Martin E M Noble

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4117461/publications.pdf

Version: 2024-02-01

132 papers	15,568 citations	21215 62 h-index	20023 121 g-index
135 all docs	135 docs citations	135 times ranked	19963 citing authors

#	Article	IF	Citations
1	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
2	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
3	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
4	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
5	Crystallographic and electrophilic fragment screening of the SARS-CoV-2 main protease. Nature Communications, 2020, 11, 5047.	5.8	376
6	Paradoxical activation of the protein kinase-transcription factor ERK5 by ERK5 kinase inhibitors. Nature Communications, 2020, 11, 1383.	5.8	30
7	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
8	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
9	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
10	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
11	Tuning the Binding Affinity and Selectivity of Perfluoroarylâ€Stapled Peptides by Cysteineâ€Editing. Chemistry - A European Journal, 2019, 25, 177-182.	1.7	23
12	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
13	CCP4i2: the new graphical user interface to theCCP4 program suite. Acta Crystallographica Section D: Structural Biology, 2018, 74, 68-84.	1.1	382
14	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
15	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
16	Aurora A regulates expression of AR-V7 in models of castrate resistant prostate cancer. Scientific Reports, 2017, 7, 40957.	1.6	30
17	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
18	Differential Regulation of G1 CDK Complexes by the Hsp90-Cdc37 Chaperone System. Cell Reports, 2017, 21, 1386-1398.	2.9	49

#	Article	IF	Citations
19	Structure-based discovery of cyclin-dependent protein kinase inhibitors. Essays in Biochemistry, 2017, 61, 439-452.	2.1	39
20	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
21	CDK1 structures reveal conserved and unique features of the essential cell cycle CDK. Nature Communications, 2015, 6, 6769.	5.8	145
22	Identification and Characterization of an Irreversible Inhibitor of CDK2. Chemistry and Biology, 2015, 22, 1159-1164.	6.2	85
23	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
24	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
25	Structural characterization of the cyclin-dependent protein kinase family. Biochemical Society Transactions, 2013, 41, 1008-1016.	1.6	35
26	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
27	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
28	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
29	Structural and functional characterization of Rpn12 identifies residues required for Rpn10 proteasome incorporation. Biochemical Journal, 2012, 448, 55-65.	1.7	23
30	The CDK9 Tail Determines the Reaction Pathway of Positive Transcription Elongation Factor b. Structure, 2012, 20, 1788-1795.	1.6	32
31	The CDK9 C-helix Exhibits Conformational Plasticity That May Explain the Selectivity of CAN508. ACS Chemical Biology, 2012, 7, 811-816.	1.6	45
32	The Structural Basis for Control of Eukaryotic Protein Kinases. Annual Review of Biochemistry, 2012, 81, 587-613.	5.0	362
33	Generation of protein lattices by fusing proteins with matching rotational symmetry. Nature Nanotechnology, 2011, 6, 558-562.	15.6	214
34	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
35	Catalysis and regulation. Current Opinion in Structural Biology, 2011, 21, 775-776.	2.6	6
36	MDM2-p53 proteinâ€“protein interaction inhibitors: A-ring substituted isoindolinones. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 5916-9.	1.0	36

#	Article	IF	Citations
37	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
38	Presenting your structures: theCCP4mgmolecular-graphics software. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 386-394.	2.5	1,133
39	Probing the architecture of the Mycobacterium marinum arylamine N-acetyltransferase active site. Protein and Cell, 2010, 1, 384-392.	4.8	24
40	Recent developments in cyclin-dependent kinase biochemical and structural studies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 511-519.	1.1	96
41	A new crystal form of Lys48-linked diubiquitin. Acta Crystallographica Section F: Structural Biology Communications, 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. Journal of Biological Chemistry, 2010, 285, 10724-10735.	1.6	45
43	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
44	Catalysis and regulation. Current Opinion in Structural Biology, 2009, 19, 641-642.	2.6	1
45	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
46	Structure of HsaD, a steroid-degrading hydrolase, fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 2-7.	0.7	31
47	Structures of P. falciparum Protein Kinase 7 Identify an Activation Motif and Leads for Inhibitor Design. Structure, 2008, 16, 228-238.	1.6	62
48	Structural Analysis of the Interactions Between Paxillin LD Motifs and Î±-Parvin. Structure, 2008, 16, 1521-1531.	1.6	32
49	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
50	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
51	Arylamine N-Acetyltransferases in Mycobacteria. Current Drug Metabolism, 2008, 9, 510-519.	0.7	38
52	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
53	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
54	Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2007, 373, 1213-1228.	2.0	66

#	Article	IF	Citations
55	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
56	Computational analyses of the surface properties of proteinâ€“protein interfaces. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 50-57.	2.5	30
57	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
58	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
59	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
60	The Role of the Phospho-CDK2/Cyclin A Recruitment Site in Substrate Recognition. Journal of Biological Chemistry, 2006, 281, 23167-23179.	1.6	79
61	Structures of the Dsk2 UBL and UBA domains and their complex. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 177-188.	2.5	69
62	Structural and kinetic mechanism of CDK2 inhibiton by Y15 phosphorylation. FASEB Journal, 2006, 20, A461.	0.2	0
63	Expression, purification, characterization and structure of Pseudomonas aeruginosa arylamine N-acetyltransferase. Biochemical Journal, 2005, 385, 605-612.	1.7	72
64	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
65	Exploiting structural principles to design cyclin-dependent kinase inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 58-64.	1.1	27
66	Mechanism of Lys48-linked polyubiquitin chain recognition by the Mud1 UBA domain. EMBO Journal, 2005, 24, 3178-3189.	3.5	87
67	Structure ofMesorhizobium lotiarylamineN-acetyltransferase 1. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 14-16.	0.7	35
68	Molecular Motions of Human Cyclin-dependent Kinase 2. Journal of Biological Chemistry, 2005, 280, 13993-14005.	1.6	44
69	Dynamite extended: two new services to simplify protein dynamic analysis. Bioinformatics, 2005, 21, 3174-3175.	1.8	20
70	Molecular Basis for the Recognition of Phosphorylated and Phosphoacetylated Histone H3 by 14-3-3. Molecular Cell, 2005, 20, 199-211.	4.5	220
71	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
72	N2-SubstitutedO6-Cyclohexylmethylguanine Derivatives:Â Potent Inhibitors of Cyclin-Dependent Kinases 1 and 2. Journal of Medicinal Chemistry, 2004, 47, 3710-3722.	2.9	116

#	Article	IF	Citations
73	Protein Kinase Inhibitors: Insights into Drug Design from Structure. Science, 2004, 303, 1800-1805.	6.0	1,164
74	Dynamite: a simple way to gain insight into protein motions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2280-2287.	2.5	81
75	Developments in theCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2288-2294.	2.5	516
76	Structure of the Regulatory Hyaluronan Binding Domain in the Inflammatory Leukocyte Homing Receptor CD44. Molecular Cell, 2004, 13, 483-496.	4.5	228
77	The role of structure in kinase-targeted inhibitor design. Current Opinion in Drug Discovery & Development, 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. Journal of Medicinal Chemistry, 2003, 46, 222-236.	2.9	139
79	Molecular Recognition of Paxillin LD Motifs by the Focal Adhesion Targeting Domain. Structure, 2003, 11, 1207-1217.	1.6	93
80	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
81	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
82	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
83	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
84	Arylamine N-acetyltransferases: a pharmacogenomic approach to drug metabolism and endogenous function. Biochemical Society Transactions, 2003, 31, 615-619.	1.6	46
85	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
86	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
87	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
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. Structure, 2002, 10, 319-327.	1.6	132

#	Article	IF	Citations
91	TheCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1955-1957.	2.5	193
92	Structure-based design of a potent purine-based cyclin-dependent kinase inhibitor. Nature Structural Biology, 2002, 9, 745-749.	9.7	198
93	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin Aâ€,â€¡. Biochemistry, 2002, 41, 15625-15634.	1.2	152
94	Xenopus Phospho-CDK7/Cyclin H Expressed in Baculoviral-Infected Insect Cells. Protein Expression and Purification, 2001, 23, 252-260.	0.6	4
95	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
96	Inhibitor Binding to Active and Inactive CDK2. Structure, 2001, 9, 389-397.	1.6	137
97	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
98	Structure of arylamine N-acetyltransferase reveals a catalytic triad. Nature Structural Biology, 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. Journal of Medicinal Chemistry, 2000, 43, 2797-2804.	2.9	203
100	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
101	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
102	The structural basis for specificity of substrate and recruitment peptides for cyclin-dependent kinases. Nature Cell Biology, 1999, 1, 438-443.	4.6	509
103	Chemical Inhibitors of Cyclin-Dependent Kinases. , 1999, 82, 269-278.		33
104	Cyclin-dependent kinases: inhibition and substrate recognition. Current Opinion in Structural Biology, 1999, 9, 738-744.	2.6	109
105	A Structural Explanation for the Binding of Multiple Ligands by the Î±-Adaptin Appendage Domain. Cell, 1999, 97, 805-815.	13.5	271
106	Structural principles in cell-cycle control: beyond the CDKs. Structure, 1998, 6, 535-541.	1.6	14
107	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
108	The structural basis for substrate recognition and control by protein kinases1. FEBS Letters, 1998, 430, 1-11.	1.3	185

#	Article	IF	Citations
109	Purification, Characterization, and Crystallization of anN-HydroxyarylamineO-Acetyltransferase fromSalmonella typhimurium. Protein Expression and Purification, 1998, 12, 371-380.	0.6	55
110	Protein kinase inhibition by staurosporine revealed in details of the molecular interaction with CDK2. Nature Structural Biology, 1997, 4, 796-801.	9.7	243
111	The cyclin box fold: protein recognition in cell-cycle and transcription control. Trends in Biochemical Sciences, 1997, 22, 482-487.	3.7	105
112	Active and Inactive Protein Kinases: Structural Basis for Regulation. Cell, 1996, 85, 149-158.	13.5	1,313
113	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
114	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
115	The crystal structure of cyclin A. Structure, 1995, 3, 1235-1247.	1.6	183
116	Expression, Purification and Crystallisation of Phosphorylase Kinase Catalytic Domain. Journal of Molecular Biology, 1995, 246, 374-381.	2.0	22
117	Analysis of the structure of Pseudomonas glumae lipase. Protein Engineering, Design and Selection, 1994, 7, 559-562.	1.0	27
118	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
119	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
120	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
121	Overexpression of trypanosomal triosephosphate isomerase in Escherichia coli and characterisation of a dimer-interface mutant. FEBS Journal, 1993, 211, 703-710.	0.2	64
122	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
123	The crystal structure of triacylglycerol lipase from Pseudomonas glumae reveals a partially redundant catalytic aspartate. FEBS Letters, 1993, 331, 123-128.	1.3	252
124	Crystallographic binding studies with triosephosphate isomerases: Conformational changes induced by substrate and substrate-analogues. FEBS Letters, 1992, 307, 34-39.	1.3	44
125	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
126	Crystal structure of a Src-homology 3 (SH3) domain. Nature, 1992, 359, 851-855.	13.7	472

#	Article	IF	Citations
127	Crystal transfer experiments carried out with crystals of tryanosomal triosephosphate isomerase (TIM). Journal of Crystal Growth, 1992, 122, 231-234.	0.7	13
128	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
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. Journal of Medicinal Chemistry, 1991, 34, 2709-2718.	2.9	32
130	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
131	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
132	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