## Anna Roujeinikova

## 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.

71
papers

2,285
citations

h-index

47
g-index

73
ext. papers

2,609
ext. citations

6
avg, IF

L-index

#	Paper	IF	Citations
71	The flagellar motor protein FliL forms a scaffold of circumferentially positioned rings required for stator activation <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	2
70	The Structure, Composition, and Role of Periplasmic Stator Scaffolds in Polar Bacterial Flagellar Motors. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 639490	5.7	1
69	Bioinformatics analysis and biochemical characterisation of ABC transporter-associated periplasmic substrate-binding proteins ModA and MetQ from Helicobacter pylori strain SS1. <i>Biophysical Chemistry</i> , <b>2021</b> , 272, 106577	3.5	1
68	The global prevalence and trend of human intestinal carriage of ESBL-producing Escherichia coli in the community. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2021</b> , 76, 22-29	5.1	29
67	Structure-Activity Relationship Study Reveals the Molecular Basis for Specific Sensing of Hydrophobic Amino Acids by the Chemoreceptor Tlp3. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	5
66	Broad Specificity of Amino Acid Chemoreceptor CtaA of Is Afforded by Plasticity of Its Amphipathic Ligand-Binding Pocket. <i>Molecular Plant-Microbe Interactions</i> , <b>2020</b> , 33, 612-623	3.6	6
65	Antibacterial activity of ethoxzolamide against strains SS1 and 26695. <i>Gut Pathogens</i> , <b>2020</b> , 12, 20	5.4	15
64	Anti- activity of ethoxzolamide. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 1660-16	<b>65</b> .6	23
63	Preliminary X-ray crystallographic studies on the Helicobacter pylori ABC transporter glutamine-binding protein GlnH. <i>Drug Discoveries and Therapeutics</i> , <b>2019</b> , 13, 52-58	5	1
62	Molecular Basis of Unexpected Specificity of ABC Transporter-Associated Substrate-Binding Protein DppA from Helicobacter pylori. <i>Journal of Bacteriology</i> , <b>2019</b> , 201,	3.5	3
61	Flagellin glycosylation with pseudaminic acid in Campylobacter and Helicobacter: prospects for development of novel therapeutics. <i>Cellular and Molecular Life Sciences</i> , <b>2018</b> , 75, 1163-1178	10.3	29
60	Purification, crystallization and preliminary X-ray crystallographic studies on the C-terminal domain of the flagellar protein FliL from Helicobacter pylori. <i>BioScience Trends</i> , <b>2018</b> , 12, 630-635	9.9	1
59	Refolding, Characterization, and Preliminary X-ray Crystallographic Studies on the Campylobacter concisus Plasmid-Encoded Secreted Protein Csep1p Associated with Crohn® Disease. <i>Crystals</i> , <b>2018</b> , 8, 391	2.3	O
58	Methyl-accepting chemotaxis proteins: a core sensing element in prokaryotes and archaea. <i>Cellular and Molecular Life Sciences</i> , <b>2017</b> , 74, 3293-3303	10.3	67
57	Structural analysis of variant of Helicobacter pylori MotB in its activated form, engineered as chimera of MotB and leucine zipper. <i>Scientific Reports</i> , <b>2017</b> , 7, 13435	4.9	8
56	Helicobacter pylori chemoreceptor TlpC mediates chemotaxis to lactate. <i>Scientific Reports</i> , <b>2017</b> , 7, 140	0849	29
55	The periplasmic sensing domain of Pseudomonas fluorescens chemotactic transducer of amino acids type B (CtaB): Cloning, refolding, purification, crystallization, and X-ray crystallographic analysis. <i>BioScience Trends</i> , <b>2017</b> , 11, 229-234	9.9	2

54	Method for Efficient Refolding and Purification of Chemoreceptor Ligand Binding Domain. <i>Journal of Visualized Experiments</i> , <b>2017</b> ,	1.6	2
53	The Middle Fragment of Helicobacter pylori CagA Induces Actin Rearrangement and Triggers Its Own Uptake into Gastric Epithelial Cells. <i>Toxins</i> , <b>2017</b> , 9,	4.9	8
52	Crystallisation and Preliminary Crystallographic Analysis of Helicobacter pylori Periplasmic Binding Protein YckK. <i>Crystals</i> , <b>2017</b> , 7, 330	2.3	3
51	Structure-Activity Relationship for Sulfonamide Inhibition of Helicobacter pylori Ecarbonic Anhydrase. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 11098-11109	8.3	40
50	The crystal structure of the tandem-PAS sensing domain of Campylobacter jejuni chemoreceptor Tlp1 suggests indirect mechanism of ligand recognition. <i>Journal of Structural Biology</i> , <b>2016</b> , 194, 205-13	3.4	23
49	Structural basis for substrate specificity of Helicobacter pylori M17 aminopeptidase. <i>Biochimie</i> , <b>2016</b> , 121, 60-71	4.6	11
48	The periplasmic sensing domain of Vibrio fischeri chemoreceptor protein A (VfcA): cloning, purification and crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2016</b> , 72, 382-5	1.1	1
47	Cloning, purification, crystallization and X-ray crystallographic analysis of the periplasmic sensing domain of Pseudomonas fluorescens chemotactic transducer of amino acids type A (CtaA). <i>BioScience Trends</i> , <b>2016</b> , 10, 320-4	9.9	2
46	Structure and Functional Diversity of GCN5-Related N-Acetyltransferases (GNAT). <i>International Journal of Molecular Sciences</i> , <b>2016</b> , 17,	6.3	82
45	Cloning, expression, refolding, purification and preliminary crystallographic analysis of the sensory domain of the Campylobacter chemoreceptor for aspartate A (CcaA). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 110-3	1.1	6
44	Cloning, refolding, purification and preliminary crystallographic analysis of the sensory domain of the Campylobacter chemoreceptor for multiple ligands (CcmL). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 211-6	1.1	5
43	Structural basis for amino-acid recognition and transmembrane signalling by tandem Per-Arnt-Sim (tandem PAS) chemoreceptor sensory domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 2127-36		41
42	Expression, refolding, purification and crystallization of the sensory domain of the TlpC chemoreceptor from Helicobacter pylori for structural studies. <i>Protein Expression and Purification</i> , <b>2015</b> , 107, 29-34	2	11
41	Crystal structure of Helicobacter pylori pseudaminic acid biosynthesis N-acetyltransferase PseH: implications for substrate specificity and catalysis. <i>PLoS ONE</i> , <b>2015</b> , 10, e0115634	3.7	15
40	Structural Basis for the Inhibition of Helicobacter pylori ECarbonic Anhydrase by Sulfonamides. <i>PLoS ONE</i> , <b>2015</b> , 10, e0127149	3.7	37
39	Phospholipid binding residues of eukaryotic membrane-remodelling F-BAR domain proteins are conserved in Helicobacter pylori CagA. <i>BMC Research Notes</i> , <b>2014</b> , 7, 525	2.3	7
38	Mechanism of Escherichia coli resistance to Pyrrhocoricin. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 2754-62	5.9	21
37	Structural and mechanistic insight into alkane hydroxylation by Pseudomonas putida AlkB. Biochemical Journal, <b>2014</b> , 460, 283-93	3.8	15

36	Purification and biochemical characterization of DnaK and its transcriptional activator RpoH from Neisseria gonorrhoeae. <i>Molecular Biology Reports</i> , <b>2014</b> , 41, 7945-53	2.8	
35	Cloning, purification and preliminary crystallographic analysis of the Helicobacter pylori pseudaminic acid biosynthesis N-acetyltransferase PseH. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1276-9	1.1	7
34	Cloning, purification and preliminary crystallographic analysis of the complex of Helicobacter pylori Etarbonic anhydrase with acetazolamide. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1252-5		7
33	Design, purification and characterization of a soluble variant of the integral membrane protein MotB for structural studies. <i>Journal of the Royal Society Interface</i> , <b>2013</b> , 10, 20120717	4.1	2
32	Cloning, purification and preliminary crystallographic analysis of the Helicobacter pylori leucyl aminopeptidase-bestatin complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1011-4		3
31	Conformational analysis of isolated domains of Helicobacter pylori CagA. <i>PLoS ONE</i> , <b>2013</b> , 8, e79367	3.7	13
30	Characterization and two-dimensional crystallization of membrane component AlkB of the medium-chain alkane hydroxylase system from Pseudomonas putida GPo1. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 7946-53	4.8	20
29	An improved procedure for the purification of catalytically active alkane hydroxylase from Pseudomonas putida GPo1. <i>Applied Biochemistry and Biotechnology</i> , <b>2011</b> , 165, 823-31	3.2	10
28	Role of the MotB linker in the assembly and activation of the bacterial flagellar motor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2011</b> , 67, 1009-16		29
27	Purification, crystallization and preliminary X-ray crystallographic analysis of the putative Vibrio parahaemolyticus resuscitation-promoting factor YeaZ. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 604-7		8
26	Crystallographic and molecular dynamics analysis of loop motions unmasking the peptidoglycan-binding site in stator protein MotB of flagellar motor. <i>PLoS ONE</i> , <b>2011</b> , 6, e18981	3.7	23
25	Structural analysis of the essential resuscitation promoting factor YeaZ suggests a mechanism of nucleotide regulation through dimer reorganization. <i>PLoS ONE</i> , <b>2011</b> , 6, e23245	3.7	18
24	Allosteric coupling between the lid and interdomain linker in DnaK revealed by inhibitor binding studies. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 1456-62	3.5	50
23	Crystal structure of the cell wall anchor domain of MotB, a stator component of the bacterial flagellar motor: implications for peptidoglycan recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 10348-53	11.5	110
22	Cloning, purification and preliminary X-ray analysis of the C-terminal domain of Helicobacter pylori MotB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 277-80		4
21	Cloning, purification and crystallization of MotB, a stator component of the proton-driven bacterial flagellar motor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 561-3		6
20	Driving force analysis of proton tunnelling across a reactivity series for an enzyme-substrate complex. <i>ChemBioChem</i> , <b>2008</b> , 9, 2839-45	3.8	18
19	Structure-Based Insight into the Asymmetric Bioreduction of the C=C Double Bond of alpha,beta-Unsaturated Nitroalkenes by Pentaerythritol Tetranitrate Reductase. <i>Advanced Synthesis and Catalysis</i> , <b>2008</b> , 350, 2789-2803	5.6	78

18	Isotope effects reveal that para-substituted benzylamines are poor reactivity probes of the quinoprotein mechanism for aromatic amine dehydrogenase. <i>Biochemistry</i> , <b>2007</b> , 46, 9250-9	3.2	5
17	New insights into the reductive half-reaction mechanism of aromatic amine dehydrogenase revealed by reaction with carbinolamine substrates. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 23766-7	7 <sup>5.4</sup>	11
16	Structural studies of fatty acyl-(acyl carrier protein) thioesters reveal a hydrophobic binding cavity that can expand to fit longer substrates. <i>Journal of Molecular Biology</i> , <b>2007</b> , 365, 135-45	6.5	121
15	Atomic level insight into the oxidative half-reaction of aromatic amine dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 40264-72	5.4	8
14	Crystal structure of the Mycobacterium tuberculosis P450 CYP121-fluconazole complex reveals new azole drug-P450 binding mode. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 39437-43	5.4	94
13	Atomic description of an enzyme reaction dominated by proton tunneling. <i>Science</i> , <b>2006</b> , 312, 237-41	33.3	278
12	Hydrogen tunnelling in enzyme-catalysed H-transfer reactions: flavoprotein and quinoprotein systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2006</b> , 361, 1375-86	5.8	59
11	Cloning, purification and preliminary crystallographic analysis of the Bacillus subtilis GTPase YphC-GDP complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2006</b> , 62, 435-	7	3
10	X-ray crystallographic studies on butyryl-ACP reveal flexibility of the structure around a putative acyl chain binding site. <i>Structure</i> , <b>2002</b> , 10, 825-35	5.2	103
9	Crystallization and preliminary X-ray crystallographic studies on acyl-(acyl carrier protein) from Escherichia coli. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 330-2		9
8	Crystal structure of Thermotoga maritima 4-alpha-glucanotransferase and its acarbose complex: implications for substrate specificity and catalysis. <i>Journal of Molecular Biology</i> , <b>2002</b> , 321, 149-62	6.5	61
7	Crystallization and preliminary X-ray crystallographic studies on 4-alpha-glucanotransferase from Thermotoga maritima. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 1046-7		2
6	The crystal structure of Thermotoga maritima maltosyltransferase and its implications for the molecular basis of the novel transfer specificity. <i>Journal of Molecular Biology</i> , <b>2001</b> , 312, 119-31	6.5	13
5	Crystallization and preliminary X-ray crystallographic studies on maltosyltransferase from Thermotoga maritima. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2000</b> , 56, 1049-50		2
4	Inhibitor binding studies on enoyl reductase reveal conformational changes related to substrate recognition. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 30811-7	5.4	50
3	Molecular basis of triclosan activity. <i>Nature</i> , <b>1999</b> , 398, 383-4	50.4	418
2	Crystallographic analysis of triclosan bound to enoyl reductase. <i>Journal of Molecular Biology</i> , <b>1999</b> , 294, 527-35	6.5	85
1	Correlation of the global spread of coronavirus disease-19 with atmospheric air temperature		1