

Kevin P Battaile

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

102
papers

2,633
citations

31
h-index

47
g-index

106
ext. papers

3,193
ext. citations

6.2
avg, IF

4.76
L-index

#	Paper	IF	Citations
102	Improving the kinetic parameters of nicotine oxidizing enzymes by homologous structure comparison and rational design.. <i>Archives of Biochemistry and Biophysics</i> , 2022 , 109122	4.1	2
101	Structure of the Anthrax Protective Antigen D425A Dominant Negative Mutant Reveals a Stalled Intermediate State of Pore Maturation.. <i>Journal of Molecular Biology</i> , 2022 , 434, 167548	6.5	0
100	Small Molecule Inhibitors of the Bacterioferritin (BfrB)-Ferredoxin (Bfd) Complex Kill Biofilm-Embedded Cells. <i>ACS Infectious Diseases</i> , 2021 , 7, 123-140	5.5	6
99	Structure-activity relationship of ipglyceramide binding to phosphoglycerate mutases. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100628	5.4	0
98	Structure-Guided Design of Conformationally Constrained Cyclohexane Inhibitors of Severe Acute Respiratory Syndrome Coronavirus-2 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 10047-10058	8.3	8
97	Postinfection treatment with a protease inhibitor increases survival of mice with a fatal SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	18
96	The Structures of SctK and SctD from <i>Pseudomonas aeruginosa</i> Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform. <i>Journal of Molecular Biology</i> , 2020 , 432, 166693	6.5	5
95	The SARS-CoV-2 conserved macrodomain is a mono-ADP-ribosylhydrolase 2020 ,		9
94	3C-like protease inhibitors block coronavirus replication in vitro and improve survival in MERS-CoV-infected mice. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	113
93	Structure-Guided Optimization of Dipeptidyl Inhibitors of Norovirus 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 11945-11963	8.3	3
92	Allosteric regulation of lysosomal enzyme recognition by the cation-independent mannose 6-phosphate receptor. <i>Communications Biology</i> , 2020 , 3, 498	6.7	7
91	Structural and ligand binding analyses of the periplasmic sensor domain of RsbU in <i>Chlamydia trachomatis</i> support a role in TCA cycle regulation. <i>Molecular Microbiology</i> , 2020 , 113, 68-88	4.1	4
90	Small Molecule Inhibitors of the BfrB-Bfd Interaction Decrease <i>Pseudomonas aeruginosa</i> Fitness and Potentiate Fluoroquinolone Activity. <i>Journal of the American Chemical Society</i> , 2019 , 141, 8171-8184	16.4	15
89	Putative structural rearrangements associated with the interaction of macrocyclic inhibitors with norovirus 3CL protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 579-587	4.2	1
88	Crystal structure of human mitochondrial trifunctional protein, a fatty acid β oxidation metabolon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 6069-6074	11.5	29
87	Crystal structures of the naturally fused CS and cytochrome b reductase (bR) domains of Ncb5or reveal an expanded CS fold, extensive CS-bR interactions and productive binding of the NAD(P) nicotinamide ring. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 628-638	5.5	2
86	Using disruptive insertional mutagenesis to identify the in situ structure-function landscape of the <i>Shigella</i> translocator protein IpaB. <i>Protein Science</i> , 2018 , 27, 1392-1406	6.3	9

85	Structure-guided design of potent and permeable inhibitors of MERS coronavirus 3CL protease that utilize a piperidine moiety as a novel design element. <i>European Journal of Medicinal Chemistry</i> , 2018 , 150, 334-346	6.8	70
84	Crystal structure of Staphylococcus aureus Zn-glyoxalase I: new subfamily of glyoxalase I family. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 376-386	3.6	4
83	Structure-guided design, synthesis and evaluation of oxazolidinone-based inhibitors of norovirus 3CL protease. <i>European Journal of Medicinal Chemistry</i> , 2018 , 143, 881-890	6.8	3
82	Bfd, a New Class of [2Fe-2S] Protein That Functions in Bacterial Iron Homeostasis, Requires a Structural Anion Binding Site. <i>Biochemistry</i> , 2018 , 57, 5533-5543	3.2	3
81	Design, synthesis, and evaluation of a novel series of macrocyclic inhibitors of norovirus 3CL protease. <i>European Journal of Medicinal Chemistry</i> , 2017 , 127, 41-61	6.8	8
80	Structural characterization of the Man5 glycoform of human IgG3 Fc. <i>Molecular Immunology</i> , 2017 , 92, 28-37	4.3	14
79	Single-domain antibodies pinpoint potential targets within invasion plasmid antigen D of the needle tip complex for inhibition of type III secretion. <i>Journal of Biological Chemistry</i> , 2017 , 292, 16677-16687	5.4	10
78	Structure-based exploration and exploitation of the S subsite of norovirus 3CL protease in the design of potent and permeable inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2017 , 126, 502-516	6.8	11
77	Oxadiazole-Based Cell Permeable Macrocyclic Transition State Inhibitors of Norovirus 3CL Protease. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 1899-913	8.3	17
76	1.65 Å resolution structure of the AraC-family transcriptional activator ToxT from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 726-31	1.1	8
75	1.45 Å resolution structure of SRPN18 from the malaria vector <i>Anopheles gambiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 853-862	1.1	2
74	Crystal structure of histone-like protein from <i>Streptococcus mutans</i> refined to 1.9 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 257-62	1.1	4
73	Replacing Arginine 33 for Alanine in the Hemophore HasA from <i>Pseudomonas aeruginosa</i> Causes Closure of the H32 Loop in the Apo-Protein. <i>Biochemistry</i> , 2016 , 55, 2622-31	3.2	12
72	Structure-based design and synthesis of triazole-based macrocyclic inhibitors of norovirus protease: Structural, biochemical, spectroscopic, and antiviral studies. <i>European Journal of Medicinal Chemistry</i> , 2016 , 119, 300-18	6.8	20
71	Structural and inhibitory effects of hinge loop mutagenesis in serpin-2 from the malaria vector <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2015 , 290, 2946-56	5.4	7
70	Characterization of the Bacterioferritin/Bacterioferritin Associated Ferredoxin Protein-Protein Interaction in Solution and Determination of Binding Energy Hot Spots. <i>Biochemistry</i> , 2015 , 54, 6162-75	3.2	18
69	Critical Evaluation of the Changes in Glutamine Synthetase Activity in Models of Cerebral Stroke. <i>Neurochemical Research</i> , 2015 , 40, 2544-56	4.6	21
68	Hypothetical protein CT398 (CdsZ) interacts with (54) (RpoN)-holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2015 , 24, 1617-32	6.3	13

67	Structure-guided design and optimization of dipeptidyl inhibitors of norovirus 3CL protease. Structure-activity relationships and biochemical, X-ray crystallographic, cell-based, and in vivo studies. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 3144-55	8.3	40
66	Spectral X-Ray Diffraction using a 6 Megapixel Photon Counting Array Detector. <i>Proceedings of SPIE</i> , 2015 , 9401, 940109	1.7	
65	Chlamydia trachomatis protein CT009 is a structural and functional homolog to the key morphogenesis component RodZ and interacts with division septal plane localized MreB. <i>Molecular Microbiology</i> , 2015 , 95, 365-82	4.1	18
64	The structure of SAV1646 from Staphylococcus aureus belonging to a new \square ribosome-associatedU subfamily of bacterial proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 332-7		2
63	Concerted motions networking pores and distant ferroxidase centers enable bacterioferritin function and iron traffic. <i>Biochemistry</i> , 2015 , 54, 1611-27	3.2	13
62	Chlamydia trachomatis CT771 (nudH) is an asymmetric Ap4A hydrolase. <i>Biochemistry</i> , 2014 , 53, 214-24	3.2	1
61	(¹⁹ F) nuclear magnetic resonance and crystallographic studies of 5-fluorotryptophan-labeled anthrax protective antigen and effects of the receptor on stability. <i>Biochemistry</i> , 2014 , 53, 690-701	3.2	9
60	Replacing the axial ligand tyrosine 75 or its hydrogen bond partner histidine 83 minimally affects heme acquisition by the hemophore HasA from Pseudomonas aeruginosa. <i>Biochemistry</i> , 2014 , 53, 2112-25	3.2	21
59	Structural and biochemical characterization of Chlamydia trachomatis hypothetical protein CT263 supports that menaquinone synthesis occurs through the futasol pathway. <i>Journal of Biological Chemistry</i> , 2014 , 289, 32214-32229	5.4	12
58	Structural insights into Noonan/LEOPARD syndrome-related mutants of protein-tyrosine phosphatase SHP2 (PTPN11). <i>BMC Structural Biology</i> , 2014 , 14, 10	2.7	39
57	Insights into the binding of PARP inhibitors to the catalytic domain of human tankyrase-2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2740-53		18
56	1.15 Å resolution structure of the proteasome-assembly chaperone Nas2 PDZ domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 418-23	1.1	7
55	High-resolution crystal structures of two crystal forms of human cyclophilin D in complex with PEG 400 molecules. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 717-22	1.1	4
54	Linear fitting of multi-threshold counting data with a pixel-array detector for spectral X-ray imaging. <i>Journal of Synchrotron Radiation</i> , 2014 , 21, 1180-7	2.4	2
53	Glutamylamines and neurodegenerative diseases. <i>Amino Acids</i> , 2013 , 44, 129-42	3.5	15
52	The designability of protein switches by chemical rescue of structure: mechanisms of inactivation and reactivation. <i>Journal of the American Chemical Society</i> , 2013 , 135, 18840-9	16.4	21
51	A conserved spiral structure for highly diverged phage tail assembly chaperones. <i>Journal of Molecular Biology</i> , 2013 , 425, 2436-49	6.5	12
50	Reconfiguration of the proteasome during chaperone-mediated assembly. <i>Nature</i> , 2013 , 497, 512-6	50.4	58

49	The hemophore HasA from <i>Yersinia pestis</i> (HasAyp) coordinates hemin with a single residue, Tyr75, and with minimal conformational change. <i>Biochemistry</i> , 2013 , 52, 2705-7	3.2	37
48	Towards protein-crystal centering using second-harmonic generation (SHG) microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 843-51		25
47	Structure of the <i>Yersinia pestis</i> tip protein LcrV refined to 1.65 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 477-81		19
46	Structure of CT584 from <i>Chlamydia trachomatis</i> refined to 3.05 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 1196-201		5
45	Crystal structure of the CN-hydrolase SA0302 from the pathogenic bacterium <i>Staphylococcus aureus</i> belonging to the Nit and NitFhit Branch of the nitrilase superfamily. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013 , 31, 1057-65	3.6	2
44	Physicochemical characterization of a thermostable alcohol dehydrogenase from <i>Pyrobaculum aerophilum</i> . <i>PLoS ONE</i> , 2013 , 8, e63828	3.7	3
43	Structural comparison of cytochromes P450 2A6, 2A13, and 2E1 with pilocarpine. <i>FEBS Journal</i> , 2012 , 279, 1621-31	5.7	52
42	Broad-spectrum antivirals against 3C or 3C-like proteases of picornaviruses, noroviruses, and coronaviruses. <i>Journal of Virology</i> , 2012 , 86, 11754-62	6.6	199
41	The structure of the BfrB-Bfd complex reveals protein-protein interactions enabling iron release from bacterioferritin. <i>Journal of the American Chemical Society</i> , 2012 , 134, 13470-81	16.4	49
40	pH effects on binding between the anthrax protective antigen and the host cellular receptor CMG2. <i>Protein Science</i> , 2012 , 21, 1467-80	6.3	9
39	Structure/function relationships of adipose phospholipase A2 containing a cys-his-his catalytic triad. <i>Journal of Biological Chemistry</i> , 2012 , 287, 35260-35274	5.4	36
38	The Min oscillator uses MinD-dependent conformational changes in MinE to spatially regulate cytokinesis. <i>Cell</i> , 2011 , 146, 396-407	56.2	117
37	Two distinct ferritin-like molecules in <i>Pseudomonas aeruginosa</i> : the product of the bfrA gene is a bacterial ferritin (FtnA) and not a bacterioferritin (Bfr). <i>Biochemistry</i> , 2011 , 50, 5236-48	3.2	37
36	Titration-based screening for evaluation of natural product extracts: identification of an aspulvinone family of luciferase inhibitors. <i>Chemistry and Biology</i> , 2011 , 18, 1442-52		32
35	X-CHIP: an integrated platform for high-throughput protein crystallization and on-the-chip X-ray diffraction data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 533-9		39
34	Crystal structure of native <i>Anopheles gambiae</i> serpin-2, a negative regulator of melanization in mosquitoes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 1999-2003	4.2	10
33	The crystal structures of the <i>Salmonella</i> type III secretion system tip protein SipD in complex with deoxycholate and chenodeoxycholate. <i>Protein Science</i> , 2011 , 20, 75-86	6.3	54
32	Ab initio structural modeling of and experimental validation for <i>Chlamydia trachomatis</i> protein CT296 reveal structural similarity to Fe(II) 2-oxoglutarate-dependent enzymes. <i>Journal of Bacteriology</i> , 2011 , 193, 6517-28	3.5	15

31	The atypical response regulator protein ChxR has structural characteristics and dimer interface interactions that are unique within the OmpR/PhoB subfamily. <i>Journal of Biological Chemistry</i> , 2011 , 286, 32606-16	5.4	11
30	Human cytochrome P450 2E1 structures with fatty acid analogs reveal a previously unobserved binding mode. <i>Journal of Biological Chemistry</i> , 2010 , 285, 22282-90	5.4	71
29	Study of the individual cytochrome b5 and cytochrome b5 reductase domains of Ncb5or reveals a unique heme pocket and a possible role of the CS domain. <i>Journal of Biological Chemistry</i> , 2010 , 285, 30181-91	5.4	21
28	Molecular basis for the high-affinity binding and stabilization of firefly luciferase by PTC124. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 4878-83	11.5	140
27	Structural, NMR spectroscopic, and computational investigation of hemin loading in the hemophore HasAp from <i>Pseudomonas aeruginosa</i> . <i>Journal of the American Chemical Society</i> , 2010 , 132, 9857-72	16.4	58
26	Evidence that histidine protonation of receptor-bound anthrax protective antigen is a trigger for pore formation. <i>Biochemistry</i> , 2010 , 49, 6973-83	3.2	23
25	The crystal structure of bacteriophage HK97 gp6: defining a large family of head-tail connector proteins. <i>Journal of Molecular Biology</i> , 2010 , 395, 754-68	6.5	49
24	Structural studies of bacterioferritin B from <i>Pseudomonas aeruginosa</i> suggest a gating mechanism for iron uptake via the ferroxidase center. <i>Biochemistry</i> , 2010 , 49, 1160-75	3.2	49
23	Crystal structure of a truncated urease accessory protein UreF from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2839-48	4.2	34
22	Transglutaminase activation in neurodegenerative diseases. <i>Future Neurology</i> , 2009 , 4, 449-467	1.5	28
21	Focusing, collimation and flux throughput at the IMCA-CAT bending-magnet beamline at the Advanced Photon Source. <i>Journal of Synchrotron Radiation</i> , 2009 , 16, 647-57	2.4	1
20	Human mevalonate diphosphate decarboxylase: characterization, investigation of the mevalonate diphosphate binding site, and crystal structure. <i>Archives of Biochemistry and Biophysics</i> , 2008 , 480, 58-67 ^{4.1}	4.1	37
19	Structural basis of allele variation of human thiopurine-S-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 198-208	4.2	31
18	Structural comparison of oxidized and reduced FKBP13 from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 789-95	4.2	18
17	Structures of isobutyryl-CoA dehydrogenase and enzyme-product complex: comparison with isovaleryl- and short-chain acyl-CoA dehydrogenases. <i>Journal of Biological Chemistry</i> , 2004 , 279, 16526-34 ^{5.4}	5.4	50
16	Lowered DHCR7 activity measured by ergosterol conversion in multiple cell types in Smith-Lemli-Opitz syndrome. <i>Molecular Genetics and Metabolism</i> , 2004 , 83, 175-83	3.7	6
15	Fanconi anemia group A and C double-mutant mice: functional evidence for a multi-protein Fanconi anemia complex. <i>Experimental Hematology</i> , 2002 , 30, 679-88	3.1	53
14	Burning fat: the structural basis of fatty acid beta-oxidation. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 721-8	8.1	61

13	Crystal structure of rat short chain acyl-CoA dehydrogenase complexed with acetoacetyl-CoA: comparison with other acyl-CoA dehydrogenases. <i>Journal of Biological Chemistry</i> , 2002 , 277, 12200-7	5.4	61
12	Carrier frequency of the common mutation IVS8-1G>C in DHCR7 and estimate of the expected incidence of Smith-Lemli-Opitz syndrome. <i>Molecular Genetics and Metabolism</i> , 2001 , 72, 67-71	3.7	72
11	Mutation analysis and description of sixteen RSH/Smith-Lemli-Opitz syndrome patients: Polymerase chain reactionBased assays to simplify genotyping. <i>American Journal of Medical Genetics Part A</i> , 2000 , 94, 214-227		56
10	Smith-Lemli-Opitz syndrome: the first malformation syndrome associated with defective cholesterol synthesis. <i>Molecular Genetics and Metabolism</i> , 2000 , 71, 154-62	3.7	42
9	Mutation analysis and description of sixteen RSH/Smith-Lemli-Opitz syndrome patients: Polymerase chain reactionBased assays to simplify genotyping 2000 , 94, 214		1
8	A simple PCR-based assay allows detection of a common mutation, IVS8-1G-->C, in DHCR7 in Smith-Lemli-Opitz syndrome. <i>Genetic Testing and Molecular Biomarkers</i> , 1999 , 3, 361-3		10
7	In Vivo Selection of Wild-Type Hematopoietic Stem Cells in a Murine Model of Fanconi Anemia. <i>Blood</i> , 1999 , 94, 2151-2158	2.2	1
6	Human long chain, very long chain and medium chain acyl-CoA dehydrogenases are specific for the S-enantiomer of 2- methylpentadecanoyl-CoA. <i>Lipids and Lipid Metabolism</i> , 1998 , 1390, 333-8		22
5	Characterization of molecular defects in isovaleryl-CoA dehydrogenase in patients with isovaleric acidemia. <i>Biochemistry</i> , 1998 , 37, 10325-35	3.2	53
4	Redesigning the active-site of an acyl-CoA dehydrogenase: new evidence supporting a one-base mechanism. <i>Bioorganic and Medicinal Chemistry</i> , 1997 , 5, 2157-64	3.4	7
3	Functional role of the active site glutamate-368 in rat short chain acyl-CoA dehydrogenase. <i>Biochemistry</i> , 1996 , 35, 15356-63	3.2	23
2	Cloning of a cDNA for short/branched chain acyl-Coenzyme A dehydrogenase from rat and characterization of its tissue expression and substrate specificity. <i>Archives of Biochemistry and Biophysics</i> , 1996 , 331, 127-33	4.1	29
1	Post-infection treatment with a protease inhibitor increases survival of mice with a fatal SARS-CoV-2 infection		3