

Patrick J Baker

List of Publications by Year in descending order

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112
papers

5,311
citations

109321

35
h-index

85541

71
g-index

113
all docs

113
docs citations

113
times ranked

5054
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of triclosan activity. <i>Nature</i> , 1999, 398, 383-384.	27.8	473
2	The structure of <i>Pyrococcus furiosus</i> glutamate dehydrogenase reveals a key role for ion-pair networks in maintaining enzyme stability at extreme temperatures. <i>Structure</i> , 1995, 3, 1147-1158.	3.3	445
3	An Inhibitor of FtsZ with Potent and Selective Anti-Staphylococcal Activity. <i>Science</i> , 2008, 321, 1673-1675.	12.6	389
4	A Mechanism of Drug Action Revealed by Structural Studies of Enoyl Reductase. <i>Science</i> , 1996, 274, 2107-2110.	12.6	239
5	Conformational Flexibility in Glutamate Dehydrogenase. <i>Journal of Molecular Biology</i> , 1993, 234, 1131-1139.	4.2	224
6	Antibiotic Activity and Characterization of BB-3497, a Novel Peptide Deformylase Inhibitor. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 563-570.	3.2	224
7	Subunit assembly and active site location in the structure of glutamate dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 75-86.	2.6	221
8	Crystal Structure of DNA Recombination Protein RuvA and a Model for Its Binding to the Holliday Junction. <i>Science</i> , 1996, 274, 415-421.	12.6	172
9	Structural consequences of sequence patterns in the fingerprint region of the nucleotide binding fold. <i>Journal of Molecular Biology</i> , 1992, 228, 662-671.	4.2	163
10	Analysis of protein solvent interactions in glucose dehydrogenase from the extreme halophile <i>Haloferax mediterranei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4846-4851.	7.1	134
11	X-Ray Crystallographic Studies on Butyryl-ACP Reveal Flexibility of the Structure around a Putative Acyl Chain Binding Site. <i>Structure</i> , 2002, 10, 825-835.	3.3	114
12	Common themes in redox chemistry emerge from the X-ray structure of oilseed rape (<i>Brassica napus</i>) enoyl acyl carrier protein reductase. <i>Structure</i> , 1995, 3, 927-938.	3.3	110
13	A <i>Burkholderia pseudomallei</i> Toxin Inhibits Helicase Activity of Translation Factor eIF4A. <i>Science</i> , 2011, 334, 821-824.	12.6	107
14	Glycerol Dehydrogenase. <i>Structure</i> , 2001, 9, 789-802.	3.3	101
15	A role for quaternary structure in the substrate specificity of leucine dehydrogenase. <i>Structure</i> , 1995, 3, 693-705.	3.3	97
16	Crystallographic analysis of triclosan bound to enoyl reductase. <i>Journal of Molecular Biology</i> , 1999, 294, 527-535.	4.2	90
17	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i> . <i>FEBS Journal</i> , 1995, 229, 688-695.	0.2	89
18	The 1.2 Å... structure of a novel quorum-sensing protein, <i>Bacillus subtilis</i> LuxS 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2001, 313, 111-122.	4.2	79

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19	Analysis of the structure and substrate binding of Phormidium lapideum alanine dehydrogenase. <i>Nature Structural Biology</i> , 1998, 5, 561-567.	9.7	78
20	Structural relationship between the hexameric and tetrameric family of glutamate dehydrogenases. <i>FEBS Journal</i> , 1992, 209, 851-859.	0.2	74
21	Evolution of Substrate Diversity in the Superfamily of Amino Acid Dehydrogenases. <i>Journal of Molecular Biology</i> , 1993, 234, 938-945.	4.2	73
22	The crystal structure and active site location of isocitrate lyase from the fungus <i>Aspergillus nidulans</i> . <i>Structure</i> , 2000, 8, 349-362.	3.3	64
23	Active site dynamics in the zinc-dependent medium chain alcohol dehydrogenase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 779-784.	7.1	61
24	The Crystal Structure of Diadenosine Tetraphosphate Hydrolase from <i>Caenorhabditis elegans</i> in Free and Binary Complex Forms. <i>Structure</i> , 2002, 10, 589-600.	3.3	57
25	Protein-protein recognition, hydride transfer and proton pumping in the transhydrogenase complex. <i>Structure with Folding & Design</i> operates a "Continuous Publication System"™ for Research Papers, this paper has been published on the internet before being printed (accessed from) https://doi.org/10.1016/j.str.2000.08.015	3.7	53
26	Substrate Specificity and Mechanism from the Structure of <i>Pyrococcus furiosus</i> Galactokinase. <i>Journal of Molecular Biology</i> , 2004, 337, 387-398.	4.2	53
27	Structure determination of the glutamate dehydrogenase from the hyperthermophile <i>Thermococcus litoralis</i> and its comparison with that from <i>Pyrococcus furiosus</i> . Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 293, 1121-1132.	4.2	52
28	Columnar Liquid Crystals in Cylindrical Nanoconfinement. <i>ACS Nano</i> , 2015, 9, 1759-1766.	14.6	51
29	The molecular basis of phosphite and hypophosphite recognition by ABC-transporters. <i>Nature Communications</i> , 2017, 8, 1746.	12.8	50
30	Substrate-Induced Conformational Changes in <i>Bacillus subtilis</i> Glutamate Racemase and Their Implications for Drug Discovery. <i>Structure</i> , 2005, 13, 1707-1713.	3.3	49
31	The mechanism of a formaldehyde-sensing transcriptional regulator. <i>Scientific Reports</i> , 2016, 6, 38879.	3.3	46
32	Determinants of Substrate Specificity in the Superfamily of Amino Acid Dehydrogenases. <i>Biochemistry</i> , 1997, 36, 16109-16115.	2.5	45
33	Insights into the mechanism of domain closure and substrate specificity of glutamate dehydrogenase from <i>Clostridium symbiosum</i> . Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 875-885.	4.2	41
34	Structural insights into the function of type VI secretion system TssA subunits. <i>Nature Communications</i> , 2018, 9, 4765.	12.8	41
35	Insights into Enzyme Evolution Revealed by the Structure of Methylaspartate Ammonia Lyase. <i>Structure</i> , 2002, 10, 105-113.	3.3	37
36	The molecular basis of endolytic activity of a multidomain alginate lyase from <i>Defluviitalea phaphyphila</i> , a representative of a new lyase family, PL39. <i>Journal of Biological Chemistry</i> , 2019, 294, 18077-18091.	3.4	37

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37	The partial amino acid sequence of the NAD -dependent glutamate dehydrogenase of <i>Clostridium symbiosum</i> : implications for the evolution and structural basis of coenzyme specificity. <i>BBA - Proteins and Proteomics</i> , 1991, 1080, 191-197.	2.1	36
38	The structure and domain organization of <i>Escherichia coli</i> isocitrate lyase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1209-1218.	2.5	35
39	Crystal Structure of <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Journal of Biological Chemistry</i> , 2003, 278, 33290-33297.	3.4	32
40	Analysis of the Open and Closed Conformations of the GTP-binding Protein YsxC from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2004, 339, 265-278.	4.2	32
41	Alteration in relative activities of phenylalanine dehydrogenase towards different substrates by site-directed mutagenesis. <i>FEBS Letters</i> , 1995, 370, 93-96.	2.8	31
42	Structure and Mechanism of Imidazoleglycerol-Phosphate Dehydratase. <i>Structure</i> , 2005, 13, 1809-1817.	3.3	31
43	Crystal Structures Reveal that the Reaction Mechanism of Imidazoleglycerol-Phosphate Dehydratase Is Controlled by Switching Mn(II) Coordination. <i>Structure</i> , 2015, 23, 1236-1245.	3.3	31
44	Evidence Supporting a cis-enediol-based Mechanism for <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Journal of Molecular Biology</i> , 2006, 358, 1353-1366.	4.2	29
45	Structural origins of pH-dependent chemical shifts in the B1 domain of protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3000-3016.	2.6	29
46	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i> . <i>FEBS Journal</i> , 1995, 229, 688-695.	0.2	28
47	Recent progress on the structure and function of glutamate dehydrogenase. <i>Biochemical Society Transactions</i> , 1987, 15, 748-751.	3.4	25
48	Purification and crystallization of the light harvesting LH1 complex from <i>Rhodobacter sphaeroides</i> . <i>Journal of Molecular Biology</i> , 1992, 228, 1259-1262.	4.2	25
49	Structure and Function of Amino Acid Ammonia-lyases. <i>Biocatalysis and Biotransformation</i> , 2004, 22, 133-140.	2.0	25
50	Effect of additives on the crystallization of glutamate dehydrogenase from <i>Clostridium symbiosum</i> . <i>Journal of Molecular Biology</i> , 1992, 224, 1181-1184.	4.2	24
51	The Structure of <i>Escherichia coli</i> RusA Endonuclease Reveals a New Holliday Junction DNA Binding Fold. <i>Structure</i> , 2003, 11, 1557-1567.	3.3	24
52	Elucidating the structural basis for differing enzyme inhibitor potency by cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1795-1800.	7.1	24
53	Analysis of the Quaternary Structure, Substrate Specificity, and Catalytic Mechanism of Valine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 1997, 272, 25105-25111.	3.4	23
54	Identification and structural analysis of the tripartite β -pore forming toxin of <i>Aeromonas hydrophila</i> . <i>Nature Communications</i> , 2019, 10, 2900.	12.8	20

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55	The Structures of Inhibitor Complexes of <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase Provide Insights into Substrate Binding and Catalysis. <i>Journal of Molecular Biology</i> , 2004, 343, 649-657.	4.2	19
56	RusA Holliday junction resolvase: DNA complex structureâ€”insights into selectivity and specificity. <i>Nucleic Acids Research</i> , 2006, 34, 5577-5584.	14.5	19
57	Alanine dehydrogenase from the psychrophilic bacterium strain PA-43: overexpression, molecular characterization, and sequence analysis. <i>Extremophiles</i> , 2003, 7, 135-143.	2.3	16
58	Pnc1 piggy-back import into peroxisomes relies on Gpd1 homodimerisation. <i>Scientific Reports</i> , 2017, 7, 42579.	3.3	16
59	The crystal structure of <i>Thermotoga maritima</i> maltosyltransferase and its implications for the molecular basis of the novel transfer specificity 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 312, 119-131.	4.2	14
60	Expression, purification and preliminary X-ray analysis of crystals of <i>Bacillus subtilis</i> glutamate racemase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2031-2034.	2.5	14
61	Crystallization of an NADP ⁺ -dependent malic enzyme from rat liver. <i>Journal of Molecular Biology</i> , 1987, 193, 233-235.	4.2	13
62	Use of chemical modification in the crystallization of isocitrate lyase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1991, 220, 13-16.	4.2	13
63	Alteration of the amino acid substrate specificity of clostridial glutamate dehydrogenase by site-directed mutagenesis of an active-site lysine residue. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 147-152.	2.1	13
64	Mirrorâ€”Image Packing Provides a Molecular Basis for the Nanomolar Equipotency of Enantiomers of an Experimental Herbicide. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 13485-13489.	13.8	13
65	Crystallization and Quaternary Structure Analysis of the NAD ⁺ -dependent Leucine Dehydrogenase from <i>Bacillus sphaericus</i> . <i>Journal of Molecular Biology</i> , 1994, 236, 663-665.	4.2	12
66	Conserved residues in Ycf54 are required for protochlorophyllide formation in <i>Synechocystis</i> sp. PCC 6803. <i>Biochemical Journal</i> , 2017, 474, 667-681.	3.7	12
67	Structural and functional studies of histidine biosynthesis in <i>Acanthamoeba</i> spp. demonstrates a novel molecular arrangement and target for antimicrobials. <i>PLoS ONE</i> , 2018, 13, e0198827.	2.5	12
68	Crystallization of the NADP ⁺ -dependent Glutamate Dehydrogenase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 1270-1273.	4.2	11
69	Crystallization and preliminary X-ray analysis of glucose dehydrogenase from <i>Haloferax mediterranei</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1887-1889.	2.5	11
70	Crystallization and preliminary X-ray crystallographic studies on acyl-(acyl carrier protein) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 330-332.	2.5	11
71	Distant Non-Obvious Mutations Influence the Activity of a Hyperthermophilic <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. <i>Biomolecules</i> , 2019, 9, 212.	4.0	11
72	Correlation of intron-exon organisation with the three-dimensional structure in glutamate dehydrogenase. <i>BBA - Proteins and Proteomics</i> , 1995, 1247, 231-238.	2.1	9

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73	From hyperthermophiles to psychrophiles: the structural basis of temperature stability of the amino acid dehydrogenases. <i>Biochemical Society Transactions</i> , 2004, 32, 264-268.	3.4	9
74	Crystal structure of <i>S. aureus</i> YlaN, an essential leucine rich protein involved in the control of cell shape. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 438-445.	2.6	9
75	The structure of a major surface antigen SAG19 from <i>Eimeria tenella</i> unifies the <i>Eimeria</i> SAG family. <i>Communications Biology</i> , 2021, 4, 376.	4.4	9
76	Purification, crystallization and preliminary crystallographic analysis of phosphoglucose isomerase from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1822-1823.	2.5	8
77	Optimization of selenium substructures as obtained from SHELXD. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1987-1994.	2.5	8
78	Crystallization and preliminary X-ray analysis of binary and ternary complexes of <i>Haloferax mediterranei</i> glucose dehydrogenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 743-746.	0.7	8
79	Crystallization and analysis of the subunit assembly and quaternary structure of imidazoleglycerol phosphate dehydratase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 845-847.	2.5	7
80	Characterisation of a tripartite β -pore forming toxin from <i>Serratia marcescens</i> . <i>Scientific Reports</i> , 2021, 11, 6447.	3.3	7
81	Crystallization of NAD ⁺ -dependent phenylalanine dehydrogenase from <i>Nocardia</i> sp239. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 269-272.	2.5	6
82	The human granulocyte/macrophage colony-stimulating factor receptor β 2 isoform influences haemopoietic lineage commitment and divergence. <i>British Journal of Haematology</i> , 2003, 122, 150-158.	2.5	6
83	Crystallization and preliminary crystallographic analysis of a surface antigen glycoprotein, SAG19, from <i>Eimeria tenella</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1380-1383.	0.7	6
84	Crystallization and preliminary X-ray studies of nitrogenase component 1 (the MoFe protein) from <i>Klebsiella pneumoniae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 227-228.	2.5	5
85	Expression, purification, crystallization and preliminary crystallographic analysis of a putative GTP-binding protein, YsxC, from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 166-168.	2.5	5
86	Cloning, purification, crystallization and preliminary crystallographic analysis of galactokinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1819-1821.	2.5	4
87	Crystallization of the NAD(P)-dependent glutamate dehydrogenase from the hyperthermophile <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 240-242.	2.5	3
88	Crystallization of the alanine dehydrogenase from <i>Phormidium lapideum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 407-408.	2.5	3
89	Purification, crystallization and quaternary structure analysis of a glycerol dehydrogenase S305C mutant from <i>Bacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 165-167.	2.5	3
90	Crystallization and preliminary X-ray analysis of substrate complexes of leucine dehydrogenase from <i>Thermoactinomyces intermedius</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1059-1062.	2.5	3

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91	Crystallization of glycerol dehydrogenase from <i>Bacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 830-832.	2.5	2
92	Isocitrate lyase from <i>Aspergillus nidulans</i> : crystallization and X-ray analysis of a glyoxylate cycle enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 488-490.	2.5	2
93	Crystallization and preliminary X-ray crystallographic studies on maltosyltransferase from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1049-1050.	2.5	2
94	Crystallization and preliminary X-ray analysis of <i>Citrobacter amalonaticus</i> methylaspartate ammonia lyase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1922-1924.	2.5	2
95	Crystallization and preliminary X-ray crystallographic studies on the class II cholesterol oxidase from <i>Burkholderia cepacia</i> containing bound flavin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2182-2183.	2.5	2
96	Purification, crystallization and preliminary crystallographic analysis of <i>Arabidopsis thaliana</i> imidazole glycerol-phosphate dehydratase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 776-778.	0.7	2
97	Cloning, purification and preliminary crystallographic analysis of a conserved hypothetical protein, SA0961 (YlaN), from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 778-780.	0.7	2
98	Cloning, purification and crystallographic analysis of a hypothetical protein, BPSL1549, from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1623-1626.	0.7	2
99	Molecular basis of specificity and deamidation of eIF4A by <i>Burkholderia</i> Lethal Factor 1. <i>Communications Biology</i> , 2022, 5, 272.	4.4	2
100	The changed pattern of substrate specificity in the K89L mutant of glutamate dehydrogenase of <i>Clostridium symbiosum</i> . <i>Biochemical Society Transactions</i> , 1994, 22, 320S-320S.	3.4	1
101	Crystallization of the dl component of transhydrogenase, a proton-translocating membrane protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1170-1172.	2.5	1
102	Mirror-Image Packing Provides a Molecular Basis for the Nanomolar Equipotency of Enantiomers of an Experimental Herbicide. <i>Angewandte Chemie</i> , 2016, 128, 13683-13687.	2.0	1
103	TssA from <i>Aeromonas hydrophila</i> : expression, purification and crystallographic studies. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 578-582.	0.8	1
104	TssA from <i>Burkholderia cenocepacia</i> : expression, purification, crystallization and crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 536-542.	0.8	1
105	The A component (SmhA) of a tripartite pore-forming toxin from <i>Serratia marcescens</i> : expression, purification and crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 577-582.	0.8	1
106	Improving the engineered activity of mutants of clostridial glutamate dehydrogenase towards monocarboxylic substrates: Substitution of Ala 163 with glycine. <i>Biochemical Society Transactions</i> , 1996, 24, 126S-126S.	3.4	0
107	The mechanism of the oxidation of glycerol to dihydroxyacetone in <i>Bacillus stearothermophilus</i> . <i>Biochemical Society Transactions</i> , 2000, 28, A331-A331.	3.4	0
108	Crystallization and preliminary X-ray analysis of the <i>tyxM</i> gene product from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2138-2140.	2.5	0

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109	Cloning, purification and preliminary crystallographic analysis of a putative DNA-binding membrane protein, YmfM, from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 656-658.	0.7	0
110	Crystallization and preliminary X-ray analysis of the receiver domain of a putative response regulator, BPSLO128, from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 917-922.	0.7	0
111	Cloning, purification, crystallization and preliminary X-ray analysis of the <i>Burkholderia pseudomallei</i> L1 ribosomal protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 347-350.	0.7	0
112	Crystallization and preliminary crystallographic analysis of the putative sugar-binding protein Msmeg_0515 (AgaE) from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 189-193.	0.8	0