

# Natalie C J Strynadka

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4339198/publications.pdf>

Version: 2024-02-01

77  
papers

4,387  
citations

117625

34  
h-index

114465

63  
g-index

77  
all docs

77  
docs citations

77  
times ranked

4817  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the <i>Propionibacterium acnes</i> surface sialidase, a drug target for <i>P. acnes</i> -associated diseases. <i>Glycobiology</i> , 2022, 32, 162-170.	2.5	2
2	The hinge region of the Israeli acute paralysis virus internal ribosome entry site directs ribosomal positioning, translational activity and virus infection. <i>Journal of Virology</i> , 2022, , JVI0133021.	3.4	2
3	The Impact of Second Coordination Sphere Methionine-Aromatic Interactions in Copper Proteins. <i>Inorganic Chemistry</i> , 2022, 61, 5563-5571.	4.0	4
4	Structural and Cellular Insights into the <i>scpI</i> , <i>scpD</i> -Transpeptidase YcbB as a Therapeutic Target in <i>Citrobacter rodentium</i> , <i>Salmonella</i> Typhimurium, and <i>Salmonella</i> Typhi Infections. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	5
5	Characterization of the Pilotin-Secretin Complex from the <i>Salmonella enterica</i> Type III Secretion System Using Hybrid Structural Methods. <i>Structure</i> , 2021, 29, 125-138.e5.	3.3	9
6	Computationally designed peptide macrocycle inhibitors of New Delhi metallo- $\beta$ -lactamase 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
7	Cryo-EM structure of the EspA filament from enteropathogenic <i>Escherichia coli</i> : Revealing the mechanism of effector translocation in the T3SS. <i>Structure</i> , 2021, 29, 479-487.e4.	3.3	7
8	CryoEM structure of the antibacterial target PBP1b at 3.3Å resolution. <i>Nature Communications</i> , 2021, 12, 2775.	12.8	10
9	The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. <i>Structure</i> , 2021, 29, 467-478.e6.	3.3	9
10	PBP4-mediated $\beta$ -lactam resistance among clinical strains of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2268-2272.	3.0	5
11	Crystallographic analysis of TarI and TarJ, a cytidyltransferase and reductase pair for CDP-ribitol synthesis in <i>Staphylococcus aureus</i> wall teichoic acid biogenesis. <i>Journal of Structural Biology</i> , 2021, 213, 107733.	2.8	1
12	Hybrid structural methods to probe atomic features of the Type III Secretion Injectisome of Pathogenic Bacteria. <i>Microscopy and Microanalysis</i> , 2021, 27, 826-827.	0.4	0
13	Structural Insights into the Inhibition of Undecaprenyl Pyrophosphate Synthase from Gram-Positive Bacteria. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13540-13550.	6.4	2
14	Automated discovery of noncovalent inhibitors of SARS-CoV-2 main protease by consensus Deep Docking of 40 billion small molecules. <i>Chemical Science</i> , 2021, 12, 15960-15974.	7.4	36
15	Structural insight into the <i>Staphylococcus aureus</i> ATP-driven exporter of virulent peptide toxins. <i>Science Advances</i> , 2020, 6, .	10.3	9
16	SPOR Proteins Are Required for Functionality of Class A Penicillin-Binding Proteins in <i>Escherichia coli</i> . <i>MBio</i> , 2020, 11, .	4.1	15
17	Crystallographic structure of wild-type SARS-CoV-2 main protease acyl-enzyme intermediate with physiological C-terminal autoprocessing site. <i>Nature Communications</i> , 2020, 11, 5877.	12.8	141
18	Cryo-EM analysis of the SctV cytosolic domain from the enteropathogenic <i>E. coli</i> T3SS injectisome. <i>Journal of Structural Biology</i> , 2020, 212, 107660.	2.8	19

#	ARTICLE	IF	CITATIONS
19	Structural analysis of avibactam-mediated activation of the bla and mec divergons in methicillin-resistant Staphylococcus aureus. Journal of Biological Chemistry, 2020, 295, 10870-10884.	3.4	7
20	Crystallographic analysis of Staphylococcus aureus LcpA, the primary wall teichoic acid ligase. Journal of Biological Chemistry, 2020, 295, 2629-2639.	3.4	23
21	A Slippery Scaffold: Synthesis and Recycling of the Bacterial Cell Wall Carrier Lipid. Journal of Molecular Biology, 2020, 432, 4964-4982.	4.2	23
22	Structure of the Peptidoglycan Synthase Activator LpoP in Pseudomonas aeruginosa. Structure, 2020, 28, 643-650.e5.	3.3	9
23	Aligning the Symmetry of the Type III Secretion System Needle Complex. Journal of Chemical Information and Modeling, 2020, 60, 2430-2435.	5.4	7
24	T3S injectisome needle complex structures in four distinct states reveal the basis of membrane coupling and assembly. Nature Microbiology, 2019, 4, 2010-2019.	13.3	58
25	A Hybrid Secretion System Facilitates Bacterial Sporulation: A Structural Perspective. Microbiology Spectrum, 2019, 7, .	3.0	10
26	On the road to structure-based development of anti-virulence therapeutics targeting the type III secretion system injectisome. MedChemComm, 2019, 10, 1273-1289.	3.4	18
27	Structural Insights into Bacteriophage GIL01 gp7 Inhibition of Host LexA Repressor. Structure, 2019, 27, 1094-1102.e4.	3.3	17
28	Structural insight into YcbB-mediated beta-lactam resistance in Escherichia coli. Nature Communications, 2019, 10, 1849.	12.8	29
29	Cryo-EM structure of the homohexameric T3SS ATPase-central stalk complex reveals rotary ATPase-like asymmetry. Nature Communications, 2019, 10, 626.	12.8	58
30	PBP4 activity and its overexpression are necessary for PBP4-mediated high-level $\beta$ -lactam resistance. Journal of Antimicrobial Chemotherapy, 2018, 73, 1177-1180.	3.0	19
31	Structural characterization of SpoIIIAB sporulation-essential protein in Bacillus subtilis. Journal of Structural Biology, 2018, 202, 105-112.	2.8	11
32	Crystal structure of an intramembranal phosphatase central to bacterial cell-wall peptidoglycan biosynthesis and lipid recycling. Nature Communications, 2018, 9, 1159.	12.8	43
33	IpdAB, a virulence factor in <i>Mycobacterium tuberculosis</i> , is a cholesterol ring-cleaving hydrolase. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3378-E3387.	7.1	28
34	Cryo-EM analysis of the T3S injectisome reveals the structure of the needle and open secretin. Nature Communications, 2018, 9, 3840.	12.8	106
35	Structural Basis for Binding of Fluorescent CMP-Neu5Ac Mimetics to Enzymes of the Human ST8Sia Family. ACS Chemical Biology, 2018, 13, 2320-2328.	3.4	6
36	Characterization of the two conformations adopted by the T3SS inner-membrane protein PrgK. Protein Science, 2018, 27, 1680-1691.	7.6	4

#	ARTICLE	IF	CITATIONS
37	Insights into Heptosyltransferase I Catalysis and Inhibition through the Structure of Its Ternary Complex. <i>Structure</i> , 2018, 26, 1399-1407.e5.	3.3	18
38	Structural and biochemical characterization of SpoIIAF, a component of a sporulation-essential channel in <i>Bacillus subtilis</i> . <i>Journal of Structural Biology</i> , 2018, 204, 1-8.	2.8	12
39	Recognition of Peptidoglycan Fragments by the Transpeptidase PBP4 From <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3223.	3.5	23
40	Structural Insights into Inhibition of <i>Escherichia coli</i> Penicillin-binding Protein 1B. <i>Journal of Biological Chemistry</i> , 2017, 292, 979-993.	3.4	42
41	High-Level Resistance of <i>Staphylococcus aureus</i> to $\beta$ -Lactam Antibiotics Mediated by Penicillin-Binding Protein 4 (PBP4). <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	44
42	Assembly, structure, function and regulation of type III secretion systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 323-337.	28.6	456
43	X-ray crystallographic structure of a bacterial polysialyltransferase provides insight into the biosynthesis of capsular polysialic acid. <i>Scientific Reports</i> , 2017, 7, 5842.	3.3	13
44	One ring to rule them all: Current trends in combating bacterial resistance to the $\beta$ -lactams. <i>Protein Science</i> , 2016, 25, 787-803.	7.6	72
45	Near-atomic-resolution cryo-EM analysis of the <i>Salmonella</i> T3S injectisome basal body. <i>Nature</i> , 2016, 540, 597-601.	27.8	127
46	Structural and Kinetic Characterization of Diazabicyclooctanes as Dual Inhibitors of Both Serine- $\beta$ -Lactamases and Penicillin-Binding Proteins. <i>ACS Chemical Biology</i> , 2016, 11, 864-868.	3.4	52
47	The Modular Structure of the Inner-Membrane Ring Component PrgK Facilitates Assembly of the Type III Secretion System Basal Body. <i>Structure</i> , 2015, 23, 161-172.	3.3	43
48	Structure of EspB from the ESX-1 Type VII Secretion System and Insights into its Export Mechanism. <i>Structure</i> , 2015, 23, 571-583.	3.3	85
49	Molecular Mechanism of Avibactam-Mediated $\beta$ -Lactamase Inhibition. <i>ACS Infectious Diseases</i> , 2015, 1, 175-184.	3.8	80
50	The <i>Salmonella</i> Type III Secretion System Virulence Effector Forms a New Hexameric Chaperone Assembly for Export of Effector/Chaperone Complexes. <i>Journal of Bacteriology</i> , 2015, 197, 672-675.	2.2	11
51	Structure of human ST8SialII sialyltransferase provides insight into cell-surface polysialylation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 627-635.	8.2	62
52	Assay for drug discovery: Synthesis and testing of nitrocefin analogues for use as $\beta$ -lactamase substrates. <i>Analytical Biochemistry</i> , 2015, 486, 75-77.	2.4	15
53	Structural Analysis of a Specialized Type III Secretion System Peptidoglycan-cleaving Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 10406-10417.	3.4	43
54	Structural analysis of SepL, an enteropathogenic <i>Escherichia coli</i> type III secretion-system gatekeeper protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1300-1308.	0.8	10

#	ARTICLE	IF	CITATIONS
55	Antagonism screen for inhibitors of bacterial cell wall biogenesis uncovers an inhibitor of undecaprenyl diphosphate synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11048-11053.	7.1	83
56	Structural Insights into the Lipoprotein Outer Membrane Regulator of Penicillin-binding Protein 1B. <i>Journal of Biological Chemistry</i> , 2014, 289, 19245-19253.	3.4	17
57	Assembly and structure of the T3SS. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1649-1663.	4.1	114
58	Fortifying the wall: synthesis, regulation and degradation of bacterial peptidoglycan. <i>Current Opinion in Structural Biology</i> , 2013, 23, 695-703.	5.7	37
59	A Refined Model of the Prototypical Salmonella SPI-1 T3SS Basal Body Reveals the Molecular Basis for Its Assembly. <i>PLoS Pathogens</i> , 2013, 9, e1003307.	4.7	76
60	Structural and Kinetic Analysis of Substrate Binding to the Sialyltransferase Cst-II from <i>Campylobacter jejuni</i> *. <i>Journal of Biological Chemistry</i> , 2011, 286, 35922-35932.	3.4	27
61	Interactions of the Transmembrane Polymeric Rings of the Salmonella enterica Serovar Typhimurium Type III Secretion System. <i>MBio</i> , 2010, 1, .	4.1	37
62	A conserved structural motif mediates formation of the periplasmic rings in the type III secretion system. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 468-476.	8.2	170
63	Structural analysis of the essential self-cleaving type III secretion proteins EscU and SpaS. <i>Nature</i> , 2008, 453, 124-127.	27.8	124
64	Identification of Dynamic Structural Motifs Involved in Peptidoglycan Glycosyltransfer. <i>Journal of Molecular Biology</i> , 2008, 383, 167-177.	4.2	44
65	High-resolution Structure of the Major Periplasmic Domain from the Cell Shape-determining Filament MreC. <i>Journal of Molecular Biology</i> , 2007, 372, 1034-1044.	4.2	25
66	Structural Insight into the Transglycosylation Step of Bacterial Cell-Wall Biosynthesis. <i>Science</i> , 2007, 315, 1402-1405.	12.6	290
67	Structural analysis of a prototypical ATPase from the type III secretion system. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 131-137.	8.2	123
68	Structural characterization of the molecular platform for type III secretion system assembly. <i>Nature</i> , 2005, 435, 702-707.	27.8	169
69	Enteropathogenic Escherichia coli translocated intimin receptor, Tir, requires a specific chaperone for stable secretion. <i>Molecular Microbiology</i> , 2002, 33, 1162-1175.	2.5	133
70	The Structure of Ribulose-5-Phosphate 4-Epimerase: An Aldolase-like Platform for Epimerization. <i>Biochemistry</i> , 2001, 40, 14763-14771.	2.5	38
71	Effect of Divalent Metal Cations on the Dimerization of OXA-10 and -14 Class D $\beta$ -Lactamases from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 2001, 40, 9412-9420.	2.5	33
72	Crystal structure of enteropathogenic Escherichia coli intimin receptor complex. <i>Nature</i> , 2000, 405, 1073-1077.	27.8	302

#	ARTICLE	IF	CITATIONS
73	The Structure of UDP-N-Acetylglucosamine 2-Epimerase Reveals Homology to Phosphoglycosyl Transferases,. <i>Biochemistry</i> , 2000, 39, 14993-15001.	2.5	108
74	The First Structure of UDP-Glucose Dehydrogenase Reveals the Catalytic Residues Necessary for the Two-fold Oxidation<sup></sup>. <i>Biochemistry</i> , 2000, 39, 7012-7023.	2.5	100
75	Common protein architecture and binding sites in proteases utilizing a Ser/Lys dyad mechanism. <i>Protein Science</i> , 1999, 8, 2533-2536.	7.6	45
76	Crystal structure of a bacterial signal peptidase in complex with a $\beta$ -lactam inhibitor. <i>Nature</i> , 1998, 396, 186-190.	27.8	291
77	Host Receptors of Bacterial Origin. , 0, , 49-68.		0