Stephen J Perkins

List of Publications by Year
in descending order

95 papers	4,590 citations	87723 38 h-index	106150 65 g-index
96 all docs	96 docs citations	96 times ranked	4184 citing authors

#	Article	IF	Citations
1	Identification of diverse lipidâ€binding modes in the groove of zinc Î±₂ glycoprotein reveals its functional versatility. FEBS Journal, 2022, 289, 1876-1896.	2.2	3
2	Solution structure of deglycosylated human IgG1 shows the role of CH2 glycans in its conformation. Biophysical Journal, 2021, 120, 1814-1834.	0.2	3
3	Solution structures of human myeloma IgG3 antibody reveal extended Fab and Fc regions relative to the other IgG subclasses. Journal of Biological Chemistry, 2021, 297, 100995.	1.6	8
4	Analysis of 272 Genetic Variants in the Upgraded Interactive FXI Web Database Reveals New Insights into FXI Deficiency. TH Open, 2021, 05, e543-e556.	0.7	8
5	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
6	Clinicopathologic Implications of Complement Genetic Variants in Kidney Transplantation. Frontiers in Medicine, 2021, 8, 775280.	1.2	4
7	Genetic and Protein Structural Evaluation of Atypical Hemolytic Uremic Syndrome and C3 Glomerulopathy. Advances in Chronic Kidney Disease, 2020, 27, 120-127.e4.	0.6	4
8	The solution structure of the complement deregulator FHR5 reveals a compact dimer and provides new insights into CFHR5 nephropathy. Journal of Biological Chemistry, 2020, 295, 16342-16358.	1.6	3
9	The European Association for Haemophilia and Allied Disorders (EAHAD) Coagulation Factor Variant Databases: Important resources for haemostasis clinicians and researchers. Haemophilia, 2020, 26, 306-313.	1.0	55
10	The EAHAD blood coagulation factor VII variant database. Human Mutation, 2020, 41, 1209-1219.	1.1	27
11	A Dimerization Site at SCR-17/18 in Factor H Clarifies a New Mechanism for Complement Regulatory Control. Frontiers in Immunology, 2020, 11, 601895.	2.2	3
12	Atomistic Modeling of Scattering Curves for Human IgG1/4 Reveals New Structure-Function Insights. Biophysical Journal, 2019, 117, 2101-2119.	0.2	7
13	The solution structure of the human IgG2 subclass is distinct from those for human IgG1 and IgG4 providing an explanation for their discrete functions. Journal of Biological Chemistry, 2019, 294, 10789-10806.	1.6	14
14	An Expanded Conformation of an Antibody Fab Region by X-Ray Scattering, Molecular Dynamics, and smFRET Identifies an Aggregation Mechanism. Journal of Molecular Biology, 2019, 431, 1409-1425.	2.0	19
15	Crystal structure of zinc-Î±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
16	Statistical Validation of Rare Complement Variants Provides Insights into the Molecular Basis of Atypical Hemolytic Uremic Syndrome and C3 Glomerulopathy. Journal of Immunology, 2018, 200, 2464-2478.	0.4	130
17	Two distinct conformations of factor H regulate discrete complement-binding functions in the fluid phase and at cell surfaces. Journal of Biological Chemistry, 2018, 293, 17166-17187.	1.6	10
18	Non-linearity of the collagen triple helix in solution and implications for collagen function. Biochemical Journal, 2017, 474, 2203-2217.	1.7	21

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19	Flexibility in Mannan-Binding Lectin-Associated Serine Proteases-1 and -2 Provides Insight on Lectin Pathway Activation. Structure, 2017, 25, 364-375.	1.6	10
20	Domain structure of human complement C4b extends with increasing NaCl concentration: implications for its regulatory mechanism. Biochemical Journal, 2016, 473, 4473-4491.	1.7	4
21	Zinc-induced oligomerization of zinc Î±2 glycoprotein reveals multiple fatty acid-binding sites. Biochemical Journal, 2016, 473, 43-54.	1.7	19
22	Atomistic modelling of scattering data in the Collaborative Computational Project for Small Angle Scattering (CCP-SAS). Journal of Applied Crystallography, 2016, 49, 1861-1875.	1.9	67
23	The solution structures of native and patient monomeric human IgA1 reveal asymmetric extended structures: implications for function and IgAN disease. Biochemical Journal, 2015, 471, 167-185.	1.7	22
24	A Revised Mechanism for the Activation of Complement C3 to C3b. Journal of Biological Chemistry, 2015, 290, 2334-2350.	1.6	41
25	SCT: a suite of programs for comparing atomistic models with small-angle scattering data. Journal of Applied Crystallography, 2015, 48, 953-961.	1.9	30
26	The Solution Structures of Two Human IgG1 Antibodies Show Conformational Stability and Accommodate Their C1q and FcÎ³R Ligands. Journal of Biological Chemistry, 2015, 290, 8420-8438.	1.6	37
27	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	1.1	71
28	Positive Selection during the Evolution of the Blood Coagulation Factors in the Context of Their Disease-Causing Mutations. Molecular Biology and Evolution, 2014, 31, 3040-3056.	3.5	22
29	New functional and structural insights from updated mutational databases for complement factor H, Factor I, membrane cofactor protein and C3. Bioscience Reports, 2014, 34, .	1.1	59
30	Molecular Interactions between Complement Factor H and Its Heparin and Heparan Sulfate Ligands. Frontiers in Immunology, 2014, 5, 126.	2.2	52
31	The Fab Conformations in the Solution Structure of Human Immunoglobulin G4 (IgG4) Restrict Access to Its Fc Region. Journal of Biological Chemistry, 2014, 289, 20740-20756.	1.6	34
32	The Solution Structure of Rabbit IgG Accounts for Its Interactions with the Fc Receptor and Complement C1q and Its Conformational Stability. Journal of Molecular Biology, 2013, 425, 506-523.	2.0	28
33	Zinc-induced Self-association of Complement C3b and Factor H. Journal of Biological Chemistry, 2013, 288, 19197-19210.	1.6	41
34	Bivalent and co-operative binding of complement Factor H to heparan sulfate and heparin. Biochemical Journal, 2012, 444, 417-428.	1.7	21
35	Near-planar Solution Structures of Mannose-binding Lectin Oligomers Provide Insight on Activation of Lectin Pathway of Complement. Journal of Biological Chemistry, 2012, 287, 3930-3945.	1.6	24
36	Solution Structure of TT30, a Novel Complement Therapeutic Agent, Provides Insight into Its Joint Binding to Complement C3b and C3d. Journal of Molecular Biology, 2012, 418, 248-263.	2.0	5

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37	Complement Factor Hâ€“ligand interactions: Self-association, multivalency and dissociation constants. Immunobiology, 2012, 217, 281-297.	0.8	75
38	Zinc Binding to the Tyr402 and His402 Allotypes of Complement Factor H: Possible Implications for Age-Related Macular Degeneration. Journal of Molecular Biology, 2011, 408, 714-735.	2.0	42
39	Analytical ultracentrifugation combined with X-ray and neutron scattering: Experiment and modelling. Methods, 2011, 54, 181-199.	1.9	30
40	Molecular architecture of heparin and heparan sulfate: Recent developments in solution structural studies. Pure and Applied Chemistry, 2011, 84, 65-76.	0.9	10
41	The Solution Structure of Heparan Sulfate Differs from That of Heparin. Journal of Biological Chemistry, 2011, 286, 24842-24854.	1.6	31
42	Self-association and domain rearrangements between complement C3 and C3u provide insight into the activation mechanism of C3. Biochemical Journal, 2010, 431, 63-72.	1.7	25
43	Unravelling proteinâ€“protein interactions between complement factor H and C-reactive protein using a multidisciplinary strategy. Biochemical Society Transactions, 2010, 38, 894-900.	1.6	19
44	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. Molecular Immunology, 2010, 47, 2263-2263.	1.0	6
45	C-reactive Protein Exists in an NaCl Concentration-dependent Pentamer-Decamer Equilibrium in Physiological Buffer. Journal of Biological Chemistry, 2010, 285, 1041-1052.	1.6	34
46	Complement Factor H Binds at Two Independent Sites to C-reactive Protein in Acute Phase Concentrations*. Journal of Biological Chemistry, 2010, 285, 1053-1065.	1.6	112
47	Masking of the Fc region in human IgG4 by constrained X-ray scattering modelling: implications for antibody function and therapy. Biochemical Journal, 2010, 432, 101-114.	1.7	40
48	Semi-Rigid Solution Structures of Heparin by Constrained X-ray Scattering Modelling: New Insight into Heparinâ€“Protein Complexes. Journal of Molecular Biology, 2010, 395, 504-521.	2.0	97
49	Multiple Interactions of Complement Factor H with Its Ligands in Solution: A Progress Report. Advances in Experimental Medicine and Biology, 2010, 703, 25-47.	0.8	29
50	Constrained solution scattering modelling of human antibodies and complement proteins reveals novel biological insights. Journal of the Royal Society Interface, 2009, 6, S679-96.	1.5	38
51	Electrostatic Interactions Contribute to the Folded-back Conformation of Wild Type Human Factor H. Journal of Molecular Biology, 2009, 391, 98-118.	2.0	57
52	Multimeric Interactions between Complement Factor H and Its C3d Ligand Provide New Insight on Complement Regulation. Journal of Molecular Biology, 2009, 391, 119-135.	2.0	20
53	Structural analysis of eight novel and 112 previously reported missense mutations in the interactive FXI mutation database reveals new insight on FXI deficiency. Thrombosis and Haemostasis, 2009, 102, 287-301.	1.8	30
54	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. Journal of Molecular Biology, 2008, 375, 80-101.	2.0	46

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55	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. Journal of Molecular Biology, 2008, 375, 102-118.	2.0	39
56	Implications of the Progressive Self-association of Wild-type Human Factor H for Complement Regulation and Disease. Journal of Molecular Biology, 2008, 375, 891-900.	2.0	35
57	Solution Structure of the Complex Formed between Human Complement C3d and Full-length Complement Receptor Type 2. Journal of Molecular Biology, 2008, 384, 137-150.	2.0	40
58	Uncontrolled Zinc- and Copper-Induced Oligomerisation of the Human Complement Regulator Factor H and Its Possible Implications for Function and Disease. Journal of Molecular Biology, 2008, 384, 1341-1352.	2.0	47
59	Xâ€Ray and Neutron Scattering Data and Their Constrained Molecular Modeling. Methods in Cell Biology, 2008, 84, 375-423.	0.5	40
60	Implications of the Near-Planar Solution Structure of Human Myeloma Dimeric IgA1 for Mucosal Immunity and IgA Nephropathy. Journal of Immunology, 2008, 180, 1008-1018.	0.4	57
61	Structure determinations of human and chimaeric antibodies by solution scattering and constrained molecular modelling. Biochemical Society Transactions, 2008, 36, 37-42.	1.6	21
62	Solution Structure of Human Secretory Component and Implications for Biological Function. Journal of Biological Chemistry, 2007, 282, 16969-16980.	1.6	41
63	Associative and Structural Properties of the Region of Complement Factor H Encompassing the Tyr402His Disease-related Polymorphism and its Interactions with Heparin. Journal of Molecular Biology, 2007, 368, 564-581.	2.0	44
64	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. Human Mutation, 2007, 28, 222-234.	1.1	160
65	An interactive web database of factor H-associated hemolytic uremic syndrome mutations: insights into the structural consequences of disease-associated mutations. Human Mutation, 2006, 27, 21-30.	1.1	79
66	Extended Flexible Linker Structures in the Complement Chimaeric Conjugate CR2-Ig by Scattering, Analytical Ultracentrifugation and Constrained Modelling: Implications for Function and Therapy. Journal of Molecular Biology, 2006, 356, 397-412.	2.0	11
67	The 15 SCR Flexible Extracellular Domains of Human Complement Receptor Type 2 can Mediate Multiple Ligand and Antigen Interactions. Journal of Molecular Biology, 2006, 362, 1132-1147.	2.0	36
68	His-384 Allotypic Variant of Factor H Associated with Age-related Macular Degeneration Has Different Heparin Binding Properties from the Non-disease-associated Form. Journal of Biological Chemistry, 2006, 281, 24713-24720.	1.6	161
69	Factor XI deficiency database: an interactive web database of mutations, phenotypes, and structural analysis tools. Human Mutation, 2005, 26, 192-198.	1.1	59
70	Solution Structure of the Complex between CR2 SCR 1-2 and C3d of Human Complement: An X-ray Scattering and Sedimentation Modelling Study. Journal of Molecular Biology, 2005, 346, 859-873.	2.0	59
71	Semi-extended Solution Structure of Human Myeloma Immunoglobulin D Determined by Constrained X-ray Scattering. Journal of Molecular Biology, 2005, 353, 155-173.	2.0	69
72	Solution Structure Determination of Monomeric Human IgA2 by X-ray and Neutron Scattering, Analytical Ultracentrifugation and Constrained Modelling: A Comparison with Monomeric Human IgA1. Journal of Molecular Biology, 2004, 338, 921-941.	2.0	100

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73	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. Journal of Molecular Biology, 2002, 316, 217-224.	2.0	70
74	Folded-back solution structure of monomeric factor H of human complement by synchrotron X-ray and neutron scattering, analytical ultracentrifugation and constrained molecular modelling. Journal of Molecular Biology, 2001, 309, 1117-1138.	2.0	134
75	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. Biochemistry, 2001, 40, 5931-5941.	1.2	55
76	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. Biochemical Journal, 2001, 357, 647-659.	1.7	42
77	X-Ray and neutron scattering analyses of hydration shells: a molecular interpretation based on sequence predictions and modelling fits. Biophysical Chemistry, 2001, 93, 129-139.	1.5	104
78	Structural models for carcinoembryonic antigen and its complex with the single-chain Fv antibody molecule MFE23. FEBS Letters, 2000, 475, 11-16.	1.3	50
79	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 1Edited by R. Huber. Journal of Molecular Biology, 1999, 286, 1421-1447.	2.0	209
80	STRUCTURE AND FUNCTION OF VWF-A DOMAINS IN COMPLEMENT AND COAGULATION. Biochemical Society Transactions, 1999, 27, A131-A131.	1.6	0
81	Analogy and solution scattering modelling: new structural strategies for the multidomain proteins of complement, cartilage and the immunoglobulin superfamily. Immunological Reviews, 1998, 163, 237-250.	2.8	6
82	The Factor I and follistatin domain families: the return of a prodigal son. Biochemical Journal, 1997, 326, 939-941.	1.7	27
83	Pentameric and decameric structures in solution of serum amyloid P component by X-ray and neutron scattering and molecular modelling analyses 1 1Edited by R. Huber. Journal of Molecular Biology, 1997, 272, 408-422.	2.0	113
84	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. FEBS Letters, 1996, 388, 211-216.	1.3	32
85	Predicted Î±-helix/Î²-sheet secondary structures for the zinc-binding motifs of human papillomavirus E7 and E6 proteins by consensus prediction averaging and spectroscopic studies of E7. Biochemical Journal, 1996, 319, 229-239.	1.7	44
86	Molecular modelling analyses of the C-type lectin domain in human aggrecan. Biochemical Society Transactions, 1996, 24, 99S-99S.	1.6	3
87	The protein fold of the von Willebrand factor type A domain is predicted to be similar to the open twisted Î²-sheet flanked by Î±-helices found in human ras-p21. FEBS Letters, 1995, 358, 283-286.	1.3	33
88	Factor VIIa and the extracellular domains of human tissue factor form a compact complex: A study by X-ray and neutron solution scattering. FEBS Letters, 1995, 374, 141-146.	1.3	16
89	Oligomeric domain structure of human complement factor H by x-ray and neutron solution scattering. Biochemistry, 1991, 30, 2847-2857.	1.2	62
90	Solution structure of human and mouse immunoglobulin M by synchrotron X-ray scattering and molecular graphics modelling. Journal of Molecular Biology, 1991, 221, 1345-1366.	2.0	178

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91	Hydrodynamic data show that C1Ì„ inhibitor of complement forms compact complexes with C1Ì„r and C1Ì„s. FEBS Letters, 1990, 271, 89-92.	1.3	7
92	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. FEBS Journal, 1989, 183, 321-329.	0.2	17
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	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. FEBS Journal, 1986, 157, 169-180.	0.2	535
95	Low-resolution structural studies of mitochondrial ubiquinol: Cytochrome c reductase in detergent solutions by neutron scattering. Journal of Molecular Biology, 1983, 168, 847-866.	2.0	98