

# Kyung-Jin Kim

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

92  
papers

1,361  
citations

17  
h-index

35  
g-index

93  
ext. papers

1,879  
ext. citations

5.8  
avg, IF

4.98  
L-index

#	Paper	IF	Citations
92	Structural insight into molecular mechanism of poly(ethylene terephthalate) degradation. <i>Nature Communications</i> , <b>2018</b> , 9, 382	17.4	247
91	CRISPR/Cas9-induced knockout and knock-in mutations in <i>Chlamydomonas reinhardtii</i> . <i>Scientific Reports</i> , <b>2016</b> , 6, 27810	4.9	227
90	Rational Protein Engineering of Thermo-Stable PETase from <i>Ideonella sakaiensis</i> for Highly Efficient PET Degradation. <i>ACS Catalysis</i> , <b>2019</b> , 9, 3519-3526	13.1	120
89	Structural Insights into Polyhydroxyalkanoates Biosynthesis. <i>Trends in Biochemical Sciences</i> , <b>2018</b> , 43, 790-805	10.3	51
88	Production of extracellular PETase from <i>Ideonella sakaiensis</i> using sec-dependent signal peptides in <i>E. coli</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 508, 250-255	3.4	51
87	Crystal structure of <i>Ralstonia eutropha</i> polyhydroxyalkanoate synthase C-terminal domain and reaction mechanisms. <i>Biotechnology Journal</i> , <b>2017</b> , 12, 1600648	5.6	48
86	Redox-switch regulatory mechanism of thiolase from <i>Clostridium acetobutylicum</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 8410	17.4	43
85	Directed evolution of the 3-hydroxypropionic acid production pathway by engineering aldehyde dehydrogenase using a synthetic selection device. <i>Metabolic Engineering</i> , <b>2018</b> , 47, 113-120	9.7	39
84	Decomposition of the PET Film by MHETase Using Exo-PETase Function. <i>ACS Catalysis</i> , <b>2020</b> , 10, 4805-4812	12.1	32
83	Structure and function of the N-terminal domain of <i>Ralstonia eutropha</i> polyhydroxyalkanoate synthase, and the proposed structure and mechanisms of the whole enzyme. <i>Biotechnology Journal</i> , <b>2017</b> , 12, 1600649	5.6	32
82	Crystal structure of (R)-3-hydroxybutyryl-CoA dehydrogenase PhaB from <i>Ralstonia eutropha</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 443, 783-8	3.4	30
81	Structural bioinformatics-based protein engineering of thermo-stable PETase from <i>Ideonella sakaiensis</i> . <i>Enzyme and Microbial Technology</i> , <b>2020</b> , 141, 109656	3.8	27
80	Enhanced succinic acid production by <i>Mannheimia</i> employing optimal malate dehydrogenase. <i>Nature Communications</i> , <b>2020</b> , 11, 1970	17.4	26
79	Microbial Polyhydroxyalkanoates and Nonnatural Polyesters. <i>Advanced Materials</i> , <b>2020</b> , 32, e1907138	24	22
78	Structural basis for cytokinin production by LOG from <i>Corynebacterium glutamicum</i> . <i>Scientific Reports</i> , <b>2016</b> , 6, 31390	4.9	20
77	Structural insights into domain movement and cofactor specificity of glutamate dehydrogenase from <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 459, 387-92	3.4	17
76	Crystal structure and biochemical characterization of beta-keto thiolase B from polyhydroxyalkanoate-producing bacterium <i>Ralstonia eutropha</i> H16. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 444, 365-9	3.4	17

75	Structural basis for a novel type of cytokinin-activating protein. <i>Scientific Reports</i> , <b>2017</b> , 7, 45985	4.9	15
74	Crystal structure and biochemical characterization of PhaA from <i>Ralstonia eutropha</i> , a polyhydroxyalkanoate-producing bacterium. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 452, 124-9	3.4	15
73	In silico-designed lignin peroxidase from shows enhanced acid stability for depolymerization of lignin. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 325	7.8	14
72	Structural basis for redox sensitivity in <i>Corynebacterium glutamicum</i> diaminopimelate epimerase: an enzyme involved in l-lysine biosynthesis. <i>Scientific Reports</i> , <b>2017</b> , 7, 42318	4.9	12
71	Crystal Structure and Pyridoxal 5-Phosphate Binding Property of Lysine Decarboxylase from <i>Selenomonas ruminantium</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0166667	3.7	12
70	Implications for the PET decomposition mechanism through similarity and dissimilarity between PETases from <i>Rhizobacter gummiphilus</i> and <i>Ideonella sakaiensis</i> . <i>Journal of Hazardous Materials</i> , <b>2021</b> , 416, 126075	12.8	12
69	Crystal structure and thermodynamic properties of d-lactate dehydrogenase from <i>Lactobacillus jensenii</i> . <i>International Journal of Biological Macromolecules</i> , <b>2014</b> , 68, 151-7	7.9	11
68	Structural basis for an atypical active site of an L-aspartate/glutamate-specific racemase from <i>Escherichia coli</i> . <i>FEBS Letters</i> , <b>2015</b> , 589, 3842-7	3.8	11
67	Structural insights into substrate specificity of crotonase from the n-butanol producing bacterium <i>Clostridium acetobutylicum</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 451, 431-5	3.4	10
66	Modeling conformational redox-switch modulation of human succinic semialdehyde dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 2217-29	4.2	10
65	Structural Basis for Highly Efficient Production of Catechol Derivatives at Acidic pH by Tyrosinase from <i>Burkholderia thailandensis</i> . <i>ACS Catalysis</i> , <b>2018</b> , 8, 10375-10382	13.1	10
64	Genome analysis of a hyper acetone-butanol-ethanol (ABE) producing <i>Clostridium acetobutylicum</i> BKM19. <i>Biotechnology Journal</i> , <b>2017</b> , 12, 1600457	5.6	9
63	Structural Insight into Dihydrodipicolinate Reductase from <i>Corynebacterium glutamicum</i> for Lysine Biosynthesis. <i>Journal of Microbiology and Biotechnology</i> , <b>2016</b> , 26, 226-32	3.3	9
62	Crystal structure of 1FOH-carotenoid 3,4-desaturase from <i>Nonlabens dokdonensis</i> DSW-6. <i>Enzyme and Microbial Technology</i> , <b>2015</b> , 77, 29-37	3.8	8
61	Crystal structure and biochemical properties of the (S)-3-hydroxybutyryl-CoA dehydrogenase PaaH1 from <i>Ralstonia eutropha</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 448, 163-8	3.4	8
60	Lysine Decarboxylase with an Enhanced Affinity for Pyridoxal 5-Phosphate by Disulfide Bond-Mediated Spatial Reconstitution. <i>PLoS ONE</i> , <b>2017</b> , 12, e0170163	3.7	8
59	Crystal Structure of Amylomaltase from <i>Corynebacterium glutamicum</i> . <i>Journal of Agricultural and Food Chemistry</i> , <b>2016</b> , 64, 5662-70	5.7	8
58	Structural insights into the production of 3-hydroxypropionic acid by aldehyde dehydrogenase from <i>Azospirillum brasilense</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 46005	4.9	7

57	Crystal Structure of Acyl-CoA Oxidase 3 from with Specificity for Short-Chain Acyl-CoA. <i>Journal of Microbiology and Biotechnology</i> , <b>2018</b> , 28, 597-605	3-3	7
56	Structural Insights into a Novel Class of Aspartate Aminotransferase from <i>Corynebacterium glutamicum</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0158402	3-7	7
55	Structural insight into molecular mechanism of cytokinin activating protein from <i>Pseudomonas aeruginosa</i> PAO1. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 3214-3223	5-2	6
54	Effects of Synergistic Inhibition on $\beta$ -glucosidase by Phytoalexins in Soybeans. <i>Biomolecules</i> , <b>2019</b> , 9,	5-9	6
53	Reply to "Conformational fitting of a flexible oligomeric substrate does not explain the enzymatic PET degradation". <i>Nature Communications</i> , <b>2019</b> , 10, 5582	17-4	6
52	Crystal structure and biochemical characterization of malate dehydrogenase from <i>Metallosphaera sedula</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 509, 833-838	3-4	5
51	Structural basis for substrate specificity of meso-diaminopimelic acid decarboxylase from <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 495, 1815-1821	3-4	5
50	Structural Insight into Substrate Specificity of 3-Hydroxypropionyl-Coenzyme A Dehydratase from <i>Metallosphaera sedula</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 10692	4-9	5
49	Crystal structure and biochemical characterization of O-acetylhomoserine acetyltransferase from <i>Mycobacterium smegmatis</i> ATCC 19420. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 517, 399-406	3-4	5
48	Crystal Structure and Biochemical Characterization of Ketol-Acid Reductoisomerase from. <i>Journal of Agricultural and Food Chemistry</i> , <b>2019</b> , 67, 8527-8535	5-7	5
47	Structural Insights into Substrate Specificity of Cystathionine $\beta$ -Synthase from <i>Corynebacterium glutamicum</i> . <i>Journal of Agricultural and Food Chemistry</i> , <b>2017</b> , 65, 6002-6008	5-7	4
46	Crystal Structure and Biochemical Characterization of Xylose Isomerase from sp. E2. <i>Journal of Microbiology and Biotechnology</i> , <b>2018</b> , 28, 571-578	3-3	4
45	Crystal Structure and Functional Characterization of a Xylose Isomerase (PbXI) from the Psychrophilic Soil Microorganism, <i>Paenibacillus</i> sp. <i>Journal of Microbiology and Biotechnology</i> , <b>2019</b> , 29, 244-255	3-3	4
44	Crystal structure of $\beta$ -aminobutyrate aminotransferase in complex with a PLP-GABA adduct from <i>Corynebacterium glutamicum</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 514, 601-606	3-4	3
43	Structural insights into the novel ARM-repeat protein CTNNBL1 and its association with the hPrp19-CDC5L complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 780-8		3
42	Structural and functional characterization of an auxiliary domain-containing PET hydrolase from Burkholderiales bacterium.. <i>Journal of Hazardous Materials</i> , <b>2022</b> , 429, 128267	12-8	3
41	Sequence, structure and function-based classification of the broadly conserved FAH superfamily reveals two distinct fumarylpyruvate hydrolase subfamilies. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 270-285	5-2	3
40	High Galacto-Oligosaccharide Production and a Structural Model for Transgalactosylation of $\beta$ -Galactosidase II from. <i>Journal of Agricultural and Food Chemistry</i> , <b>2020</b> , 68, 13806-13814	5-7	3

39	Structural insight into the substrate specificity of acyl-CoA oxidase1 from <i>Yarrowia lipolytica</i> for short-chain dicarboxyl-CoAs. <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 495, 1628-1634	3-4	3
38	Structural insight into -xylose utilization by xylose reductase from <i>Scheffersomyces stipitis</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 17442	4-9	3
37	Structural insights into a maleylpyruvate hydrolase from <i>sphingobium</i> sp. SYK-6, a bacterium degrading lignin-derived aryls. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 514, 765-771	3-4	2
36	Crystal structure and biochemical properties of msed_0281, the citrate synthase from <i>Metallosphaera sedula</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 509, 722-727	3-4	2
35	Structural insights into the inhibition properties of archaeon citrate synthase from <i>Metallosphaera sedula</i> . <i>PLoS ONE</i> , <b>2019</b> , 14, e0212807	3-7	2
34	Crystal structure and biochemical properties of ReH16_A1887, the 3-ketoacyl-CoA thiolase from <i>Ralstonia eutropha</i> H16. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 459, 547-52	3-4	2
33	Biochemical properties and crystal structure of formate-tetrahydrofolate ligase from <i>Methylobacterium extorquens</i> CM4. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 528, 426-431	3-4	2
32	Crystal structure of a substrate-binding protein from <i>Rhodothermus marinus</i> reveals a single $\beta$ domain. <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 497, 368-373	3-4	2
31	Structural and biochemical characterization of the type-II LOG protein from <i>Streptomyces coelicolor</i> A3. <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 499, 577-583	3-4	2
30	Crystal structure and biochemical characterization of a 3-ketoacyl-CoA thiolase from <i>Ralstonia eutropha</i> H16. <i>International Journal of Biological Macromolecules</i> , <b>2016</b> , 82, 425-31	7-9	2
29	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of (S)-3-hydroxybutyryl-CoA dehydrogenase from <i>Clostridium butyricum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 485-8	1-1	2
28	Metabolic engineering of <i>Escherichia coli</i> for production of non-natural acetins from glycerol. <i>Green Chemistry</i> , <b>2020</b> , 22, 7788-7802	10	2
27	Dual $\beta$ 1,4- and $\beta$ 1,4-Glycosidase Activities by the Novel Carbohydrate-Binding Module in $\beta$ -Fucosidase from sp. Strain EJY3. <i>Journal of Agricultural and Food Chemistry</i> , <b>2021</b> , 69, 3380-3389	5-7	2
26	Structural basis for nucleotide-independent regulation of acyl-CoA thioesterase from <i>Bacillus cereus</i> ATCC 14579. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 170, 390-396	7-9	2
25	Crystal Structure of a Novel Type Isomerase of Enoyl-CoA Hydratase/Isomerase Family Protein from <i>Cupriavidus necator</i> H16. <i>Biotechnology and Bioprocess Engineering</i> , <b>2019</b> , 24, 155-162	3-1	1
24	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of the (S)-3-hydroxybutyryl-CoA dehydrogenase PaaH1 from <i>Ralstonia eutropha</i> H16. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 955-8	1-1	1
23	Small angle X-ray scattering studies of CTNNBL1 dimerization and CTNNBL1/CDC5L complex. <i>Scientific Reports</i> , <b>2015</b> , 5, 14251	4-9	1
22	Crystal Structure and Biochemical Characterization of Tetrahydrodipicolinate N-Succinyltransferase from <i>Corynebacterium glutamicum</i> . <i>Journal of Agricultural and Food Chemistry</i> , <b>2015</b> , 63, 10641-6	5-7	1

21	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of D-lactate dehydrogenase from <i>Lactobacillus jensenii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1046-8	1.1	1
20	Structural insight into a molecular mechanism of methenyltetrahydrofolate cyclohydrolase from <i>Methylobacterium extorquens</i> AM1.. <i>International Journal of Biological Macromolecules</i> , <b>2022</b> , 202, 234-240	7.8	1
19	Structural and Functional Characterization of Cystathionine $\beta$ -lyase from ATCC 14579. <i>Journal of Agricultural and Food Chemistry</i> , <b>2020</b> , 68, 15267-15274	5.7	1
18	Crystal structure of an acetyl-CoA acetyltransferase from PHB producing bacterium <i>Bacillus cereus</i> ATCC 14579. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 533, 442-448	3.4	1
17	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of $\beta$ -ketothiolase B from <i>Ralstonia eutropha</i> H16. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 316-9	1.1	0
16	Structural analysis of the peptidoglycan editing factor PdeF from <i>Bacillus cereus</i> ATCC 14579. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 583, 43-48	3.4	0
15	Structural insight into bi-functional malonyl-CoA reductase. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 752-765	6.5	0
14	Biochemical properties and crystal structure of isocitrate lyase from <i>Bacillus cereus</i> ATCC 14579. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 533, 1177-1183	3.4	0
13	Structural basis for stereospecificity to d-amino acid of glycine oxidase from <i>Bacillus cereus</i> ATCC 14579. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 533, 824-830	3.4	0
12	Bacterial Polyesters: Microbial Polyhydroxyalkanoates and Nonnatural Polyesters (Adv. Mater. 35/2020). <i>Advanced Materials</i> , <b>2020</b> , 32, 2070264	24	0
11	CE Selective Aldol Addition of d-Threonine Aldolase by Spatial Constraint of Aldehyde Binding. <i>ACS Catalysis</i> , <b>2021</b> , 11, 6892-6899	13.1	0
10	Crystal Structure and Regiospecificity of Catechol -Methyltransferase from. <i>Journal of Agricultural and Food Chemistry</i> , <b>2021</b> , 69, 2531-2538	5.7	0
9	Extra disulfide and ionic salt bridge improves the thermostability of lignin peroxidase H8 under acidic condition. <i>Enzyme and Microbial Technology</i> , <b>2021</b> , 148, 109803	3.8	0
8	Crystal structure of geranylgeranyl pyrophosphate synthase (crtE) from <i>Nonlabens dokdonensis</i> DSW-6. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 518, 479-485	3.4	
7	Structure and biochemical studies of a pseudomonad maleylpyruvate isomerase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 514, 991-997	3.4	
6	Purification, crystallization and preliminary X-ray diffraction analysis of 3-ketoacyl-CoA thiolase A1887 from <i>Ralstonia eutropha</i> H16. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 758-62	1.1	
5	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of PhaA from <i>Ralstonia eutropha</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1566-9	1.1	
4	Crystal Structure and Functional Characterization of the Bifunctional -(5TPPhosphoribosyl)anthranilate Isomerase-indole-3-glycerol-phosphate Synthase from. <i>Journal of Agricultural and Food Chemistry</i> , <b>2021</b> , 69, 12485-12493	5.7	

- 3 Crystal Structure and Molecular Mechanism of Phosphotransbutyrylase from. *Journal of Microbiology and Biotechnology*, **2021**, 31, 1393-1400 3:3
- 2 Purification, crystallization and X-ray crystallographic analysis of feruloyl-CoA hydratase/lyase of *Pseudomonas putida* KT2440. *Biodesign*, **2022**, 10, 12-15 0
- 1 Endoplasmic reticulum regulates differentiation of tonsil-derived mesenchymal stem cells into chondrocytes through ERK signaling. *BMB Reports*, **2022**, 55, 226-231 5:5