CD200 Receptor Family and Implications for Topology, Regulation, and Evolution. <i>Structure</i> , 2013, 21, 820-832.	1.6	52
42	Structural Basis for Recognition of the Pore-Forming Toxin Intermedilysin by Human Complement Receptor CD59. <i>Cell Reports</i> , 2013, 3, 1369-1377.	2.9	60
43	Defining a protective epitope on factor H binding protein, a key meningococcal virulence factor and vaccine antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3304-3309.	3.3	125
44	Distinct Binding and Immunogenic Properties of the Gonococcal Homologue of Meningococcal Factor H Binding Protein. <i>PLoS Pathogens</i> , 2013, 9, e1003528.	2.1	37
45	Biochemical Analysis of the Plasmodium falciparum Erythrocyte-binding Antigen-175 (EBA175)-Glycophorin-A Interaction. <i>Journal of Biological Chemistry</i> , 2013, 288, 32106-32117.	1.6	40
46	Abnormal accumulation and recycling of glycoproteins visualized in Niemann-Pick type C cells using the chemical reporter strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10207-10212.	3.3	29
47	ErpC, a member of the complement regulator-acquiring family of surface proteins from <i>Borrelia burgdorferi</i> , possesses an architecture previously unseen in this protein family. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 624-628.	0.7	12
48	Investigating the structure of the factor B vWF-A domain/CD55 protein complex using DEER spectroscopy: successes and pitfalls. <i>Molecular Physics</i> , 2013, 111, 2865-2872.	0.8	2
49	Dimerization of complement factor H-related proteins modulates complement activation in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4685-4690.	3.3	243
50	Crystal structures of the CPAP/STIL complex reveal its role in centriole assembly and human microcephaly. <i>ELife</i> , 2013, 2, e01071.	2.8	90
51	Semaphorin-7A Is an Erythrocyte Receptor for <i>P. falciparum</i> Merozoite-Specific TRAP Homolog, MTRAP. <i>PLoS Pathogens</i> , 2012, 8, e1003031.	2.1	68
52	Design and Evaluation of Meningococcal Vaccines through Structure-Based Modification of Host and Pathogen Molecules. <i>PLoS Pathogens</i> , 2012, 8, e1002981.	2.1	53
53	Crystal Structure and Functional Characterization of the Complement Regulator Mannose-binding Lectin (MBL)/Ficolin-associated Protein-1 (MAP-1). <i>Journal of Biological Chemistry</i> , 2012, 287, 32913-32921.	1.6	35
54	Excessive activity of cathepsin K is associated with cartilage defects in a zebrafish model of mucopolidosis II. <i>DMM Disease Models and Mechanisms</i> , 2012, 5, 177-190.	1.2	36

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55	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012, 492, 210-214.	13.7	164
56	Putting the structure into complement. <i>Immunobiology</i> , 2012, 217, 1117-1121.	0.8	9
57	Tetartohedral twinning could happen to you too. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 418-424.	2.5	14
58	A case of community-acquired <i>Acinetobacter junii-johnsonii</i> cellulitis. <i>Biomedica</i> , 2012, 32, 179-81.	0.3	14
59	<i>Shigella flexneri</i> Spa15 Crystal Structure Verified in Solution by Double Electron Electron Resonance. <i>Journal of Molecular Biology</i> , 2011, 405, 427-435.	2.0	21
60	Mislocalization of large ARF-GEFs as a potential mechanism for BFA resistance in COG-deficient cells. <i>Experimental Cell Research</i> , 2011, 317, 2342-2352.	1.2	7
61	Structures of the rat complement regulator CrrY. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 739-743.	0.7	6
62	Structural basis for complement factor I control and its disease-associated sequence polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12839-12844.	3.3	118
63	Structural and Functional Studies on the N-terminal Domain of the <i>Shigella</i> Type III Secretion Protein MxiG. <i>Journal of Biological Chemistry</i> , 2011, 286, 30606-30614.	1.6	30
64	Timing is everything: the regulation of type III secretion. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 1065-1075.	2.4	87
65	With phases: how two wrongs can sometimes make a right. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 420-425.	2.5	4
66	The Extreme C Terminus of <i>Shigella flexneri</i> IpaB Is Required for Regulation of Type III Secretion, Needle Tip Composition, and Binding. <i>Infection and Immunity</i> , 2010, 78, 1682-1691.	1.0	40
67	SepL Resembles an Aberrant Effector in Binding to a Class 1 Type III Secretion Chaperone and Carrying an N-Terminal Secretion Signal. <i>Journal of Bacteriology</i> , 2010, 192, 6093-6098.	1.0	23
68	A Mechanism of Release of Calreticulin from Cells During Apoptosis. <i>Journal of Molecular Biology</i> , 2010, 401, 799-812.	2.0	87
69	<i>Neisseria meningitidis</i> recruits factor H using protein mimicry of host carbohydrates. <i>Nature</i> , 2009, 458, 890-893.	13.7	287
70	Three-dimensional reconstruction of the <i>Shigella</i> T3SS transmembrane regions reveals 12-fold symmetry and novel features throughout. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 477-485.	3.6	100
71	Towards the crystal structure of intact Human Complement Factor I. <i>Molecular Immunology</i> , 2009, 46, 2864-2865.	1.0	3
72	Characterization of soluble complexes of the <i>Shigella flexneri</i> type III secretion system ATPase. <i>FEMS Microbiology Letters</i> , 2008, 286, 274-278.	0.7	40

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73	A conserved face of the Jagged/Serrate DSL domain is involved in Notch trans-activation and cis-inhibition. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 849-857.	3.6	222
74	Crystal structure of Spa40, the specificity switch for the <i>Shigella flexneri</i> type III secretion system. <i>Molecular Microbiology</i> , 2008, 69, 267-276.	1.2	55
75	Structures of the <i>Shigella flexneri</i> Type 3 Secretion System Protein MxiC Reveal Conformational Variability Amongst Homologues. <i>Journal of Molecular Biology</i> , 2008, 377, 985-992.	2.0	32
76	What's the point of the type III secretion system needle?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6507-6513.	3.3	125
77	Self-chaperoning of the Type III Secretion System Needle Tip Proteins IpaD and BipD. <i>Journal of Biological Chemistry</i> , 2007, 282, 4035-4044.	1.6	129
78	Identification of minor inner-membrane components of the <i>Shigella</i> type III secretion system "needle complex". <i>Microbiology (United Kingdom)</i> , 2007, 153, 2405-2415.	0.7	21
79	The Structure of OMCI, a Novel Lipocalin Inhibitor of the Complement System. <i>Journal of Molecular Biology</i> , 2007, 369, 784-793.	2.0	50
80	Towards a structural basis for complement factor H linked age-related macular degeneration. <i>Molecular Immunology</i> , 2007, 44, 3930-3931.	1.0	1
81	Structural basis for complement factor H-linked age-related macular degeneration. <i>Journal of Experimental Medicine</i> , 2007, 204, 2277-2283.	4.2	168
82	Expression, purification, cocrystallization and preliminary crystallographic analysis of sucrose octasulfate/human complement regulator factor H SCRs 6-8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 480-483.	0.7	14
83	High-resolution structures of bacterially expressed soluble human CD59. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 648-652.	0.7	25
84	Expression, purification, crystallization and preliminary crystallographic analysis of MxiH, a subunit of the <i>Shigella flexneri</i> type III secretion system needle. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 302-305.	0.7	22
85	Expression, purification, crystallization and preliminary crystallographic analysis of BipD, a component of the <i>Burkholderia pseudomallei</i> type III secretion system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 861-864.	0.7	5
86	Expression, limited proteolysis and preliminary crystallographic analysis of IpaD, a component of the <i>Shigella flexneri</i> type III secretion system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 865-868.	0.7	12
87	Molecular model of a type III secretion system needle: Implications for host-cell sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12529-12533.	3.3	149
88	The type III needle and the damage done. <i>Current Opinion in Structural Biology</i> , 2005, 15, 700-707.	2.6	25
89	The ins and outs of calreticulin: from the ER lumen to the extracellular space. <i>Trends in Cell Biology</i> , 2001, 11, 122-129.	3.6	303
90	Fine specificity of autoantibodies to calreticulin: epitope mapping and characterization. <i>Clinical and Experimental Immunology</i> , 2000, 120, 384-391.	1.1	51

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91	The conformation of calreticulin is influenced by the endoplasmic reticulum lumenal environment. <i>Journal of Biological Chemistry</i> , 2000, 275, 27177-85.	1.6	61
92	Expression and Purification of Mammalian Calreticulin in <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2000, 20, 207-215.	0.6	16
93	Evidence That C1q Binds Specifically to CH2-like Immunoglobulin $\hat{3}$ Motifs Present in the Autoantigen Calreticulin and Interferes with Complement Activation. <i>Biochemistry</i> , 1998, 37, 17865-17874.	1.2	64