

Yorgo Modis

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76 papers	7,361 citations	40 h-index	85 g-index
90 ext. papers	8,475 ext. citations	11.7 avg, IF	5.91 L-index

#	Paper	IF	Citations
76	X-ray structure of a protein-conducting channel. <i>Nature</i> , 2004 , 427, 36-44	50.4	994
75	Structure of the dengue virus envelope protein after membrane fusion. <i>Nature</i> , 2004 , 427, 313-9	50.4	866
74	A ligand-binding pocket in the dengue virus envelope glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6986-91	11.5	806
73	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021 , 592, 277-282	50.4	390
72	Variable surface epitopes in the crystal structure of dengue virus type 3 envelope glycoprotein. <i>Journal of Virology</i> , 2005 , 79, 1223-31	6.6	338
71	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. <i>Cancer Cell</i> , 2015 , 27, 617-30	24.3	337
70	Quantification of the affinities and kinetics of protein interactions using silicon nanowire biosensors. <i>Nature Nanotechnology</i> , 2012 , 7, 401-7	28.7	273
69	Pattern Recognition and Signaling Mechanisms of RIG-I and MDA5. <i>Frontiers in Immunology</i> , 2014 , 5, 3428.4		238
68	Atomic model of the papillomavirus capsid. <i>EMBO Journal</i> , 2002 , 21, 4754-62	13	197
67	Crystal structure of west nile virus envelope glycoprotein reveals viral surface epitopes. <i>Journal of Virology</i> , 2006 , 80, 11000-8	6.6	191
66	Chitinase 3-like 1 regulates cellular and tissue responses via IL-13 receptor α . <i>Cell Reports</i> , 2013 , 4, 830-410.6		175
65	MDA5 cooperatively forms dimers and ATP-sensitive filaments upon binding double-stranded RNA. <i>EMBO Journal</i> , 2012 , 31, 1714-26	13	136
64	Virus-like particle-based human vaccines: quality assessment based on structural and functional properties. <i>Trends in Biotechnology</i> , 2013 , 31, 654-63	15.1	135
63	RNA:DNA hybrids are a novel molecular pattern sensed by TLR9. <i>EMBO Journal</i> , 2014 , 33, 542-58	13	111
62	Crystal structure of dengue virus type 1 envelope protein in the postfusion conformation and its implications for membrane fusion. <i>Journal of Virology</i> , 2009 , 83, 4338-44	6.6	107
61	The 1.8 Å crystal structure of the dimeric peroxisomal 3-ketoacyl-CoA thiolase of <i>Saccharomyces cerevisiae</i> : implications for substrate binding and reaction mechanism. <i>Journal of Molecular Biology</i> , 1997 , 273, 714-28	6.5	98
60	Crystallographic analysis of the reaction pathway of <i>Zoogloea ramigera</i> biosynthetic thiolase. <i>Journal of Molecular Biology</i> , 2000 , 297, 1171-82	6.5	92

59	MDA5 assembles into a polar helical filament on dsRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18437-41	11.5	91
58	Crystal structure of glycoprotein E2 from bovine viral diarrhea virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 6805-10	11.5	90
57	Crystal structure of glycoprotein C from Rift Valley fever virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1696-701	11.5	87
56	The crystal structure of dienoyl-CoA isomerase at 1.5 Å resolution reveals the importance of aspartate and glutamate sidechains for catalysis. <i>Structure</i> , 1998 , 6, 957-70	5.2	80
55	Crystal structure of an insect antifreeze protein and its implications for ice binding. <i>Journal of Biological Chemistry</i> , 2013 , 288, 12295-304	5.4	79
54	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016 , 7, 10882	17.4	78
53	Disassembly and reassembly of human papillomavirus virus-like particles produces more virion-like antibody reactivity. <i>Virology Journal</i> , 2012 , 9, 52	6.1	73
52	A biosynthetic thiolase in complex with a reaction intermediate: the crystal structure provides new insights into the catalytic mechanism. <i>Structure</i> , 1999 , 7, 1279-90	5.2	68
51	Hyperactivation of HUSH complex function by Charcot-Marie-Tooth disease mutation in MORC2. <i>Nature Genetics</i> , 2017 , 49, 1035-1044	36.3	65
50	The mu2 subunit of the clathrin adaptor AP-2 binds to FDNPVY and Ypp3 sorting signals at distinct sites. <i>Traffic</i> , 2002 , 3, 590-600	5.7	65
49	West Nile virus envelope protein inhibits dsRNA-induced innate immune responses. <i>Journal of Immunology</i> , 2007 , 179, 8403-9	5.3	58
48	IL-13Rα uses TMEM219 in chitinase 3-like-1-induced signalling and effector responses. <i>Nature Communications</i> , 2016 , 7, 12752	17.4	53
47	Viral membrane fusion and nucleocapsid delivery into the cytoplasm are distinct events in some flaviviruses. <i>PLoS Pathogens</i> , 2013 , 9, e1003585	7.6	51
46	N-glycosylation at the SynCAM (synaptic cell adhesion molecule) immunoglobulin interface modulates synaptic adhesion. <i>Journal of Biological Chemistry</i> , 2010 , 285, 34864-74	5.4	49
45	Structural basis of innate immune recognition of viral RNA. <i>Cellular Microbiology</i> , 2013 , 15, 386-94	3.9	48
44	DNA binding to proteolytically activated TLR9 is sequence-independent and enhanced by DNA curvature. <i>EMBO Journal</i> , 2012 , 31, 919-31	13	47
43	Structural studies of viperin, an antiviral radical SAM enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 6806-6811	11.5	46
42	Structure-based analysis of <i>Toxoplasma gondii</i> profilin: a parasite-specific motif is required for recognition by Toll-like receptor 11. <i>Journal of Molecular Biology</i> , 2010 , 403, 616-29	6.5	45

41	Endosomal vesicles as vehicles for viral genomes. <i>Trends in Cell Biology</i> , 2014 , 24, 449-54	18.3	44
40	Selective pressure causes an RNA virus to trade reproductive fitness for increased structural and thermal stability of a viral enzyme. <i>PLoS Genetics</i> , 2012 , 8, e1003102	6	44
39	Relating structure to evolution in class II viral membrane fusion proteins. <i>Current Opinion in Virology</i> , 2014 , 5, 34-41	7.5	43
38	Utilizing protein structure to identify non-random somatic mutations. <i>BMC Bioinformatics</i> , 2013 , 14, 190	3.6	42
37	Human interleukin-2 receptor 1 mutations associated with defects in immunity and peripheral tolerance. <i>Journal of Experimental Medicine</i> , 2019 , 216, 1311-1327	16.6	41
36	Crystal Structure of Glycoprotein C from a Hantavirus in the Post-fusion Conformation. <i>PLoS Pathogens</i> , 2016 , 12, e1005948	7.6	39
35	Neuropathic MORC2 mutations perturb GHKL ATPase dimerization dynamics and epigenetic silencing by multiple structural mechanisms. <i>Nature Communications</i> , 2018 , 9, 651	17.4	38
34	Cryo-EM Structures of MDA5-dsRNA Filaments at Different Stages of ATP Hydrolysis. <i>Molecular Cell</i> , 2018 , 72, 999-1012.e6	17.6	32
33	Toll-like receptor 5 forms asymmetric dimers in the absence of flagellin. <i>Journal of Structural Biology</i> , 2012 , 177, 402-9	3.4	31
32	A novel membrane fusion protein family in Flaviviridae?. <i>Trends in Microbiology</i> , 2014 , 22, 176-82	12.4	30
31	Peroxiredoxin-1 from the human hookworm <i>Ancylostoma ceylanicum</i> forms a stable oxidized decamer and is covalently inhibited by conoidin A. <i>Chemistry and Biology</i> , 2013 , 20, 991-1001		30
30	Class II fusion proteins. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 790, 150-66	3.6	28
29	Structure of KAP1 tripartite motif identifies molecular interfaces required for retroelement silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15042-15051	11.5	26
28	Two crystal structures of N-acetyltransferases reveal a new fold for CoA-dependent enzymes. <i>Structure</i> , 1998 , 6, 1345-50	5.2	25
27	A graph theoretic approach to utilizing protein structure to identify non-random somatic mutations. <i>BMC Bioinformatics</i> , 2014 , 15, 86	3.6	22
26	TASOR is a pseudo-PARP that directs HUSH complex assembly and epigenetic transposon control. <i>Nature Communications</i> , 2020 , 11, 4940	17.4	21
25	A spatial simulation approach to account for protein structure when identifying non-random somatic mutations. <i>BMC Bioinformatics</i> , 2014 , 15, 231	3.6	18
24	Physico-chemical requirements and kinetics of membrane fusion of flavivirus-like particles. <i>Journal of General Virology</i> , 2015 , 96, 1702-11	4.9	18

23	Protein crystallization for X-ray crystallography. <i>Journal of Visualized Experiments</i> , 2011 ,	1.6	13
22	Crystal structure of the dimeric coiled-coil domain of the cytosolic nucleic acid sensor LRRFIP1. <i>Journal of Structural Biology</i> , 2013 , 181, 82-8	3.4	12
21	Ancylostoma ceylanicum excretory-secretory protein 2 adopts a netrin-like fold and defines a novel family of nematode proteins. <i>Journal of Molecular Biology</i> , 2011 , 408, 9-17	6.5	12
20	MAVS polymers smaller than 80 nm induce mitochondrial membrane remodeling and interferon signaling. <i>FEBS Journal</i> , 2019 , 286, 1543-1560	5.7	11
19	FAMIN Is a Multifunctional Purine Enzyme Enabling the Purine Nucleotide Cycle. <i>Cell</i> , 2020 , 180, 278-295	6.23	11
18	Functional assessment and structural basis of antibody binding to human papillomavirus capsid. <i>Reviews in Medical Virology</i> , 2016 , 26, 115-28	11.7	10
17	P(I) Release Limits the Intrinsic and RNA-Stimulated ATPase Cycles of DEAD-Box Protein 5 (Dbp5). <i>Journal of Molecular Biology</i> , 2016 , 428, 492-508	6.5	9
16	Structural models of the membrane anchors of envelope glycoproteins E1 and E2 from pestiviruses. <i>Virology</i> , 2014 , 454-455, 93-101	3.6	8
15	Leveraging protein quaternary structure to identify oncogenic driver mutations. <i>BMC Bioinformatics</i> , 2016 , 17, 137	3.6	6
14	How influenza virus is locked out of the cell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18647-8	11.5	5
13	Exploiting structural biology in the fight against parasitic diseases. <i>Trends in Parasitology</i> , 2012 , 28, 124-30	3.4	4
12	Crystallization and X-ray diffraction analysis of peroxisomal Delta3-Delta2-enoyl-CoA isomerase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1020-3		3
11	Periphilin self-association underpins epigenetic silencing by the HUSH complex. <i>Nucleic Acids Research</i> , 2020 , 48, 10313-10328	20.1	3
10	Equilibrium Binding Model for CpG DNA-Dependent Dimerization of Toll-like Receptor 9 Ectodomain. <i>Biochemistry</i> , 2020 , 59, 4155-4162	3.2	3
9	Exploiting subtle structural differences in heavy-atom derivatives for experimental phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1873-83		2
8	Periphilin self-association underpins epigenetic silencing by the HUSH complex		2
7	TASOR is a pseudo-PARP that directs HUSH complex assembly and epigenetic transposon control		2
6	Imaging and visualizing SARS-CoV-2 in a new era for structural biology.. <i>Interface Focus</i> , 2021 , 11, 202100319	3.19	1

5	Structure of the tripartite motif of KAP1/TRIM28 identifies molecular interfaces required for transcriptional silencing of retrotransposons	1
4	MDA5 disease variant M854K prevents ATP-dependent structural discrimination of viral and cellular RNA. <i>Nature Communications</i> , 2021 , 12, 6668	17.4 ○
3	Molecular Mechanisms of Flaviviral Membrane Fusion 2009 , 265-286	○
2	A bioactive phlebovirus-like envelope protein in a hookworm endogenous virus.. <i>Science Advances</i> , 2022 , 8, eabj6894	14.3 ○
1	An Endogenous Retrovirus from Human Hookworm Encodes an Ancient Phlebovirus-Like Class II Envelope Fusion Protein. <i>Proceedings (mdpi)</i> , 2020 , 50, 33	0.3