

David J Scott

List of Publications by Year in descending order

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88
papers

2,510
citations

201385

27
h-index

223531

46
g-index

90
all docs

90
docs citations

90
times ranked

3872
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of filopodia formation induced by the IRSp53/MIM homology domain of human IRSp53. <i>EMBO Journal</i> , 2005, 24, 240-250.	3.5	214
2	Insulin at pH 2: Structural Analysis of the Conditions Promoting Insulin Fibre Formation. <i>Journal of Molecular Biology</i> , 2002, 318, 479-490.	2.0	196
3	Screening Transthyretin Amyloid Fibril Inhibitors. <i>Structure</i> , 2002, 10, 851-863.	1.6	106
4	Structure of the intact transactivation domain of the human papillomavirus E2 protein. <i>Nature</i> , 2000, 403, 805-809.	13.7	95
5	FtsZ Polymer-bundling by the Escherichia coli ZapA Orthologue, YgfE, Involves a Conformational Change in Bound GTP. <i>Journal of Molecular Biology</i> , 2007, 369, 210-221.	2.0	83
6	Crystal Structures of the Liganded and Unliganded Nickel-binding Protein NikA from Escherichia coli. <i>Journal of Biological Chemistry</i> , 2003, 278, 50322-50329.	1.6	77
7	Dimer formation and transcription activation in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2002, 316, 235-245.	2.0	68
8	Multifunctional Xylooligosaccharide/Cephalosporin C Deacetylase Revealed by the Hexameric Structure of the Bacillus subtilis Enzyme at 1.9Å... Resolution. <i>Journal of Molecular Biology</i> , 2003, 330, 593-606.	2.0	67
9	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
10	Heterocomplex formation between metastasis-related protein S100A4 (Mts1) and S100A1 as revealed by the yeast two-hybrid system. <i>FEBS Letters</i> , 2000, 475, 187-191.	1.3	60
11	STAT2 Is a Pervasive Cytokine Regulator due to Its Inhibition of STAT1 in Multiple Signaling Pathways. <i>PLoS Biology</i> , 2016, 14, e2000117.	2.6	55
12	Metastasis-associated protein Mts1 (S100A4) inhibits CK2-mediated phosphorylation and self-assembly of the heavy chain of nonmuscle myosin. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2000, 1498, 252-263.	1.9	53
13	The Dimerization Interface of the Metastasis-associated Protein S100A4 (Mts1). <i>Journal of Biological Chemistry</i> , 2001, 276, 24212-24222.	1.6	53
14	Isolation and Characterisation of Mutants of GroEL that are Fully Functional as Single Rings. <i>Journal of Molecular Biology</i> , 2003, 332, 715-728.	2.0	52
15	Structural modeling of an outer membrane electron conduit from a metal-reducing bacterium suggests electron transfer via periplasmic redox partners. <i>Journal of Biological Chemistry</i> , 2018, 293, 8103-8112.	1.6	51
16	The lipidome and proteome of oil bodies from Helianthus annuus (common sunflower). <i>Journal of Chemical Biology</i> , 2013, 6, 63-76.	2.2	42
17	Subunit Assembly for DNA Cleavage by Restriction Endonuclease SgrAI. <i>Journal of Molecular Biology</i> , 2003, 327, 579-591.	2.0	41
18	Cleavage of Individual DNA Strands by the Different Subunits of the Heterodimeric Restriction Endonuclease BbvCI. <i>Journal of Molecular Biology</i> , 2005, 348, 641-653.	2.0	40

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19	SilE is an intrinsically disordered periplasmic α -molecular sponge β involved in bacterial silver resistance. <i>Molecular Microbiology</i> , 2016, 101, 731-742.	1.2	38
20	Structural Characterisation of the Insecticidal Toxin XptA1, Reveals a 1.15ÅMDa Tetramer with a Cage-like Structure. <i>Journal of Molecular Biology</i> , 2007, 366, 1558-1568.	2.0	37
21	Oligomerization of the <i>Bacillus subtilis</i> division protein DivIVA. <i>Microbiology (United Kingdom)</i> , 2002, 148, 807-813.	0.7	37
22	The Vip3Ag4 Insecticidal Protoxin from <i>Bacillus thuringiensis</i> Adopts A Tetrameric Configuration That Is Maintained on Proteolysis. <i>Toxins</i> , 2017, 9, 165.	1.5	36
23	Conformational Properties of \hat{I}^2 -PrP. <i>Journal of Biological Chemistry</i> , 2009, 284, 21981-21990.	1.6	34
24	Structure and Catalytic Regulatory Function of Ubiquitin Specific Protease 11 N-Terminal and Ubiquitin-like Domains. <i>Biochemistry</i> , 2014, 53, 2966-2978.	1.2	34
25	The DNA-remodelling activity of DnaD is the sum of oligomerization and DNA-binding activities on separate domains. <i>Molecular Microbiology</i> , 2006, 60, 917-924.	1.2	33
26	An Undecided Coiled Coil. <i>Journal of Biological Chemistry</i> , 2011, 286, 27537-27547.	1.6	33
27	A Hydrodynamic Comparison of Solution and Gas Phase Proteins and Their Complexes. <i>Journal of Physical Chemistry B</i> , 2014, 118, 8489-8495.	1.2	31
28	Analytical ultracentrifugation: A versatile tool for the characterisation of macromolecular complexes in solution. <i>Methods</i> , 2016, 95, 55-61.	1.9	29
29	Synthesis of \hat{I}^{\pm} -Glucan in <i>Mycobacteria</i> Involves a Hetero-octameric Complex of Trehalose Synthase TreS and Maltokinase Pep2. <i>ACS Chemical Biology</i> , 2013, 8, 2245-2255.	1.6	27
30	Concentration dependence of translational diffusion coefficients for globular proteins. <i>Analyst</i> , 2014, 139, 6242-6248.	1.7	27
31	The <i>Bacillus subtilis</i> DnaD protein: a putative link between DNA remodeling and initiation of DNA replication. <i>FEBS Letters</i> , 2004, 577, 460-464.	1.3	26
32	The $2\hat{\alpha}$ -oxoacid dehydrogenase multi β -enzyme complex of the archaeon <i>Thermoplasma acidophilum</i> recombinant expression, assembly and characterization. <i>FEBS Journal</i> , 2007, 274, 5406-5415.	2.2	26
33	Quaternary re-arrangement analysed by spectral enhancement: the interaction of a sporulation repressor with its antagonist 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 293, 997-1004.	2.0	25
34	Low resolution solution structure of the apo form of <i>Escherichia coli</i> haemoglobin protease Hbp. <i>Journal of Molecular Biology</i> , 2002, 315, 1179-1187.	2.0	25
35	Structure of the USP15 N-Terminal Domains: A \hat{I}^2 -Hairpin Mediates Close Association between the DUSP and UBL Domains. <i>Biochemistry</i> , 2011, 50, 7995-8004.	1.2	25
36	Dynamic Allostery in the Ring Protein TRAP. <i>Journal of Molecular Biology</i> , 2007, 371, 154-167.	2.0	24

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37	Role of Odorant Binding Proteins: Comparing Hypothetical Mechanisms with Experimental Data. <i>Chemosensory Perception</i> , 2008, 1, 153-162.	0.7	24
38	Characterisation of a GroEL Single-Ring Mutant that Supports Growth of <i>Escherichia coli</i> and Has GroES-Dependent ATPase Activity. <i>Journal of Molecular Biology</i> , 2010, 396, 1271-1283.	2.0	24
39	Creating Hetero-11-mers Composed of Wild-type and Mutant Subunits to Study RNA Binding to TRAP. <i>Journal of Biological Chemistry</i> , 2002, 277, 11838-11844.	1.6	22
40	N-terminal Domain of Prion Protein Directs Its Oligomeric Association. <i>Journal of Biological Chemistry</i> , 2014, 289, 25497-25508.	1.6	20
41	Enthalpy/Entropy Compensation Effects from Cavity Desolvation Underpin Broad Ligand Binding Selectivity for Rat Odorant Binding Protein 3. <i>Biochemistry</i> , 2014, 53, 2371-2379.	1.2	20
42	Structural Insights into the β -Mannosidase from <i>T. reesei</i> Obtained by Synchrotron Small-Angle X-ray Solution Scattering Enhanced by X-ray Crystallography. <i>Biochemistry</i> , 2002, 41, 9370-9375.	1.2	19
43	Comparison of Methods for Characterizing Nonideal Solute Self-Association by Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2009, 97, 886-896.	0.2	18
44	Effects of the Oncogenic V ⁶⁶⁴ E Mutation on Membrane Insertion, Structure, and Sequence-Dependent Interactions of the Neu Transmembrane Domain in Micelles and Model Membranes: An Integrated Biophysical and Simulation Study. <i>Biochemistry</i> , 2012, 51, 2558-2568.	1.2	18
45	The osmotic second virial coefficient for protein self-interaction: Use and misuse to describe thermodynamic nonideality. <i>Analytical Biochemistry</i> , 2015, 490, 55-65.	1.1	18
46	Remodeling of the AB site of rat parvalbumin and oncomodulin into a canonical EF-hand. <i>FEBS Journal</i> , 1999, 264, 790-799.	0.2	17
47	Structure of rat odorant-binding protein OBP1 at 1.6 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 403-410.	2.5	17
48	Interaction of λ 70 with <i>Escherichia coli</i> RNA polymerase core enzyme studied by surface plasmon resonance. <i>FEBS Letters</i> , 2000, 481, 281-284.	1.3	16
49	A simpler analysis for the measurement of second virial coefficients by self-interaction chromatography. <i>Analytical Biochemistry</i> , 2007, 371, 21-25.	1.1	16
50	Rapid Odorant Release in Mammalian Odour Binding Proteins Facilitates Their Temporal Coupling to Odorant Signals. <i>Journal of Molecular Biology</i> , 2010, 404, 372-380.	2.0	16
51	Dimerization of inositol monophosphatase <i>Mycobacterium tuberculosis</i> SuhB is not constitutive, but induced by binding of the activator Mg ²⁺ . <i>BMC Structural Biology</i> , 2007, 7, 55.	2.3	15
52	Domain swapping reveals that the C- and N-terminal domains of DnaG and DnaB, respectively, are functional homologues. <i>Molecular Microbiology</i> , 2007, 63, 1629-1639.	1.2	15
53	DnaB proteolysis in vivo regulates oligomerization and its localization at oriC in <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2010, 38, 2851-2864.	6.5	15
54	Dynamics of Odorant Binding to Thin Aqueous Films of Rat-OBP3. <i>Chemical Senses</i> , 2011, 36, 659-671.	1.1	15

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55	When a module is not a domain: the case of the REJ module and the redefinition of the architecture of polycystin-1. <i>Biochemical Journal</i> , 2011, 435, 651-660.	1.7	14
56	Allowance for the effect of protein charge in the characterization of nonideal solute self-association by sedimentation equilibrium. <i>Biophysical Chemistry</i> , 2010, 149, 83-91.	1.5	13
57	RepD-mediated recruitment of PcrA helicase at the <i>Staphylococcus aureus</i> pC221 plasmid replication origin, oriD. <i>Nucleic Acids Research</i> , 2010, 38, 1874-1888.	6.5	13
58	Defining the Intrinsically Disordered C-Terminal Domain of SSB Reveals DNA-Mediated Compaction. <i>Journal of Molecular Biology</i> , 2016, 428, 357-364.	2.0	12
59	Order and Disorder in the Domain Organization of the Plasmid Partition Protein KorB. <i>Journal of Biological Chemistry</i> , 2010, 285, 15440-15449.	1.6	11
60	DyBOBS: A Dynamic Biomimetic Assay for Odorant-Binding to Odor-Binding Protein. <i>Chemosensory Perception</i> , 2010, 3, 108-117.	0.7	10
61	Examination of the Discrepancy between Size Estimates for Ovalbumin from Small-Angle X-ray Scattering and Other Physicochemical Measurements. <i>Journal of Physical Chemistry B</i> , 2011, 115, 10725-10729.	1.2	10
62	Crystal structure of signal regulatory protein gamma (SIRP γ) in complex with an antibody Fab fragment. <i>BMC Structural Biology</i> , 2013, 13, 13.	2.3	10
63	Anomalous Small Angle X-Ray Scattering Simulations: Proof of Concept for Distance Measurements for Nanoparticle-Labelled Biomacromolecules in Solution. <i>PLoS ONE</i> , 2014, 9, e95664.	1.1	10
64	Effect of Protein Kinase A-mediated Phosphorylation on the Structure and Association Properties of the Enteropathogenic <i>Escherichia coli</i> Tir Virulence Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 25839-25846.	1.6	9
65	A potential for overestimating the absolute magnitudes of second virial coefficients by small-angle X-ray scattering. <i>Analytical Biochemistry</i> , 2013, 435, 159-165.	1.1	9
66	Allowance for radial dilution in evaluating the concentration dependence of sedimentation coefficients for globular proteins. <i>European Biophysics Journal</i> , 2018, 47, 291-295.	1.2	9
67	The role of the jaw subdomain of peptidoglycan glycosyltransferases for lipid II polymerization. <i>Cell Surface</i> , 2018, 2, 54-66.	1.5	8
68	Quantifying the concentration dependence of sedimentation coefficients for globular macromolecules: a continuing age-old problem. <i>Biophysical Reviews</i> , 2021, 13, 273-288.	1.5	8
69	Allowance for effects of thermodynamic nonideality in sedimentation equilibrium distributions reflecting protein dimerization. <i>Analytical Biochemistry</i> , 2012, 422, 28-32.	1.1	7
70	Engineering the Human Fc Region Enables Direct Cell Killing by Cancer Glycan-Targeting Antibodies without the Need for Immune Effector Cells or Complement. <i>Cancer Research</i> , 2020, 80, 3399-3412.	0.4	7
71	Interaction of sigma factor σ^{70} with <i>Escherichia coli</i> RNA polymerase core enzyme. <i>Biochemical Journal</i> , 2000, 352, 539-547.	1.7	7
72	Engineering a reagentless biosensor for single-stranded DNA to measure real-time helicase activity in <i>Bacillus</i> . <i>Biosensors and Bioelectronics</i> , 2014, 61, 579-586.	5.3	6

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73	Characterization of Intrinsically Disordered Proteins by Analytical Ultracentrifugation. <i>Methods in Enzymology</i> , 2015, 562, 225-239.	0.4	6
74	Flexibility of KorA, a plasmid-encoded, global transcription regulator, in the presence and the absence of its operator. <i>Nucleic Acids Research</i> , 2016, 44, 4947-4956.	6.5	6
75	Intrinsic disorder in the partitioning protein KorB persists after co-operative complex formation with operator DNA and KorA. <i>Biochemical Journal</i> , 2017, 474, 3121-3135.	1.7	6
76	Structure-Guided Enhancement of Selectivity of Chemical Probe Inhibitors Targeting Bacterial Seryl-tRNA Synthetase. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9703-9717.	2.9	5
77	Evaluation of diffusion coefficients by means of an approximate steady-state condition in sedimentation velocity distributions. <i>Analytical Biochemistry</i> , 2015, 490, 20-25.	1.1	4
78	Allowance for boundary sharpening in the determination of diffusion coefficients by sedimentation velocity: a historical perspective. <i>Biophysical Reviews</i> , 2018, 10, 3-13.	1.5	4
79	Thermodynamics of semi-specific ligand recognition: the binding of dipeptides to the E.coli dipeptide binding protein DppA. <i>European Biophysics Journal</i> , 2021, 50, 1103-1110.	1.2	4
80	Interaction of sigma factor σ^{70} with Escherichia coli RNA polymerase core enzyme. <i>Biochemical Journal</i> , 2000, 352, 539.	1.7	3
81	The shock of the old: hydrodynamics for the masses. <i>Biochemical Society Transactions</i> , 2008, 36, 766-770.	1.6	2
82	Accounting for thermodynamic non-ideality in the Guinier region of small-angle scattering data of proteins. <i>Biophysical Reviews</i> , 2016, 8, 441-444.	1.5	2
83	Use of molecular crowding for the detection of protein self-association by size-exclusion chromatography. <i>Analytical Biochemistry</i> , 2019, 584, 113392.	1.1	2
84	Sedimentation velocity of intrinsically disordered proteins: what information can we actually obtain?. <i>Molecular BioSystems</i> , 2012, 8, 378-380.	2.9	1
85	Expression, purification and crystallization of the cell-division protein YgfE from Escherichia coli. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 305-307.	0.7	0
86	Oligomerisation of TBP1 from <i>Haloferax volcanii</i> . , 0, , 93-96.		0
87	Experimental determination of second virial coefficients by small-angle X-ray scattering: a problem revisited. <i>European Biophysics Journal</i> , 2019, 48, 781-787.	1.2	0
88	Thermodynamics and Thermodynamic Nonideality. , 2018, , 1-8.		0