

# Henriette J Rozeboom

## List of Publications by Year in descending order

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73  
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136950

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citing authors

#	ARTICLE	IF	CITATIONS
1	Abstract: Gene Fusion and Directed Evolution to Break Structural Symmetry and Boost Catalysis by an Oligomeric C-C Bond-Forming Enzyme (Angew. Chem. 8/2022). Angewandte Chemie, 2022, 134, .	2.0	0
2	Gene Fusion and Directed Evolution to Break Structural Symmetry and Boost Catalysis by an Oligomeric C-C Bond-Forming Enzyme. Angewandte Chemie, 2022, 134, .	2.0	9
3	Gene Fusion and Directed Evolution to Break Structural Symmetry and Boost Catalysis by an Oligomeric C-C Bond-Forming Enzyme. Angewandte Chemie - International Edition, 2022, 61, .	13.8	17
4	From thiol-subtilisin to omniligase: Design and structure of a broadly applicable peptide ligase. Computational and Structural Biotechnology Journal, 2021, 19, 1277-1287.	4.1	11
5	Engineering Thermostability in Artificial Metalloenzymes to Increase Catalytic Activity. ACS Catalysis, 2021, 11, 3620-3627.	11.2	16
6	Catalytic and structural properties of <i>ATP</i> -dependent caprolactamase from <i>Pseudomonas jessenii</i> . Proteins: Structure, Function and Bioinformatics, 2021, 89, 1079-1098.	2.6	6
7	Computational Redesign of an $\alpha$ -Transaminase from <i>Pseudomonas jessenii</i> for Asymmetric Synthesis of Enantiopure Bulky Amines. ACS Catalysis, 2021, 11, 10733-10747.	11.2	28
8	Unlocking Asymmetric Michael Additions in an Archetypical Class I Aldolase by Directed Evolution. ACS Catalysis, 2021, 11, 13236-13243.	11.2	14
9	Kinetic and Structural Properties of a Robust Bacterial L-Amino Acid Oxidase. Catalysts, 2021, 11, 1309.	3.5	3
10	Structure of a robust bacterial protein cage and its application as a versatile biocatalytic platform through enzyme encapsulation. Biochemical and Biophysical Research Communications, 2020, 529, 548-553.	2.1	33
11	Characterization of the starch surface binding site on <i>Bacillus paralicheniformis</i> $\alpha$ -amylase. International Journal of Biological Macromolecules, 2020, 165, 1529-1539.	7.5	18
12	Structure-based directed evolution improves <i>S. cerevisiae</i> growth on xylose by influencing in vivo enzyme performance. Biotechnology for Biofuels, 2020, 13, 5.	6.2	20
13	Robust $\alpha$ -Transaminases by Computational Stabilization of the Subunit Interface. ACS Catalysis, 2020, 10, 2915-2928.	11.2	52
14	Biochemical properties of a <i>Pseudomonas</i> aminotransferase involved in caprolactam metabolism. FEBS Journal, 2019, 286, 4086-4102.	4.7	10
15	Characterization of a New DyP-Peroxidase from the Alkaliphilic Cellulomonad, <i>Cellulomonas bogoriensis</i> . Molecules, 2019, 24, 1208.	3.8	29
16	Design of a substrate-tailored peptidase variant for the efficient synthesis of thymosin- $\beta$ 1. Organic and Biomolecular Chemistry, 2018, 16, 609-618.	2.8	25
17	Characterization of Two VAO-Type Flavoprotein Oxidases from <i>Myceliophthora thermophila</i> . Molecules, 2018, 23, 111.	3.8	7
18	Metal Dependence of the Xylose Isomerase from <i>Piromyces</i> sp. E2 Explored by Activity Profiling and Protein Crystallography. Biochemistry, 2017, 56, 5991-6005.	2.5	30

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19	Versatile Peptide C-Terminal Functionalization via a Computationally Engineered Peptide Amidase. <i>ACS Catalysis</i> , 2016, 6, 5405-5414.	11.2	60
20	Discovery of a Xylooligosaccharide Oxidase from <i>Myceliophthora thermophila</i> C1. <i>Journal of Biological Chemistry</i> , 2016, 291, 23709-23718.	3.4	26
21	Crystal structure of quinone-dependent alcohol dehydrogenase from <i>Pseudogluconobacter saccharoketogenes</i> . A versatile dehydrogenase oxidizing alcohols and carbohydrates. <i>Protein Science</i> , 2015, 24, 2044-2054.	7.6	17
22	Picosecond Fluorescence Dynamics of Tryptophan and 5-Fluorotryptophan in Monellin: Slow Water-Protein Relaxation Unmasked. <i>Journal of Physical Chemistry B</i> , 2015, 119, 4230-4239.	2.6	20
23	Functional and Structural Characterization of an Unusual Cofactor-Independent Oxygenase. <i>Biochemistry</i> , 2015, 54, 1219-1232.	2.5	11
24	Crystal structures of two <i>Bacillus</i> carboxylesterases with different enantioselectivities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 567-575.	2.3	20
25	Crystal structure of endo-xylogalacturonan hydrolase from <i>Aspergillus tubingensis</i> . <i>FEBS Journal</i> , 2013, 280, 6061-6069.	4.7	14
26	Crystal Structure of $\alpha$ -1,4-Glucan Lyase, a Unique Glycoside Hydrolase Family Member with a Novel Catalytic Mechanism. <i>Journal of Biological Chemistry</i> , 2013, 288, 26764-26774.	3.4	22
27	Enhancement of the enantioselectivity of carboxylesterase A by structure-based mutagenesis. <i>Journal of Biotechnology</i> , 2012, 158, 36-43.	3.8	23
28	Engineering methylaspartate ammonia lyase for the asymmetric synthesis of unnatural amino acids. <i>Nature Chemistry</i> , 2012, 4, 478-484.	13.6	77
29	Crystal Structure of <i>Agaricus bisporus</i> Mushroom Tyrosinase: Identity of the Tetramer Subunits and Interaction with Tropolone. <i>Biochemistry</i> , 2011, 50, 5477-5486.	2.5	648
30	Crystallization and preliminary X-ray crystallographic analysis of tyrosinase from the mushroom <i>Agaricus bisporus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 575-578.	0.7	26
31	Structural and Functional Characterization of a Macrophage Migration Inhibitory Factor Homologue from the Marine Cyanobacterium <i>Prochlorococcus marinus</i> . <i>Biochemistry</i> , 2010, 49, 7572-7581.	2.5	20
32	Crystallization and preliminary X-ray analysis of carnein, a serine protease from <i>Pomoea carnea</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 383-385.	0.7	1
33	Elimination of competing hydrolysis and coupling side reactions of a cyclodextrin glucanotransferase by directed evolution. <i>Biochemical Journal</i> , 2008, 413, 517-525.	3.7	47
34	Structural and Mutational Characterization of the Catalytic A-module of the Mannuronan C-5-epimerase AlgE4 from <i>Azotobacter vinelandii</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 23819-23828.	3.4	44
35	Structure and mechanism of a bacterial haloalcohol dehalogenase: a new variation of the short-chain dehydrogenase/reductase fold without an NAD(P)H binding site. <i>EMBO Journal</i> , 2003, 22, 4933-4944.	7.8	102
36	Improved thermostability of <i>Bacillus circulans</i> cyclodextrin glycosyltransferase by the introduction of a salt bridge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 128-134.	2.6	38

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37	Conversion of Cyclodextrin Glycosyltransferase into a Starch Hydrolase by Directed Evolution: The Role of Alanine 230 in Acceptor Subsite +1. <i>Biochemistry</i> , 2003, 42, 7518-7526.	2.5	57
38	The fully conserved Asp residue in conserved sequence region I of the $\alpha$ -amylase family is crucial for the catalytic site architecture and activity. <i>FEBS Letters</i> , 2003, 541, 47-51.	2.8	25
39	Crystal Structure of Quinohemoprotein Alcohol Dehydrogenase from <i>Comamonas testosteroni</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 3727-3732.	3.4	78
40	Structure of Human Chitotriosidase. <i>Journal of Biological Chemistry</i> , 2002, 277, 25537-25544.	3.4	185
41	The Remote Substrate Binding Subsite $\alpha$ 6 in Cyclodextrin-glycosyltransferase Controls the Transferase Activity of the Enzyme via an Induced-fit Mechanism. <i>Journal of Biological Chemistry</i> , 2002, 277, 1113-1119.	3.4	43
42	Crystal Structure of the Copper-Containing Quercetin 2,3-Dioxygenase from <i>Aspergillus japonicus</i> . <i>Structure</i> , 2002, 10, 259-268.	3.3	216
43	Expression and characterization of active site mutants of hevamine, a chitinase from the rubber tree <i>Hevea brasiliensis</i> . <i>FEBS Journal</i> , 2002, 269, 893-901.	0.2	72
44	Crystallization and preliminary X-ray analysis of an enantioselective halohydrin dehalogenase from <i>Agrobacterium radiobacter</i> AD1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 176-178.	2.5	17
45	X-ray structure of bovine pancreatic phospholipase A2 at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 516-526.	2.5	26
46	Crystallization of quinohaemoprotein alcohol dehydrogenase from <i>Comamonas testosteroni</i> : crystals with unique optical properties. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1732-1734.	2.5	2
47	Active-site structure of the soluble quinoprotein glucose dehydrogenase complexed with methylhydrazine: A covalent cofactor-inhibitor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11787-11791.	7.1	63
48	The X-ray Structure of Epoxide Hydrolase from <i>Agrobacterium radiobacter</i> AD1. <i>Journal of Biological Chemistry</i> , 1999, 274, 14579-14586.	3.4	160
49	Crystal Structures of Intermediates in the Dehalogenation of Haloalkanoates by l-2-Haloacid Dehalogenase. <i>Journal of Biological Chemistry</i> , 1999, 274, 30672-30678.	3.4	71
50	Haloalkane dehalogenase from <i>Xanthobacter autotrophicus</i> GJ10 refined at 1.15 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1273-1290.	2.5	30
51	Structure and mechanism of soluble quinoprotein glucose dehydrogenase. <i>EMBO Journal</i> , 1999, 18, 5187-5194.	7.8	148
52	Crystallographic and Kinetic Evidence of a Collision Complex Formed during Halide Import in Haloalkane Dehalogenase. <i>Biochemistry</i> , 1999, 38, 12052-12061.	2.5	20
53	The 1.7 Å crystal structure of the apo form of the soluble quinoprotein glucose dehydrogenase from <i>Acinetobacter calcoaceticus</i> reveals a novel internal conserved sequence repeat. <i>Journal of Molecular Biology</i> , 1999, 289, 319-333.	4.2	80
54	Kinetic Analysis and X-ray Structure of Haloalkane Dehalogenase with a Modified Halide-Binding Site. <i>Biochemistry</i> , 1998, 37, 15013-15023.	2.5	57

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55	Three-dimensional Structure of I-2-Haloacid Dehalogenase from Xanthobacter autotrophicus GJ10 Complexed with the Substrate-analogue Formate. Journal of Biological Chemistry, 1997, 272, 33015-33022.	3.4	97
56	Structure of Cyclodextrin Glycosyltransferase Complexed with a Maltononaose Inhibitor at 2.6 Å... Resolution. Implications for Product Specificity. Biochemistry, 1996, 35, 4241-4249.	2.5	149
57	Crystal Structure at 2.3 Å... Resolution and Revised Nucleotide Sequence of the Thermostable Cyclodextrin Glycosyltransferase from Thermoanaerobacterium thermosulfurigenes EM1. Journal of Molecular Biology, 1996, 256, 611-622.	4.2	84
58	Crystallization and preliminary crystallographic analysis of endo-1,4-xyloxyase I from Aspergillus niger. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 571-576.	2.5	3
59	The Raw Starch Binding Domain of Cyclodextrin Glycosyltransferase from Bacillus circulans Strain 251. Journal of Biological Chemistry, 1996, 271, 32777-32784.	3.4	172
60	Crystallization and preliminary X-ray analysis of haloalkane dehalogenase from Xanthobacter autotrophicus GJ10. Protein Science, 1995, 4, 2619-2620.	7.6	13
61	Structure of the 70-kDa Soluble Lytic Transglycosylase Complexed with Bulgecin A. Implications for the Enzymic Mechanism. Biochemistry, 1995, 34, 12729-12737.	2.5	110
62	Crystallographic Studies of the Interaction of Cyclodextrin Glycosyltransferase from Bacillus circulans Strain 251 with Natural Substrates and Products. Journal of Biological Chemistry, 1995, 270, 29256-29264.	3.4	131
63	Doughnut-shaped structure of a bacterial muramidase revealed by X-ray crystallography. Nature, 1994, 367, 750-753.	27.8	164
64	Nucleotide Sequence and X-ray Structure of Cyclodextrin Glycosyltransferase from Bacillus circulans Strain 251 in a Maltose-dependent Crystal Form. Journal of Molecular Biology, 1994, 236, 590-600.	4.2	228
65	Crystallographic analysis of the catalytic mechanism of haloalkane dehalogenase. Nature, 1993, 363, 693-698.	27.8	496
66	Non-covalent binding of the heavy atom compound [Au(CN) <sub>2</sub> ] <sup>-</sup> at the halide binding site of haloalkane dehalogenase from Xanthobacter autotrophicus GJ10. FEBS Letters, 1993, 323, 267-270.	2.8	8
67	Refined X-ray Structures of Haloalkane Dehalogenase at pH 6.2 and pH 8.2 and Implications for the Reaction Mechanism. Journal of Molecular Biology, 1993, 232, 856-872.	4.2	143
68	Crystallographic and fluorescence studies of the interaction of haloalkane dehalogenase with halide ions. Studies with halide compounds reveal a halide binding site in the active site. Biochemistry, 1993, 32, 9031-9037.	2.5	92
69	Crystallization of the soluble lytic transglycosylase from Escherichia coli K12. Journal of Molecular Biology, 1990, 212, 557-559.	4.2	12
70	Crystallization of hevamine, an enzyme with lysozyme/chitinase activity from Hevea brasiliensis latex. Journal of Molecular Biology, 1990, 212, 441-443.	4.2	31
71	Structure Determination of Haloalkane Dehalogenase. , 1990, , 583-587.		0
72	Use of electron microscopy in the examination of lattice defects in crystals of alcohol oxidase. FEBS Letters, 1989, 244, 213-216.	2.8	14

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73	Crystallization of haloalkane dehalogenase from Xanthobacter autotrophicus GJ10. Journal of Molecular Biology, 1988, 200, 611-612.	4.2	34