Alan Berry

List of Publications by Year
in descending order

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49 papers	2,539 citations	218677 26 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	2550 citing authors

#	Article	IF	Citations
1	C-type cytochrome-initiated reduction of bacterial lytic polysaccharide monooxygenases. Biochemical Journal, 2021, 478, 2927-2944.	3.7	9
2	Crystal structure of the putative cyclase IdmH from the indanomycin nonribosomal peptide synthase/polyketide synthase. IUCrJ, 2019, 6, 1120-1133.	2.2	8
3	Aldolase-catalysed stereoselective synthesis of fluorinated small molecules. Current Opinion in Chemical Biology, 2017, 37, 33-38.	6.1	12
4	Extending enzyme molecular recognition with an expanded amino acid alphabet. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2610-2615.	7.1	30
5	Towards designer organelles by subverting the peroxisomal import pathway. Nature Communications, 2017, 8, 454.	12.8	16
6	An Enantioâ€•and Diastereoselective Chemoenzymatic Synthesis of Îâ€Fluoro Î²â€Hydroxy Carboxylic Esters. Angewandte Chemie - International Edition, 2016, 55, 6767-6770.	13.8	35
7	An Enantioâ€•and Diastereoselective Chemoenzymatic Synthesis of Îâ€Fluoro Î²â€Hydroxy Carboxylic Esters. Angewandte Chemie, 2016, 128, 6879-6882.	2.0	18
8	Evaluation of fluoropyruvate as nucleophile in reactions catalysed by N-acetyl neuraminic acid lyase variants: scope, limitations and stereoselectivity. Organic and Biomolecular Chemistry, 2016, 14, 105-112.	2.8	19
9	Advances in Pathway Engineering for Natural Product Biosynthesis. ChemCatChem, 2015, 7, 3078-3093.	3.7	16
10	Reaction Mechanism of N-Acetylneuraminic Acid Lyase Revealed by a Combination of Crystallography, QM/MM Simulation, and Mutagenesis. ACS Chemical Biology, 2014, 9, 1025-1032.	3.4	41
11	Engineering aldolases as biocatalysts. Current Opinion in Chemical Biology, 2014, 19, 25-33.	6.1	84
12	Engineering of a Cytidine 5â€²â€Monophosphateâ€Sialic Acid Synthetase for Improved Tolerance to Functional Sialic Acids. Advanced Synthesis and Catalysis, 2013, 355, 3597-3612.	4.3	18
13	Structural Insights into the Recovery of Aldolase Activity in Nâ€Acetylneuraminic Acid Lyase by Replacement of the Catalytically Active Lysine with Î³â€Thialysine by Using a Chemical Mutagenesis Strategy. ChemBioChem, 2013, 14, 474-481.	2.6	26
14	Development of an organo- and enzyme-catalysed one-pot, sequential three-component reaction. Tetrahedron, 2012, 68, 7719-7722.	1.9	16
15	Identification and characterization of important residues in the catalytic mechanism of CMPâ€Neu5Ac synthetase from Neisseriaâ€fmeningitidis. FEBS Journal, 2010, 277, 2779-2790.	4.7	19
16	The moonlighting protein fructose-1, 6-bisphosphate aldolase of Neisseria meningitidis: surface localization and role in host cell adhesion. Molecular Microbiology, 2010, 76, 605-615.	2.5	101
17	Structural Insights into Substrate Specificity in Variants of N-Acetylneuraminic Acid Lyase Produced by Directed Evolution. Journal of Molecular Biology, 2010, 404, 56-69.	4.2	28
18	Structure of anEscherichia coli N-acetyl-<scp>D</scp>-neuraminic acid lyase mutant, E192N, in complex with pyruvate at 1.45â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1088-1090.	0.7	9

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19	Directed evolution of aldolases for exploitation in synthetic organic chemistry. Archives of Biochemistry and Biophysics, 2008, 474, 318-330.	3.0	77
20	Hadamard NMR spectroscopy for relaxation measurements of large (>35ÂkDa) proteins. Journal of Biomolecular NMR, 2007, 39, 239-245.	2.8	2
21	Creation of a Pair of Stereochemically Complementary Biocatalysts. Journal of the American Chemical Society, 2006, 128, 16238-16247.	13.7	68
22	Creation of a Tailored Aldolase for the Parallel Synthesis of Sialic Acid Mimetics. Angewandte Chemie - International Edition, 2005, 44, 2109-2112.	13.8	47
23	Synthesis of screening substrates for the directed evolution of sialic acid aldolase: towards tailored enzymes for the preparation of influenza A sialidase inhibitor analogues. Organic and Biomolecular Chemistry, 2005, 3, 1795.	2.8	13
24	A thermostable variant of fructose bisphosphate aldolase constructed by directed evolution also shows increased stability in organic solvents. Protein Engineering, Design and Selection, 2004, 17, 689-697.	2.1	78
25	Directed evolution of enzymes for biocatalysis and the life sciences. Cellular and Molecular Life Sciences, 2004, 61, 3034-3046.	5.4	64
26	The organization of divalent cations in the active site of cadmiumEscherichia colifructose-1,6-bisphosphate aldolase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 611-614.	2.5	8
27	Cloning, over-expression, purification, and characterisation of N-acetylneuraminate synthase from Streptococcus agalactiae. Protein Expression and Purification, 2003, 27, 346-356.	1.3	22
28	Modifying the stereochemistry of an enzyme-catalyzed reaction by directed evolution. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3143-3148.	7.1	110
29	Structure of Tagatose-1,6-bisphosphate Aldolase. Journal of Biological Chemistry, 2002, 277, 22018-22024.	3.4	55
30	Exploring substrate binding and discrimination in fructose1,6-bisphosphate and tagatose 1,6-bisphosphate aldolases. FEBS Journal, 2000, 267, 1858-1868.	0.2	58
31	The crystal structure of Escherichia coli class II fructose-1,6-bisphosphate aldolase in complex with phosphoglycolohydroxamate reveals details of mechanism and specificity 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 287, 383-394.	4.2	117
32	The dhnA gene of Escherichia coli encodes a Class I fructose bisphosphate aldolase. Biochemical Journal, 1998, 331, 437-445.	3.7	65
33	The oxidative and reductive half reactions of subunit interface mutants of Escherichia coli glutathione reductase. Biochemical Society Transactions, 1996, 24, 9S-9S.	3.4	2
34	The crystal structure of a class II fructose-1,6-bisphosphate aldolase shows a novel binuclear metal-binding active site embedded in a familiar fold. Structure, 1996, 4, 1303-1315.	3.3	112
35	Identification of arginine 331 as an important active site residue in the Class II fructoseâ€1,6â€bisphosphate aldolase of Escherichia coli. Protein Science, 1996, 5, 154-161.	7.6	35
36	A Reactive, Surface Cysteine Residue of the Class-II Fructose-1,6-Bisphosphate Aldolase of Escherichia coli Revealed by Electrospray Ionisation Mass Spectrometry. FEBS Journal, 1995, 227, 510-515.	0.2	19

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37	A quantitative methodology for the de novo design of proteins. Protein Science, 1994, 3, 1871-1882.	7.6	11
38	Identification of zinc-binding ligands in the Class II fructose- 1,6-bisphosphate aldolase of Escherichia coli. FEBS Letters, 1993, 318, 11-16.	2.8	47
39	Structural Differences between Wild-type NADP-dependent Glutathione Reductase from Escherichia coli and a Redesigned NAD-dependent Mutant. Journal of Molecular Biology, 1993, 231, 191-195.	4.2	32
40	New enzymes for old: Redesigning the coenzyme and substrate specificities of glutathione reductase. BioEssays, 1991, 13, 515-525.	2.5	34
41	Redesign of the coenzyme specificity of a dehydrogenase by protein engineering. Nature, 1990, 343, 38-43.	27.8	764
42	Switching kinetic mechanism and putative proton donor by directed mutagenesis of glutathione reductase. Biochemistry, 1989, 28, 1264-1269.	2.5	68
43	Alternative proton donors/acceptors in the catalytic mechanism of the glutathione reductase of Escherichia coli: the role of histidine-439 and tyrosine-99. Biochemistry, 1989, 28, 9602-9607.	2.5	49
44	Site-Directed Mutagenesis and the Mechanism of Flavoprotein Disulphide Oxidoreductases. , 1989, , 333-346.		0
45	Engineering of an intersubunit disulphide bridge in glutathione reductase fromEscherichia coli. FEBS Letters, 1988, 241, 46-50.	2.8	29
46	Flavoprotein disulphide oxidoreductases: protein engineering of glutathione reductase from Escherichia coli. Biochemical Society Transactions, 1988, 16, 84-87.	3.4	3
47	Protein engineering of glutathione reductase: over-expression of the gene from Escherichia coli. Biochemical Society Transactions, 1986, 14, 1229-1230.	3.4	0
48	The isolation and characterization of catalytically competent porphobilinogen deaminase-intermediate complexes. FEBS Letters, 1981, 129, 220-224.	2.8	36
49	Porphobilinogen Deaminase: Involvement of stable covalent enzyme intermediate complexes in the enzyme from Rhodopseudomonas spheroides. Biochemical Society Transactions, 1981, 9, 231-232.	3.4	3