

# Svetlana Antonyuk

## List of Publications by Year in descending order

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97  
papers

4,407  
citations

126708

33  
h-index

114278

63  
g-index

104  
all docs

104  
docs citations

104  
times ranked

5246  
citing authors

#	ARTICLE	IF	CITATIONS
1	CPVT-associated calmodulin variants N53I and A102V dysregulate Ca <sup>2+</sup> signalling via different mechanisms. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	7
2	Reverse protein engineering of a novel 4 $\alpha$ -domain copper nitrite reductase reveals functional regulation by proteinâ€“protein interaction. <i>FEBS Journal</i> , 2021, 288, 262-280.	2.2	12
3	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. <i>Science Advances</i> , 2021, 7, .	4.7	25
4	Nature of the copper-nitrosyl intermediates of copper nitrite reductases during catalysis. <i>Chemical Science</i> , 2020, 11, 12485-12492.	3.7	6
5	AcGI1, a novel genomic island carrying antibiotic resistance integron In687 in multidrug resistant <i>Achromobacter xylosoxidans</i> in a teaching hospital in Thailand. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	4
6	Potent Tetrahydroquinolone Eliminates Apicomplexan Parasites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 203.	1.8	21
7	Ebselen as template for stabilization of A4V mutant dimer for motor neuron disease therapy. <i>Communications Biology</i> , 2020, 3, 97.	2.0	30
8	Purification and Structural Characterization of Aggregation-Prone Human TDP-43 Involved in Neurodegenerative Diseases. <i>IScience</i> , 2020, 23, 101159.	1.9	19
9	<i>Prevotella intermedia</i> produces two proteins homologous to <i>Porphyromonas gingivalis</i> HmuY but with different heme coordination mode. <i>Biochemical Journal</i> , 2020, 477, 381-405.	1.7	21
10	The active form of quinol-dependent nitric oxide reductase from <i>Neisseria meningitidis</i> is a dimer. <i>IUCr</i> , 2020, 7, 404-415.	1.0	10
11	Structures of substrate- and product-bound forms of a multi-domain copper nitrite reductase shed light on the role of domain tethering in protein complexes. <i>IUCr</i> , 2020, 7, 557-565.	1.0	5
12	Structural basis of the dominant inheritance of hypermethioninemia associated with the Arg264His mutation in the <i>MAT1A</i> gene. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 594-607.	1.1	5
13	Crystal Structure of the Japanese Encephalitis Virus Capsid Protein. <i>Viruses</i> , 2019, 11, 623.	1.5	32
14	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. <i>IUCr</i> , 2019, 6, 761-772.	1.0	24
15	<i>Talaromyces marneffeii</i> Mp1 Protein, a Novel Virulence Factor, Carries Two Arachidonic Acid-Binding Domains To Suppress Inflammatory Responses in Hosts. <i>Infection and Immunity</i> , 2019, 87, .	1.0	13
16	Unexpected Roles of a Tether Harboring a Tyrosine Gatekeeper Residue in Modular Nitrite Reductase Catalysis. <i>ACS Catalysis</i> , 2019, 9, 6087-6099.	5.5	17
17	Molecular recognition and maturation of SOD1 by its evolutionarily destabilised cognate chaperone hCCS. <i>PLoS Biology</i> , 2019, 17, e3000141.	2.6	38
18	Control and regulation of S $\alpha$ -Adenosylmethionine biosynthesis by the regulatory $\hat{2}$ subunit and quinoloneâ€“based compounds. <i>FEBS Journal</i> , 2019, 286, 2135-2154.	2.2	9

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19	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryo-electron microscopy. <i>Science Advances</i> , 2019, 5, eaax1803.	4.7	14
20	The biophysics of superoxide dismutase-1 and amyotrophic lateral sclerosis. <i>Quarterly Reviews of Biophysics</i> , 2019, 52, e12.	2.4	51
21	Noncovalent Complexes Formed between Metal-Substituted Polyoxometalates and Hen Egg White Lysozyme. <i>European Journal of Inorganic Chemistry</i> , 2019, 2019, 506-511.	1.0	18
22	The expanding toolkit for structural biology: synchrotrons, X-ray lasers and cryoEM. <i>IUCrJ</i> , 2019, 6, 167-177.	1.0	36
23	LAT1 (SLC7A5) and CD98hc (SLC3A2) complex dynamics revealed by single-particle cryo-EM. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 660-669.	1.1	16
24	Architecture of the complete oxygen-sensing FixL-FixJ two-component signal transduction system. <i>Science Signaling</i> , 2018, 11, .	1.6	38
25	Structural Study of the C-Terminal Domain of Nonstructural Protein 1 from Japanese Encephalitis Virus. <i>Journal of Virology</i> , 2018, 92, .	1.5	24
26	The cysteine-reactive small molecule ebselen facilitates effective SOD1 maturation. <i>Nature Communications</i> , 2018, 9, 1693.	5.8	71
27	Dystonia-Associated Hippocalcin Mutants Dysregulate Cellular Calcium Influx. <i>Biophysical Journal</i> , 2018, 114, 467a-468a.	0.2	0
28	<i>Tannerella forsythia</i> Tfo belongs to <i>Porphyromonas gingivalis</i> HmuY-like family of proteins but differs in heme-binding properties. <i>Bioscience Reports</i> , 2018, 38, .	1.1	24
29	Potent Antimalarial 2-Pyrazolyl Quinolone <i>bc</i> <sub>1</sub> (Q <sub>i</sub> ) Inhibitors with Improved Drug-like Properties. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 1205-1210.	1.3	28
30	X-ray and cryo-EM structures of inhibitor-bound cytochrome <i>bc</i> <sub>1</sub> complexes for structure-based drug discovery. <i>IUCrJ</i> , 2018, 5, 200-210.	1.0	23
31	Characterization of the quinol-dependent nitric oxide reductase from the pathogen <i>Neisseria meningitidis</i> , an electrogenic enzyme. <i>Scientific Reports</i> , 2018, 8, 3637.	1.6	22
32	Structural and functional insights into the unique CBS-CP12 fusion protein family in cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7141-7146.	3.3	20
33	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCrJ</i> , 2018, 5, 22-31.	1.0	27
34	Enzyme catalysis captured using multiple structures from one crystal at varying temperatures. <i>IUCrJ</i> , 2018, 5, 283-292.	1.0	26
35	Identification of a tyrosine switch in copper-haem nitrite reductases. <i>IUCrJ</i> , 2018, 5, 510-518.	1.0	10
36	Modulation of LAT1 (SLC7A5) transporter activity and stability by membrane cholesterol. <i>Scientific Reports</i> , 2017, 7, 43580.	1.6	59

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37	Biophysical and functional characterization of hippocalcin mutants responsible for human dystonia. <i>Human Molecular Genetics</i> , 2017, 26, 2426-2435.	1.4	29
38	MSEX crystallography and simulations to capture redox enzyme catalysis. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C651-C651.	0.0	0
39	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. <i>Scientific Reports</i> , 2016, 6, 29179.	1.6	40
40	Serial crystallography captures enzyme catalysis in copper nitrite reductase at atomic resolution from one crystal. <i>IUCr</i> , 2016, 3, 271-281.	1.0	56
41	A faulty interaction between SOD1 and hCCS in neurodegenerative disease. <i>Scientific Reports</i> , 2016, 6, 27691.	1.6	34
42	Fresh insight to functioning of selected enzymes of the nitrogen cycle. <i>Current Opinion in Chemical Biology</i> , 2016, 31, 103-112.	2.8	13
43	Crystallography captures catalytic steps in human methionine adenosyltransferase enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2104-2109.	3.3	35
44	Single-crystal serial crystallography to capture redox enzyme catalysis and dynamics. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s38-s38.	0.0	0
45	Sub-atomic resolution X-ray crystallography and neutron crystallography: promise, challenges and potential. <i>IUCr</i> , 2015, 2, 464-474.	1.0	104
46	Antimalarial 4(1H)-pyridones bind to the Q site of cytochrome <i>b<sub>5</sub>h<sub>6</sub></i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 755-760.	3.3	90
47	Impact of residues remote from the catalytic centre on enzyme catalysis of copper nitrite reductase. <i>Nature Communications</i> , 2014, 5, 4395.	5.8	36
48	Disease causing mutants of TDP-43 nucleic acid binding domains are resistant to aggregation and have increased stability and half-life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4309-4314.	3.3	68
49	Fingerprinting redox and ligand states in haemprotein crystal structures using resonance Raman spectroscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1289-1296.	2.5	18
50	The structure of a purple acid phosphatase involved in plant growth and pathogen defence exhibits a novel immunoglobulin-like fold. <i>IUCr</i> , 2014, 1, 101-109.	1.0	26
51	Structure and function study of the complex that synthesizes <i>S-adenosylmethionine</i> . <i>IUCr</i> , 2014, 1, 240-249.	1.0	36
52	Transport of gabapentin by LAT1 (SLC7A5). <i>Biochemical Pharmacology</i> , 2013, 85, 1672-1683.	2.0	120
53	Structures of protein-protein complexes involved in electron transfer. <i>Nature</i> , 2013, 496, 123-126.	13.7	65
54	Ligand binding and aggregation of pathogenic SOD1. <i>Nature Communications</i> , 2013, 4, 1758.	5.8	90

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55	Structure of the hypothetical DUF1811-family protein GK0453 from <i>Geobacillus kaustophilus</i> HTA426. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 342-345.	0.7	0
56	X-ray Crystallography and Computational Docking for the Detection and Development of Protein-Ligand Interactions. <i>Current Medicinal Chemistry</i> , 2013, 20, 569-575.	1.2	14
57	Crystal structure of D-serine dehydratase from <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 422-432.	1.1	20
58	Structural Evidence for a Copper-Bound Carbonate Intermediate in the Peroxidase and Dismutase Activities of Superoxide Dismutase. <i>PLoS ONE</i> , 2012, 7, e44811.	1.1	20
59	Proton-Coupled Electron Transfer in the Catalytic Cycle of <i>Alcaligenes xylosoxidans</i> Copper-Dependent Nitrite Reductase. <i>Biochemistry</i> , 2011, 50, 4121-4131.	1.2	64
60	Distal-to-Proximal NO Conversion in Hemoproteins: The Role of the Proximal Pocket. <i>Journal of Molecular Biology</i> , 2011, 405, 395-409.	2.0	30
61	Monitoring and validating active site redox states in protein crystals. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 778-784.	1.1	38
62	Carbon monoxide poisoning is prevented by the energy costs of conformational changes in gas-binding haemproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15780-15785.	3.3	34
63	Structural Discovery of Small Molecule Binding Sites in Cu <sup>2+</sup> Zn Human Superoxide Dismutase Familial Amyotrophic Lateral Sclerosis Mutants Provides Insights for Lead Optimization. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 1402-1406.	2.9	31
64	Structure of hypothetical Mo-cofactor biosynthesis protein B (ST2315) from <i>Sulfolobus tokodaii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1200-1203.	0.7	2
65	Structure of SurE protein from <i>Aquifex aeolicus</i> VF5 at 1.5 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1204-1208.	0.7	6
66	The structure of an archaeal ribose-5-phosphate isomerase from <i>Methanocaldococcus jannaschii</i> (MJ1603). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1214-1217.	0.7	5
67	Structure of D-lactate dehydrogenase from <i>Aquifex aeolicus</i> complexed with NAD <sup>+</sup> and lactic acid (or pyruvate). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1209-1213.	0.7	20
68	Structure of a putative Î <sup>2</sup> -phosphoglucomutase (TM1254) from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1218-1221.	0.7	2
69	Structure of dihydrodipicolinate synthase from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1222-1226.	0.7	14
70	Structure of glyceraldehyde-3-phosphate dehydrogenase from the archaeal hyperthermophile <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1227-1233.	0.7	11
71	Structure of putative 4-amino-4-deoxychorismate lyase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1234-1239.	0.7	7
72	The Structure of Human Extracellular Copper-Zinc Superoxide Dismutase at 1.7 Å Resolution: Insights into Heparin and Collagen Binding. <i>Journal of Molecular Biology</i> , 2009, 388, 310-326.	2.0	104

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73	Structural and biophysical properties of metal-free pathogenic SOD1 mutants A4V and G93A. Archives of Biochemistry and Biophysics, 2009, 492, 40-47.	1.4	74
74	Crystal structure of human prion protein bound to a therapeutic antibody. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2554-2558.	3.3	108
75	Crystallography with Online Optical and X-ray Absorption Spectroscopies Demonstrates an Ordered Mechanism in Copper Nitrite Reductase. Journal of Molecular Biology, 2008, 378, 353-361.	2.0	82
76	Structures of the G85R Variant of SOD1 in Familial Amyotrophic Lateral Sclerosis. Journal of Biological Chemistry, 2008, 283, 16169-16177.	1.6	85
77	Variable Metallation of Human Superoxide Dismutase: Atomic Resolution Crystal Structures of Cu <sup>2+</sup> Zn, Zn <sup>2+</sup> Zn and As-isolated Wild-type Enzymes. Journal of Molecular Biology, 2006, 356, 1152-1162.	2.0	156
78	Insight into Catalysis of Nitrous Oxide Reductase from High-resolution Structures of Resting and Inhibitor-bound Enzyme from Achromobacter cycloclastes. Journal of Molecular Biology, 2006, 362, 55-65.	2.0	85
79	X-ray diffraction study of the complex of the enzyme SAICAR synthase with the reaction product. Crystallography Reports, 2006, 51, 824-827.	0.1	3
80	A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. Journal of Synchrotron Radiation, 2005, 12, 455-466.	1.0	39
81	Atomic resolution structures of resting-state, substrate- and product-complexed Cu-nitrite reductase provide insight into catalytic mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12041-12046.	3.3	173
82	High Resolution Structural Studies of Mutants Provide Insights into Catalysis and Electron Transfer Processes in Copper Nitrite Reductase. Journal of Molecular Biology, 2005, 350, 300-309.	2.0	42
83	Structural consequences of the familial amyotrophic lateral sclerosis SOD1 mutant His46Arg. Protein Science, 2005, 14, 1201-1213.	3.1	75
84	Dimer destabilization in superoxide dismutase may result in disease-causing properties: Structures of motor neuron disease mutants. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5976-5981.	3.3	198
85	Observation of an Unprecedented Cu Bis-His Site: Crystal Structure of the H129V Mutant of Nitrite Reductase. Inorganic Chemistry, 2004, 43, 7591-7593.	1.9	10
86	Insights into Redox Partner Interactions and Substrate Binding in Nitrite Reductase from Alcaligenes xylosoxidans: Crystal Structures of the Trp138His and His313Gln Mutants. Biochemistry, 2004, 43, 16311-16319.	1.2	25
87	The structure of glyceraldehyde 3-phosphate dehydrogenase from Alcaligenes xylosoxidans at 1.7 Å resolution. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 835-842.	2.5	12
88	Amyloid-like filaments and water-filled nanotubes formed by SOD1 mutant proteins linked to familial ALS. Nature Structural and Molecular Biology, 2003, 10, 461-467.	3.6	311
89	X-ray diffraction study of the complex of the enzyme SAICAR synthase with substrate analogues. Crystallography Reports, 2003, 48, 763-767.	0.1	6
90	The Structure of Holo and Metal-deficient Wild-type Human Cu, Zn Superoxide Dismutase and its Relevance to Familial Amyotrophic Lateral Sclerosis. Journal of Molecular Biology, 2003, 328, 877-891.	2.0	222

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91	Crystal Structures of the Met148Leu and Ser86Asp Mutants of Rusticyanin from Thiobacillus ferrooxidans: Insights into the Structural Relationship with the Cupredoxins and the Multi Copper Proteins. <i>Journal of Molecular Biology</i> , 2002, 320, 263-275.	2.0	43
92	Resolution improvement from 'in situ annealing' of copper nitrite reductase crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 456-458.	2.5	12
93	X-ray diffraction study of the complexes of SAICAR synthase with adenosinetriphosphate. <i>Crystallography Reports</i> , 2001, 46, 620-625.	0.1	6
94	Crystal Structure of Manganese Catalase from <i>Lactobacillus plantarum</i> . <i>Structure</i> , 2001, 9, 725-738.	1.6	314
95	Improving the X-ray resolution by reversible flash-cooling combined with concentration screening, as exemplified with PPase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 595-603.	2.5	17
96	Three-dimensional structure of the enzyme dimanganese catalase from <i>Thermus Thermophilus</i> at 1 Å resolution. <i>Crystallography Reports</i> , 2000, 45, 105-116.	0.1	136
97	The Oxidized (3,3) State of Manganese Catalase. Comparison of Enzymes from <i>Thermus thermophilus</i> and <i>Lactobacillus plantarum</i> . <i>Biochemistry</i> , 1999, 38, 9126-9136.	1.2	84