

Hideaki Tsuge

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7260619/publications.pdf>

Version: 2024-02-01

77
papers

2,172
citations

218677

26
h-index

243625

44
g-index

81
all docs

81
docs citations

81
times ranked

2480
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM Structural Analysis of Binary Toxin: Nihon Kessho Gakkaishi, 2022, 64, 69-76.	0.0	0
2	Preparation of Clostridium perfringens binary iota-toxin pore complex for structural analysis using cryo-EM. Methods in Enzymology, 2021, 649, 125-148.	1.0	1
3	Common Mechanism for Target Specificity of Protein- and DNA-Targeting ADP-Ribosyltransferases. Toxins, 2021, 13, 40.	3.4	9
4	A myelin sheath protein forming its lattice. Journal of Biological Chemistry, 2020, 295, 8706-8707.	3.4	1
5	Cryo-EM structures reveal translocational unfolding in the clostridial binary iota toxin complex. Nature Structural and Molecular Biology, 2020, 27, 288-296.	8.2	21
6	Substrate N2 atom recognition mechanism in pierisin family DNA-targeting, guanine-specific ADP-ribosyltransferase ScARP. Journal of Biological Chemistry, 2018, 293, 13768-13774.	3.4	13
7	Precipitant-Free Lysozyme Crystals Grown by Centrifugal Concentration Reveal Structural Changes. Crystal Growth and Design, 2018, 18, 4226-4229.	3.0	5
8	Crystal structure and structure-based mutagenesis of actin-specific ADP-ribosylating toxin CPILe-a as novel enterotoxin. PLoS ONE, 2017, 12, e0171278.	2.5	9
9	Involvement of the Arg566 residue of Aeromonas sobria serine protease in substrate specificity. PLoS ONE, 2017, 12, e0186392.	2.5	3
10	<i>Anabaena</i> sp. DyP-type peroxidase is a tetramer consisting of two asymmetric dimers. Proteins: Structure, Function and Bioinformatics, 2016, 84, 31-42.	2.6	14
11	Comparative Studies of Actin- and Rho-Specific ADP-Ribosylating Toxins: Insight from Structural Biology. Current Topics in Microbiology and Immunology, 2016, 399, 69-86.	1.1	6
12	Conformational plasticity is crucial for C3-RhoA complex formation by ARTT-loop. Pathogens and Disease, 2015, 73, ftv094.	2.0	8
13	Structural Basis for Action of the External Chaperone for a Propeptide-deficient Serine Protease from Aeromonas sobria. Journal of Biological Chemistry, 2015, 290, 11130-11143.	3.4	7
14	Rho GTPase Recognition by C3 Exoenzyme Based on C3-RhoA Complex Structure. Journal of Biological Chemistry, 2015, 290, 19423-19432.	3.4	24
15	Enteric Toxins of Clostridium perfringens. , 2015, , 997-1013.		1
16	Crystallization and preliminary X-ray diffraction studies of a surface mutant of the middle domain of PB2 from human influenza A (H1N1) virus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 72-75.	0.8	3
17	Reaction Mechanism of Mono-ADP-Ribosyltransferase Based on Structures of the Complex of Enzyme and Substrate Protein. Current Topics in Microbiology and Immunology, 2014, 384, 69-87.	1.1	8
18	Substrate selectivity of bacterial monoacylglycerol lipase based on crystal structure. Journal of Structural and Functional Genomics, 2014, 15, 83-89.	1.2	6

#	ARTICLE	IF	CITATIONS
19	Arginine ADP-ribosylation mechanism based on structural snapshots of iota-toxin and actin complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4267-4272.	7.1	73
20	Conformational Polymorphism of m7GTP in Crystal Structure of the PB2 Middle Domain from Human Influenza A Virus. PLoS ONE, 2013, 8, e82020.	2.5	8
21	Crystal structures of dye-decolorizing peroxidase with ascorbic acid and 2,6-dimethoxyphenol. FEBS Letters, 2012, 586, 4351-4356.	2.8	43
22	Role of side-edge site of sphingomyelinase from Bacillus cereus. Biochemical and Biophysical Research Communications, 2012, 422, 128-132.	2.1	5
23	Role of Sphingomyelinase in Infectious Diseases Caused by Bacillus cereus. PLoS ONE, 2012, 7, e38054.	2.5	59
24	The catalytic mechanism of dye-decolorizing peroxidase DyP may require the swinging movement of an aspartic acid residue. FEBS Journal, 2011, 278, 2387-2394.	4.7	72
25	Structure and stability of Gyuba, a β -lactoglobulin chimera. Protein Science, 2011, 20, 1867-1875.	7.6	8
26	Structural Basis of Free Reduced Flavin Generation by Flavin Reductase from Thermus thermophilus HB8. Journal of Biological Chemistry, 2011, 286, 44078-44085.	3.4	9
27	Nucleolin as cell surface receptor for tumor necrosis factor- α inducing protein: a carcinogenic factor of Helicobacter pylori. Journal of Cancer Research and Clinical Oncology, 2010, 136, 911-921.	2.5	52
28	Clostridium perfringens Iota-Toxin: Structure and Function. Toxins, 2009, 1, 208-228.	3.4	64
29	Structural Basis for the Kexin-like Serine Protease from Aeromonas sobria as Sepsis-causing Factor. Journal of Biological Chemistry, 2009, 284, 27655-27663.	3.4	24
30	Structural analysis of human glutamine:fructose-6-phosphate amidotransferase, a key regulator in type 2 diabetes. FEBS Letters, 2009, 583, 163-167.	2.8	29
31	Non-native β -helix formation is not necessary for folding of lipocalin: Comparison of burst-phase folding between tear lipocalin and β -lactoglobulin. Proteins: Structure, Function and Bioinformatics, 2009, 76, 226-236.	2.6	11
32	Crystallization and X-ray diffraction analysis of the RNA primer/promoter-binding domain of influenza A virus RNA-dependent RNA polymerase PB2. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 144-146.	0.7	7
33	The carboxy-terminal tail of <i>Aeromonas sobria</i> serine protease is associated with the chaperone. Microbiology and Immunology, 2009, 53, 647-657.	1.4	5
34	Refolding, characterization and crystal structure of (S)-malate dehydrogenase from the hyperthermophilic archaeon Aeropyrum pernix. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1496-1504.	2.3	10
35	Crystal structure of the ADP-dependent glucokinase from Pyrococcus horikoshii at 2.0-Å... resolution: A large conformational change in ADP-dependent glucokinase. Protein Science, 2009, 11, 2456-2463.	7.6	40
36	Structural Basis of the Influenza A Virus RNA Polymerase PB2 RNA-binding Domain Containing the Pathogenicity-determinant Lysine 627 Residue. Journal of Biological Chemistry, 2009, 284, 6855-6860.	3.4	86

#	ARTICLE	IF	CITATIONS
37	Structural basis for the <i>Helicobacter pylori</i> -carcinogenic TNF- α -inducing protein. <i>Biochemical and Biophysical Research Communications</i> , 2009, 388, 193-198.	2.1	16
38	3P-004 Crystal structure of influenza virus RNA polymerase PB2 including host determinant residue K627(Protein:Structure,The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009, 49, S151.	0.1	0
39	Structure of an archaeal alanine:glyoxylate aminotransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 696-699.	2.5	4
40	Structure of L-aspartate oxidase from the hyperthermophilic archaeon <i>Sulfolobus tokodaii</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 563-571.	2.3	18
41	Crystal structure of the YdjC-family protein TTHB029 from <i>Thermus thermophilus</i> HB8: Structural relationship with peptidoglycan N-acetylglucosamine deacetylase. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 535-541.	2.1	10
42	Structural basis of actin recognition and arginine ADP-ribosylation by <i>Clostridium perfringens</i> β -toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7399-7404.	7.1	104
43	Sequential Aldol Condensation Catalyzed by Hyperthermophilic 2-Deoxy-5-Phosphate Aldolase. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7427-7434.	3.1	62
44	1P030 Molecular Mechanism of Actin Recognition by Arginine ADP-ribosylating Toxin(Proteins-functions, methodology, and protein engineering,Oral Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S31.	0.1	0
45	Structural basis of d-DOPA oxidation by d-amino acid oxidase: Alternative pathway for dopamine biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 385-391.	2.1	61
46	Structure of a Hyperthermophilic Archaeal Homing Endonuclease, I-Tsp061: Contribution of Cross-domain Polar Networks to Thermostability. <i>Journal of Molecular Biology</i> , 2007, 365, 362-378.	4.2	11
47	Human D-amino acid oxidase: an update and review. <i>Chemical Record</i> , 2007, 7, 305-315.	5.8	49
48	Crystal structure of archaeal highly thermostable L-aspartate dehydrogenase/NAD/citrate ternary complex. <i>FEBS Journal</i> , 2007, 274, 4315-4325.	4.7	14
49	Crystal structure of human D-amino acid oxidase: Context-dependent variability of the backbone conformation of the VAAGL hydrophobic stretch located at the face of the flavin ring. <i>Protein Science</i> , 2006, 15, 2708-2717.	7.6	102
50	Structural Basis of the Sphingomyelin Phosphodiesterase Activity in Neutral Sphingomyelinase from <i>Bacillus cereus</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 16157-16167.	3.4	82
51	Presence of a Motif Conserved between <i>Helicobacter pylori</i> TNF- α -Inducing Protein (Tip.ALPHA.) and Penicillin-Binding Proteins. <i>Biological and Pharmaceutical Bulletin</i> , 2005, 28, 2133-2137.	1.4	9
52	A second novel dye-linked L-proline dehydrogenase complex is present in the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT-3. <i>FEBS Journal</i> , 2005, 272, 4044-4054.	4.7	25
53	The first crystal structure of an archaeal helical repeat protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 636-639.	0.7	2
54	Crystal Structure of a Novel FAD-, FMN-, and ATP-containing L-Proline Dehydrogenase Complex from <i>Pyrococcus horikoshii</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 31045-31049.	3.4	39

#	ARTICLE	IF	CITATIONS
55	Crystal Structure of the NAD Biosynthetic Enzyme Quinolate Synthase. <i>Journal of Biological Chemistry</i> , 2005, 280, 26645-26648.	3.4	36
56	The First Crystal Structure of Hyperthermostable NAD-dependent Glutamate Dehydrogenase from <i>Pyrobaculum islandicum</i> . <i>Journal of Molecular Biology</i> , 2005, 345, 325-337.	4.2	47
57	Crystallization and preliminary X-ray diffraction analysis of the hyperthermostable NAD-dependent glutamate dehydrogenase from <i>Pyrobaculum islandicum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 715-717.	2.5	1
58	Crystallization and preliminary X-ray diffraction analysis of homing endonuclease I-Tsp0611. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2006-2008.	2.5	2
59	<i>Clostridium perfringens</i> $\hat{1}$ -toxin, ADP-ribosyltransferase: structure and mechanism of action. <i>Advances in Enzyme Regulation</i> , 2003, 43, 361-377.	2.6	26
60	Identification of 16 novel mutations in the argininosuccinate synthetase gene and genotype-phenotype correlation in 38 classical citrullinemia patients. <i>Human Mutation</i> , 2003, 22, 24-34.	2.5	71
61	Crystal Structure and Site-directed Mutagenesis of Enzymatic Components from <i>Clostridium perfringens</i> Iota-toxin. <i>Journal of Molecular Biology</i> , 2003, 325, 471-483.	4.2	94
62	The First Crystal Structure of Archaeal Aldolase. <i>Journal of Biological Chemistry</i> , 2003, 278, 10799-10806.	3.4	42
63	Crystal Structure and Function of Actin-Specific ADP Ribosyl Toxin.. <i>Seibutsu Butsuri</i> , 2003, 43, 168-173.	0.1	0
64	Chondroitin Sulfate Proteoglycan Is a Potent Enhancer in the Processing of Procathepsin L. <i>Biological Chemistry</i> , 2002, 383, 1925-9.	2.5	11
65	Crystallization and preliminary X-ray crystallographic studies of monoacylglycerol lipase of the moderately thermophilic <i>Bacillus</i> sp. H-257. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1232-1233.	2.5	2
66	Crystallization and preliminary X-ray diffraction analysis of glutamate dehydrogenase from an aerobic hyperthermophilic archaeon, <i>Aeropyrum pernix</i> K1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1338-1339.	2.5	1
67	Crystallization and Preliminary X-Ray Studies of the Ia Component of <i>Clostridium perfringens</i> Iota Toxin Complexed with NADPH. <i>Journal of Structural Biology</i> , 1999, 126, 175-177.	2.8	6
68	Inhibition Mechanism of Cathepsin L-Specific Inhibitors Based on the Crystal Structure of Papain \hat{c} CLIK148 Complex. <i>Biochemical and Biophysical Research Communications</i> , 1999, 266, 411-416.	2.1	81
69	Structure of the Human Cytomegalovirus Protease Catalytic Domain Reveals a Novel Serine Protease Fold and Catalytic Triad. <i>Cell</i> , 1996, 86, 835-843.	28.9	171
70	X-ray Structure of a Pokeweed Antiviral Protein, Coded by a New Genomic Clone, at 0.23 nm Resolution. A Model Structure Provides a Suitable Electrostatic Field for Substrate Binding. <i>FEBS Journal</i> , 1994, 225, 369-374.	0.2	26
71	Crystallization and Preliminary X-ray Crystallographic Studies of Recombinant Human Leukotriene A4 Hydrolase Complexed with Bestatin. <i>Journal of Molecular Biology</i> , 1994, 238, 854-856.	4.2	24
72	Nucleotide sequence of a genomic gene encoding tritin, a ribosome-inactivating protein from <i>Triticum aestivum</i> . <i>Plant Molecular Biology</i> , 1993, 22, 171-176.	3.9	25

#	ARTICLE	IF	CITATIONS
73	Comparative study of the stability of the folding intermediates of the calcium-binding lysozymes. International Journal of Peptide and Protein Research, 1993, 41, 118-123.	0.1	23
74	Crystallization and preliminary X-ray crystallographic analysis of Mirabilis antiviral protein. Journal of Molecular Biology, 1992, 226, 281-283.	4.2	8
75	A structural study of calcium-binding equine lysozyme by two-dimensional 1H-NMR. BBA - Proteins and Proteomics, 1991, 1078, 77-84.	2.1	18
76	Calcium-Binding Lysozymes. Biological Chemistry Hoppe-Seyler, 1988, 369, 671-676.	1.4	41
77	The calcium-binding property of equine lysozyme. FEBS Letters, 1987, 223, 405-408.	2.8	63