

# Michail N Isupov

## List of Publications by Year in descending order

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98  
papers

5,942  
citations

117453

34  
h-index

74018

75  
g-index

108  
all docs

108  
docs citations

108  
times ranked

8338  
citing authors

#	ARTICLE	IF	CITATIONS
1	An archaellum filament composed of two alternating subunits. <i>Nature Communications</i> , 2022, 13, 710.	5.8	18
2	Structural Insights into a Novel Esterase from the East Pacific Rise and Its Improved Thermostability by a Semirational Design. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 1079-1090.	2.4	12
3	Biochemical and Structural Characterisation of a Novel D-Lyxose Isomerase From the Hyperthermophilic Archaeon <i>Thermofilum</i> sp.. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 711487.	2.0	3
4	Structural basis for UFM1 transfer from UBA5 to UFC1. <i>Nature Communications</i> , 2021, 12, 5708.	5.8	21
5	Using enzyme cascades in biocatalysis: Highlight on transaminases and carboxylic acid reductases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140322.	1.1	31
6	A "Split-Gene"™ Transketolase From the Hyper-Thermophilic Bacterium <i>Carboxydotherrmus hydrogenoformans</i> : Structure and Biochemical Characterization. <i>Frontiers in Microbiology</i> , 2020, 11, 592353.	1.5	3
7	Structural insights into the NAD <sup>+</sup> -dependent formate dehydrogenase mechanism revealed from the NADH complex and the formate NAD <sup>+</sup> ternary complex of the <i>Chaetomium thermophilum</i> enzyme. <i>Journal of Structural Biology</i> , 2020, 212, 107657.	1.3	14
8	The crystal structure of <i>Arabidopsis</i> BON1 provides insights into the copine protein family. <i>Plant Journal</i> , 2020, 103, 1215-1232.	2.8	8
9	Structural basis for SARM1 inhibition and activation under energetic stress. <i>ELife</i> , 2020, 9, .	2.8	83
10	Structural Evidence for an Octameric Ring Arrangement of SARM1. <i>Journal of Molecular Biology</i> , 2019, 431, 3591-3605.	2.0	59
11	X-ray structure of <i>Fasciola hepatica</i> Sigma class glutathione transferase 1 reveals a disulfide bond to support stability in gastro-intestinal environment. <i>Scientific Reports</i> , 2019, 9, 902.	1.6	2
12	Structural Principles in Robo Activation and Auto-inhibition. <i>Cell</i> , 2019, 177, 272-285.e16.	13.5	34
13	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea <i>Geoglobus acetivorans</i> and <i>Archaeoglobus fulgidus</i> : Biochemical and Structural Characterization. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 7.	2.0	26
14	Structural basis for the Target <sc>DNA</sc> recognition and binding by the <sc>MYB</sc> domain of phosphate starvation response 1. <i>FEBS Journal</i> , 2019, 286, 2809-2821.	2.2	23
15	The crystal structure of human microsomal triglyceride transfer protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17251-17260.	3.3	47
16	An N-Terminal Extension to UBA5 Adenylation Domain Boosts UFM1 Activation: Isoform-Specific Differences in Ubiquitin-like Protein Activation. <i>Journal of Molecular Biology</i> , 2019, 431, 463-478.	2.0	24
17	A high-sensitivity electrochemiluminescence-based ELISA for the measurement of the oxidative stress biomarker, 3-nitrotyrosine, in human blood serum and cells. <i>Free Radical Biology and Medicine</i> , 2018, 120, 246-254.	1.3	20
18	New Thermophilic $\hat{1}\hat{2}$ Class Epoxide Hydrolases Found in Metagenomes From Hot Environments. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 144.	2.0	19

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19	The molecular basis of protein toxin HicA-dependent binding of the protein antitoxin HicB to DNA. <i>Journal of Biological Chemistry</i> , 2018, 293, 19429-19440.	1.6	10
20	Structural History of Human SRGAP2 Proteins. <i>Molecular Biology and Evolution</i> , 2017, 34, 1463-1478.	3.5	31
21	The Crystal Structure and Conformations of an Unbranched Mixed Tri-Ubiquitin Chain Containing K48 and K63 Linkages. <i>Journal of Molecular Biology</i> , 2017, 429, 3801-3813.	2.0	3
22	Molecular mechanism for the subversion of the retromer coat by the <i>Legionella</i> effector RidL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11151-E11160.	3.3	42
23	Crystal structure of the type IV secretion system component CagX from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 167-173.	0.4	8
24	Cloning retinoid and peroxisome proliferator-activated nuclear receptors of the Pacific oyster and in silico binding to environmental chemicals. <i>PLoS ONE</i> , 2017, 12, e0176024.	1.1	29
25	Discovery and Characterization of a Thermostable and Highly Halotolerant GH5 Cellulase from an Icelandic Hot Spring Isolate. <i>PLoS ONE</i> , 2016, 11, e0146454.	1.1	61
26	Molecular symmetry-constrained systematic search approach to structure solution of the coiled-coil SRGAP2 F-BARx domain. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1241-1253.	1.1	11
27	Structural and biochemical characterisation of <i>Archaeoglobus fulgidus</i> esterase reveals a bound CoA molecule in the vicinity of the active site. <i>Scientific Reports</i> , 2016, 6, 25542.	1.6	8
28	Unraveling the <i>B. pseudomallei</i> Heptokinase WcbL: From Structure to Drug Discovery. <i>Chemistry and Biology</i> , 2015, 22, 1622-1632.	6.2	7
29	Discovery and characterization of thermophilic limonene-1,2-epoxide hydrolases from hot spring metagenomic libraries. <i>FEBS Journal</i> , 2015, 282, 2879-2894.	2.2	43
30	Structural studies of a thermophilic esterase from a new Planctomycetes species, <i>Thermogutta terrifontis</i> . <i>FEBS Journal</i> , 2015, 282, 2846-2857.	2.2	27
31	The Structure of a Novel Thermophilic Esterase from the Planctomycetes Species, <i>Thermogutta terrifontis</i> Reveals an Open Active Site Due to a Minimal $\hat{c}$ Cap <sup>TM</sup> Domain. <i>Frontiers in Microbiology</i> , 2015, 6, 1294.	1.5	20
32	The oxygenating constituent of 3,6-diketocamphane monooxygenase from the CAM plasmid of <i>Pseudomonas putida</i> : the first crystal structure of a type II Baeyer-Villiger monooxygenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2344-2353.	2.5	20
33	Space-group and origin ambiguity in macromolecular structures with pseudo-symmetry and its treatment with the program <i>Zanuda</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2430-2443.	2.5	83
34	The structure of a tetrameric $\hat{L}$ -carbonic anhydrase from <i>Thermovibrio ammonificans</i> reveals a core formed around intermolecular disulfides that contribute to its thermostability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2607-2618.	2.5	47
35	The substrate specificity, enantioselectivity and structure of the ( <i>R</i> )-selective amine:pyruvate transaminase from <i>Nectria haematococca</i> . <i>FEBS Journal</i> , 2014, 281, 2240-2253.	2.2	60
36	Biochemical and structural characterisation of a haloalkane dehalogenase from a marine <i>Rhodobacteraceae</i> . <i>FEBS Letters</i> , 2014, 588, 1616-1622.	1.3	27

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37	Structural insights into Wcbl, a novel polysaccharide-biosynthesis enzyme. IUCrJ, 2014, 1, 28-38.	1.0	5
38	Functional and structural characterisation of a viral cytochrome <i>b<sub>5</sub></i> . FEBS Letters, 2013, 587, 3633-3639.	1.3	7
39	Structural studies of <i>Pseudomonas</i> and <i>Chromobacterium</i> $\gamma$ -aminotransferases provide insights into their differing substrate specificity. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 564-576.	2.5	51
40	Marine <i>Rhodobacteraceae</i> <i>Halorubrum</i> haloacid dehalogenase contains a novel His/Glu dyad that could activate the catalytic water. FEBS Journal, 2013, 280, 1664-1680.	2.2	36
41	Crystal structure of D-serine dehydratase from Escherichia coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 422-432.	1.1	20
42	<i>Ligand</i> : a graphical tool for the CCP4 template-restraint library. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 431-440.	2.5	373
43	Crystal structure and substrate specificity of the thermophilic serine:pyruvate aminotransferase from <i>Sulfolobus solfataricus</i> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 763-772.	2.5	30
44	Thermophilic enzymes and their applications in biocatalysis: a robust aldo-keto reductase. Environmental Technology (United Kingdom), 2010, 31, 1159-1167.	1.2	10
45	<i>Bacillus licheniformis</i> Anti-TRAP can assemble into two types of dodecameric particles with the same symmetry but inverted orientation of trimers. Journal of Structural Biology, 2010, 170, 127-133.	1.3	4
46	Crystal structure of a thermostable Old Yellow Enzyme from <i>Thermus scotoductus</i> SA-01. Biochemical and Biophysical Research Communications, 2010, 393, 426-431.	1.0	76
47	The binding of haem and zinc in the 1.9 Å X-ray structure of Escherichia coli bacterioferritin. Journal of Biological Inorganic Chemistry, 2009, 14, 201-207.	1.1	20
48	Biochemical and structural studies of a l-haloacid dehalogenase from the thermophilic archaeon <i>Sulfolobus tokodaii</i> . Extremophiles, 2009, 13, 179-190.	0.9	34
49	Conformational flexibility and molecular interactions of an archaeal homologue of the Shwachman-Bodian-Diamond syndrome protein. BMC Structural Biology, 2009, 9, 32.	2.3	27
50	Vanadium containing bromoperoxidase – Insights into the enzymatic mechanism using X-ray crystallography. Journal of Inorganic Biochemistry, 2009, 103, 617-621.	1.5	37
51	NCS-constrained exhaustive search using oligomeric models. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 90-98.	2.5	17
52	The <i>Fasciola hepatica</i> thioredoxin: High resolution structure reveals two oxidation states. Molecular and Biochemical Parasitology, 2008, 161, 44-48.	0.5	9
53	Natural methods of protein stabilization: thermostable biocatalysts. Biochemical Society Transactions, 2007, 35, 1558-1563.	1.6	47
54	Papillomavirus E1 helicase assembly maintains an asymmetric state in the absence of DNA and nucleotide cofactors. Nucleic Acids Research, 2007, 35, 6451-6457.	6.5	36

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55	An order-disorder twin crystal of L-2-haloacid dehalogenase from <i>Sulfolobus tokodaii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 926-930.	2.5	28
56	Crystallization and preliminary X-ray diffraction analysis of L-amino acid:pyruvate transaminase from <i>Chromobacterium violaceum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 117-119.	0.7	11
57	<i>Arabidopsis thaliana</i> VTC4 Encodes L-Galactose-1-P Phosphatase, a Plant Ascorbic Acid Biosynthetic Enzyme. <i>Journal of Biological Chemistry</i> , 2006, 281, 15662-15670.	1.6	154
58	Synthesis and characterisation of a ligand that forms a stable tetrahedral intermediate in the active site of the <i>Aureobacterium</i> species ( $\beta$ -lactamase. <i>Organic and Biomolecular Chemistry</i> , 2005, 3, 3260.	1.5	11
59	Modification of halogen specificity of a vanadium-dependent bromoperoxidase. <i>Protein Science</i> , 2004, 13, 1566-1571.	3.1	37
60	Crystallization and preliminary X-ray diffraction studies of a fungal hydrolase from <i>Ophiostoma novo-ulmi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1879-1882.	2.5	9
61	The Crystal Structure of a $\beta$ -Lactamase from an <i>Aureobacterium</i> Species Reveals a Tetrahedral Intermediate in the Active Site. <i>Journal of Molecular Biology</i> , 2004, 338, 519-532.	2.0	62
62	The Crystal Structure of YloQ, a Circularly Permuted GTPase Essential for <i>Bacillus subtilis</i> Viability. <i>Journal of Molecular Biology</i> , 2004, 340, 767-782.	2.0	50
63	Conformational Changes Induced by Nucleotide Binding in Cdc6/ORC From <i>Aeropyrum pernix</i> . <i>Journal of Molecular Biology</i> , 2004, 343, 547-557.	2.0	73
64	Hyperthermophilic dehydrogenase enzymes. <i>Biochemical Society Transactions</i> , 2004, 32, 255-258.	1.6	28
65	Crystallization and preliminary X-ray diffraction studies of a novel alcohol dehydrogenase from the hyperthermophilic archaeon <i>Aeropyrum pernix</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 174-176.	2.5	10
66	The Structure of an Alcohol Dehydrogenase from the Hyperthermophilic Archaeon <i>Aeropyrum pernix</i> . <i>Journal of Molecular Biology</i> , 2003, 331, 1041-1051.	2.0	67
67	Structural and functional comparisons between vanadium haloperoxidase and acid phosphatase enzymes. <i>Journal of Molecular Recognition</i> , 2002, 15, 291-296.	1.1	55
68	Crystallization and preliminary X-ray diffraction analysis of L-aminoacylase from the hyperthermophilic archaeon <i>Thermococcus litoralis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 507-510.	2.5	8
69	[9] Glyceraldehyde-3-phosphate dehydrogenase from <i>Sulfolobus solfataricus</i> . <i>Methods in Enzymology</i> , 2001, 331, 105-117.	0.4	7
70	Use of TLS parameters to model anisotropic displacements in macromolecular refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 122-133.	2.5	1,563
71	Crystallization and preliminary X-ray analysis of a $\beta$ -lactamase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 284-286.	2.5	20
72	Spherically averaged phased translation function and its application to the search for molecules and fragments in electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1451-1456.	2.5	195

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73	Comparison of the decameric structure of peroxiredoxin-II by transmission electron microscopy and X-ray crystallography. <i>BBA - Proteins and Proteomics</i> , 2001, 1547, 221-234.	2.1	63
74	Chloroplast Glyceraldehyde-3-phosphate Dehydrogenase Contains a Single Disulfide Bond Located in the C-terminal Extension to the B Subunit. <i>Journal of Biological Chemistry</i> , 2001, 276, 35247-35252.	1.6	30
75	Structure and mechanism of decameric 2-cys peroxiredoxin from human erythrocytes. <i>Biochemical Society Transactions</i> , 2000, 28, A75-A75.	1.6	0
76	Cloning, Expression & Purification of a Thermostable Aminoacylase from <i>Thermococcus litoralis</i> . <i>Biochemical Society Transactions</i> , 2000, 28, A78-A78.	1.6	0
77	The atomic-resolution structure of a novel bacterial esterase. <i>Structure</i> , 2000, 8, 143-151.	1.6	72
78	Crystal structure of decameric 2-Cys peroxiredoxin from human erythrocytes at 1.7Å... resolution. <i>Structure</i> , 2000, 8, 605-615.	1.6	301
79	The crystal structure of d-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon <i>Methanothermus fervidus</i> in the presence of NADP+ at 2.1 Å... resolution. <i>Journal of Molecular Biology</i> , 2000, 297, 481-500.	2.0	31
80	Crystal structure of dodecameric vanadium-dependent bromoperoxidase from the red algae <i>Corallina officinalis</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 1035-1049.	2.0	185
81	Crystallization and preliminary X-ray analysis of human thioredoxin peroxidase-B from red blood cells. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 536-538.	2.5	3
82	Crystallization and preliminary X-ray diffraction studies of pyrrolidone carboxyl peptidase from the hyperthermophilic archaeon <i>Thermococcus litoralis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 702-703.	2.5	7
83	Crystallization and preliminary X-ray diffraction studies of a novel bacterial esterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 915-917.	2.5	3
84	Crystallization and preliminary X-ray diffraction studies of D-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon <i>Methanothermus fervidus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1353-1355.	2.5	5
85	Structure of a phosphoglycerate mutase:3-phosphoglyceric acid complex at 1.7Å... <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1822-1826.	2.5	20
86	X-ray structure of pyrrolidone carboxyl peptidase from the hyperthermophilic archaeon <i>Thermococcus litoralis</i> . <i>Structure</i> , 1999, 7, 237-244.	1.6	60
87	Structure of Human Pro-Matrix Metalloproteinase-2: Activation Mechanism Revealed. <i>Science</i> , 1999, 284, 1667-1670.	6.0	505
88	Crystal structure of the glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 291, 651-660.	2.0	62
89	Preliminary X-ray analysis of a new crystal form of the vanadium-dependent bromoperoxidase from <i>Corallina officinalis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 454-457.	2.5	14
90	Characterization, crystallization and preliminary X-ray investigation of glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 671-674.	2.5	7

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91	Crystallization and preliminary X-ray diffraction studies of the oxygenating subunit of 3,6-diketocamphane monooxygenase from <i>Pseudomonas putida</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1035-1038.	2.5	11
92	Crystal structure of tryptophanase. <i>Journal of Molecular Biology</i> , 1998, 276, 603-623.	2.0	114
93	Two glycolytic enzymes from <i>Sulfolobus solfataricus</i> . <i>Biochemical Society Transactions</i> , 1998, 26, S275-S275.	1.6	3
94	Carbon-Carbon Bond Synthesis: The Impact of rDNA Technology on the Production and Use of <i>E. coli</i> Transketolase. <i>Annals of the New York Academy of Sciences</i> , 1996, 782, 513-525.	1.8	28
95	Substrate binding is required for assembly of the active conformation of the catalytic site in Ntn amidotransferases: evidence from the 1.8 Å crystal structure of the glutaminase domain of glucosamine 6-phosphate synthase. <i>Structure</i> , 1996, 4, 801-810.	1.6	146
96	Crystallization and Preliminary X-ray Investigation of Holotryptophanases from <i>Escherichia coli</i> and <i>Proteus vulgaris</i> . <i>Journal of Molecular Biology</i> , 1994, 235, 780-782.	2.0	26
97	Crystallization and Preliminary Crystallographic Characterization of Bacteriophage T4 Baseplate Protein Encoded by Gene 9. <i>Journal of Molecular Biology</i> , 1993, 234, 493-495.	2.0	4
98	The polypeptide chain fold in tyrosine phenol-lyase, a pyridoxal-5-phosphate-dependent enzyme. <i>FEBS Letters</i> , 1992, 302, 256-260.	1.3	17