

Charles W Carter Jr

List of Publications by Year in descending order

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78
papers

3,289
citations

126907

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161849

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88
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88
docs citations

88
times ranked

1693
citing authors

#	ARTICLE	IF	CITATIONS
1	Cognition, Mechanism, and Evolutionary Relationships in Aminoacyl-tRNA Synthetases. Annual Review of Biochemistry, 1993, 62, 715-748.	11.1	353
2	Crystal structure of estrogen sulphotransferase. Nature Structural and Molecular Biology, 1997, 4, 904-908.	8.2	263
3	Tryptophanyl-tRNA synthetase crystal structure reveals an unexpected homology to tyrosyl-tRNA synthetase. Structure, 1995, 3, 17-31.	3.3	181
4	Four-body potentials reveal protein-specific correlations to stability changes caused by hydrophobic core mutations. Journal of Molecular Biology, 2001, 311, 625-638.	4.2	122
5	A Minimal TrpRS Catalytic Domain Supports Sense/Antisense Ancestry of Class I and II Aminoacyl-tRNA Synthetases. Molecular Cell, 2007, 25, 851-862.	9.7	87
6	The mutation \hat{I}^{299} Asp-Tyr stabilizes $Y\hat{A}^{\epsilon}$ A new, composite quaternary state of human hemoglobin. Proteins: Structure, Function and Bioinformatics, 1991, 10, 81-91.	2.6	86
7	Cytidine Deaminase Complexed to 3-Deazacytidine: A $\hat{\epsilon}$ Valence Buffer $\hat{\epsilon}$ in Zinc Enzyme Catalysis. Biochemistry, 1996, 35, 1335-1341.	2.5	85
8	Interconversion of ATP Binding and Conformational Free Energies by Tryptophanyl-tRNA Synthetase: Structures of ATP Bound to Open and Closed, Pre-Transition-state Conformations. Journal of Molecular Biology, 2003, 325, 39-63.	4.2	84
9	Aminoacylating Urzymes Challenge the RNA World Hypothesis. Journal of Biological Chemistry, 2013, 288, 26856-26863.	3.4	77
10	What RNA World? Why a Peptide/RNA Partnership Merits Renewed Experimental Attention. Life, 2015, 5, 294-320.	2.4	73
11	2.9 Å... crystal structure of ligand-free tryptophanyl-tRNA synthetase: Domain movements fragment the adenine nucleotide binding site. Protein Science, 2000, 9, 218-231.	7.6	70
12	Temperature dependence of amino acid hydrophobicities. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7484-7488.	7.1	68
13	tRNA acceptor stem and anticodon bases form independent codes related to protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7489-7494.	7.1	64
14	Functional Class I and II Amino Acid-activating Enzymes Can Be Coded by Opposite Strands of the Same Gene. Journal of Biological Chemistry, 2015, 290, 19710-19725.	3.4	62
15	Did tRNA Synthetase Classes Arise on Opposite Strands of the Same Gene?. Molecular Cell, 2002, 10, 705-708.	9.7	59
16	Tryptophanyl-tRNA Synthetase Urzyme. Journal of Biological Chemistry, 2010, 285, 38590-38601.	3.4	58
17	The Rodin-Ohno hypothesis that two enzyme superfamilies descended from one ancestral gene: an unlikely scenario for the origins of translation that will not be dismissed. Biology Direct, 2014, 9, 11.	4.6	56
18	Histidyl-tRNA Synthetase Urzymes. Journal of Biological Chemistry, 2011, 286, 10387-10395.	3.4	55

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19	Computational Studies of Tryptophanyl-tRNA Synthetase: Activation of ATP by Induced-Fit. <i>Journal of Molecular Biology</i> , 2006, 362, 1159-1180.	4.2	51
20	Interdependence, Reflexivity, Fidelity, Impedance Matching, and the Evolution of Genetic Coding. <i>Molecular Biology and Evolution</i> , 2018, 35, 269-286.	8.9	50
21	Insuperable problems of the genetic code initially emerging in an RNA world. <i>BioSystems</i> , 2018, 164, 155-166.	2.0	49
22	Statistical Evaluation of the Rodinâ€“Ohno Hypothesis: Sense/Antisense Coding of Ancestral Class I and II Aminoacyl-tRNA Synthetases. <i>Molecular Biology and Evolution</i> , 2013, 30, 1588-1604.	8.9	47
23	Urzymology: Experimental Access to a Key Transition in the Appearance of Enzymes. <i>Journal of Biological Chemistry</i> , 2014, 289, 30213-30220.	3.4	46
24	Cytidine Deaminases from <i>B. subtilis</i> and <i>E. coli</i> : Compensating Effects of Changing Zinc Coordination and Quaternary Structure. <i>Biochemistry</i> , 1999, 38, 12258-12265.	2.5	43
25	Crystal Structure of Tryptophanyl-tRNA Synthetase Complexed with Adenosine-5â€² Tetraphosphate: Evidence for Distributed Use of Catalytic Binding Energy in Amino Acid Activation by Class I Aminoacyl-tRNA Synthetases. <i>Journal of Molecular Biology</i> , 2007, 369, 108-128.	4.2	42
26	Six Rossmannoid folds, including the Class I aminoacyl-tRNA synthetases, share a partial core with the anti-codon-binding domain of a Class II aminoacyl-tRNA synthetase. <i>Bioinformatics</i> , 2010, 26, 709-714.	4.1	41
27	On Primordial Senseâ€“Antisense Coding. <i>Journal of Molecular Evolution</i> , 2009, 69, 555-67.	1.8	40
28	Coding of Class I and II Aminoacyl-tRNA Synthetases. <i>Advances in Experimental Medicine and Biology</i> , 2017, 966, 103-148.	1.6	40
29	Selective Inhibition of Bacterial Tryptophanyl-tRNA Synthetases by Indolmycin Is Mechanism-based. <i>Journal of Biological Chemistry</i> , 2016, 291, 255-265.	3.4	38
30	Hierarchical groove discrimination by Class I and II aminoacyl-tRNA synthetases reveals a palimpsest of the operational RNA code in the tRNA acceptor-stem bases. <i>Nucleic Acids Research</i> , 2018, 46, 9667-9683.	14.5	38
31	A Conformational Transition State Accompanies Tryptophan Activation by <i>B. stearothermophilus</i> Tryptophanyl-tRNA Synthetase. <i>Structure</i> , 2007, 15, 1272-1284.	3.3	37
32	A Master Switch Couples Mg ²⁺ -Assisted Catalysis to Domain Motion in <i>B. stearothermophilus</i> Tryptophanyl-tRNA Synthetase. <i>Structure</i> , 2012, 20, 128-138.	3.3	37
33	Simplicial Neighborhood Analysis of Protein Packing (SNAPP): A Computational Geometry Approach to Studying Proteins. <i>Methods in Enzymology</i> , 2003, 374, 509-544.	1.0	36
34	Ancient Adaptation of the Active Site of Tryptophanyl-tRNA Synthetase for Tryptophan Binding. <i>Biochemistry</i> , 2000, 39, 13136-13143.	2.5	35
35	Full Implementation of the Genetic Code by Tryptophanyl-tRNA Synthetase Requires Intermodular Coupling. <i>Journal of Biological Chemistry</i> , 2013, 288, 34736-34745.	3.4	34
36	Enhanced Amino Acid Selection in Fully Evolved Tryptophanyl-tRNA Synthetase, Relative to Its Urzyme, Requires Domain Motion Sensed by the D1 Switch, a Remote Dynamic Packing Motif. <i>Journal of Biological Chemistry</i> , 2014, 289, 4367-4376.	3.4	33

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37	Quantitative Analysis of Crystal Growth. <i>Journal of Molecular Biology</i> , 1994, 238, 346-365.	4.2	32
38	tRNA acceptor-stem and anticodon bases embed separate features of amino acid chemistry. <i>RNA Biology</i> , 2016, 13, 145-151.	3.1	32
39	[5] Response surface methods for optimizing and improving reproducibility of crystal growth. <i>Methods in Enzymology</i> , 1997, 276, 74-99.	1.0	31
40	Models for protein-zinc ion binding sites. II. The catalytic sites. <i>International Journal of Quantum Chemistry</i> , 2001, 83, 150-165.	2.0	30
41	Structure alignment via Delaunay tetrahedralization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 66-81.	2.6	30
42	High-resolution experimental phases for tryptophanyl-tRNA synthetase (TrpRS) complexed with tryptophanyl-5â€²AMP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1595-1608.	2.5	28
43	Independent saturation of three TrpRS subsites generates a partially assembled state similar to those observed in molecular simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1790-1795.	7.1	28
44	Class I and II aminoacyl-tRNA synthetase tRNA groove discrimination created the first synthetase-tRNA cognate pairs and was therefore essential to the origin of genetic coding. <i>IUBMB Life</i> , 2019, 71, 1088-1098.	3.4	28
45	Mg ²⁺ -Assisted Catalysis by <i>B. Stearothermophilus</i> TrpRS Is Promoted by Allosteric Effects. <i>Structure</i> , 2009, 17, 952-964.	3.3	26
46	A modified PATH algorithm rapidly generates transition states comparable to those found by other well established algorithms. <i>Structural Dynamics</i> , 2016, 3, 012101.	2.3	26
47	High-Dimensional Mutant and Modular Thermodynamic Cycles, Molecular Switching, and Free Energy Transduction. <i>Annual Review of Biophysics</i> , 2017, 46, 433-453.	10.0	24
48	Crystals of <i>Bacillus stearothermophilus</i> tryptophanyl-tRNA synthetase containing enzymatically formed acyl transfer product tryptophanyl-ATP, an active site marker for the 3' CCA terminus of tryptophanyl-tRNA ^{Trp} . <i>Biochemistry</i> , 1984, 23, 381-385.	2.5	23
49	A Concerted Tryptophanyl-adenylate-dependent Conformational Change in <i>Bacillus subtilis</i> Tryptophanyl-tRNA Synthetase Revealed by the Fluorescence of Trp92. <i>Journal of Molecular Biology</i> , 1996, 260, 446-466.	4.2	21
50	Mg ²⁺ -Free <i>Bacillus stearothermophilus</i> Tryptophanyl-tRNA Synthetase Retains a Major Fraction of the Overall Rate Enhancement for Tryptophan Activation. <i>Journal of the American Chemical Society</i> , 2008, 130, 1488-1494.	13.7	21
51	An Ancestral Tryptophanyl-tRNA Synthetase Precursor Achieves High Catalytic Rate Enhancement without Ordered Ground-State Tertiary Structures. <i>ACS Chemical Biology</i> , 2016, 11, 1661-1668.	3.4	21
52	The Roots of Genetic Coding in Aminoacyl-tRNA Synthetase Duality. <i>Annual Review of Biochemistry</i> , 2021, 90, 349-373.	11.1	21
53	Experimental solutions to problems defining the origin of codon-directed protein synthesis. <i>BioSystems</i> , 2019, 183, 103979.	2.0	20
54	Cloning heterologous genes into <i>E. Coli</i> for enzyme production and crystal growth: Problems of expression and microheterogeneity. <i>Journal of Crystal Growth</i> , 1988, 90, 168-179.	1.5	18

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55	Combining multi-mutant and modular thermodynamic cycles to measure energetic coupling networks in enzyme catalysis. <i>Structural Dynamics</i> , 2017, 4, 032101.	2.3	17
56	Escapement mechanisms: Efficient free energy transduction by reciprocally-coupled gating. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 710-717.	2.6	17
57	Augmenting the anisotropic network model with torsional potentials improves PATH performance, enabling detailed comparison with experimental rate data. <i>Structural Dynamics</i> , 2017, 4, 032103.	2.3	15
58	An Alternative to the RNA World. <i>Natural History</i> , 2016, 125, 28-33.	0.2	15
59	Simultaneous codon usage, the origin of the proteome, and the emergence of de-novo proteins. <i>Current Opinion in Structural Biology</i> , 2021, 68, 142-148.	5.7	14
60	Enzymatic conformational fluctuations along the reaction coordinate of cytidine deaminase. <i>Protein Science</i> , 2002, 11, 1424-1434.	7.6	13
61	HIV-1 Protease Uses Bi-Specific S2/S2' Subsites to Optimize Cleavage of Two Classes of Target Sites. <i>Journal of Molecular Biology</i> , 2018, 430, 5182-5195.	4.2	13
62	Impedance Matching and the Choice Between Alternative Pathways for the Origin of Genetic Coding. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7392.	4.1	11
63	Reciprocally-Coupled Gating: Strange Loops in Bioenergetics, Genetics, and Catalysis. <i>Biomolecules</i> , 2021, 11, 265.	4.0	11
64	Identification of Sequence-Specific Tertiary Packing Motifs in Protein Structures using Delaunay Tessellation. <i>Lecture Notes in Computational Science and Engineering</i> , 2002, , 477-494.	0.3	10
65	A Leucyl-tRNA Synthetase Urzyme: Authenticity of tRNA Synthetase Catalytic Activities and Promiscuous Phosphorylation of Leucyl-5'AMP. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4229.	4.1	9
66	Nucleoside Deaminases for Cytidine and Adenosine: Comparison with Deaminases Acting on RNA. , 0, , 363-375.		8
67	Multidimensional Phylogenetic Metrics Identify Class I Aminoacyl-tRNA Synthetase Evolutionary Mosaicity and Inter-Modular Coupling. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1520.	4.1	5
68	[6] Phase improvement using conditional probability methods: Maximum entropy solvent flattening and phase permutation. <i>Methods in Enzymology</i> , 1997, 277, 79-109.	1.0	4
69	Improving Marginal Crystals. <i>Methods in Molecular Biology</i> , 2007, 363, 153-174.	0.9	3
70	Did Gene Expression Co-evolve with Gene Replication?. , 2018, , 293-313.		3
71	Did Class 1 and Class 2 Aminoacyl Trna Synthetases Descend from Genetically Complimentary, Catalytically Active ATP-Binding Motifs?. <i>Biophysical Journal</i> , 2014, 106, 675a.	0.5	2
72	E Pluribus Tres: The 2009 Nobel Prize in Chemistry. <i>Structure</i> , 2009, 17, 1558-1561.	3.3	1

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73	Energetics of enzyme stability: Response from Carter, Tropsha and Edgell. Trends in Biotechnology, 2002, 20, 2-3.	9.3	0
74	Tryptophan activation activity of a minimal TrpRS catalytic domain. FASEB Journal, 2006, 20, A504.	0.5	0
75	Mg ²⁺ -Assisted Catalysis by B. stearothermophilus TrpRS is Promoted by Allosteric Effects. FASEB Journal, 2008, 22, 1009.4.	0.5	0
76	Solving a Heavy-Atom Substructure by Direct Methods. , 1998, , 253-273.		0
77	Ab Initio Determination of a Low Resolution Molecular Envelope by Direct Methods. , 1998, , 413-419.		0
78	10.1063/1.4974218.1. , 2017, , .		0