## Pravindra Kumar

List of Publications by Year in descending order

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126 papers 2,402 citations

28 h-index 288905 40 g-index

131 all docs

131 docs citations

131 times ranked

2288 citing authors

#	Article	IF	CITATIONS
1	Structure of a Serine Protease Proteinase K from Tritirachium album limber at 0.98 Å Resolution. Biochemistry, 2001, 40, 3080-3088.	1.2	128
2	Biodegradation of phthalic acid esters (PAEs) and in silico structural characterization of mono-2-ethylhexyl phthalate (MEHP) hydrolase on the basis of close structural homolog. Journal of Hazardous Materials, 2017, 338, 11-22.	6.5	96
3	Camel Lactoferrin, a Transferrin-cum-Lactoferrin: Crystal Structure of Camel Apolactoferrin at 2.6Ã Resolution and Structural Basis of its Dual Role. Journal of Molecular Biology, 2001, 309, 751-761.	2.0	80
4	Structure and function of proteins involved in milk allergies. Biomedical Applications, 2001, 756, 183-187.	1.7	77
5	Crystal Structure of a Novel Regulatory 40-kDa Mammary Gland Protein (MGP-40) Secreted during Involution. Journal of Biological Chemistry, 2003, 278, 14451-14460.	1.6	61
6	Characterization of dye-decolorizing peroxidase from Bacillus subtilis. Archives of Biochemistry and Biophysics, 2020, 693, 108590.	1.4	61
7	Purification and characterization of a trypsin inhibitor from Putranjiva roxburghii seeds. Phytochemistry, 2008, 69, 2120-2126.	1.4	59
8	Inhibition of chikungunya virus by picolinate that targets viral capsid protein. Virology, 2016, 498, 265-276.	1.1	57
9	Characterization of Biphenyl Dioxygenase of Pandoraea pnomenusa B-356 As a Potent Polychlorinated Biphenyl-Degrading Enzyme. Journal of Bacteriology, 2007, 189, 5705-5715.	1.0	53
10	Repurposing an Ancient Protein Core Structure: Structural Studies on FmtA, a Novel Esterase of Staphylococcus aureus. Journal of Molecular Biology, 2019, 431, 3107-3123.	2.0	51
11	Emerging SARS-CoV-2 Variants: Genetic Variability and Clinical Implications. Current Microbiology, 2022, 79, 20.	1.0	48
12	Evaluation of antiviral activity of piperazine against Chikungunya virus targeting hydrophobic pocket of alphavirus capsid protein. Antiviral Research, 2017, 146, 102-111.	1.9	47
13	Structure-Based Identification of Potential Drugs Against FmtA of Staphylococcus aureus: Virtual Screening, Molecular Dynamics, MM-GBSA, and QM/MM. Protein Journal, 2021, 40, 148-165.	0.7	47
14	Structural Insight into the Expanded PCB-Degrading Abilities of a Biphenyl Dioxygenase Obtained by Directed Evolution. Journal of Molecular Biology, 2011, 405, 531-547.	2.0	45
15	Structure-function insights into chikungunya virus capsid protein: Small molecules targeting capsid hydrophobic pocket. Virology, 2018, 515, 223-234.	1.1	45
16	Antiviral strategies targeting host factors and mechanisms obliging +ssRNA viral pathogens. Bioorganic and Medicinal Chemistry, 2021, 46, 116356.	1.4	45
17	Kinetic characterization of trans-proteolytic activity of Chikungunya virus capsid protease and development of a FRET-based HTS assay. Scientific Reports, 2015, 5, 14753.	1.6	44
18	Crystal structure of chikungunya virus nsP2 cysteine protease reveals a putative flexible loop blocking its active site. International Journal of Biological Macromolecules, 2018, 116, 451-462.	3.6	44

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19	Structural and functional evolution of chitinaseâ€like proteins from plants. Proteomics, 2015, 15, 1693-1705.	1.3	39
20	i In-silico i approach to identify novel potent inhibitors against GraR of i S aureus i. Frontiers in Bioscience - Landmark, 2020, 25, 1337-1360.	3.0	39
21	Structure based mimicking of Phthalic acid esters (PAEs) and inhibition of hACMSD, an important enzyme of the tryptophan kynurenine metabolism pathway. International Journal of Biological Macromolecules, 2018, 108, 214-224.	3.6	38
22	The Tautomeric Half-reaction of BphD, a C-C Bond Hydrolase. Journal of Biological Chemistry, 2007, 282, 19894-19904.	1.6	34
23	Retuning Rieske-type Oxygenases to Expand Substrate Range. Journal of Biological Chemistry, 2011, 286, 27612-27621.	1.6	32
24	Structural Characterization of Pandoraea pnomenusa B-356 Biphenyl Dioxygenase Reveals Features of Potent Polychlorinated Biphenyl-Degrading Enzymes. PLoS ONE, 2013, 8, e52550.	1.1	32
25	Structural characterization and in-silico analysis of Momordica charantia 7S globulin for stability and ACE inhibition. Scientific Reports, 2020, 10, 1160.	1.6	32
26	Computational guided identification of novel potent inhibitors of N-terminal domain of nucleocapsid protein of severe acute respiratory syndrome coronavirus 2. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4084-4099.	2.0	31
27	Biochemical Studies and Ligand-bound Structures of Biphenyl Dehydrogenase from Pandoraea pnomenusa Strain B-356 Reveal a Basis for Broad Specificity of the Enzyme. Journal of Biological Chemistry, 2011, 286, 37011-37022.	1.6	29
28	Structural basis for dual inhibitory role of tamarind <scp>K</scp> unitz inhibitor ( <scp>TKI</scp> ) against factor <scp>X</scp> a and trypsin. FEBS Journal, 2012, 279, 4547-4564.	2.2	29
29	Glycan-dependent chikungunya viral infection divulged by antiviral activity of NAG specific chi-like lectin. Virology, 2019, 526, 91-98.	1.1	29
30	Molecular docking and dynamic approach to virtual screen inhibitors against Esbp of Candidatus Liberibacter asiaticus. Journal of Molecular Graphics and Modelling, 2019, 92, 329-340.	1.3	28
31	Structure of dye-decolorizing peroxidase from Bacillus subtilis in complex with veratryl alcohol. International Journal of Biological Macromolecules, 2021, 193, 601-608.	3.6	27
32	Crystal Structure of Aura Virus Capsid Protease and Its Complex with Dioxane: New Insights into Capsid-Glycoprotein Molecular Contacts. PLoS ONE, 2012, 7, e51288.	1.1	26
33	<i>trans</i> -Protease Activity and Structural Insights into the Active Form of the Alphavirus Capsid Protease. Journal of Virology, 2014, 88, 12242-12253.	1.5	24
34	Molecular docking and simulation analysis for elucidation of toxic effects of dicyclohexyl phthalate (DCHP) in glucocorticoid receptor-mediated adipogenesis. Molecular Simulation, 2020, 46, 9-21.	0.9	24
35	Characterization of phthalate reductase from Ralstonia eutropha CH34 and in silico study of phthalate dioxygenase and phthalate reductase interaction. Journal of Molecular Graphics and Modelling, 2019, 90, 161-170.	1.3	23
36	Mutation studies and structure-based identification of potential inhibitor molecules against periplasmic amino acid binding protein of Candidatus Liberibacter asiaticus (CLasTcyA). International Journal of Biological Macromolecules, 2020, 147, 1228-1238.	3.6	23

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37	Quantum Mechanics/Molecular Mechanics Studies on the Catalytic Mechanism of a Novel Esterase (FmtA) of <i>Staphylococcus aureus</i> Journal of Chemical Information and Modeling, 2022, 62, 2409-2420.	2.5	23
38	In-silico functional and structural annotation of hypothetical protein from Klebsiella pneumonia: A potential drug target. Journal of Molecular Graphics and Modelling, 2022, 116, 108262.	1.3	23
39	Cloning, sequence analysis and crystal structure determination of a miraculin-like protein from Murraya koenigii. Archives of Biochemistry and Biophysics, 2010, 494, 15-22.	1.4	22
40	Multifunctional inhibitors of SARS-CoV-2 by MM/PBSA, essential dynamics, and molecular dynamic investigations. Journal of Molecular Graphics and Modelling, 2021, 107, 107969.	1.3	21
41	Protein Intermediate Trapped by the Simultaneous Crystallization Process. Journal of Biological Chemistry, 2001, 276, 36817-36823.	1.6	20
42	Structure and Function of Enzymes of Shikimate Pathway. Current Bioinformatics, 2012, 7, 374-391.	0.7	19
43	Structural insights into the metabolism of 2-chlorodibenzofuran by an evolved biphenyl dioxygenase. Biochemical and Biophysical Research Communications, 2012, 421, 757-762.	1.0	19
44	Structure-Function Studies of DNA Binding Domain of Response Regulator KdpE Reveals Equal Affinity Interactions at DNA Half-Sites. PLoS ONE, 2012, 7, e30102.	1.1	19
45	X-Ray crystallographic structural characteristics of Arabidopsis hemoglobin I and their functional implications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1944-1956.	1.1	19
46	Structural Investigation of a Novel N-Acetyl Glucosamine Binding Chi-Lectin Which Reveals Evolutionary Relationship with Class III Chitinases. PLoS ONE, 2013, 8, e63779.	1.1	19
47	Structural Basis of the Enhanced Pollutant-Degrading Capabilities of an Engineered Biphenyl Dioxygenase. Journal of Bacteriology, 2016, 198, 1499-1512.	1.0	19
48	Antagonistic interaction between TTA-A2 and paclitaxel for anti-cancer effects by complex formation with T-type calcium channel. Journal of Biomolecular Structure and Dynamics, 2022, 40, 2395-2406.	2.0	19
49	Crystal structure of a periplasmic solute binding protein in metal-free, intermediate and metal-bound states from Candidatus Liberibacter asiaticus. Journal of Structural Biology, 2015, 189, 184-194.	1.3	18
50	A molecular docking and dynamic approach to screen inhibitors against ZnuA1 of <i>Candidatus</i> Liberibacter asiaticus. Molecular Simulation, 2021, 47, 510-525.	0.9	18
51	Active-Site Plasticity Is Essential to Carbapenem Hydrolysis by OXA-58 Class D $\hat{l}^2$ -Lactamase of Acinetobacter baumannii. Antimicrobial Agents and Chemotherapy, 2016, 60, 75-86.	1.4	17
52	Molecular insights into substrate recognition and catalysis by phthalate dioxygenase from Comamonas testosteroni. Journal of Biological Chemistry, 2021, 297, 101416.	1.6	17
53	Structural analysis of chorismate synthase from Plasmodium falciparum: A novel target for antimalaria drug discovery. International Journal of Biological Macromolecules, 2011, 49, 767-777.	3.6	16
54	Conformer and pharmacophore based identification of peptidomimetic inhibitors of chikungunya virus nsP2 protease. Journal of Biomolecular Structure and Dynamics, 2017, 35, 3522-3539.	2.0	15

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55	Structural Insight into DFMO Resistant Ornithine Decarboxylase from Entamoeba histolytica: An Inkling to Adaptive Evolution. PLoS ONE, 2013, 8, e53397.	1.1	15
56	Structural, Functional and Evolutionary Aspects of Seed Globulins. Protein and Peptide Letters, 2017, 24, 267-277.	0.4	15
57	Design of peptides with $\hat{l}\pm,\hat{l}^2$ -dehydro-residues: synthesis, crystal structure and molecular conformation of a tetrapeptide Z- $\hat{l}$ "Val-Val- $\hat{l}$ "Phe-lle-Ome. Journal of Molecular Structure, 2003, 654, 119-124.	1.8	13
58	Enhanced performance of FSO link using OFDM and comparison with traditional TDM-FSO link. , 2015, , .		13
59	Characterization of recombinant pumpkin 2S albumin and mutation studies to unravel potential DNA/RNA binding site. Biochemical and Biophysical Research Communications, 2021, 580, 28-34.	1.0	13
60	Isolation, purification, crystallization and preliminary crystallographic studies of chitinase from tamarind ( <i>Tamarindus indica</i> ) seeds. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 343-345.	0.7	12
61	Structure of Chorismate Mutase-like Domain of DAHPS from Bacillus subtilis Complexed with Novel Inhibitor Reveals Conformational Plasticity of Active Site. Scientific Reports, 2017, 7, 6364.	1.6	12
62	Structural and Biochemical Analyses Reveal that Chlorogenic Acid Inhibits the Shikimate Pathway. Journal of Bacteriology, 2020, 202, .	1.0	12
63	Purification and Characterization of 2S Albumin from Seeds of Wrightia tinctoria Exhibiting Antibacterial and DNase Activity. Protein and Peptide Letters, 2017, 24, 368-378.	0.4	12
64	Characterization of the heavy metal binding properties of periplasmic metal uptake protein CLas-ZnuA2. Metallomics, 2020, 12, 280-289.	1.0	11
65	Purification, bio-chemical characterization, homology modeling and active site binding mode interactions of thermo-alkali-tolerant $\hat{l}^2$ -1,4 endoxylanase from Coprinus cinereus LK-D-NCIM-1369. Biocatalysis and Agricultural Biotechnology, 2013, 2, 267-277.	1.5	10
66	Acyl chain preference and inhibitor identification of Moraxella catarrhalis LpxA: Insight through crystal structure and computational studies. International Journal of Biological Macromolecules, 2017, 96, 759-765.	3.6	10
67	Biophysical and in silico interaction studies of aporphine alkaloids with Malonyl-CoA: ACP transacylase (FabD) from drug resistant Moraxella catarrhalis. Biochimie, 2018, 149, 18-33.	1.3	10
68	In-silico screening and identification of potential inhibitors against 2Cys peroxiredoxin of <i>Candidatus</i> Liberibacter asiaticus. Journal of Biomolecular Structure and Dynamics, 2022, 40, 8725-8739.	2.0	10
69	Design of peptides with $\hat{l}\pm,\hat{l}^2$ -dehydro residues: a dipeptide with a branched $\hat{l}^2$ -carbon dehydro residue at the (i+1) position, methylN-(benzyloxycarbonyl)- $\hat{l}\pm,\hat{l}^2$ -didehydrovalyl-L-tryptophanate. Acta Crystallographica Section C: Crystal Structure Communications, 2001, 57, 1220-1221.	0.4	9
70	Crystal structure of equine apolactoferrin at 303â€K providing further evidence of closed conformations of N and C lobes. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 225-232.	2.5	9
71	Anaerobic crystallization and initial X-ray diffraction data of biphenyl 2,3-dioxygenase from <i>Burkholderia xenovorans </i>  i>LB400: addition of agarose improved the quality of the crystals. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 59-63.	0.7	9
72	Performance analysis of next generation OFDM based optical access networks using multi-level modulation under various system impairments. , $2013, \dots$		9

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73	Performance improvement of OFDM-FSO multi-user communication system with combined transmit frequency diversity and receive space diversity. Optics Communications, 2016, 366, 410-418.	1.0	9
74	Biochemical and biophysical characterization of 1,4-naphthoquinone as a dual inhibitor of two key enzymes of type II fatty acid biosynthesis from Moraxella catarrhalis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1131-1142.	1.1	9
75	Purification, crystallization and preliminary crystallographic studies of a Kunitz-type proteinase inhibitor from tamarind ( <i>Tamarindus indica</i> ) seeds. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 736-738.	0.7	8
76	Biochemical, Mutational and In Silico Structural Evidence for a Functional Dimeric Form of the Ornithine Decarboxylase from Entamoeba histolytica. PLoS Neglected Tropical Diseases, 2012, 6, e1559.	1.3	8
77	Crystal structure of pentapeptide-independent chemotaxis receptor methyltransferase (CheR) reveals idiosyncratic structural determinants for receptor recognition. Journal of Structural Biology, 2016, 196, 364-374.	1.3	8
78	Structural and Functional Significance of the N- and C-Terminal Appendages in <i>Arabidopsis</i> Truncated Hemoglobin. Biochemistry, 2016, 55, 1724-1740.	1.2	8
79	Characterization of isoflavonoids as inhibitors of $\hat{l}^2$ -hydroxyacyl-acyl carrier protein dehydratase (FabZ) from Moraxella catarrhalis : Kinetics, spectroscopic, thermodynamics and in silico studies. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 726-744.	1.1	8
80	Crystallization and structure determination of goat lactoferrin at 4.0 A resolution: a new form of packing in lactoferrins with a high solvent content in crystals. Indian Journal of Biochemistry and Biophysics, 2002, 39, 16-21.	0.2	8
81	Crystallization and preliminary X-ray diffraction studies of Murraya koenigiitrypsin inhibitor. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 318-319.	0.7	7
82	A novel function for globulin in sequestering plant hormone: Crystal structure of Wrightia tinctoria 11S globulin in complex with auxin. Scientific Reports, 2017, 7, 4705.	1.6	7
83	Crystal structures of a putative periplasmic cystineâ€binding protein from ⟨i⟩Candidatus⟨/i⟩ Liberibacter asiaticus: insights into an adapted mechanism of ligand binding. FEBS Journal, 2019, 286, 3450-3472.	2.2	7
84	Structural insights into dihydroxylation of terephthalate, a product of polyethylene terephthalate degradation. Journal of Bacteriology, 2022, , JB0054321.	1.0	7
85	Crystallization, high-resolution data collection and preliminary crystallographic analysis of Aura virus capsid protease and its complex with dioxane. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1394-1398.	0.7	6
86	An insilico approach to structural elucidation of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase from Arabidopsis thaliana: Hints for herbicide design. Phytochemistry, 2012, 73, 7-14.	1.4	6
87	In vitro metal catalyzed oxidative stress in DAH7PS: Methionine modification leads to structure destabilization and induce amorphous aggregation. International Journal of Biological Macromolecules, 2018, 106, 1089-1106.	3.6	6
88	Performance of OFDM-FSO link with analog network coding. Photonic Network Communications, 2018, 35, 210-224.	1.4	6
89	The analysis of subtle internal communications through mutation studies in periplasmic metal uptake protein CLas-ZnuA2. Journal of Structural Biology, 2018, 204, 228-239.	1.3	6
90	Biophysical and In-Silico Studies of Phytochemicals Targeting Chorismate Synthase from Drug-Resistant Moraxella Catarrhalis. Protein Journal, 2020, 39, 449-460.	0.7	6

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91	Chikungunya virus titration, detection and diagnosis using N-Acetylglucosamine (GlcNAc) specific lectin based virus capture assay. Virus Research, 2021, 302, 198493.	1.1	6
92	Design, Synthesis and Structural Aspects of Acyclic N3E2(E=Se or Te) Type Donors and its Complexes with Group 12 Metals. Phosphorus, Sulfur and Silicon and the Related Elements, 2001, 172, 223-230.	0.8	5
93	Design of peptides with $\hat{l}\pm,\hat{l}^2$ -dehydro-residues: syntheses, crystal structures and molecular conformations of two $\hat{l}$ Phe-Trp containing peptides. Journal of Molecular Structure, 2003, 654, 103-110.	1.8	5
94	Crystallization and preliminary X-ray diffraction analysis of the complex of Kunitz-type tamarind trypsin inhibitor and porcine pancreatic trypsin. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1179-1181.	0.7	5
95	Performance analysis of next generation 3-D OFDM based optical access networks under various system impairments., 2013,,.		5
96	MD simulation and MM/PBSA identifies phytochemicals as bifunctional inhibitors of SARS-CoV-2. Journal of Biomolecular Structure and Dynamics, 2022, 40, 12048-12061.	2.0	5
97	<i>In silico</i> identification of potential phytochemical inhibitors targeting farnesyl diphosphate synthase of cotton bollworm ( <i>Helicoverpa armigera</i> ). Journal of Biomolecular Structure and Dynamics, 2023, 41, 1978-1987.	2.0	5
98	Purification, crystallization and preliminary X-ray diffraction studies of disintegrin (schistatin) from saw-scaled viper (Echis carinatus). Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1669-1670.	2.5	4
99	Synthesis and structural studies of some copper-benzoate complexes. Transition Metal Chemistry, 2013, 38, 573-585.	0.7	4
100	Receiver sensitivity improvement of OFDM-FSO link using SRM device. , 2015, , .		4
101	Optical power budget enhancement in next-generation DDO-OFDM-based optical access networks using square root module. Photonic Network Communications, 2016, 31, 48-55.	1.4	4
102	Biochemical characterization and structure-based (i) in silico (i) screening of potent inhibitor molecules against the 1 cys peroxiredoxin of bacterioferritin comigratory protein family from (i) Candidatus Liberibacter asiaticus (i). Journal of Biomolecular Structure and Dynamics, 2023, 41, 5776-5788.	2.0	4
103	Expression, purification, crystallization and preliminary crystallographic studies ofcis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase fromPandoraea pnomenusaB-356. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1517-1520.	0.7	3
104	Ligand-bound structures of 3-deoxy- <scp>D</scp> - <i>manno</i> -octulosonate 8-phosphate phosphatase from <i>Moraxella catarrhalis</i> reveal a water channel connecting to the active site for the second step of catalysis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 239-255.	2.5	3
105	OBI reduction and optical power budget enhancement in OFDM-PON system using spreading code in electrical domain. Optics Communications, 2016, 361, 79-85.	1.0	3
106	The inhibitory and binding studies of methyl-sulfone hydroxamate based inhibitors against LpxC from drug resistant Moraxella catarrhalis using biophysical, biochemical and in silico approaches. International Journal of Biological Macromolecules, 2018, 118, 1747-1762.	3.6	3
107	Purification and Biophysical Characterization of an 11S Globulin from Wrightia tinctoria Exhibiting Hemagglutinating Activity. Protein and Peptide Letters, 2013, 20, 499-509.	0.4	3
108	Deciphering the enigma of missing DNA binding domain of LacI family transcription factors. Archives of Biochemistry and Biophysics, 2021, 713, 109060.	1.4	3

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109	A novel 40 kDa protein from goat mammary secretions: purification, crystallization and preliminary X-ray diffraction studies. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1332-1333.	2.5	2
110	Next generation 3-D OFDM based optical access networks using FEC under various system impairments. Proceedings of SPIE, 2013, , .	0.8	2
111	Improvement in error performance of optical communication system using quantum detection theory. Journal of Optics (India), 2022, 51, 505-513.	0.8	2
112	Alphavirus antivirals targeting RNAâ€dependent RNA polymerase domain of nsP4 divulged using surface plasmon resonance. FEBS Journal, 2022, 289, 4901-4924.	2.2	2
113	Conformational flexibility enables catalysis of phthalate cis-4,5-dihydrodiol dehydrogenase. Archives of Biochemistry and Biophysics, 2022, 727, 109314.	1.4	2
114	Biophysical and modeling-based approach for the identification of inhibitors against DOHH from <i>Leishmania donovani  Ii&gt;. Briefings in Functional Genomics, 2023, 22, 217-226.</i>	1.3	2
115	Design, Synthesis and Structural Aspects of Terdentate (N,O,Se/Te) Donors and their Competitive Coordination Behavior towards Pt(II). Phosphorus, Sulfur and Silicon and the Related Elements, 2001, 172, 231-238.	0.8	1
116	Design of peptides with α,β-dehydro residues: pseudo-tripeptideN-benzyloxycarbonyl–ΔLeu–L-Ala–L-Leu–OCH3. Acta Crystallographica Section C: Crystal Structure Communications, 2002, 58, o212-o214.	0.4	1
117	Crimean-Congo Hemorrhagic Fever Virus: Strategies to Combat with an Emerging Threat to Human. Current Bioinformatics, 2012, 7, 467-477.	0.7	1
118	Characterization of substrate binding and enzymatic removal of a 3-methyladenine lesion from genomic DNA with TAG of MDR A. baumannii. Molecular BioSystems, 2016, 12, 3259-3265.	2.9	1
119	Bioremediation of synthetic dyes: Dye decolorizing peroxidases (DyPs). , 2020, , 453-486.		1
120	Biochemical and structural basis for Moraxella catarrhalis enoyl-acyl carrier protein reductase (Fabl) inhibition by triclosan and estradiol. Biochimie, 2022, 198, 8-22.	1.3	1
121	Bacterial histidine kinases as potential antibacterial drug targets. , 2022, , 711-734.		1
122	Enhanced optical power budget in DDO-OFDM-PON and CO-OFDM-PON system using frequency diversity. , 2014, , .		0
123	Structural insights into the aggregation behavior of <i>Murraya koenigii</i> miraculin″ike protein below pH 7.5. Proteins: Structure, Function and Bioinformatics, 2014, 82, 830-840.	1.5	0
124	Electrical Spreading Code-Based OFDM Optical Access Networks for Budget Enhancement and Reduced System Bandwidth Requirement. Journal of Optical Communications, 2015, 36, .	4.0	0
125	Performance of 3T-ANC based orthogonal frequency-division-multiplexed optical wireless link with pointing error. Journal of Optics (India), 2019, 48, 400-411.	0.8	0
126	Phthalatesâ€"A class of ubiquitous pollutant: Microbial and enzymatic degradation perspectives. , 2020, , 487-513.		0