

# Stephen J Perkins

## List of Publications by Year in descending order

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95  
papers

4,590  
citations

87723

38  
h-index

106150

65  
g-index

96  
all docs

96  
docs citations

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times ranked

4184  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein volumes and hydration effects. The calculations of partial specific volumes, neutron scattering matchpoints and 280-nm absorption coefficients for proteins and glycoproteins from amino acid sequences. <i>FEBS Journal</i> , 1986, 157, 169-180.	0.2	535
2	The fab and fc fragments of IgA1 exhibit a different arrangement from that in IgG: a study by X-ray and neutron solution scattering and homology modelling 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 286, 1421-1447.	2.0	209
3	Solution structure of human and mouse immunoglobulin M by synchrotron X-ray scattering and molecular graphics modelling. <i>Journal of Molecular Biology</i> , 1991, 221, 1345-1366.	2.0	178
4	His-384 Allotypic Variant of Factor H Associated with Age-related Macular Degeneration Has Different Heparin Binding Properties from the Non-disease-associated Form. <i>Journal of Biological Chemistry</i> , 2006, 281, 24713-24720.	1.6	161
5	The interactive Factor H-atypical hemolytic uremic syndrome mutation database and website: update and integration of membrane cofactor protein and Factor I mutations with structural models. <i>Human Mutation</i> , 2007, 28, 222-234.	1.1	160
6	Folded-back solution structure of monomeric factor H of human complement by synchrotron X-ray and neutron scattering, analytical ultracentrifugation and constrained molecular modelling. <i>Journal of Molecular Biology</i> , 2001, 309, 1117-1138.	2.0	134
7	Statistical Validation of Rare Complement Variants Provides Insights into the Molecular Basis of Atypical Hemolytic Uremic Syndrome and C3 Glomerulopathy. <i>Journal of Immunology</i> , 2018, 200, 2464-2478.	0.4	130
8	Pentameric and decameric structures in solution of serum amyloid P component by X-ray and neutron scattering and molecular modelling analyses 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 272, 408-422.	2.0	113
9	Complement Factor H Binds at Two Independent Sites to C-reactive Protein in Acute Phase Concentrations*. <i>Journal of Biological Chemistry</i> , 2010, 285, 1053-1065.	1.6	112
10	X-Ray and neutron scattering analyses of hydration shells: a molecular interpretation based on sequence predictions and modelling fits. <i>Biophysical Chemistry</i> , 2001, 93, 129-139.	1.5	104
11	Solution Structure Determination of Monomeric Human IgA2 by X-ray and Neutron Scattering, Analytical Ultracentrifugation and Constrained Modelling: A Comparison with Monomeric Human IgA1. <i>Journal of Molecular Biology</i> , 2004, 338, 921-941.	2.0	100
12	Low-resolution structural studies of mitochondrial ubiquinol: Cytochrome c reductase in detergent solutions by neutron scattering. <i>Journal of Molecular Biology</i> , 1983, 168, 847-866.	2.0	98
13	Semi-Rigid Solution Structures of Heparin by Constrained X-ray Scattering Modelling: New Insight into Heparin-Protein Complexes. <i>Journal of Molecular Biology</i> , 2010, 395, 504-521.	2.0	97
14	An interactive web database of factor H-associated hemolytic uremic syndrome mutations: insights into the structural consequences of disease-associated mutations. <i>Human Mutation</i> , 2006, 27, 21-30.	1.1	79
15	Complement Factor H ligand interactions: Self-association, multivalency and dissociation constants. <i>Immunobiology</i> , 2012, 217, 281-297.	0.8	75
16	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	1.1	71
17	Molecular modelling of the C-terminal domains of factor H of human complement: a correlation between haemolytic uraemic syndrome and a predicted heparin binding site. <i>Journal of Molecular Biology</i> , 2002, 316, 217-224.	2.0	70
18	Semi-extended Solution Structure of Human Myeloma Immunoglobulin D Determined by Constrained X-ray Scattering. <i>Journal of Molecular Biology</i> , 2005, 353, 155-173.	2.0	69

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19	Atomistic modelling of scattering data in the Collaborative Computational Project for Small Angle Scattering (CCP-SAS). <i>Journal of Applied Crystallography</i> , 2016, 49, 1861-1875.	1.9	67
20	Oligomeric domain structure of human complement factor H by x-ray and neutron solution scattering. <i>Biochemistry</i> , 1991, 30, 2847-2857.	1.2	62
21	Factor XI deficiency database: an interactive web database of mutations, phenotypes, and structural analysis tools. <i>Human Mutation</i> , 2005, 26, 192-198.	1.1	59
22	Solution Structure of the Complex between CR2 SCR 1-2 and C3d of Human Complement: An X-ray Scattering and Sedimentation Modelling Study. <i>Journal of Molecular Biology</i> , 2005, 346, 859-873.	2.0	59
23	New functional and structural insights from updated mutational databases for complement factor H, Factor I, membrane cofactor protein and C3. <i>Bioscience Reports</i> , 2014, 34, .	1.1	59
24	Implications of the Near-Planar Solution Structure of Human Myeloma Dimeric IgA1 for Mucosal Immunity and IgA Nephropathy. <i>Journal of Immunology</i> , 2008, 180, 1008-1018.	0.4	57
25	Electrostatic Interactions Contribute to the Folded-back Conformation of Wild Type Human Factor H. <i>Journal of Molecular Biology</i> , 2009, 391, 98-118.	2.0	57
26	Structural Studies in Solution of the Recombinant N-Terminal Pair of Short Consensus/Complement Repeat Domains of Complement Receptor Type 2 (CR2/CD21) and Interactions with Its Ligand C3dg. <i>Biochemistry</i> , 2001, 40, 5931-5941.	1.2	55
27	The European Association for Haemophilia and Allied Disorders (EAHAD) Coagulation Factor Variant Databases: Important resources for haemostasis clinicians and researchers. <i>Haemophilia</i> , 2020, 26, 306-313.	1.0	55
28	Molecular Interactions between Complement Factor H and Its Heparin and Heparan Sulfate Ligands. <i>Frontiers in Immunology</i> , 2014, 5, 126.	2.2	52
29	Structural models for carcinoembryonic antigen and its complex with the single-chain Fv antibody molecule MFE23. <i>FEBS Letters</i> , 2000, 475, 11-16.	1.3	50
30	Uncontrolled Zinc- and Copper-Induced Oligomerisation of the Human Complement Regulator Factor H and Its Possible Implications for Function and Disease. <i>Journal of Molecular Biology</i> , 2008, 384, 1341-1352.	2.0	47
31	The Regulatory SCR-1/5 and Cell Surface-binding SCR-16/20 Fragments of Factor H Reveal Partially Folded-back Solution Structures and Different Self-associative Properties. <i>Journal of Molecular Biology</i> , 2008, 375, 80-101.	2.0	46
32	Predicted $\alpha$ -helix/ $\beta$ -sheet secondary structures for the zinc-binding motifs of human papillomavirus E7 and E6 proteins by consensus prediction averaging and spectroscopic studies of E7. <i>Biochemical Journal</i> , 1996, 319, 229-239.	1.7	44
33	Associative and Structural Properties of the Region of Complement Factor H Encompassing the Tyr402His Disease-related Polymorphism and its Interactions with Heparin. <i>Journal of Molecular Biology</i> , 2007, 368, 564-581.	2.0	44
34	Molecular modelling and experimental studies of mutation and cell-adhesion sites in the fibronectin type III and whey acidic protein domains of human anosmin-1. <i>Biochemical Journal</i> , 2001, 357, 647-659.	1.7	42
35	Zinc Binding to the Tyr402 and His402 Allotypes of Complement Factor H: Possible Implications for Age-Related Macular Degeneration. <i>Journal of Molecular Biology</i> , 2011, 408, 714-735.	2.0	42
36	Solution Structure of Human Secretory Component and Implications for Biological Function. <i>Journal of Biological Chemistry</i> , 2007, 282, 16969-16980.	1.6	41

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37	Zinc-induced Self-association of Complement C3b and Factor H. <i>Journal of Biological Chemistry</i> , 2013, 288, 19197-19210.	1.6	41
38	A Revised Mechanism for the Activation of Complement C3 to C3b. <i>Journal of Biological Chemistry</i> , 2015, 290, 2334-2350.	1.6	41
39	Solution Structure of the Complex Formed between Human Complement C3d and Full-length Complement Receptor Type 2. <i>Journal of Molecular Biology</i> , 2008, 384, 137-150.	2.0	40
40	X-ray and Neutron Scattering Data and Their Constrained Molecular Modeling. <i>Methods in Cell Biology</i> , 2008, 84, 375-423.	0.5	40
41	Masking of the Fc region in human IgG4 by constrained X-ray scattering modelling: implications for antibody function and therapy. <i>Biochemical Journal</i> , 2010, 432, 101-114.	1.7	40
42	The Partly Folded Back Solution Structure Arrangement of the 30 SCR Domains in Human Complement Receptor Type 1 (CR1) Permits Access to its C3b and C4b Ligands. <i>Journal of Molecular Biology</i> , 2008, 375, 102-118.	2.0	39
43	Constrained solution scattering modelling of human antibodies and complement proteins reveals novel biological insights. <i>Journal of the Royal Society Interface</i> , 2009, 6, S679-96.	1.5	38
44	The Solution Structures of Two Human IgG1 Antibodies Show Conformational Stability and Accommodate Their C1q and Fcγ3R Ligands. <i>Journal of Biological Chemistry</i> , 2015, 290, 8420-8438.	1.6	37
45	The 15 SCR Flexible Extracellular Domains of Human Complement Receptor Type 2 can Mediate Multiple Ligand and Antigen Interactions. <i>Journal of Molecular Biology</i> , 2006, 362, 1132-1147.	2.0	36
46	Implications of the Progressive Self-association of Wild-type Human Factor H for Complement Regulation and Disease. <i>Journal of Molecular Biology</i> , 2008, 375, 891-900.	2.0	35
47	C-reactive Protein Exists in an NaCl Concentration-dependent Pentamer-Decamer Equilibrium in Physiological Buffer. <i>Journal of Biological Chemistry</i> , 2010, 285, 1041-1052.	1.6	34
48	The Fab Conformations in the Solution Structure of Human Immunoglobulin G4 (IgG4) Restrict Access to Its Fc Region. <i>Journal of Biological Chemistry</i> , 2014, 289, 20740-20756.	1.6	34
49	The protein fold of the von Willebrand factor type A domain is predicted to be similar to the open twisted β <sup>2</sup> -sheet flanked by β <sub>1</sub> -helices found in human ras-p21. <i>FEBS Letters</i> , 1995, 358, 283-286.	1.3	33
50	The protein fold of the hyaluronate-binding proteoglycan tandem repeat domain of link protein, aggrecan and CD44 is similar to that of the C-type lectin superfamily. <i>FEBS Letters</i> , 1996, 388, 211-216.	1.3	32
51	The Solution Structure of Heparan Sulfate Differs from That of Heparin. <i>Journal of Biological Chemistry</i> , 2011, 286, 24842-24854.	1.6	31
52	Structural analysis of eight novel and 112 previously reported missense mutations in the interactive FXI mutation database reveals new insight on FXI deficiency. <i>Thrombosis and Haemostasis</i> , 2009, 102, 287-301.	1.8	30
53	Analytical ultracentrifugation combined with X-ray and neutron scattering: Experiment and modelling. <i>Methods</i> , 2011, 54, 181-199.	1.9	30
54	<i>SCT</i>: a suite of programs for comparing atomistic models with small-angle scattering data. <i>Journal of Applied Crystallography</i> , 2015, 48, 953-961.	1.9	30

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55	Multiple Interactions of Complement Factor H with Its Ligands in Solution: A Progress Report. <i>Advances in Experimental Medicine and Biology</i> , 2010, 703, 25-47.	0.8	29
56	The Solution Structure of Rabbit IgG Accounts for Its Interactions with the Fc Receptor and Complement C1q and Its Conformational Stability. <i>Journal of Molecular Biology</i> , 2013, 425, 506-523.	2.0	28
57	The Factor I and follistatin domain families: the return of a prodigal son. <i>Biochemical Journal</i> , 1997, 326, 939-941.	1.7	27
58	The EAHAD blood coagulation factor VII variant database. <i>Human Mutation</i> , 2020, 41, 1209-1219.	1.1	27
59	Self-association and domain rearrangements between complement C3 and C3u provide insight into the activation mechanism of C3. <i>Biochemical Journal</i> , 2010, 431, 63-72.	1.7	25
60	Near-planar Solution Structures of Mannose-binding Lectin Oligomers Provide Insight on Activation of Lectin Pathway of Complement. <i>Journal of Biological Chemistry</i> , 2012, 287, 3930-3945.	1.6	24
61	Positive Selection during the Evolution of the Blood Coagulation Factors in the Context of Their Disease-Causing Mutations. <i>Molecular Biology and Evolution</i> , 2014, 31, 3040-3056.	3.5	22
62	The solution structures of native and patient monomeric human IgA1 reveal asymmetric extended structures: implications for function and IgAN disease. <i>Biochemical Journal</i> , 2015, 471, 167-185.	1.7	22
63	Structure determinations of human and chimaeric antibodies by solution scattering and constrained molecular modelling. <i>Biochemical Society Transactions</i> , 2008, 36, 37-42.	1.6	21
64	Bivalent and co-operative binding of complement Factor H to heparan sulfate and heparin. <i>Biochemical Journal</i> , 2012, 444, 417-428.	1.7	21
65	Non-linearity of the collagen triple helix in solution and implications for collagen function. <i>Biochemical Journal</i> , 2017, 474, 2203-2217.	1.7	21
66	Multimeric Interactions between Complement Factor H and Its C3d Ligand Provide New Insight on Complement Regulation. <i>Journal of Molecular Biology</i> , 2009, 391, 119-135.	2.0	20
67	Unravelling protein-protein interactions between complement factor H and C-reactive protein using a multidisciplinary strategy. <i>Biochemical Society Transactions</i> , 2010, 38, 894-900.	1.6	19
68	Zinc-induced oligomerization of zinc $\beta$ 2 glycoprotein reveals multiple fatty acid-binding sites. <i>Biochemical Journal</i> , 2016, 473, 43-54.	1.7	19
69	An Expanded Conformation of an Antibody Fab Region by X-Ray Scattering, Molecular Dynamics, and smFRET Identifies an Aggregation Mechanism. <i>Journal of Molecular Biology</i> , 2019, 431, 1409-1425.	2.0	19
70	Structural changes in oxidised low-density lipoproteins and of the effect of the anti-atherosclerotic drug probucol observed by synchrotron X-ray and neutron solution scattering. <i>FEBS Journal</i> , 1989, 183, 321-329.	0.2	17
71	Factor VIIa and the extracellular domains of human tissue factor form a compact complex: A study by X-ray and neutron solution scattering. <i>FEBS Letters</i> , 1995, 374, 141-146.	1.3	16
72	The solution structure of the human IgG2 subclass is distinct from those for human IgG1 and IgG4 providing an explanation for their discrete functions. <i>Journal of Biological Chemistry</i> , 2019, 294, 10789-10806.	1.6	14

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73	Extended Flexible Linker Structures in the Complement Chimaeric Conjugate CR2-Ig by Scattering, Analytical Ultracentrifugation and Constrained Modelling: Implications for Function and Therapy. <i>Journal of Molecular Biology</i> , 2006, 356, 397-412.	2.0	11
74	Molecular architecture of heparin and heparan sulfate: Recent developments in solution structural studies. <i>Pure and Applied Chemistry</i> , 2011, 84, 65-76.	0.9	10
75	Flexibility in Mannan-Binding Lectin-Associated Serine Proteases-1 and -2 Provides Insight on Lectin Pathway Activation. <i>Structure</i> , 2017, 25, 364-375.	1.6	10
76	Two distinct conformations of factor H regulate discrete complement-binding functions in the fluid phase and at cell surfaces. <i>Journal of Biological Chemistry</i> , 2018, 293, 17166-17187.	1.6	10
77	Solution structures of human myeloma IgG3 antibody reveal extended Fab and Fc regions relative to the other IgG subclasses. <i>Journal of Biological Chemistry</i> , 2021, 297, 100995.	1.6	8
78	Analysis of 272 Genetic Variants in the Upgraded Interactive FXI Web Database Reveals New Insights into FXI Deficiency. <i>TH Open</i> , 2021, 05, e543-e556.	0.7	8
79	Hydrodynamic data show that C1 $\lambda$ , inhibitor of complement forms compact complexes with C1 $\lambda$ ,r and C1 $\lambda$ ,s. <i>FEBS Letters</i> , 1990, 271, 89-92.	1.3	7
80	Atomistic Modeling of Scattering Curves for Human IgG1/4 Reveals New Structure-Function Insights. <i>Biophysical Journal</i> , 2019, 117, 2101-2119.	0.2	7
81	Analogy and solution scattering modelling: new structural strategies for the multidomain proteins of complement, cartilage and the immunoglobulin superfamily. <i>Immunological Reviews</i> , 1998, 163, 237-250.	2.8	6
82	The His402 allotype of complement factor H show similar self-association to the Tyr402 allotype but exhibits greater self-association in the presence of zinc. <i>Molecular Immunology</i> , 2010, 47, 2263-2263.	1.0	6
83	Solution Structure of TT30, a Novel Complement Therapeutic Agent, Provides Insight into Its Joint Binding to Complement C3b and C3d. <i>Journal of Molecular Biology</i> , 2012, 418, 248-263.	2.0	5
84	Domain structure of human complement C4b extends with increasing NaCl concentration: implications for its regulatory mechanism. <i>Biochemical Journal</i> , 2016, 473, 4473-4491.	1.7	4
85	Genetic and Protein Structural Evaluation of Atypical Hemolytic Uremic Syndrome and C3 Glomerulopathy. <i>Advances in Chronic Kidney Disease</i> , 2020, 27, 120-127.e4.	0.6	4
86	Clinicopathologic Implications of Complement Genetic Variants in Kidney Transplantation. <i>Frontiers in Medicine</i> , 2021, 8, 775280.	1.2	4
87	Molecular modelling analyses of the C-type lectin domain in human aggrecan. <i>Biochemical Society Transactions</i> , 1996, 24, 99S-99S.	1.6	3
88	The solution structure of the complement deregulator FHR5 reveals a compact dimer and provides new insights into CFHR5 nephropathy. <i>Journal of Biological Chemistry</i> , 2020, 295, 16342-16358.	1.6	3
89	Solution structure of deglycosylated human IgG1 shows the role of CH2 glycans in its conformation. <i>Biophysical Journal</i> , 2021, 120, 1814-1834.	0.2	3
90	A Dimerization Site at SCR-17/18 in Factor H Clarifies a New Mechanism for Complement Regulatory Control. <i>Frontiers in Immunology</i> , 2020, 11, 601895.	2.2	3

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91	Identification of diverse lipid-binding modes in the groove of zinc $\beta$ 2-glycoprotein reveals its functional versatility. FEBS Journal, 2022, 289, 1876-1896.	2.2	3
92	Analysis of 180 Genetic Variants in a New Interactive FX Variant Database Reveals Novel Insights into FX Deficiency. TH Open, 2021, 05, e557-e569.	0.7	3
93	Synchrotron X-ray and neutron solution scattering studies of structural changes in low-density lipoproteins. Biochemical Society Transactions, 1989, 17, 680-681.	1.6	2
94	Crystal structure of zinc- $\beta$ 2-glycoprotein in complex with a fatty acid reveals multiple different modes of protein-lipid binding. Biochemical Journal, 2019, 476, 2815-2834.	1.7	2
95	STRUCTURE AND FUNCTION OF VWF-A DOMAINS IN COMPLEMENT AND COAGULATION. Biochemical Society Transactions, 1999, 27, A131-A131.	1.6	0