Martin E M Noble

List of Publications by Year
in descending order

132 papers	15,568 citations	18465 62 h-index	17580 121 g-index
135 all docs	135 docs citations	135 times ranked	17992 citing authors

#	Article	IF	Citations
1	Active and Inactive Protein Kinases: Structural Basis for Regulation. Cell, 1996, 85, 149-158.	13.5	1,313
2	Protein Kinase Inhibitors: Insights into Drug Design from Structure. Science, 2004, 303, 1800-1805.	6.0	1,164
3	Presenting your structures: theCCP4mgmolecular-graphics software. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 386-394.	2.5	1,133
4	Developments in theCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2288-2294.	2.5	516
5	The structural basis for specificity of substrate and recruitment peptides for cyclin-dependent kinases. Nature Cell Biology, 1999, 1, 438-443.	4.6	509
6	Crystal structure of a Src-homology 3 (SH3) domain. Nature, 1992, 359, 851-855.	13.7	472
7	CCP4i2: the new graphical user interface to theCCP4 program suite. Acta Crystallographica Section D: Structural Biology, 2018, 74, 68-84.	1.1	382
8	Crystallographic and electrophilic fragment screening of the SARS-CoV-2 main protease. Nature Communications, 2020, 11, 5047.	5.8	376
9	The Structural Basis for Control of Eukaryotic Protein Kinases. Annual Review of Biochemistry, 2012, 81, 587-613.	5.0	362
10	Structures of the Cd44â€“hyaluronan complex provide insight into a fundamental carbohydrate-protein interaction. Nature Structural and Molecular Biology, 2007, 14, 234-239.	3.6	314
11	A Structural Explanation for the Binding of Multiple Ligands by the Î±-Adaptin Appendage Domain. Cell, 1999, 97, 805-815.	13.5	271
12	The crystal structure of triacylglycerol lipase from Pseudomonas glumae reveals a partially redundant catalytic aspartate. FEBS Letters, 1993, 331, 123-128.	1.3	252
13	Protein kinase inhibition by staurosporine revealed in details of the molecular interaction with CDK2. Nature Structural Biology, 1997, 4, 796-801.	9.7	243
14	Structure of the Regulatory Hyaluronan Binding Domain in the Inflammatory Leukocyte Homing Receptor CD44. Molecular Cell, 2004, 13, 483-496.	4.5	228
15	Molecular Basis for the Recognition of Phosphorylated and Phosphoacetylated Histone H3 by 14-3-3. Molecular Cell, 2005, 20, 199-211.	4.5	220
16	Generation of protein lattices by fusing proteins with matching rotational symmetry. Nature Nanotechnology, 2011, 6, 558-562.	15.6	214
17	Identification of Novel Purine and Pyrimidine Cyclin-Dependent Kinase Inhibitors with Distinct Molecular Interactions and Tumor Cell Growth Inhibition Profiles. Journal of Medicinal Chemistry, 2000, 43, 2797-2804.	2.9	203
18	Effects of Phosphorylation of Threonine 160 on Cyclin-dependent Kinase 2 Structure and Activity. Journal of Biological Chemistry, 1999, 274, 8746-8756.	1.6	198

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19	Structure-based design of a potent purine-based cyclin-dependent kinase inhibitor. Nature Structural Biology, 2002, 9, 745-749.	9.7	198
20	TheCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1955-1957.	2.5	193
21	The structural basis for substrate recognition and control by protein kinases1. FEBS Letters, 1998, 430, 1-11.	1.3	185
22	The crystal structure of cyclin A. Structure, 1995, 3, 1235-1247.	1.6	183
23	Structure of arylamine N-acetyltransferase reveals a catalytic triad. Nature Structural Biology, 2000, 7, 560-564.	9.7	179
24	Refined 1.83 Ã... structure of trypanosomal triosephosphate isomerase crystallized in the presence of 2.4 m-ammonium sulphate. Journal of Molecular Biology, 1991, 220, 995-1015.	2.0	163
25	Phosphoproteinâ€“Protein Interactions Revealed by the Crystal Structure of Kinase-Associated Phosphatase in Complex with PhosphoCDK2. Molecular Cell, 2001, 7, 615-626.	4.5	163
26	Two structures of the catalytic domain of phosphorylase kinase: an active protein kinase complexed with substrate analogue and product. Structure, 1995, 3, 467-482.	1.6	162
27	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin Aâ€‚â€¡. Biochemistry, 2002, 41, 15625-15634.	1.2	152
28	CDK1 structures reveal conserved and unique features of the essential cell cycle CDK. Nature Communications, 2015, 6, 6769.	5.8	145
29	Aloisines, a New Family of CDK/GSK-3 Inhibitors. SAR Study, Crystal Structure in Complex with CDK2, Enzyme Selectivity, and Cellular Effects. Journal of Medicinal Chemistry, 2003, 46, 222-236.	2.9	139
30	Inhibitor Binding to Active and Inactive CDK2. Structure, 2001, 9, 389-397.	1.6	137
31	The Structural Basis of Localization and Signaling by the Focal Adhesion Targeting Domain. Structure, 2002, 10, 319-327.	1.6	132
32	Isoindolinone Inhibitors of the Murine Double Minute 2 (MDM2)-p53 Proteinâ^'Protein Interaction: Structureâ^'Activity Studies Leading to Improved Potency. Journal of Medicinal Chemistry, 2011, 54, 1233-1243.	2.9	130
33	N2-SubstitutedO6-CyclohexylmethylguanineÂ Derivatives:Â Potent Inhibitors of Cyclin-Dependent Kinases 1 and 2. Journal of Medicinal Chemistry, 2004, 47, 3710-3722.	2.9	116
34	Comparison of the refined crystal structures of liganded and unliganded chicken, yeast and trypanosomal triosephosphate isomerase. Journal of Molecular Biology, 1992, 224, 1115-1126.	2.0	113
35	Substituted 4-(Thiazol-5-yl)-2-(phenylamino)pyrimidines Are Highly Active CDK9 Inhibitors: Synthesis, X-ray Crystal Structures, Structureâ€“Activity Relationship, and Anticancer Activities. Journal of Medicinal Chemistry, 2013, 56, 640-659.	2.9	111
36	Cyclin-dependent kinases: inhibition and substrate recognition. Current Opinion in Structural Biology, 1999, 9, 738-744.	2.6	109

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37	The cyclin box fold: protein recognition in cell-cycle and transcription control. Trends in Biochemical Sciences, 1997, 22, 482-487.	3.7	105
38	Analysis of Chemical Shift Changes Reveals the Binding Modes of Isoindolinone Inhibitors of the MDM2-p53 Interaction. Journal of the American Chemical Society, 2008, 130, 16038-16044.	6.6	102
39	The structure of CDK4/cyclin D3 has implications for models of CDK activation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4171-4176.	3.3	102
40	The Structure of Arylamine N-acetyltransferase from Mycobacterium smegmatisâ€"An Enzyme which Inactivates the Anti-tubercular Drug, Isoniazid. Journal of Molecular Biology, 2002, 318, 1071-1083.	2.0	100
41	Structure-based design of cyclin-dependent kinase inhibitors. , 2002, 93, 125-133.		96
42	Recent developments in cyclin-dependent kinase biochemical and structural studies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 511-519.	1.1	96
43	Molecular Recognition of Paxillin LD Motifs by the Focal Adhesion Targeting Domain. Structure, 2003, 11, 1207-1217.	1.6	93
44	Structures of P. falciparum PfPK5 Test the CDK Regulation Paradigm and Suggest Mechanisms of Small Molecule Inhibition. Structure, 2003, 11, 1329-1337.	1.6	91
45	Probing the ATP Ribose-Binding Domain of Cyclin-Dependent Kinases 1 and 2 withO6-Substituted Guanine Derivatives. Journal of Medicinal Chemistry, 2002, 45, 3381-3393.	2.9	90
46	Mechanism of Lys48-linked polyubiquitin chain recognition by the Mud1 UBA domain. EMBO Journal, 2005, 24, 3178-3189.	3.5	87
47	Cyclin-Dependent Kinase Inhibition by New C-2 Alkynylated Purine Derivatives and Molecular Structure of a CDK2â^'Inhibitor Complex. Journal of Medicinal Chemistry, 2000, 43, 1282-1292.	2.9	86
48	The crystal structure of the â€œopenâ€•and the â€œclosedâ€•conformation of the flexible loop of trypanosomal triosephosphate isomerase. Proteins: Structure, Function and Bioinformatics, 1991, 10, 33-49.	1.5	85
49	The structure of a glycogen phosphorylase glucopyranose spirohydantoin complex at 1.8 Ã... resolution and 100 K: The role of the water structure and its contribution to binding. Protein Science, 1998, 7, 915-927.	3.1	85
50	How Tyrosine 15 Phosphorylation Inhibits the Activity of Cyclin-dependent Kinase 2-Cyclin A. Journal of Biological Chemistry, 2007, 282, 3173-3181.	1.6	85
51	Identification and Characterization of an Irreversible Inhibitor of CDK2. Chemistry and Biology, 2015, 22, 1159-1164.	6.2	85
52	Dynamite: a simple way to gain insight into protein motions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2280-2287.	2.5	81
53	The Role of the Src Homology 3-Src Homology 2 Interface in the Regulation of Src Kinases. Journal of Biological Chemistry, 2001, 276, 17199-17205.	1.6	79
54	The Role of the Phospho-CDK2/Cyclin A Recruitment Site in Substrate Recognition. Journal of Biological Chemistry, 2006, 281, 23167-23179.	1.6	79

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55	The adaptability of the active site of trypanosomal triosephosphate isomerase as observed in the crystal structures of three different complexes. Proteins: Structure, Function and Bioinformatics, 1991, 10, 50-69.	1.5	77
56	Cyclin-Dependent Kinase (CDK) Inhibitors: Structureâ€“Activity Relationships and Insights into the CDK-2 Selectivity of 6-Substituted 2-Arylaminopurines. Journal of Medicinal Chemistry, 2017, 60, 1746-1767.	2.9	77
57	Reversal of Growth Suppression by p107 via Direct Phosphorylation by Cyclin D1/Cyclin-Dependent Kinase 4. Molecular and Cellular Biology, 2002, 22, 2242-2254.	1.1	75
58	Expression, purification, characterization and structure of Pseudomonas aeruginosa arylamine N-acetyltransferase. Biochemical Journal, 2005, 385, 605-612.	1.7	72
59	Differences in the Conformational Energy Landscape of CDK1 and CDK2 Suggest a Mechanism for Achieving Selective CDK Inhibition. Cell Chemical Biology, 2019, 26, 121-130.e5.	2.5	72
60	Crystal structure of the cell cycle-regulatory protein suc1 reveals a beta-hinge conformational switch.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 10232-10236.	3.3	70
61	Structure-Based design of 2-Arylamino-4-cyclohexylmethyl-5-nitroso-6-aminopyrimidine inhibitors of cyclin-Dependent kinases 1 and 2. Bioorganic and Medicinal Chemistry Letters, 2003, 13, 3079-3082.	1.0	69
62	Structures of the Dsk2 UBL and UBA domains and their complex. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 177-188.	2.5	69
63	Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2007, 373, 1213-1228.	2.0	66
64	Overexpression of trypanosomal triosephosphate isomerase in Escherichia coli and characterisation of a dimer-interface mutant. FEBS Journal, 1993, 211, 703-710.	0.2	64
65	Searching for Cyclin-Dependent Kinase Inhibitors Using a New Variant of the Cope Elimination. Journal of the American Chemical Society, 2006, 128, 6012-6013.	6.6	64
66	Structures of P. falciparum Protein Kinase 7 Identify an Activation Motif and Leads for Inhibitor Design. Structure, 2008, 16, 228-238.	1.6	62
67	FragLitesâ€”Minimal, Halogenated Fragments Displaying Pharmacophore Doublets. An Efficient Approach to Druggability Assessment and Hit Generation. Journal of Medicinal Chemistry, 2019, 62, 3741-3752.	2.9	62
68	Structural studies with inhibitors of the cell cycle regulatory kinase cyclin-dependent protein kinase 2. , 2002, 93, 113-124.		61
69	Structure of Rpn10 and Its Interactions with Polyubiquitin Chains and the Proteasome Subunit Rpn12*. Journal of Biological Chemistry, 2010, 285, 33992-34003.	1.6	61
70	Investigation of the catalytic triad of arylamine N-acetyltransferases: essential residues required for acetyl transfer to arylamines. Biochemical Journal, 2005, 390, 115-123.	1.7	60
71	The structure of an MDM2â€“Nutlin-3a complex solved by the use of a validated MDM2 surface-entropy reduction mutant. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1358-1366.	2.5	59
72	Structures of the â€œopenâ€•and â€œclosedâ€•state of trypanosomal triosephosphate isomerase, as observed in a new crystal form: Implications for the reaction mechanism. Proteins: Structure, Function and Bioinformatics, 1993, 16, 311-326.	1.5	56

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73	Binding of the anti-tubercular drug isoniazid to the arylamine N-acetyltransferase protein from Mycobacterium smegmatis. Protein Science, 2005, 14, 775-782.	3.1	56
74	Divergence of Cofactor Recognition across Evolution: Coenzyme A Binding in a Prokaryotic Arylamine N-Acetyltransferase. Journal of Molecular Biology, 2008, 375, 178-191.	2.0	56
75	Purification, Characterization, and Crystallization of anN-HydroxyarylamineO-Acetyltransferase fromSalmonella typhimurium. Protein Expression and Purification, 1998, 12, 371-380.	0.6	55
76	4-Alkoxy-2,6-diaminopyrimidine derivatives: inhibitors of cyclin dependent kinases 1 and 2. Bioorganic and Medicinal Chemistry Letters, 2003, 13, 217-222.	1.0	54
77	Comparative Structural and Functional Studies of 4-(Thiazol-5-yl)-2-(phenylamino)pyrimidine-5-carbonitrile CDK9 Inhibitors Suggest the Basis for Isotype Selectivity. Journal of Medicinal Chemistry, 2013, 56, 660-670.	2.9	51
78	Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. Cell Reports, 2017, 21, 1386-1398.	2.9	49
79	Arylamine N-acetyltransferases: a pharmacogenomic approach to drug metabolism and endogenous function. Biochemical Society Transactions, 2003, 31, 615-619.	1.6	46
80	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). Acta Crystallographica Section D: Structural Biology, 2019, 75, 451-454.	1.1	46
81	Distinctive Properties of the Hyaluronan-binding Domain in the Lymphatic Endothelial Receptor Lyve-1 and Their Implications for Receptor Function. Journal of Biological Chemistry, 2010, 285, 10724-10735.	1.6	45
82	The CDK9 C-helix Exhibits Conformational Plasticity That May Explain the Selectivity of CAN508. ACS Chemical Biology, 2012, 7, 811-816.	1.6	45
83	Benzene Probes in Molecular Dynamics Simulations Reveal Novel Binding Sites for Ligand Design. Journal of Physical Chemistry Letters, 2016, 7, 3452-3457.	2.1	45
84	Crystallographic binding studies with triosephosphate isomerases: Conformational changes induced by substrate and substrate-analogues. FEBS Letters, 1992, 307, 34-39.	1.3	44
85	Molecular Motions of Human Cyclin-dependent Kinase 2. Journal of Biological Chemistry, 2005, 280, 13993-14005.	1.6	44
86	Dissecting the Determinants of Cyclin-Dependent Kinase 2 and Cyclin-Dependent Kinase 4 Inhibitor Selectivityâ€. Journal of Medicinal Chemistry, 2006, 49, 5470-5477.	2.9	39
87	Structure-based discovery of cyclin-dependent protein kinase inhibitors. Essays in Biochemistry, 2017, 61, 439-452.	2.1	39
88	Arylamine N-Acetyltransferases in Mycobacteria. Current Drug Metabolism, 2008, 9, 510-519.	0.7	38
89	MDM2-p53 proteinâ€“protein interaction inhibitors: A-ring substituted isoindolinones. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 5916-9.	1.0	36
90	Structure ofMesorhizobium lotiarylamineN-acetyltransferase 1. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 14-16.	0.7	35

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91	Structural characterization of the cyclin-dependent protein kinase family. Biochemical Society Transactions, 2013, 41, 1008-1016.	1.6	35
92	Chemical Inhibitors of Cyclin-Dependent Kinases. , 1999, 82, 269-278.		33
93	Molecular profiling and combinatorial activity of <scp>CCT</scp>068127: a potent <scp>CDK</scp>2 and <scp>CDK</scp>9 inhibitor. Molecular Oncology, 2018, 12, 287-304.	2.1	33
94	Crystallographic and molecular modeling studies on trypanosomal triosephosphate isomerase: a critical assessment of the predicted and observed structures of the complex with 2-phosphoglycerate. Journal of Medicinal Chemistry, 1991, 34, 2709-2718.	2.9	32
95	Structural Analysis of the Interactions Between Paxillin LD Motifs and Î±-Parvin. Structure, 2008, 16, 1521-1531.	1.6	32
96	The CDK9 Tail Determines the Reaction Pathway of Positive Transcription Elongation Factor b. Structure, 2012, 20, 1788-1795.	1.6	32
97	Structure of HsaD, a steroid-degrading hydrolase, fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 2-7.	0.7	31
98	Computational analyses of the surface properties of proteinâ€“protein interfaces. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 50-57.	2.5	30
99	Aurora A regulates expression of AR-V7 in models of castrate resistant prostate cancer. Scientific Reports, 2017, 7, 40957.	1.6	30
100	Paradoxical activation of the protein kinase-transcription factor ERK5 by ERK5 kinase inhibitors. Nature Communications, 2020, 11, 1383.	5.8	30
101	Structure-Based Design of Potent and Orally Active Isoindolinone Inhibitors of MDM2-p53 Proteinâ€“Protein Interaction. Journal of Medicinal Chemistry, 2021, 64, 4071-4088.	2.9	30
102	Anion binding at the active site of trypanosomal triosephosphate isomerase. Monohydrogen phosphate does not mimic sulphate. FEBS Journal, 1991, 198, 53-57.	0.2	28
103	Analysis of the structure of Pseudomonas glumae lipase. Protein Engineering, Design and Selection, 1994, 7, 559-562.	1.0	27
104	Exploiting structural principles to design cyclin-dependent kinase inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 58-64.	1.1	27
105	An Inhibitorâ€™s-Eye View of the ATP-Binding Site of CDKs in Different Regulatory States. ACS Chemical Biology, 2014, 9, 1251-1256.	1.6	27
106	A new crystal form of Lys48-linked diubiquitin. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 994-998.	0.7	26
107	Validating and enabling phosphoglycerate dehydrogenase (PHGDH) as a target for fragment-based drug discovery in PHGDH-amplified breast cancer. Oncotarget, 2018, 9, 13139-13153.	0.8	25
108	Plasticity of the TSG-6 HA-binding Loop and Mobility in the TSG-6-HA Complex Revealed by NMR and X-ray Crystallography. Journal of Molecular Biology, 2007, 371, 669-684.	2.0	24

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109	Probing the architecture of the Mycobacterium marinum arylamine N-acetyltransferase active site. Protein and Cell, 2010, 1, 384-392.	4.8	24
110	Structural and functional characterization of Rpn12 identifies residues required for Rpn10 proteasome incorporation. Biochemical Journal, 2012, 448, 55-65.	1.7	23
111	Tuning the Binding Affinity and Selectivity of Perfluoroarylâ€Stapled Peptides by Cysteineâ€Editing. Chemistry - A European Journal, 2019, 25, 177-182.	1.7	23
112	Expression, Purification and Crystallisation of Phosphorylase Kinase Catalytic Domain. Journal of Molecular Biology, 1995, 246, 374-381.	2.0	22
113	Comparison of the structures and the crystal contacts of trypanosomal triosephosphate isomerase in four different crystal forms. Protein Science, 1994, 3, 779-787.	3.1	20
114	Dynamite extended: two new services to simplify protein dynamic analysis. Bioinformatics, 2005, 21, 3174-3175.	1.8	20
115	Structure-based design of 2-arylamino-4-cyclohexylmethoxy-5-nitroso-6-aminopyrimidine inhibitors of cyclin-dependent kinase 2. Organic and Biomolecular Chemistry, 2007, 5, 1577.	1.5	16
116	Understanding Smallâ€Molecule Binding to MDM2: Insights into Structural Effects of Isoindolinone Inhibitors from NMR Spectroscopy. Chemical Biology and Drug Design, 2011, 77, 301-308.	1.5	15
117	8-Substituted O⁶-Cyclohexylmethylguanine CDK2 Inhibitors: Using Structure-Based Inhibitor Design to Optimize an Alternative Binding Mode. Journal of Medicinal Chemistry, 2014, 57, 56-70.	2.9	15
118	Identification of a novel ligand for the ATAD2 bromodomain with selectivity over BRD4 through a fragment growing approach. Organic and Biomolecular Chemistry, 2018, 16, 1843-1850.	1.5	15
119	Identification of a novel orally bioavailable ERK5 inhibitor with selectivity over p38Î± and BRD4. European Journal of Medicinal Chemistry, 2019, 178, 530-543.	2.6	15
120	Structural principles in cell-cycle control: beyond the CDKs. Structure, 1998, 6, 535-541.	1.6	14
121	Structural investigation of mutant Mycobacterium smegmatis arylamine N-acetyltransferase: a model for a naturally occurring functional polymorphism in Mycobacterium tuberculosis arylamine N-acetyltransferase. Protein Expression and Purification, 2003, 27, 75-84.	0.6	14
122	Crystal transfer experiments carried out with crystals of tryanosomal triosephosphate isomerase (TIM). Journal of Crystal Growth, 1992, 122, 231-234.	0.7	13
123	Discriminative SKP2 Interactions with CDK-Cyclin Complexes Support a Cyclin A-Specific Role in p27KIP1 Degradation. Journal of Molecular Biology, 2021, 433, 166795.	2.0	10
124	An Alkynylpyrimidine-Based Covalent Inhibitor That Targets a Unique Cysteine in NF-ÎºB-Inducing Kinase. Journal of Medicinal Chemistry, 2021, 64, 10001-10018.	2.9	9
125	Replacing the (Î²Î±)-unit 8 of E.coli TIM with its chicken homologue leads to a stable and active hybrid enzyme. Protein Engineering, Design and Selection, 1993, 6, 893-900.	1.0	8
126	Catalysis and regulation. Current Opinion in Structural Biology, 2011, 21, 775-776.	2.6	6

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127	The role of structure in kinase-targeted inhibitor design. Current Opinion in Drug Discovery & Development, 2004, 7, 428-36.	1.9	6
128	Xenopus Phospho-CDK7/Cyclin H Expressed in Baculoviral-Infected Insect Cells. Protein Expression and Purification, 2001, 23, 252-260.	0.6	4
129	Parallel Optimization of Potency and Pharmacokinetics Leading to the Discovery of a Pyrrole Carboxamide ERK5 Kinase Domain Inhibitor. Journal of Medicinal Chemistry, 2022, 65, 6513-6540.	2.9	3
130	Modular mutagenesis of a TEM-barrel enzyme: the crystal structure of a chimeric E.coli TIM having the eighth Î²Î±-unit replaced by the equivalent unit of chicken TIM. Protein Engineering, Design and Selection, 1994, 7, 945-951.	1.0	2
131	Catalysis and regulation. Current Opinion in Structural Biology, 2009, 19, 641-642.	2.6	1
132	Structural and kinetic mechanism of CDK2 inhibiton by Y15 phosphorylation. FASEB Journal, 2006, 20, A461.	0.2	0