

# Douglas C Rees

## List of Publications by Year in descending order

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109  
papers

15,399  
citations

38742

50  
h-index

27406

106  
g-index

131  
all docs

131  
docs citations

131  
times ranked

10872  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fluorescence activation mechanism and imaging of drug permeation with new sensors for smoking-cessation ligands. <i>ELife</i> , 2022, 11, .	6.0	14
2	Glutathione binding to the plant AtAtm3 transporter and implications for the conformational coupling of ABC transporters. <i>ELife</i> , 2022, 11, .	6.0	8
3	Modeling the stimulation by glutathione of the steady state kinetics of an adenosine triphosphate binding cassette transporter. <i>Protein Science</i> , 2022, 31, 752-757.	7.6	1
4	Structural Characterization of Two CO Molecules Bound to the Nitrogenase Active Site. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 5704-5707.	13.8	47
5	Structural Characterization of Two CO Molecules Bound to the Nitrogenase Active Site. <i>Angewandte Chemie</i> , 2021, 133, 5768-5771.	2.0	7
6	Microcrystal Electron Diffraction Elucidates Water-Specific Polymorphism-Induced Emission Enhancement of Bis-arylacylhydrazone. <i>ACS Applied Materials &amp; Interfaces</i> , 2021, 13, 7546-7555.	8.0	8
7	Mechanism of molybdate insertion into pterin-based molybdenum cofactors. <i>Nature Chemistry</i> , 2021, 13, 758-765.	13.6	19
8	CaMn <sub>3</sub> IVO <sub>4</sub> Cubane Models of the Oxygen-Evolving Complex: Spin Ground States $S < 9/2$ and the Effect of Oxo Protonation. <i>Angewandte Chemie</i> , 2021, 133, 17812-17820.	2.0	1
9	CaMn <sub>3</sub> IVO <sub>4</sub> Cubane Models of the Oxygen-Evolving Complex: Spin Ground States $S < 9/2$ and the Effect of Oxo Protonation. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 17671-17679.	13.8	14
10	Characterization of the ABC methionine transporter from <i>Neisseria meningitidis</i> reveals that lipidated MetQ is required for interaction. <i>ELife</i> , 2021, 10, .	6.0	2
11	Titrateable transmembrane residues and a hydrophobic plug are essential for manganese import via the <i>Bacillus anthracis</i> ABC transporter MntBC-A. <i>Journal of Biological Chemistry</i> , 2021, 297, 101087.	3.4	1
12	A structural framework for unidirectional transport by a bacterial ABC exporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19228-19236.	7.1	21
13	Structural Enzymology of Nitrogenase Enzymes. <i>Chemical Reviews</i> , 2020, 120, 4969-5004.	47.7	194
14	Crystal structure of the <i>Escherichia coli</i> transcription termination factor Rho. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 398-405.	0.8	3
15	Structures of the <i>Neisseria meningitidis</i> methionine-binding protein MetQ in substrate-free form and bound to methionine isomers. <i>Protein Science</i> , 2019, 28, 1750-1757.	7.6	10
16	Localized Electronic Structure of Nitrogenase FeMoco Revealed by Selenium K-Edge High Resolution X-ray Absorption Spectroscopy. <i>Journal of the American Chemical Society</i> , 2019, 141, 13676-13688.	13.7	47
17	Rethinking the Nitrogenase Mechanism: Activating the Active Site. <i>Joule</i> , 2019, 3, 2662-2678.	24.0	62
18	Site-Specific Oxidation State Assignments of the Iron Atoms in the [4Fe:4S] <sup>2+/1+/0/</sup> States of the Nitrogenase Fe-Protein. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 3894-3897.	13.8	30

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19	Site-specific Oxidation State Assignments of the Iron Atoms in the [4Fe:4S] <sup>2+/1+/0</sup> States of the Nitrogenase Fe-Protein. <i>Angewandte Chemie</i> , 2019, 131, 3934-3937.	2.0	1
20	Elucidating a role for the cytoplasmic domain in the <i>Mycobacterium tuberculosis</i> mechanosensitive channel of large conductance. <i>Scientific Reports</i> , 2018, 8, 14566.	3.3	7
21	Noncanonical role for the binding protein in substrate uptake by the MetNI methionine ATP Binding Cassette (ABC) transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10596-E10604.	7.1	36
22	The "speed limit" for macromolecular crystal growth. <i>Protein Science</i> , 2018, 27, 1837-1841.	7.6	3
23	Electrochemical and structural characterization of <i>Azotobacter vinelandii</i> flavodoxin II. <i>Protein Science</i> , 2017, 26, 1984-1993.	7.6	22
24	Reversible Protonated Resting State of the Nitrogenase Active Site. <i>Journal of the American Chemical Society</i> , 2017, 139, 10856-10862.	13.7	29
25	The role of MscL amphipathic N terminus indicates a blueprint for bilayer-mediated gating of mechanosensitive channels. <i>Nature Communications</i> , 2016, 7, 11984.	12.8	87
26	Nitrogenase FeMoco investigated by spatially resolved anomalous dispersion refinement. <i>Nature Communications</i> , 2016, 7, 10902.	12.8	131
27	A sulfur-based transport pathway in <i>Cupressus</i> ATPases. <i>EMBO Reports</i> , 2015, 16, 728-740.	4.5	41
28	The Effect of Detergent, Temperature, and Lipid on the Oligomeric State of MscL Constructs: Insights from Mass Spectrometry. <i>Chemistry and Biology</i> , 2015, 22, 593-603.	6.0	72
29	Powering brain power: GLUT1 and the era of structure based human transporter biology. <i>National Science Review</i> , 2015, 2, 3-4.	9.5	1
30	Structural Evidence for Asymmetrical Nucleotide Interactions in Nitrogenase. <i>Journal of the American Chemical Society</i> , 2015, 137, 146-149.	13.7	44
31	Nitrogenase MoFe protein from <i>Clostridium pasteurianum</i> at 1.08 Å resolution: comparison with the <i>Azotobacter vinelandii</i> MoFe protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 274-282.	2.5	32
32	Substrate Pathways in the Nitrogenase MoFe Protein by Experimental Identification of Small Molecule Binding Sites. <i>Biochemistry</i> , 2015, 54, 2052-2060.	2.5	41
33	The Allosteric Regulatory Mechanism of the <i>Escherichia coli</i> MetNI Methionine ATP Binding Cassette (ABC) Transporter. <i>Journal of Biological Chemistry</i> , 2015, 290, 9135-9140.	3.4	24
34	The contribution of methionine to the stability of the <i>Escherichia coli</i> MetNIQ ABC transporter-substrate binding protein complex. <i>Biological Chemistry</i> , 2015, 396, 1127-1134.	2.5	15
35	MscL: channeling membrane tension. <i>Pflügers Archiv European Journal of Physiology</i> , 2015, 467, 15-25.	2.8	23
36	Catalysis-dependent selenium incorporation and migration in the nitrogenase active site iron-molybdenum cofactor. <i>ELife</i> , 2015, 4, e11620.	6.0	116

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37	Structural Basis for Heavy Metal Detoxification by an Atm1-Type ABC Exporter. <i>Science</i> , 2014, 343, 1133-1136.	12.6	152
38	Turnover-Dependent Inactivation of the Nitrogenase MoFe-Protein at High pH. <i>Biochemistry</i> , 2014, 53, 333-343.	2.5	23
39	Ligand binding to the FeMo-cofactor: Structures of CO-bound and reactivated nitrogenase. <i>Science</i> , 2014, 345, 1620-1623.	12.6	343
40	Structure and mechanism of Zn <sup>2+</sup> -transporting P-type ATPases. <i>Nature</i> , 2014, 514, 518-522.	27.8	107
41	The Structure of a Conserved Piezo Channel Domain Reveals a Topologically Distinct $\beta^2$ Sandwich Fold. <i>Structure</i> , 2014, 22, 1520-1527.	3.3	41
42	The Sixteenth Iron in the Nitrogenase MoFe Protein. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 10529-10532.	13.8	28
43	Open and shut: Crystal structures of the dodecylmaltoside solubilized mechanosensitive channel of small conductance from <i>Escherichia coli</i> and <i>Helicobacter pylori</i> at 4.4 Å... and 4.1 Å... resolutions. <i>Protein Science</i> , 2013, 22, 502-509.	7.6	63
44	Structure and stability of the C-terminal helical bundle of the <i>E. coli</i> mechanosensitive channel of large conductance. <i>Protein Science</i> , 2013, 22, 1592-1601.	7.6	18
45	Multiple Amino Acid Sequence Alignment Nitrogenase Component 1: Insights into Phylogenetics and Structure-Function Relationships. <i>PLoS ONE</i> , 2013, 8, e72751.	2.5	23
46	Inward facing conformations of the MetNI methionine ABC transporter: Implications for the mechanism of transinhibition. <i>Protein Science</i> , 2012, 21, 84-96.	7.6	39
47	Structure of Precursor-Bound NifEN: A Nitrogenase FeMo Cofactor Maturase/Insertase. <i>Science</i> , 2011, 331, 91-94.	12.6	115
48	Mechanosensitive Channels: What Can They Do and How Do They Do It?. <i>Structure</i> , 2011, 19, 1356-1369.	3.3	303
49	Evidence for Interstitial Carbon in Nitrogenase FeMo Cofactor. <i>Science</i> , 2011, 334, 940-940.	12.6	774
50	OCAM: A new tool for studying the oligomeric diversity of MscL channels. <i>Protein Science</i> , 2011, 20, 313-326.	7.6	23
51	A reported archaeal mechanosensitive channel is a structural homolog of MarR-like transcriptional regulators. <i>Protein Science</i> , 2010, 19, 808-814.	7.6	7
52	A distinct mechanism for the ABC transporter BtuCD-BtuF revealed by the dynamics of complex formation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 332-338.	8.2	105
53	Structural and mechanistic diversity of ABC transporters. <i>FASEB Journal</i> , 2010, 24, 405.1.	0.5	0
54	A P-type ATPase importer that discriminates between essential and toxic transition metals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4677-4682.	7.1	88

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55	Structure of a tetrameric MscL in an expanded intermediate state. <i>Nature</i> , 2009, 461, 120-124.	27.8	105
56	ABC transporters: the power to change. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 218-227.	37.0	1,105
57	The Funnel Approach to the Precrystallization Production of Membrane Proteins. <i>Journal of Molecular Biology</i> , 2008, 377, 62-73.	4.2	58
58	The High-Affinity <i>E. coli</i> Methionine ABC Transporter: Structure and Allosteric Regulation. <i>Science</i> , 2008, 321, 250-253.	12.6	187
59	Opening the Molecular Floodgates. <i>Science</i> , 2008, 321, 1166-1167.	12.6	7
60	The Future of Biological X-Ray Analysis. , 2008, , 145-164.		0
61	Structures of the Prokaryotic Mechanosensitive Channels MscL and MscS. <i>Current Topics in Membranes</i> , 2007, 58, 1-24.	0.9	176
62	Assignment of Individual Metal Redox States in a Metalloprotein by Crystallographic Refinement at Multiple X-ray Wavelengths. <i>Journal of the American Chemical Society</i> , 2007, 129, 2210-2211.	13.7	47
63	How many metals does it take to fix N <sub>2</sub> ? A mechanistic overview of biological nitrogen fixation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17088-17093.	7.1	225
64	Structural basis of biological nitrogen fixation. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2005, 363, 971-984.	3.4	852
65	Functional Analysis of Detergent-Solubilized and Membrane-Reconstituted ATP-Binding Cassette Transporters. <i>Methods in Enzymology</i> , 2005, 400, 429-459.	1.0	31
66	Nitrogenase Complexes: Multiple Docking Sites for a Nucleotide Switch Protein. <i>Science</i> , 2005, 309, 1377-1380.	12.6	216
67	In Vitro Functional Characterization of BtuCD-F, the <i>Escherichia coli</i> ABC Transporter for Vitamin B12 Uptake. <i>Biochemistry</i> , 2005, 44, 16301-16309.	2.5	146
68	Structure and mechanism in prokaryotic mechanosensitive channels. <i>Current Opinion in Structural Biology</i> , 2003, 13, 432-442.	5.7	151
69	The Interface Between the Biological and Inorganic Worlds: Iron-Sulfur Metalloclusters. <i>Science</i> , 2003, 300, 929-931.	12.6	214
70	The structures of BtuCD and MscS and their implications for transporter and channel function. <i>FEBS Letters</i> , 2003, 555, 111-115.	2.8	22
71	STRUCTURAL BIOLOGY: Enhanced: Breaching the Barrier. <i>Science</i> , 2003, 301, 603-604.	12.6	34
72	Prokaryotic mechanosensitive channels. <i>Advances in Protein Chemistry</i> , 2003, 63, 177-209.	4.4	26

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73	High Resolution Crystal Structures of the Wild Type and Cys-55 → Ser and Cys-59 → Ser Variants of the Thioredoxin-like [2Fe-2S] Ferredoxin from Aquifex aeolicus. Journal of Biological Chemistry, 2002, 277, 34499-34507.	3.4	31
74	Structure of a Cofactor-Deficient Nitrogenase MoFe Protein. Science, 2002, 296, 352-356.	12.6	176
75	The Î±-Helix and the Organization and Gating of Channels. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 207-233.	18.3	65
76	The structure of Escherichia coli BtuF and binding to its cognate ATP binding cassette transporter. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16642-16647.	7.1	209
77	Crystallographic Studies of the Escherichia coli Quinol-Fumarate Reductase with Inhibitors Bound to the Quinol-binding Site. Journal of Biological Chemistry, 2002, 277, 16124-16130.	3.4	98
78	Nitrogenase MoFe-Protein at 1.16 Å Resolution: A Central Ligand in the FeMo-Cofactor. Science, 2002, 297, 1696-1700.	12.6	1,041
79	Crystal Structure of Escherichia coli MscS, a Voltage-Modulated and Mechanosensitive Channel. Science, 2002, 298, 1582-1587.	12.6	574
80	Metalloproteins to Membrane Proteins: Biological Energy Transduction Mechanisms. ACS Symposium Series, 2002, , 202-215.	0.5	0
81	Biochemical and Structural Characterization of the Cross-Linked Complex of Nitrogenase: A Comparison to the ADP-AlF <sub>4</sub> -Stabilized Structure. Biochemistry, 2002, 41, 15557-15565.	2.5	81
82	The <i>E. coli</i> BtuCD Structure: A Framework for ABC Transporter Architecture and Mechanism. Science, 2002, 296, 1091-1098.	12.6	1,039
83	Great Metalloclusters in Enzymology. Annual Review of Biochemistry, 2002, 71, 221-246.	11.1	198
84	MgATP-Bound and Nucleotide-Free Structures of a Nitrogenase Protein Complex between the Leu 1271 <sup>Fe</sup> -Protein and the MoFe-Protein. Biochemistry, 2001, 40, 641-650.	2.5	85
85	Crystal Structure of the All-Ferrous [4Fe-4S] Form of the Nitrogenase Iron Protein from <i>Azotobacter vinelandii</i> . Biochemistry, 2001, 40, 651-656.	2.5	135
86	Crystal structure of the <i>Acidaminococcus fermentans</i> 2-hydroxyglutaryl-CoA dehydratase component A. Journal of Molecular Biology, 2001, 307, 297-308.	4.2	70
87	Some thermodynamic implications for the thermostability of proteins. Protein Science, 2001, 10, 1187-1194.	7.6	152
88	High-resolution structures of the oxidized and reduced states of cytochrome c554 from <i>Nitrosomonas europaea</i> . Journal of Biological Inorganic Chemistry, 2001, 6, 390-397.	2.6	44
89	Turning a reference inside-out: Commentary on an article by Stevens and Arkin entitled: 'Are membrane proteins 'inside-out' proteins?' (Proteins 1999;36:135-143). Proteins: Structure, Function and Bioinformatics, 2000, 38, 121-122.	2.6	18
90	Nitrogenase: standing at the crossroads. Current Opinion in Chemical Biology, 2000, 4, 559-566.	6.1	287

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91	Analyzing your complexes: structure of the quinol-fumarate reductase respiratory complex. <i>Current Opinion in Structural Biology</i> , 2000, 10, 448-455.	5.7	32
92	Crystallographic Analyses of Ion Channels: Lessons and Challenges. <i>Journal of Biological Chemistry</i> , 2000, 275, 713-716.	3.4	41
93	Overexpression, Purification, and Crystallization of the Membrane-Bound Fumarate Reductase from <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2000, 19, 188-196.	1.3	23
94	Structures of the Superoxide Reductase from <i>Pyrococcus furiosus</i> in the Oxidized and Reduced States. <i>Biochemistry</i> , 2000, 39, 2499-2508.	2.5	164
95	Comparing crystallographic and solution structures of nitrogenase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 727-728.	2.5	12
96	“Feeling the pressure”: structural insights into a gated mechanosensitive channel. <i>Current Opinion in Structural Biology</i> , 1999, 9, 448-454.	5.7	43
97	Structure of the <i>Escherichia coli</i> Fumarate Reductase Respiratory Complex. <i>Science</i> , 1999, 284, 1961-1966.	12.6	400
98	Structural bioenergetics and energy transduction mechanisms. <i>Journal of Molecular Biology</i> , 1999, 293, 343-350.	4.2	50
99	Heme packing motifs revealed by the crystal structure of the tetra-heme cytochrome c554 from <i>Nitrosomonas europaea</i> . <i>Nature Structural Biology</i> , 1998, 5, 1005-1012.	9.7	102
100	Conformational variability in structures of the nitrogenase iron proteins from <i>Azotobacter vinelandii</i> and <i>Clostridium pasteurianum</i> . <i>Journal of Molecular Biology</i> , 1998, 280, 669-685.	4.2	152
101	MOLYBDENUM-COFACTOR-CONTAINING ENZYMES: Structure and Mechanism. <i>Annual Review of Biochemistry</i> , 1997, 66, 233-267.	11.1	489
102	Redox-Dependent Structural Changes in the Nitrogenase P-Cluster. <i>Biochemistry</i> , 1997, 36, 1181-1187.	2.5	498
103	Crystal structure of the molybdate binding protein ModA. <i>Nature Structural Biology</i> , 1997, 4, 703-707.	9.7	72
104	Structure of ADP-ATP-stabilized nitrogenase complex and its implications for signal transduction. <i>Nature</i> , 1997, 387, 370-376.	27.8	517
105	Structural Basis of Biological Nitrogen Fixation. <i>Chemical Reviews</i> , 1996, 96, 2965-2982.	47.7	1,015
106	A leucine-rich repeat variant with a novel repetitive protein structural motif. <i>Nature Structural Biology</i> , 1996, 3, 991-994.	9.7	49
107	Macromolecular solvation energies derived from small molecule crystal morphology. <i>Protein Science</i> , 1993, 2, 1882-1889.	7.6	11
108	X-ray crystal structures of the oxidized and reduced forms of the rubredoxin from the marine hyperthermophilic archaeobacterium <i>pyrococcus furiosus</i> . <i>Protein Science</i> , 1992, 1, 1494-1507.	7.6	238

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109	Comparison of the X-ray structure of native rubredoxin from pyrococcus furiosus with the NMR structure of the zinc-substituted protein. Protein Science, 1992, 1, 1522-1525.	7.6	47