

# 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	Crystal Structure of Manganese Catalase from <i>Lactobacillus plantarum</i> . <i>Structure</i> , 2001, 9, 725-738.	1.6	314
2	Amyloid-like filaments and water-filled nanotubes formed by SOD1 mutant proteins linked to familial ALS. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 461-467.	3.6	311
3	The Structure of Holo and Metal-deficient Wild-type Human Cu, Zn Superoxide Dismutase and its Relevance to Familial Amyotrophic Lateral Sclerosis. <i>Journal of Molecular Biology</i> , 2003, 328, 877-891.	2.0	222
4	Dimer destabilization in superoxide dismutase may result in disease-causing properties: Structures of motor neuron disease mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5976-5981.	3.3	198
5	Atomic resolution structures of resting-state, substrate- and product-complexed Cu-nitrite reductase provide insight into catalytic mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12041-12046.	3.3	173
6	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. <i>Journal of Molecular Biology</i> , 2006, 356, 1152-1162.	2.0	156
7	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
8	Transport of gabapentin by LAT1 (SLC7A5). <i>Biochemical Pharmacology</i> , 2013, 85, 1672-1683.	2.0	120
9	Crystal structure of human prion protein bound to a therapeutic antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2554-2558.	3.3	108
10	The Structure of Human Extracellular Copper <sup>2+</sup> 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
11	Sub-atomic resolution X-ray crystallography and neutron crystallography: promise, challenges and potential. <i>IUCr</i> , 2015, 2, 464-474.	1.0	104
12	Ligand binding and aggregation of pathogenic SOD1. <i>Nature Communications</i> , 2013, 4, 1758.	5.8	90
13	Antimalarial 4(1H)-pyridones bind to the Q <sub>i</sub> site of cytochrome <sub>bc<sub>1</sub></sub> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 755-760.	3.3	90
14	Insight into Catalysis of Nitrous Oxide Reductase from High-resolution Structures of Resting and Inhibitor-bound Enzyme from <i>Achromobacter cycloclastes</i> . <i>Journal of Molecular Biology</i> , 2006, 362, 55-65.	2.0	85
15	Structures of the G85R Variant of SOD1 in Familial Amyotrophic Lateral Sclerosis. <i>Journal of Biological Chemistry</i> , 2008, 283, 16169-16177.	1.6	85
16	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
17	Crystallography with Online Optical and X-ray Absorption Spectroscopies Demonstrates an Ordered Mechanism in Copper Nitrite Reductase. <i>Journal of Molecular Biology</i> , 2008, 378, 353-361.	2.0	82
18	Structural consequences of the familial amyotrophic lateral sclerosis SOD1 mutant His46Arg. <i>Protein Science</i> , 2005, 14, 1201-1213.	3.1	75

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19	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
20	The cysteine-reactive small molecule ebselen facilitates effective SOD1 maturation. Nature Communications, 2018, 9, 1693.	5.8	71
21	Disease causing mutants of TDP-43 nucleic acid binding domains are resistant to aggregation and have increased stability and half-life. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4309-4314.	3.3	68
22	Structures of proteinâ€“protein complexes involved in electron transfer. Nature, 2013, 496, 123-126.	13.7	65
23	Proton-Coupled Electron Transfer in the Catalytic Cycle of <i>Alcaligenes xylosoxidans</i> Copper-Dependent Nitrite Reductase. Biochemistry, 2011, 50, 4121-4131.	1.2	64
24	Modulation of LAT1 (SLC7A5) transporter activity and stability by membrane cholesterol. Scientific Reports, 2017, 7, 43580.	1.6	59
25	Serial crystallography captures enzyme catalysis in copper nitrite reductase at atomic resolution from one crystal. IUCr, 2016, 3, 271-281.	1.0	56
26	The biophysics of superoxide dismutase-1 and amyotrophic lateral sclerosis. Quarterly Reviews of Biophysics, 2019, 52, e12.	2.4	51
27	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. Journal of Molecular Biology, 2002, 320, 263-275.	2.0	43
28	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
29	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. Scientific Reports, 2016, 6, 29179.	1.6	40
30	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
31	Monitoring and validating active site redox states in protein crystals. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 778-784.	1.1	38
32	Architecture of the complete oxygen-sensing FixL-FixJ two-component signal transduction system. Science Signaling, 2018, 11, .	1.6	38
33	Molecular recognition and maturation of SOD1 by its evolutionarily destabilised cognate chaperone hCCS. PLoS Biology, 2019, 17, e3000141.	2.6	38
34	Impact of residues remote from the catalytic centre on enzyme catalysis of copper nitrite reductase. Nature Communications, 2014, 5, 4395.	5.8	36
35	Structure and function study of the complex that synthesizes <i>S</i> -adenosylmethionine. IUCr, 2014, 1, 240-249.	1.0	36
36	The expanding toolkit for structural biology: synchrotrons, X-ray lasers and cryoEM. IUCr, 2019, 6, 167-177.	1.0	36

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37	Crystallography captures catalytic steps in human methionine adenosyltransferase enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2104-2109.	3.3	35
38	Carbon monoxide poisoning is prevented by the energy costs of conformational changes in gas-binding haemproteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15780-15785.	3.3	34
39	A faulty interaction between SOD1 and hCCS in neurodegenerative disease. Scientific Reports, 2016, 6, 27691.	1.6	34
40	Crystal Structure of the Japanese Encephalitis Virus Capsid Protein. Viruses, 2019, 11, 623.	1.5	32
41	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. Journal of Medicinal Chemistry, 2010, 53, 1402-1406.	2.9	31
42	Distal-to-Proximal NO Conversion in Hemoproteins: The Role of the Proximal Pocket. Journal of Molecular Biology, 2011, 405, 395-409.	2.0	30
43	Ebselen as template for stabilization of A4V mutant dimer for motor neuron disease therapy. Communications Biology, 2020, 3, 97.	2.0	30
44	Biophysical and functional characterization of hippocalcin mutants responsible for human dystonia. Human Molecular Genetics, 2017, 26, 2426-2435.	1.4	29
45	Potent Antimalarial 2-Pyrazolyl Quinolone <i>bc</i> ( <i>Q</i> ) Inhibitors with Improved Drug-like Properties. ACS Medicinal Chemistry Letters, 2018, 9, 1205-1210.	1.3	28
46	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. IUCr, 2018, 5, 22-31.	1.0	27
47	The structure of a purple acid phosphatase involved in plant growth and pathogen defence exhibits a novel immunoglobulin-like fold. IUCr, 2014, 1, 101-109.	1.0	26
48	Enzyme catalysis captured using multiple structures from one crystal at varying temperatures. IUCr, 2018, 5, 283-292.	1.0	26
49	Insights into Redox Partner Interactions and Substrate Binding in Nitrite Reductase from <i>Alcaligenes xylosoxidans</i> : Crystal Structures of the Trp138His and His313Gln Mutants. Biochemistry, 2004, 43, 16311-16319.	1.2	25
50	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. Science Advances, 2021, 7, .	4.7	25
51	Structural Study of the C-Terminal Domain of Nonstructural Protein 1 from Japanese Encephalitis Virus. Journal of Virology, 2018, 92, .	1.5	24
52	<i>Tannerella forsythia</i> Tfo belongs to <i>Porphyromonas gingivalis</i> HmuY-like family of proteins but differs in heme-binding properties. Bioscience Reports, 2018, 38, .	1.1	24
53	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. IUCr, 2019, 6, 761-772.	1.0	24
54	X-ray and cryo-EM structures of inhibitor-bound cytochrome <i>bc</i> <sub>1</sub> complexes for structure-based drug discovery. IUCr, 2018, 5, 200-210.	1.0	23

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55	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
56	Potent Tetrahydroquinolone Eliminates Apicomplexan Parasites. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 203.	1.8	21
57	<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
58	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
59	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
60	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
61	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
62	Purification and Structural Characterization of Aggregation-Prone Human TDP-43 Involved in Neurodegenerative Diseases. <i>IScience</i> , 2020, 23, 101159.	1.9	19
63	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
64	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
65	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
66	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
67	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
68	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
69	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryo-electron microscopy. <i>Science Advances</i> , 2019, 5, eaax1803.	4.7	14
70	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
71	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
72	<i>Talaromyces marneffei</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

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73	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
74	The structure of glyceraldehyde 3-phosphate dehydrogenase from <i>Alcaligenes xylosoxidans</i> at 1.7 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 835-842.	2.5	12
75	Reverse protein engineering of a novel domain copper nitrite reductase reveals functional regulation by protein-protein interaction. <i>FEBS Journal</i> , 2021, 288, 262-280.	2.2	12
76	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
77	Observation of an Unprecedented Cu Bis-His Site: Crystal Structure of the H129V Mutant of Nitrite Reductase. <i>Inorganic Chemistry</i> , 2004, 43, 7591-7593.	1.9	10
78	Identification of a tyrosine switch in copper-haem nitrite reductases. <i>IUCr</i> , 2018, 5, 510-518.	1.0	10
79	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
80	Control and regulation of S-adenosylmethionine biosynthesis by the regulatory $\beta^2$ subunit and quinolone-based compounds. <i>FEBS Journal</i> , 2019, 286, 2135-2154.	2.2	9
81	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
82	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
83	X-ray diffraction study of the complexes of SAICAR synthase with adenosinetriphosphate. <i>Crystallography Reports</i> , 2001, 46, 620-625.	0.1	6
84	X-ray diffraction study of the complex of the enzyme SAICAR synthase with substrate analogues. <i>Crystallography Reports</i> , 2003, 48, 763-767.	0.1	6
85	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
86	Nature of the copper-nitrosyl intermediates of copper nitrite reductases during catalysis. <i>Chemical Science</i> , 2020, 11, 12485-12492.	3.7	6
87	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
88	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
89	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
90	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

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91	X-ray diffraction study of the complex of the enzyme SAICAR synthase with the reaction product. <i>Crystallography Reports</i> , 2006, 51, 824-827.	0.1	3
92	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
93	Structure of a putative $\hat{\text{I}}^2$ -phosphoglucomutase (TM1254) from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1218-1221.	0.7	2
94	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
95	Dystonia-Associated Hippocalcin Mutants Dysregulate Cellular Calcium Influx. <i>Biophysical Journal</i> , 2018, 114, 467a-468a.	0.2	0
96	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
97	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