

Kyriacos Petratos

List of Publications by Year in descending order

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56
papers

2,561
citations

361045

20
h-index

197535

49
g-index

57
all docs

57
docs citations

57
times ranked

2096
citing authors

#	ARTICLE	IF	CITATIONS
1	The first non-helical Aib-containing hexapeptide: The crystal structure of Z-Gly-Aib-Gly-Aib-Gly-Aib-OtBu. <i>Journal of Peptide Science</i> , 2021, 27, e3307.	0.8	2
2	Structure and Dynamics of a Thermostable Alcohol Dehydrogenase from the Antarctic Psychrophile <i>Moraxella</i> sp. TAE123. <i>ACS Omega</i> , 2020, 5, 14523-14534.	1.6	12
3	Removing the C-terminal protecting group enlarges the crystal size: Z-(Gly-Aib) ₂ -OH·H ₂ O. <i>Acta Crystallographica Section C, Structural Chemistry</i> , 2020, 76, 1057-1061.	0.2	2
4	Polysaccharide deacetylases serve as new targets for the design of inhibitors against <i>Bacillus anthracis</i> and <i>Bacillus cereus</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 3845-3851.	1.4	5
5	The crystal structure of the lipoaminopeptaibol helioferin, an antibiotic peptide from <i>Mycogone rosea</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 315-320.	1.1	4
6	Crystal structures of Z-(Gly-Aib) ₂ -O·0.5Ca ²⁺ ·H ₂ O and Z-(Gly-Aib)-OH. <i>Acta Crystallographica Section E: Crystallographic Communications</i> , 2018, 74, 1173-1177.	0.2	0
7	A natural, single-residue substitution yields a less active peptaibiotic: the structure of bergofungin A at atomic resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 95-100.	0.4	7
8	Diphenylalanine in tetrahydrofuran: a highly potent candidate for the development of novel nanomaterials. <i>Acta Crystallographica Section C, Structural Chemistry</i> , 2017, 73, 447-450.	0.2	2
9	The crystal structure of Z-(Aib) ₁₀ -OH at 0.65 Å resolution: three complete turns of 3 ₁₀ -helix. <i>Journal of Peptide Science</i> , 2016, 22, 76-81.	0.8	13
10	HU histone-like DNA-binding protein from <i>Thermus thermophilus</i> : structural and evolutionary analyses. <i>Extremophiles</i> , 2016, 20, 695-709.	0.9	21
11	The crystal structure of Z-Gly-Aib-Gly-Aib-OtBu. <i>Journal of Peptide Science</i> , 2015, 21, 476-479.	0.8	7
12	Biophysical and enzymatic properties of aminoglycoside adenylyltransferase AadA6 from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry and Biophysics Reports</i> , 2015, 4, 152-157.	0.7	8
13	The first N-terminal unprotected (Gly-Aib) _n peptide: H-Gly-Aib-Gly-Aib-OtBu. <i>Acta Crystallographica Section C, Structural Chemistry</i> , 2015, 71, 1114-1117.	0.2	4
14	Zinc-substituted pseudoazurin solved by S/Zn-SAD phasing. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 19-23.	0.4	3
15	The peptide Z-Aib-Aib-Aib-L-Ala-OtBu. <i>Acta Crystallographica Section C, Structural Chemistry</i> , 2014, 70, 405-407.	0.2	4
16	The achiral tetrapeptide Z-Aib-Aib-Aib-Gly-OtBu. <i>Acta Crystallographica Section C, Structural Chemistry</i> , 2014, 70, 1046-1049.	0.2	1
17	The crystal structure of samarosporin I at atomic resolution. <i>Journal of Peptide Science</i> , 2012, 18, 678-684.	0.8	12
18	Four complete turns of a curved 310-helix at atomic resolution; the crystal structure of the peptaibol trichovirin I-4A in a polar environment suggests a transition to 1 ₂ -helix for membrane function. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 109-116.	2.5	21

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19	The crystal structure of cobalt-substituted pseudoazurin from <i>Alcaligenes faecalis</i> . <i>Biopolymers</i> , 2011, 95, 202-207.	1.2	5
20	Molecular Modeling of Mechanosensory Ion Channel Structural and Functional Features. <i>PLoS ONE</i> , 2010, 5, e12814.	1.1	9
21	Structure of Dimeric SecA, the <i>Escherichia coli</i> Preprotein Translocase Motor. <i>Journal of Molecular Biology</i> , 2007, 366, 1545-1557.	2.0	127
22	Novel Mutations in Smad Proteins That Inhibit Signaling by the Transforming Growth Factor \hat{I}^2 in Mammalian Cells. <i>Biochemistry</i> , 2007, 46, 13775-13786.	1.2	7
23	Equilibrium heat-induced denaturation of chitinase 40 from <i>Streptomyces thermoviolaceus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 513-523.	1.5	6
24	Isolation, characterization, sequencing and crystal structure of charybдин, a type 1 ribosome-inactivating protein from <i>Charybdis maritima</i> agg.. <i>FEBS Journal</i> , 2006, 273, 2684-2692.	2.2	16
25	Crystallization and preliminary X-ray diffraction studies of an alcohol dehydrogenase from the Antarctic psychrophile <i>Moraxella</i> sp. TAE123. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 246-248.	0.7	4
26	The tetrapeptide Z-Leu-Aib-Pro-Val-OBg monohydrate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2003, 59, o413-o415.	0.4	2
27	De novopurification scheme and crystallization conditions yield high-resolution structures of chitinase A and its complex with the inhibitor allosamidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 400-403.	2.5	39
28	Three complete turns of a 310-helix at atomic resolution: the crystal structure of Z-(Aib) ₁₁ -Ot Bu. <i>Journal of Peptide Science</i> , 2003, 9, 753-762.	0.8	71
29	Application of the effects of ionic strength reducing agents in the purification and crystallization of chitinase A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1593-1596.	2.5	0
30	High Resolution Structural Analyses of Mutant Chitinase A Complexes with Substrates Provide New Insight into the Mechanism of Catalysis. <i>Biochemistry</i> , 2001, 40, 11338-11343.	1.2	156
31	Crystallization of the <i>E. coli</i> polyamine-induced protein: a novel procedure based on the concept of ionic strength reducers. <i>Journal of Crystal Growth</i> , 2000, 210, 761-766.	0.7	3
32	Structures of chitinase mutants complexed with the substrate di-N-acetyl-d-glucosamine: the catalytic role of the conserved acidic pair, aspartate 539 and glutamate 540. <i>Journal of Molecular Biology</i> , 2000, 300, 611-617.	2.0	80
33	Structural studies of chitinase A from <i>S. marcescens</i> complexed with substrates and the inhibitor allosamidin. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2000, 56, s259-s259.	0.3	0
34	Purification, crystallization and preliminary X-ray analysis of the <i>M. BseCI</i> DNA methyltransferase from <i>Bacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 477-479.	2.5	1
35	Novel Structural Features of the Human Histocompatibility Molecules HLA-DQ as Revealed by Modeling Based on the Published Structure of the Related Molecule HLA-DR. <i>Journal of Structural Biology</i> , 1996, 117, 145-163.	1.3	29
36	The crystal structure of apo-pseudoazurin from <i>Alcaligenes faecalis</i> S-6. <i>FEBS Letters</i> , 1995, 368, 432-434.	1.3	19

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37	Refined crystal structure of liver alcohol dehydrogenaseâ€™NADH complex at 1.8 Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 793-807.	2.5	54
38	The crystal structures of reduced pseudoazurin from Alcaligenes faecalis S-6 at two pH values. FEBS Letters, 1994, 347, 203-206.	1.3	71
39	The crystal structure of EcoRV endonuclease and of its complexes with cognate and non-cognate DNA fragments.. EMBO Journal, 1993, 12, 1781-1795.	3.5	422
40	THE CRYSTAL STRUCTURE OF ECORV ENDONUCLEASE AND OF ITS COMPLEXES WITH COGNATE AND NON-COGNATE DNA SEGMENTS. , 1993, 12, 1781-95.		155
41	High-resolution x-ray structures of pig metmyoglobin and two CD3 mutants: Mb(Lys45 .fwdarw. Arg) and Mb(Lys45 .fwdarw. Ser). Biochemistry, 1992, 31, 8732-8739.	1.2	31
42	Structure of oxidized bacteriophage T4 glutaredoxin (thioredoxin). Journal of Molecular Biology, 1992, 228, 596-618.	2.0	68
43	Structure of 2-amino-6-dimethylamino-4-(tricyclo[3.3.1.1 ^{3,7}]dec-1-yl)-1,3,5-triazine. Acta Crystallographica Section C: Crystal Structure Communications, 1992, 48, 347-350.	0.4	1
44	Observation of the light-triggered binding of pyrone to chymotrypsin by Laue x-ray crystallography.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 5503-5507.	3.3	43
45	Time-resolved X-ray crystallographic study of the conformational change in Ha-Ras p21 protein on GTP hydrolysis. Nature, 1990, 345, 309-315.	13.7	520
46	Structure of quinoprotein methylamine dehydrogenase at 2.25 Å resolution.. EMBO Journal, 1989, 8, 2171-2178.	3.5	125
47	A 2.0-Å... structure of the blue copper protein (cupredoxin) from Alcaligenes faecalis S-6. Journal of Biological Chemistry, 1989, 264, 87-99.	1.6	94
48	Structure of quinoprotein methylamine dehydrogenase at 2.25 Å resolution. EMBO Journal, 1989, 8, 2171-8.	3.5	24
49	A 2.0-Å structure of the blue copper protein (cupredoxin) from Alcaligenes faecalis S-6. Journal of Biological Chemistry, 1989, 264, 87-99.	1.6	64
50	Refinement of the structure of pseudoazurin from Alcaligenes faecalis S-6 at 1.55 Å... resolution. Acta Crystallographica Section B: Structural Science, 1988, 44, 628-636.	1.8	93
51	Preliminary X-ray crystallographic study of amicyanin from Thiobacillus versutus. Journal of Molecular Biology, 1988, 199, 545-546.	2.0	10
52	Protein Crystallography Using Synchrotron Radiation at the EMBL Outstation Hamburg. , 1988, , 568-568.		0
53	Refinement of the structure of pseudoazurin from Alcaligenes faecalis S-6 at 1.55 Å resolution. Acta Crystallographica Section B: Structural Science, 1988, 44 (Pt 6), 628-36.	1.8	11
54	The crystal structure of pseudoazurin fromAlcaligenes faecalisS-6 determined at 2.9 Å... resolution. FEBS Letters, 1987, 218, 209-214.	1.3	62

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55	Preliminary characterization of crystals of nitrite reductase isolated from <i>Alcaligenes faecalis</i> strain S-6. <i>Journal of Molecular Biology</i> , 1986, 190, 135.	2.0	7
56	Preliminary characterization of crystals of the protein insecticyanin from the tobacco hornworm <i>Manduca sexta</i> L.. <i>Journal of Molecular Biology</i> , 1986, 189, 727.	2.0	4