

Martin E M Noble

List of Publications by Year in descending order

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132
papers

15,568
citations

18482

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docs citations

135
times ranked

17992
citing authors

#	ARTICLE	IF	CITATIONS
1	Parallel Optimization of Potency and Pharmacokinetics Leading to the Discovery of a Pyrrole Carboxamide ERK5 Kinase Domain Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 6513-6540.	6.4	3
2	Discriminative SKP2 Interactions with CDK-Cyclin Complexes Support a Cyclin A-Specific Role in p27KIP1 Degradation. <i>Journal of Molecular Biology</i> , 2021, 433, 166795.	4.2	10
3	Structure-Based Design of Potent and Orally Active Isoindolinone Inhibitors of MDM2-p53 Protein-Protein Interaction. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4071-4088.	6.4	30
4	An Alkynylpyrimidine-Based Covalent Inhibitor That Targets a Unique Cysteine in NF- κ B-Inducing Kinase. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10001-10018.	6.4	9
5	Crystallographic and electrophilic fragment screening of the SARS-CoV-2 main protease. <i>Nature Communications</i> , 2020, 11, 5047.	12.8	376
6	Paradoxical activation of the protein kinase-transcription factor ERK5 by ERK5 kinase inhibitors. <i>Nature Communications</i> , 2020, 11, 1383.	12.8	30
7	Identification of a novel orally bioavailable ERK5 inhibitor with selectivity over p38 β and BRD4. <i>European Journal of Medicinal Chemistry</i> , 2019, 178, 530-543.	5.5	15
8	FragLites—Minimal, Halogenated Fragments Displaying Pharmacophore Doublets. An Efficient Approach to Druggability Assessment and Hit Generation. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 3741-3752.	6.4	62
9	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46
10	Differences in the Conformational Energy Landscape of CDK1 and CDK2 Suggest a Mechanism for Achieving Selective CDK Inhibition. <i>Cell Chemical Biology</i> , 2019, 26, 121-130.e5.	5.2	72
11	Tuning the Binding Affinity and Selectivity of Perfluoroaryl-Stapled Peptides by Cysteine Editing. <i>Chemistry - A European Journal</i> , 2019, 25, 177-182.	3.3	23
12	Identification of a novel ligand for the ATAD2 bromodomain with selectivity over BRD4 through a fragment growing approach. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 1843-1850.	2.8	15
13	CCP4: the new graphical user interface to the CCP4 program suite. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 68-84.	2.3	382
14	Molecular profiling and combinatorial activity of CCTO68127: a potent CDK2 and CDK9 inhibitor. <i>Molecular Oncology</i> , 2018, 12, 287-304.	4.6	33
15	Validating and enabling phosphoglycerate dehydrogenase (PHGDH) as a target for fragment-based drug discovery in PHGDH-amplified breast cancer. <i>Oncotarget</i> , 2018, 9, 13139-13153.	1.8	25
16	Aurora A regulates expression of AR-V7 in models of castrate resistant prostate cancer. <i>Scientific Reports</i> , 2017, 7, 40957.	3.3	30
17	Cyclin-Dependent Kinase (CDK) Inhibitors: Structure-Activity Relationships and Insights into the CDK-2 Selectivity of 6-Substituted 2-Arylamino-purines. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 1746-1767.	6.4	77
18	Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. <i>Cell Reports</i> , 2017, 21, 1386-1398.	6.4	49

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19	Structure-based discovery of cyclin-dependent protein kinase inhibitors. <i>Essays in Biochemistry</i> , 2017, 61, 439-452.	4.7	39
20	Benzene Probes in Molecular Dynamics Simulations Reveal Novel Binding Sites for Ligand Design. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 3452-3457.	4.6	45
21	CDK1 structures reveal conserved and unique features of the essential cell cycle CDK. <i>Nature Communications</i> , 2015, 6, 6769.	12.8	145
22	Identification and Characterization of an Irreversible Inhibitor of CDK2. <i>Chemistry and Biology</i> , 2015, 22, 1159-1164.	6.0	85
23	8-Substituted <i>O</i> ⁶ -Cyclohexylmethylguanine CDK2 Inhibitors: Using Structure-Based Inhibitor Design to Optimize an Alternative Binding Mode. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 56-70.	6.4	15
24	An Inhibitor's-Eye View of the ATP-Binding Site of CDKs in Different Regulatory States. <i>ACS Chemical Biology</i> , 2014, 9, 1251-1256.	3.4	27
25	Structural characterization of the cyclin-dependent protein kinase family. <i>Biochemical Society Transactions</i> , 2013, 41, 1008-1016.	3.4	35
26	The structure of an MDM2-Nutlin-3a complex solved by the use of a validated MDM2 surface-entropy reduction mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1358-1366.	2.5	59
27	Comparative Structural and Functional Studies of 4-(Thiazol-5-yl)-2-(phenylamino)pyrimidine-5-carbonitrile CDK9 Inhibitors Suggest the Basis for Isotype Selectivity. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 660-670.	6.4	51
28	Substituted 4-(Thiazol-5-yl)-2-(phenylamino)pyrimidines Are Highly Active CDK9 Inhibitors: Synthesis, X-ray Crystal Structures, Structure-Activity Relationship, and Anticancer Activities. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 640-659.	6.4	111
29	Structural and functional characterization of Rpn12 identifies residues required for Rpn10 proteasome incorporation. <i>Biochemical Journal</i> , 2012, 448, 55-65.	3.7	23
30	The CDK9 Tail Determines the Reaction Pathway of Positive Transcription Elongation Factor b. <i>Structure</i> , 2012, 20, 1788-1795.	3.3	32
31	The CDK9 C-helix Exhibits Conformational Plasticity That May Explain the Selectivity of CAN508. <i>ACS Chemical Biology</i> , 2012, 7, 811-816.	3.4	45
32	The Structural Basis for Control of Eukaryotic Protein Kinases. <i>Annual Review of Biochemistry</i> , 2012, 81, 587-613.	11.1	362
33	Generation of protein lattices by fusing proteins with matching rotational symmetry. <i>Nature Nanotechnology</i> , 2011, 6, 558-562.	31.5	214
34	Understanding Small-Molecule Binding to MDM2: Insights into Structural Effects of Isoindolinone Inhibitors from NMR Spectroscopy. <i>Chemical Biology and Drug Design</i> , 2011, 77, 301-308.	3.2	15
35	Catalysis and regulation. <i>Current Opinion in Structural Biology</i> , 2011, 21, 775-776.	5.7	6
36	MDM2-p53 protein-protein interaction inhibitors: A-ring substituted isoindolinones. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 5916-9.	2.2	36

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37	Isoindolinone Inhibitors of the Murine Double Minute 2 (MDM2)-p53 Protein-Protein Interaction: Structure-Activity Studies Leading to Improved Potency. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 1233-1243.	6.4	130
38	Presenting your structures: the CCP4 molecular-graphics software. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 386-394.	2.5	1,133
39	Probing the architecture of the <i>Mycobacterium marinum</i> arylamine N-acetyltransferase active site. <i>Protein and Cell</i> , 2010, 1, 384-392.	11.0	24
40	Recent developments in cyclin-dependent kinase biochemical and structural studies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 511-519.	2.3	96
41	A new crystal form of Lys48-linked diubiquitin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 994-998.	0.7	26
42	Distinctive Properties of the Hyaluronan-binding Domain in the Lymphatic Endothelial Receptor Lyve-1 and Their Implications for Receptor Function. <i>Journal of Biological Chemistry</i> , 2010, 285, 10724-10735.	3.4	45
43	Structure of Rpn10 and Its Interactions with Polyubiquitin Chains and the Proteasome Subunit Rpn12*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33992-34003.	3.4	61
44	Catalysis and regulation. <i>Current Opinion in Structural Biology</i> , 2009, 19, 641-642.	5.7	1
45	The structure of CDK4/cyclin D3 has implications for models of CDK activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4171-4176.	7.1	102
46	Structure of HsaD, a steroid-degrading hydrolase, from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 2-7.	0.7	31
47	Structures of <i>P. falciparum</i> Protein Kinase 7 Identify an Activation Motif and Leads for Inhibitor Design. <i>Structure</i> , 2008, 16, 228-238.	3.3	62
48	Structural Analysis of the Interactions Between Paxillin LD Motifs and β -Parvin. <i>Structure</i> , 2008, 16, 1521-1531.	3.3	32
49	Divergence of Cofactor Recognition across Evolution: Coenzyme A Binding in a Prokaryotic Arylamine N-Acetyltransferase. <i>Journal of Molecular Biology</i> , 2008, 375, 178-191.	4.2	56
50	Analysis of Chemical Shift Changes Reveals the Binding Modes of Isoindolinone Inhibitors of the MDM2-p53 Interaction. <i>Journal of the American Chemical Society</i> , 2008, 130, 16038-16044.	13.7	102
51	Arylamine N-Acetyltransferases in <i>Mycobacteria</i> . <i>Current Drug Metabolism</i> , 2008, 9, 510-519.	1.2	38
52	How Tyrosine 15 Phosphorylation Inhibits the Activity of Cyclin-dependent Kinase 2-Cyclin A. <i>Journal of Biological Chemistry</i> , 2007, 282, 3173-3181.	3.4	85
53	Plasticity of the TSG-6 HA-binding Loop and Mobility in the TSG-6-HA Complex Revealed by NMR and X-ray Crystallography. <i>Journal of Molecular Biology</i> , 2007, 371, 669-684.	4.2	24
54	Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2007, 373, 1213-1228.	4.2	66

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55	Structure-based design of 2-arylamino-4-cyclohexylmethoxy-5-nitroso-6-aminopyrimidine inhibitors of cyclin-dependent kinase 2. <i>Organic and Biomolecular Chemistry</i> , 2007, 5, 1577.	2.8	16
56	Computational analyses of the surface properties of protein-protein interfaces. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 50-57.	2.5	30
57	Structures of the Cd44-hyaluronan complex provide insight into a fundamental carbohydrate-protein interaction. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 234-239.	8.2	314
58	Searching for Cyclin-Dependent Kinase Inhibitors Using a New Variant of the Cope Elimination. <i>Journal of the American Chemical Society</i> , 2006, 128, 6012-6013.	13.7	64
59	Dissecting the Determinants of Cyclin-Dependent Kinase 2 and Cyclin-Dependent Kinase 4 Inhibitor Selectivity. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5470-5477.	6.4	39
60	The Role of the Phospho-CDK2/Cyclin A Recruitment Site in Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2006, 281, 23167-23179.	3.4	79
61	Structures of the Dsk2 UBL and UBA domains and their complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 177-188.	2.5	69
62	Structural and kinetic mechanism of CDK2 inhibition by Y15 phosphorylation. <i>FASEB Journal</i> , 2006, 20, A461.	0.5	0
63	Expression, purification, characterization and structure of <i>Pseudomonas aeruginosa</i> arylamine N-acetyltransferase. <i>Biochemical Journal</i> , 2005, 385, 605-612.	3.7	72
64	Investigation of the catalytic triad of arylamine N-acetyltransferases: essential residues required for acetyl transfer to arylamines. <i>Biochemical Journal</i> , 2005, 390, 115-123.	3.7	60
65	Exploiting structural principles to design cyclin-dependent kinase inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1754, 58-64.	2.3	27
66	Mechanism of Lys48-linked polyubiquitin chain recognition by the Mud1 UBA domain. <i>EMBO Journal</i> , 2005, 24, 3178-3189.	7.8	87
67	Structure of <i>Mesorhizobium lotii</i> arylamine N-acetyltransferase 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 14-16.	0.7	35
68	Molecular Motions of Human Cyclin-dependent Kinase 2. <i>Journal of Biological Chemistry</i> , 2005, 280, 13993-14005.	3.4	44
69	Dynamite extended: two new services to simplify protein dynamic analysis. <i>Bioinformatics</i> , 2005, 21, 3174-3175.	4.1	20
70	Molecular Basis for the Recognition of Phosphorylated and Phosphoacetylated Histone H3 by 14-3-3. <i>Molecular Cell</i> , 2005, 20, 199-211.	9.7	220
71	Binding of the anti-tubercular drug isoniazid to the arylamine N-acetyltransferase protein from <i>Mycobacterium smegmatis</i> . <i>Protein Science</i> , 2005, 14, 775-782.	7.6	56
72	N2-Substituted O6-Cyclohexylmethylguanidine Derivatives: Potent Inhibitors of Cyclin-Dependent Kinases 1 and 2. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 3710-3722.	6.4	116

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73	Protein Kinase Inhibitors: Insights into Drug Design from Structure. <i>Science</i> , 2004, 303, 1800-1805.	12.6	1,164
74	Dynamite: a simple way to gain insight into protein motions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2280-2287.	2.5	81
75	Developments in the CCP4 molecular-graphics project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2288-2294.	2.5	516
76	Structure of the Regulatory Hyaluronan Binding Domain in the Inflammatory Leukocyte Homing Receptor CD44. <i>Molecular Cell</i> , 2004, 13, 483-496.	9.7	228
77	The role of structure in kinase-targeted inhibitor design. <i>Current Opinion in Drug Discovery & Development</i> , 2004, 7, 428-36.	1.9	6
78	Aloisines, a New Family of CDK/GSK-3 Inhibitors. SAR Study, Crystal Structure in Complex with CDK2, Enzyme Selectivity, and Cellular Effects. <i>Journal of Medicinal Chemistry</i> , 2003, 46, 222-236.	6.4	139
79	Molecular Recognition of Paxillin LD Motifs by the Focal Adhesion Targeting Domain. <i>Structure</i> , 2003, 11, 1207-1217.	3.3	93
80	Structures of <i>P. falciparum</i> PfPK5 Test the CDK Regulation Paradigm and Suggest Mechanisms of Small Molecule Inhibition. <i>Structure</i> , 2003, 11, 1329-1337.	3.3	91
81	4-Alkoxy-2,6-diaminopyrimidine derivatives: inhibitors of cyclin dependent kinases 1 and 2. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 217-222.	2.2	54
82	Structure-Based design of 2-Arylamino-4-cyclohexylmethyl-5-nitroso-6-aminopyrimidine inhibitors of cyclin-Dependent kinases 1 and 2. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 3079-3082.	2.2	69
83	Structural investigation of mutant <i>Mycobacterium smegmatis</i> arylamine N-acetyltransferase: a model for a naturally occurring functional polymorphism in <i>Mycobacterium tuberculosis</i> arylamine N-acetyltransferase. <i>Protein Expression and Purification</i> , 2003, 27, 75-84.	1.3	14
84	Arylamine N-acetyltransferases: a pharmacogenomic approach to drug metabolism and endogenous function. <i>Biochemical Society Transactions</i> , 2003, 31, 615-619.	3.4	46
85	Reversal of Growth Suppression by p107 via Direct Phosphorylation by Cyclin D1/Cyclin-Dependent Kinase 4. <i>Molecular and Cellular Biology</i> , 2002, 22, 2242-2254.	2.3	75
86	Probing the ATP Ribose-Binding Domain of Cyclin-Dependent Kinases 1 and 2 with O6-Substituted Guanine Derivatives. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 3381-3393.	6.4	90
87	The Structure of Arylamine N-acetyltransferase from <i>Mycobacterium smegmatis</i> An Enzyme which Inactivates the Anti-tubercular Drug, Isoniazid. <i>Journal of Molecular Biology</i> , 2002, 318, 1071-1083.	4.2	100
88	Structural studies with inhibitors of the cell cycle regulatory kinase cyclin-dependent protein kinase 2. , 2002, 93, 113-124.		61
89	Structure-based design of cyclin-dependent kinase inhibitors. , 2002, 93, 125-133.		96
90	The Structural Basis of Localization and Signaling by the Focal Adhesion Targeting Domain. <i>Structure</i> , 2002, 10, 319-327.	3.3	132

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91	TheCCP4 molecular-graphics project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1955-1957.	2.5	193
92	Structure-based design of a potent purine-based cyclin-dependent kinase inhibitor. <i>Nature Structural Biology</i> , 2002, 9, 745-749.	9.7	198
93	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin A. <i>Biochemistry</i> , 2002, 41, 15625-15634.	2.5	152
94	Xenopus Phospho-CDK7/Cyclin H Expressed in Baculoviral-Infected Insect Cells. <i>Protein Expression and Purification</i> , 2001, 23, 252-260.	1.3	4
95	Phosphoprotein-Protein Interactions Revealed by the Crystal Structure of Kinase-Associated Phosphatase in Complex with PhosphoCDK2. <i>Molecular Cell</i> , 2001, 7, 615-626.	9.7	163
96	Inhibitor Binding to Active and Inactive CDK2. <i>Structure</i> , 2001, 9, 389-397.	3.3	137
97	The Role of the Src Homology 3-Src Homology 2 Interface in the Regulation of Src Kinases. <i>Journal of Biological Chemistry</i> , 2001, 276, 17199-17205.	3.4	79
98	Structure of arylamine N-acetyltransferase reveals a catalytic triad. <i>Nature Structural Biology</i> , 2000, 7, 560-564.	9.7	179
99	Identification of Novel Purine and Pyrimidine Cyclin-Dependent Kinase Inhibitors with Distinct Molecular Interactions and Tumor Cell Growth Inhibition Profiles. <i>Journal of Medicinal Chemistry</i> , 2000, 43, 2797-2804.	6.4	203
100	Cyclin-Dependent Kinase Inhibition by New C-2 Alkynylated Purine Derivatives and Molecular Structure of a CDK2-Inhibitor Complex. <i>Journal of Medicinal Chemistry</i> , 2000, 43, 1282-1292.	6.4	86
101	Effects of Phosphorylation of Threonine 160 on Cyclin-dependent Kinase 2 Structure and Activity. <i>Journal of Biological Chemistry</i> , 1999, 274, 8746-8756.	3.4	198
102	The structural basis for specificity of substrate and recruitment peptides for cyclin-dependent kinases. <i>Nature Cell Biology</i> , 1999, 1, 438-443.	10.3	509
103	Chemical Inhibitors of Cyclin-Dependent Kinases. , 1999, 82, 269-278.		33
104	Cyclin-dependent kinases: inhibition and substrate recognition. <i>Current Opinion in Structural Biology</i> , 1999, 9, 738-744.	5.7	109
105	A Structural Explanation for the Binding of Multiple Ligands by the $\hat{\pm}$ -Adaptin Appendage Domain. <i>Cell</i> , 1999, 97, 805-815.	28.9	271
106	Structural principles in cell-cycle control: beyond the CDKs. <i>Structure</i> , 1998, 6, 535-541.	3.3	14
107	The structure of a glycogen phosphorylase glucopyranose spirohydantoin complex at 1.8 Å... resolution and 100 K: The role of the water structure and its contribution to binding. <i>Protein Science</i> , 1998, 7, 915-927.	7.6	85
108	The structural basis for substrate recognition and control by protein kinases1. <i>FEBS Letters</i> , 1998, 430, 1-11.	2.8	185

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109	Purification, Characterization, and Crystallization of an N-Hydroxyarylamine O-Acetyltransferase from <i>Salmonella typhimurium</i> . <i>Protein Expression and Purification</i> , 1998, 12, 371-380.	1.3	55
110	Protein kinase inhibition by staurosporine revealed in details of the molecular interaction with CDK2. <i>Nature Structural Biology</i> , 1997, 4, 796-801.	9.7	243
111	The cyclin box fold: protein recognition in cell-cycle and transcription control. <i>Trends in Biochemical Sciences</i> , 1997, 22, 482-487.	7.5	105
112	Active and Inactive Protein Kinases: Structural Basis for Regulation. <i>Cell</i> , 1996, 85, 149-158.	28.9	1,313
113	Crystal structure of the cell cycle-regulatory protein <i>suc1</i> reveals a beta-hinge conformational switch.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 10232-10236.	7.1	70
114	Two structures of the catalytic domain of phosphorylase kinase: an active protein kinase complexed with substrate analogue and product. <i>Structure</i> , 1995, 3, 467-482.	3.3	162
115	The crystal structure of cyclin A. <i>Structure</i> , 1995, 3, 1235-1247.	3.3	183
116	Expression, Purification and Crystallisation of Phosphorylase Kinase Catalytic Domain. <i>Journal of Molecular Biology</i> , 1995, 246, 374-381.	4.2	22
117	Analysis of the structure of <i>Pseudomonas glumae</i> lipase. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 559-562.	2.1	27
118	Comparison of the structures and the crystal contacts of trypanosomal triosephosphate isomerase in four different crystal forms. <i>Protein Science</i> , 1994, 3, 779-787.	7.6	20
119	Modular mutagenesis of a TEM-barrel enzyme: the crystal structure of a chimeric <i>E.coli</i> TIM having the eighth β -sheet-unit replaced by the equivalent unit of chicken TIM. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 945-951.	2.1	2
120	Structures of the "open" and "closed" state of trypanosomal triosephosphate isomerase, as observed in a new crystal form: Implications for the reaction mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 311-326.	2.6	56
121	Overexpression of trypanosomal triosephosphate isomerase in <i>Escherichia coli</i> and characterisation of a dimer-interface mutant. <i>FEBS Journal</i> , 1993, 211, 703-710.	0.2	64
122	Replacing the β -sheet-unit 8 of <i>E.coli</i> TIM with its chicken homologue leads to a stable and active hybrid enzyme. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 893-900.	2.1	8
123	The crystal structure of triacylglycerol lipase from <i>Pseudomonas glumae</i> reveals a partially redundant catalytic aspartate. <i>FEBS Letters</i> , 1993, 331, 123-128.	2.8	252
124	Crystallographic binding studies with triosephosphate isomerases: Conformational changes induced by substrate and substrate-analogues. <i>FEBS Letters</i> , 1992, 307, 34-39.	2.8	44
125	Comparison of the refined crystal structures of liganded and unliganded chicken, yeast and trypanosomal triosephosphate isomerase. <i>Journal of Molecular Biology</i> , 1992, 224, 1115-1126.	4.2	113
126	Crystal structure of a Src-homology 3 (SH3) domain. <i>Nature</i> , 1992, 359, 851-855.	27.8	472

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127	Crystal transfer experiments carried out with crystals of trypanosomal triosephosphate isomerase (TIM). <i>Journal of Crystal Growth</i> , 1992, 122, 231-234.	1.5	13
128	Refined 1.83 Å... structure of trypanosomal triosephosphate isomerase crystallized in the presence of 2.4 M-ammonium sulphate. <i>Journal of Molecular Biology</i> , 1991, 220, 995-1015.	4.2	163
129	Crystallographic and molecular modeling studies on trypanosomal triosephosphate isomerase: a critical assessment of the predicted and observed structures of the complex with 2-phosphoglycerate. <i>Journal of Medicinal Chemistry</i> , 1991, 34, 2709-2718.	6.4	32
130	Anion binding at the active site of trypanosomal triosephosphate isomerase. Monohydrogen phosphate does not mimic sulphate. <i>FEBS Journal</i> , 1991, 198, 53-57.	0.2	28
131	The crystal structure of the "open" and the "closed" conformation of the flexible loop of trypanosomal triosephosphate isomerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 33-49.	2.6	85
132	The adaptability of the active site of trypanosomal triosephosphate isomerase as observed in the crystal structures of three different complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 50-69.	2.6	77