

Salam Al-Karadaghi

List of Publications by Year in descending order

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73
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126907

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#	ARTICLE	IF	CITATIONS
1	Targeting Acute Myelogenous Leukemia Using Potent Human Dihydroorotate Dehydrogenase Inhibitors Based on the 2-Hydroxypyrazolo[1,5- <i>a</i>]pyridine Scaffold: SAR of the Biphenyl Moiety. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 5404-5428.	6.4	19
2	Hydroxazole scaffold-based Plasmodium falciparum dihydroorotate dehydrogenase inhibitors: Synthesis, biological evaluation and X-ray structural studies. <i>European Journal of Medicinal Chemistry</i> , 2019, 163, 266-280.	5.5	23
3	N-Acetyl-3-aminopyrazoles block the non-canonical NF- κ B cascade by selectively inhibiting NIK. <i>MedChemComm</i> , 2018, 9, 963-968.	3.4	27
4	Structural modelling of the DNAJB6 oligomeric chaperone shows a peptide-binding cleft lined with conserved S/T-residues at the dimer interface. <i>Scientific Reports</i> , 2018, 8, 5199.	3.3	43
5	Targeting Myeloid Differentiation Using Potent 2-Hydroxypyrazolo[1,5- <i>a</i>]pyridine Scaffold-Based Human Dihydroorotate Dehydrogenase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 6034-6055.	6.4	57
6	Design, synthesis, biological evaluation and X-ray structural studies of potent human dihydroorotate dehydrogenase inhibitors based on hydroxylated azole scaffolds. <i>European Journal of Medicinal Chemistry</i> , 2017, 129, 287-302.	5.5	46
7	4-Hydroxy-N-[3,5-bis(trifluoromethyl)phenyl]-1,2,5-thiadiazole-3-carboxamide: a novel inhibitor of the canonical NF- κ B cascade. <i>MedChemComm</i> , 2017, 8, 1850-1855.	3.4	23
8	SAXS and stability studies of iron-induced oligomers of bacterial frataxin CyaY. <i>PLoS ONE</i> , 2017, 12, e0184961.	2.5	1
9	Iron-induced oligomerization of human FXN81-210 and bacterial CyaY frataxin and the effect of iron chelators. <i>PLoS ONE</i> , 2017, 12, e0188937.	2.5	16
10	The S/T-Rich Motif in the DNAJB6 Chaperone Delays Polyglutamine Aggregation and the Onset of Disease in a Mouse Model. <i>Molecular Cell</i> , 2016, 62, 272-283.	9.7	140
11	The Structure of the Complex between Yeast Frataxin and Ferrochelatase. <i>Journal of Biological Chemistry</i> , 2016, 291, 11887-11898.	3.4	22
12	Architecture of the Human Mitochondrial Iron-Sulfur Cluster Assembly Machinery. <i>Journal of Biological Chemistry</i> , 2016, 291, 21296-21321.	3.4	24
13	Architecture of the Yeast Mitochondrial Iron-Sulfur Cluster Assembly Machinery. <i>Journal of Biological Chemistry</i> , 2016, 291, 10378-10398.	3.4	17
14	Three-dimensional structures of Plasmodium falciparum spermidine synthase with bound inhibitors suggest new strategies for drug design. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 484-493.	2.5	15
15	The Molecular Basis of Iron-induced Oligomerization of Frataxin and the Role of the Ferroxidation Reaction in Oligomerization. <i>Journal of Biological Chemistry</i> , 2013, 288, 8156-8167.	3.4	21
16	Magnesium Chelatase: The Molecular Motor of Chlorophyll Biosynthesis. <i>Handbook of Porphyrin Science</i> , 2013, , 41-84.	0.8	12
17	Structure of the Cyanobacterial Magnesium Chelatase H Subunit Determined by Single Particle Reconstruction and Small-angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2012, 287, 4946-4956.	3.4	19
18	Oligomerization Propensity and Flexibility of Yeast Frataxin Studied by X-ray Crystallography and Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 414, 783-797.	4.2	21

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19	Biochemical characterisation and novel classification of monofunctional S-adenosylmethionine decarboxylase of <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2011, 180, 17-26.	1.1	9
20	Bacterial ferrochelatase turns human: Tyr13 determines the apparent metal specificity of <i>Bacillus subtilis</i> ferrochelatase. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 235-242.	2.6	14
21	Resonance Raman spectroscopic examination of ferrochelatase-induced porphyrin distortion. <i>Journal of Porphyrins and Phthalocyanines</i> , 2011, 15, 357-363.	0.8	13
22	Ferrochelatase: the convergence of the porphyrin biosynthesis and iron transport pathways. <i>Journal of Porphyrins and Phthalocyanines</i> , 2011, 15, 350-356.	0.8	18
23	ATP-Induced Conformational Dynamics in the AAA+ Motor Unit of Magnesium Chelatase. <i>Structure</i> , 2010, 18, 354-365.	3.3	70
24	Inhibition of Human DHODH by 4-Hydroxycoumarins, Fenamic Acids, and (Alkylcarbonyl)anthranilic Acids Identified by Structure-Guided Fragment Selection. <i>ChemMedChem</i> , 2010, 5, 608-617.	3.2	26
25	The AAA+ motor complex of subunits CobS and CobT of cobaltochelatase visualized by single particle electron microscopy. <i>Journal of Structural Biology</i> , 2009, 167, 227-234.	2.8	38
26	The Structures of Human Dihydroorotate Dehydrogenase with and without Inhibitor Reveal Conformational Flexibility in the Inhibitor and Substrate Binding Sites. <i>Biochemistry</i> , 2008, 47, 8929-8936.	2.5	69
27	A New Cryo-EM Single-Particle Ab Initio Reconstruction Method Visualizes Secondary Structure Elements in an ATP-Fueled AAA+ Motor. <i>Journal of Molecular Biology</i> , 2008, 375, 934-947.	4.2	44
28	Porphyrin Binding and Distortion and Substrate Specificity in the Ferrochelatase Reaction: The Role of Active Site Residues. <i>Journal of Molecular Biology</i> , 2008, 378, 1074-1083.	4.2	62
29	Structural Basis of the Iron Storage Function of Frataxin from Single-Particle Reconstruction of the Iron-Loaded Oligomer. <i>Biochemistry</i> , 2008, 47, 4948-4954.	2.5	40
30	Substrate-binding Model of the Chlorophyll Biosynthetic Magnesium Chelatase BchH Subunit. <i>Journal of Biological Chemistry</i> , 2008, 283, 11652-11660.	3.4	49
31	Recessiveness and Dominance in Barley Mutants Deficient in Mg-Chelatase Subunit D, an AAA Protein Involved in Chlorophyll Biosynthesis. <i>Plant Cell</i> , 2007, 18, 3606-3616.	6.6	49
32	Crystal Structure of <i>Plasmodium falciparum</i> Spermidine Synthase in Complex with the Substrate Decarboxylated S-adenosylmethionine and the Potent Inhibitors 4MCHA and AdoDATO. <i>Journal of Molecular Biology</i> , 2007, 373, 167-177.	4.2	53
33	Amino Acid Residues His183 and Glu264 in <i>Bacillus subtilis</i> Ferrochelatase Direct and Facilitate the Insertion of Metal Ion into Protoporphyrin IX. <i>Biochemistry</i> , 2007, 46, 87-94.	2.5	60
34	ATPase activity associated with the magnesium chelatase H-subunit of the chlorophyll biosynthetic pathway is an artefact. <i>Biochemical Journal</i> , 2006, 400, 477-484.	3.7	24
35	Structural Aspects of Protein Synthesis. By Anders Liljas. Pp. 290. Singapore: World Scientific, 2004. Price (paperback) USD 44/GBP 27. ISBN 981-238-867-2.. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1101-1101.	2.5	0
36	Characterization of insulin microcrystals using powder diffraction and multivariate data analysis. <i>Journal of Applied Crystallography</i> , 2006, 39, 391-400.	4.5	37

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37	Transmembrane topology of FRO2, a ferric chelate reductase from <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2006, 62, 215-221.	3.9	42
38	The Structures of Frataxin Oligomers Reveal the Mechanism for the Delivery and Detoxification of Iron. <i>Structure</i> , 2006, 14, 1535-1546.	3.3	78
39	Chelataes: distort to select?. <i>Trends in Biochemical Sciences</i> , 2006, 31, 135-142.	7.5	94
40	Immunolocalization of the saposin-like insert of plant aspartic proteinases exhibiting saposin C activity. Expression in young flower tissues and in barley seeds. <i>Physiologia Plantarum</i> , 2005, 125, 051020045109003-???	5.2	2
41	Metallation of the Transition-state Inhibitor N-methyl Mesoporphyrin by Ferrochelatase: Implications for the Catalytic Reaction Mechanism. <i>Journal of Molecular Biology</i> , 2005, 352, 1081-1090.	4.2	36
42	Cloning, expression, characterisation and three-dimensional structure determination of <i>Caenorhabditis elegans</i> spermidine synthase. <i>FEBS Letters</i> , 2005, 579, 6037-6043.	2.8	25
43	Structural Basis for Interactions between Tenascins and Lectican C-Type Lectin Domains. <i>Structure</i> , 2004, 12, 1495-1506.	3.3	113
44	EM single particle analysis of the ATP-dependent Bchl complex of magnesium chelatase: an AAA+ hexamer. <i>Journal of Structural Biology</i> , 2004, 146, 227-233.	2.8	47
45	Metal binding to <i>Bacillus subtilis</i> ferrochelatase and interaction between metal sites. <i>Journal of Biological Inorganic Chemistry</i> , 2003, 8, 452-458.	2.6	48
46	In Vivo and In Vitro Studies of <i>Bacillus subtilis</i> Ferrochelatase Mutants Suggest Substrate Channeling in the Heme Biosynthesis Pathway. <i>Journal of Bacteriology</i> , 2002, 184, 4018-4024.	2.2	33
47	Metal Binding to <i>Saccharomyces cerevisiae</i> Ferrochelatase. <i>Biochemistry</i> , 2002, 41, 13499-13506.	2.5	61
48	Occurrence, conformational features and amino acid propensities for the α -helix. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 353-358.	2.1	227
49	Interplay between an AAA module and an integrin I domain may regulate the function of magnesium chelatase. <i>Journal of Molecular Biology</i> , 2001, 311, 111-122.	4.2	175
50	Structure of ribosomal protein TL5 complexed with RNA provides new insights into the CTC family of stress proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 968-976.	2.5	38
51	Archaeal ribosomal protein L1: the structure provides new insights into RNA binding of the L1 protein family. <i>Structure</i> , 2000, 8, 363-371.	3.3	35
52	A decade of progress in understanding the structural basis of protein synthesis. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 167-193.	2.9	16
53	Structural and mechanistic basis of porphyrin metallation by ferrochelatase. <i>Journal of Molecular Biology</i> , 2000, 297, 221-232.	4.2	122
54	Crystallization and preliminary X-ray analysis of the <i>Rhodobacter capsulatus</i> magnesium chelatase Bchl subunit. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 689-690.	2.5	11

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55	Crystallization and preliminary X-ray analysis of <i>Thermotoga maritima</i> ribosome recycling factor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2049-2050.	2.5	5
56	Crystal Structure of <i>Thermotoga maritima</i> Ribosome Recycling Factor: A tRNA Mimic. <i>Science</i> , 1999, 286, 2349-2352.	12.6	184
57	Iron superoxide dismutase from the archaeon <i>Sulfolobus solfataricus</i> : analysis of structure and thermostability. <i>Journal of Molecular Biology</i> , 1999, 286, 189-205.	4.2	86
58	Crystal structure of ribosomal protein S8 from <i>Thermus thermophilus</i> reveals a high degree of structural conservation of a specific RNA binding site 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 279, 233-244.	4.2	29
59	A mutant form of the ribosomal protein L1 reveals conformational flexibility. <i>FEBS Letters</i> , 1997, 411, 53-59.	2.8	17
60	Structural aspects of protein synthesis. <i>Nature Structural Biology</i> , 1997, 4, 767-771.	9.7	31
61	Crystal structure of ferrochelatase: the terminal enzyme in heme biosynthesis. <i>Structure</i> , 1997, 5, 1501-1510.	3.3	180
62	The structure of elongation factor G in complex with GDP: conformational flexibility and nucleotide exchange. <i>Structure</i> , 1996, 4, 555-565.	3.3	137
63	Crystallization and structural studies of components of the protein-synthesizing system from <i>Thermus thermophilus</i> . <i>Journal of Crystal Growth</i> , 1996, 168, 301-307.	1.5	3
64	Refined structure of Cu-substituted alcohol dehydrogenase at 2.1 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 805-813.	2.5	9
65	Purification, crystallization, and preliminary X-ray analysis of <i>Bacillus subtilis</i> ferrochelatase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 607-609.	2.6	16
66	Crystallographic studies of elongation factor G. <i>Biochemistry and Cell Biology</i> , 1995, 73, 1209-1216.	2.0	20
67	Ribosomal protein L22 from <i>Thermus thermophilus</i> : sequencing overexpression and crystallisation. <i>FEBS Letters</i> , 1995, 369, 229-232.	2.8	7
68	Refined crystal structure of liver alcohol dehydrogenase-NADH complex at 1.8 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 793-807.	2.5	54
69	Crystallization and preliminary investigation of single crystals of deoxyuridine triphosphate nucleotidohydrolase from <i>Escherichia coli</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 71-75.	2.6	7
70	Three-dimensional structure of the crystalline surface layer from <i>Aeromonas hydrophila</i> . <i>Journal of Structural Biology</i> , 1988, 101, 92-97.	0.8	15
71	Interaction of influenza virus proteins with planar bilayer lipid membranes II. Effects of rimantadine and amantadine. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1984, 778, 276-280.	2.6	7
72	The States, Conformational Dynamics, and Fusidic Acid-Resistant Mutants of Elongation Factor G. , 0, , 359-365.		1

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73	Ribosomal Proteins and Their Structural Transitions on and off the Ribosome. , 0, , 63-72.		0