

# John Kuriyan

## List of Publications by Year in descending order

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137  
papers

30,684  
citations

8172

76  
h-index

11303

136  
g-index

165  
all docs

165  
docs citations

165  
times ranked

22028  
citing authors

#	ARTICLE	IF	CITATIONS
1	A saturation-mutagenesis analysis of the interplay between stability and activation in Ras. <i>ELife</i> , 2022, 11, .	2.8	13
2	A two-component protein condensate of the EGFR cytoplasmic tail and Grb2 regulates Ras activation by SOS at the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122531119.	3.3	33
3	Allosteric communication in DNA polymerase clamp loaders relies on a critical hydrogen-bonded junction. <i>ELife</i> , 2021, 10, .	2.8	19
4	GHB analogs confer neuroprotection through specific interaction with the CaMKII $\beta$ hub domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	31
5	Structural basis and regulation of the reductive stress response. <i>Cell</i> , 2021, 184, 5375-5390.e16.	13.5	58
6	New insights into Raf regulation from structural analyses. <i>Current Opinion in Structural Biology</i> , 2021, 71, 223-231.	2.6	4
7	Differences in the dynamics of the tandem SH2 modules of the Syk and ZAP $\beta$ tyrosine kinases. <i>Protein Science</i> , 2021, 30, 2373-2384.	3.1	10
8	Relating cellular signaling timescales to single-molecule kinetics: A first-passage time analysis of Ras activation by SOS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
9	A molecular mechanism for the generation of ligand-dependent differential outputs by the epidermal growth factor receptor. <i>ELife</i> , 2021, 10, .	2.8	44
10	Structural Insights into the Regulation of Ca <sup>2+</sup> /Calmodulin-Dependent Protein Kinase II (CaMKII). <i>Cold Spring Harbor Perspectives in Biology</i> , 2020, 12, a035147.	2.3	54
11	Structural basis for dimerization quality control. <i>Nature</i> , 2020, 586, 452-456.	13.7	36
12	Flexible linkers in CaMKII control the balance between activating and inhibitory autophosphorylation. <i>ELife</i> , 2020, 9, .	2.8	41
13	CRISPR-Cas12a exploits R-loop asymmetry to form double-strand breaks. <i>ELife</i> , 2020, 9, .	2.8	80
14	Breakage of the oligomeric CaMKII hub by the regulatory segment of the kinase. <i>ELife</i> , 2020, 9, .	2.8	25
15	Slow phosphorylation of a tyrosine residue in LAT optimizes T cell ligand discrimination. <i>Nature Immunology</i> , 2019, 20, 1481-1493.	7.0	64
16	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. <i>Science</i> , 2019, 366, 109-115.	6.0	127
17	Switch-like activation of Bruton's tyrosine kinase by membrane-mediated dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10798-10803.	3.3	37
18	A molecular assembly phase transition and kinetic proofreading modulate Ras activation by SOS. <i>Science</i> , 2019, 363, 1098-1103.	6.0	268

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19	Prospective discovery of small molecule enhancers of an E3 ligase-substrate interaction. <i>Nature Communications</i> , 2019, 10, 1402.	5.8	110
20	Variation in assembly stoichiometry in non-metazoan homologs of the hub domain of Ca <sup>2+</sup> /calmodulin-dependent protein kinase II. <i>Protein Science</i> , 2019, 28, 1071-1082.	3.1	16
21	Understanding molecular mechanisms in cell signaling through natural and artificial sequence variation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 25-34.	3.6	28
22	The Interdependent Activation of Son-of-Sevenless and Ras. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a031534.	2.9	46
23	Phosphorylation control of the ubiquitin ligase Cbl is conserved in choanoflagellates. <i>Protein Science</i> , 2018, 27, 923-932.	3.1	7
24	The Src module: an ancient scaffold in the evolution of cytoplasmic tyrosine kinases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2018, 53, 535-563.	2.3	62
25	Fine-tuning of substrate preferences of the Src-family kinase Lck revealed through a high-throughput specificity screen. <i>ELife</i> , 2018, 7, .	2.8	51
26	Deep mutational analysis reveals functional trade-offs in the sequences of EGFR autophosphorylation sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7303-E7312.	3.3	28
27	Lck promotes Zap70-dependent LAT phosphorylation by bridging Zap70 to LAT. <i>Nature Immunology</i> , 2018, 19, 733-741.	7.0	115
28	Identification of Inhibitors of the Association of ZAP-70 with the T Cell Receptor by High-Throughput Screen. <i>SLAS Discovery</i> , 2017, 22, 324-331.	1.4	14
29	Multiple interactions between an Arf/GEF complex and charged lipids determine activation kinetics on the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11416-11421.	3.3	38
30	A Phosphosite within the SH2 Domain of Lck Regulates Its Activation by CD45. <i>Molecular Cell</i> , 2017, 67, 498-511.e6.	4.5	51
31	Deconstruction of the Ras switching cycle through saturation mutagenesis. <i>ELife</i> , 2017, 6, .	2.8	95
32	A Histidine pH sensor regulates activation of the Ras-specific guanine nucleotide exchange factor RasGRP1. <i>ELife</i> , 2017, 6, .	2.8	32
33	An electrostatic selection mechanism controls sequential kinase signaling downstream of the T cell receptor. <i>ELife</i> , 2016, 5, .	2.8	85
34	Phosphotyrosine-mediated LAT assembly on membranes drives kinetic bifurcation in recruitment dynamics of the Ras activator SOS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8218-8223.	3.3	101
35	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. <i>Journal of Experimental Medicine</i> , 2016, 213, 155-165.	4.2	83
36	Crystal Structure of a Ube2S-Ubiquitin Conjugate. <i>PLoS ONE</i> , 2016, 11, e0147550.	1.1	24

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37	Molecular mechanism of activation-triggered subunit exchange in Ca <sup>2+</sup> /calmodulin-dependent protein kinase II. <i>ELife</i> , 2016, 5, .	2.8	89
38	Molecular basis for multimerization in the activation of the epidermal growth factor receptor. <i>ELife</i> , 2016, 5, .	2.8	144
39	Crystal Structure of the FLT3 Kinase Domain Bound to the Inhibitor Quizartinib (AC220). <i>PLoS ONE</i> , 2015, 10, e0121177.	1.1	75
40	The catalytic activity of the kinase ZAP-70 mediates basal signaling and negative feedback of the T cell receptor pathway. <i>Science Signaling</i> , 2015, 8, ra49.	1.6	50
41	A Structural Perspective on the Regulation of the Epidermal Growth Factor Receptor. <i>Annual Review of Biochemistry</i> , 2015, 84, 739-764.	5.0	266
42	Crystal structure of an SH2 <sup>+</sup> kinase construct of c-Abl and effect of the SH2 domain on kinase activity. <i>Biochemical Journal</i> , 2015, 468, 283-291.	1.7	27
43	Analysis of the Role of the C-Terminal Tail in the Regulation of the Epidermal Growth Factor Receptor. <i>Molecular and Cellular Biology</i> , 2015, 35, 3083-3102.	1.1	74
44	Modification by covalent reaction or oxidation of cysteine residues in the tandem-SH2 domains of ZAP-70 and Syk can block phosphopeptide binding. <i>Biochemical Journal</i> , 2015, 465, 149-161.	1.7	21
45	Autoinhibition of Bruton's tyrosine kinase (Btk) and activation by soluble inositol hexakisphosphate. <i>ELife</i> , 2015, 4, .	2.8	82
46	Activation-triggered subunit exchange between CaMKII holoenzymes facilitates the spread of kinase activity. <i>ELife</i> , 2014, 3, e01610.	2.8	87
47	A Structural Atlas of Kinases Inhibited by Clinically Approved Drugs. <i>Methods in Enzymology</i> , 2014, 548, 23-67.	0.4	44
48	Emerging concepts in the regulation of the EGF receptor and other receptor tyrosine kinases. <i>Trends in Biochemical Sciences</i> , 2014, 39, 437-446.	3.7	68
49	Structural insights into the role of iron <sup>+</sup> histidine bond cleavage in nitric oxide-induced activation of H-NOX gas sensor proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4156-64.	3.3	87
50	Ras activation by SOS: Allosteric regulation by altered fluctuation dynamics. <i>Science</i> , 2014, 345, 50-54.	6.0	126
51	Structural studies on the regulation of Ca <sup>2+</sup> /calmodulin dependent protein kinase II. <i>Current Opinion in Structural Biology</i> , 2013, 23, 292-301.	2.6	72
52	Macromolecular juggling by ubiquitylation enzymes. <i>BMC Biology</i> , 2013, 11, 65.	1.7	56
53	Monovalent and Multivalent Ligation of the B Cell Receptor Exhibit Differential Dependence upon Syk and Src Family Kinases. <i>Science Signaling</i> , 2013, 6, ra1.	1.6	73
54	Architecture and Membrane Interactions of the EGF Receptor. <i>Cell</i> , 2013, 152, 557-569.	13.5	417

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55	Conformational Coupling across the Plasma Membrane in Activation of the EGF Receptor. <i>Cell</i> , 2013, 152, 543-556.	13.5	423
56	A highly efficient peptide substrate for EGFR activates the kinase by inducing aggregation. <i>Biochemical Journal</i> , 2013, 453, 337-344.	1.7	4
57	Structural Basis for Activation of ZAP-70 by Phosphorylation of the SH2-Kinase Linker. <i>Molecular and Cellular Biology</i> , 2013, 33, 2188-2201.	1.1	90
58	Structural analysis of autoinhibition in the Ras-specific exchange factor RasGRP1. <i>ELife</i> , 2013, 2, e00813.	2.8	78
59	Oncogenic Mutations Counteract Intrinsic Disorder in the EGFR Kinase and Promote Receptor Dimerization. <i>Cell</i> , 2012, 149, 860-870.	13.5	304
60	Clamp loader ATPases and the evolution of DNA replication machinery. <i>BMC Biology</i> , 2012, 10, 34.	1.7	82
61	Molecular Mechanisms of DNA Polymerase Clamp Loaders. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 103-114.	0.5	2
62	A Mechanism for Tunable Autoinhibition in the Structure of a Human Ca <sup>2+</sup> /Calmodulin- Dependent Kinase II Holoenzyme. <i>Cell</i> , 2011, 146, 732-745.	13.5	230
63	Catalytic Control in the EGF Receptor and Its Connection to General Kinase Regulatory Mechanisms. <i>Molecular Cell</i> , 2011, 42, 9-22.	4.5	265
64	Regulation of the catalytic activity of the EGF receptor. <i>Current Opinion in Structural Biology</i> , 2011, 21, 777-784.	2.6	87
65	How a DNA Polymerase Clamp Loader Opens a Sliding Clamp. <i>Science</i> , 2011, 334, 1675-1680.	6.0	155
66	Analysis of the role of PCNA-DNA contacts during clamp loading. <i>BMC Structural Biology</i> , 2010, 10, 3.	2.3	97
67	Intersubunit capture of regulatory segments is a component of cooperative CaMKII activation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 264-272.	3.6	108
68	Molecular mechanisms in signal transduction at the membrane. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 659-665.	3.6	248
69	Role of the histone domain in the autoinhibition and activation of the Ras activator Son of Sevenless. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3430-3435.	3.3	81
70	A conserved protonation-dependent switch controls drug binding in the Abl kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 139-144.	3.3	240
71	Stability of an autoinhibitory interface in the structure of the tyrosine kinase ZAP-70 impacts T cell receptor response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20699-20704.	3.3	32
72	Equally Potent Inhibition of c-Src and Abl by Compounds that Recognize Inactive Kinase Conformations. <i>Cancer Research</i> , 2009, 69, 2384-2392.	0.4	134

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73	Structural analysis of the catalytically inactive kinase domain of the human EGF receptor 3. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21608-21613.	3.3	278
74	The structure, regulation, and function of ZAP-70. Immunological Reviews, 2009, 228, 41-57.	2.8	203
75	Comparative Analysis of Mutant Tyrosine Kinase Chemical Rescue. Biochemistry, 2009, 48, 3378-3386.	1.2	19
76	The Mechanism of ATP-Dependent Primer-Template Recognition by a Clamp Loader Complex. Cell, 2009, 137, 659-671.	13.5	151
77	Mechanism for Activation of the EGF Receptor Catalytic Domain by the Juxtamembrane Segment. Cell, 2009, 137, 1293-1307.	13.5	506
78	The Tyrosine Kinase Csk Dimerizes through Its SH3 Domain. PLoS ONE, 2009, 4, e7683.	1.1	28
79	Allosteric Mechanisms in Receptor Tyrosine Kinase Activation. FASEB Journal, 2009, 23, 313.1.	0.2	0
80	Membrane-dependent signal integration by the Ras activator Son of sevenless. Nature Structural and Molecular Biology, 2008, 15, 452-461.	3.6	222
81	Activation of tyrosine kinases by mutation of the gatekeeper threonine. Nature Structural and Molecular Biology, 2008, 15, 1109-1118.	3.6	366
82	Structure of a Sliding Clamp on DNA. Cell, 2008, 132, 43-54.	13.5	209
83	Structural Basis for the Recognition of c-Src by Its Inactivator Csk. Cell, 2008, 134, 124-134.	13.5	119
84	Structural Basis for the Inhibition of Tyrosine Kinase Activity of ZAP-70. Cell, 2007, 129, 735-746.	13.5	217
85	Inhibition of the EGF receptor by binding of MIG6 to an activating kinase domain interface. Nature, 2007, 450, 741-744.	13.7	311
86	The origin of protein interactions and allostery in colocalization. Nature, 2007, 450, 983-990.	13.7	351
87	c-Src Binds to the Cancer Drug Imatinib with an Inactive Abl/c-Kit Conformation and a Distributed Thermodynamic Penalty. Structure, 2007, 15, 299-311.	1.6	203
88	An Allosteric Mechanism for Activation of the Kinase Domain of Epidermal Growth Factor Receptor. Cell, 2006, 125, 1137-1149.	13.5	1,358
89	Crystal Structure of the Catalytic $\beta$ Subunit of E. coli Replicative DNA Polymerase III. Cell, 2006, 126, 881-892.	13.5	155
90	A Dimeric Kinase Assembly Underlying Autophosphorylation in the p21 Activated Kinases. Journal of Molecular Biology, 2006, 361, 312-326.	2.0	82

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91	Organization of the SH3-SH2 Unit in Active and Inactive Forms of the c-Abl Tyrosine Kinase. <i>Molecular Cell</i> , 2006, 21, 787-798.	4.5	192
92	A Src-Like Inactive Conformation in the Abl Tyrosine Kinase Domain. <i>PLoS Biology</i> , 2006, 4, e144.	2.6	277
93	Oligomerization states of the association domain and the holoenzyme of Ca <sup>2+</sup> /CaM kinase II. <i>FEBS Journal</i> , 2006, 273, 682-694.	2.2	92
94	Regulation of Ras Signaling Dynamics by Sos-Mediated Positive Feedback. <i>Current Biology</i> , 2006, 16, 2173-2179.	1.8	106
95	Protein-protein interactions in the allosteric regulation of protein kinases. <i>Current Opinion in Structural Biology</i> , 2006, 16, 702-709.	2.6	99
96	Mechanism of Proliferating Cell Nuclear Antigen Clamp Opening by Replication Factor C. <i>Journal of Biological Chemistry</i> , 2006, 281, 17528-17539.	1.6	66
97	Structure of the Kinase Domain of an Imatinib-Resistant Abl Mutant in Complex with the Aurora Kinase Inhibitor VX-680. <i>Cancer Research</i> , 2006, 66, 1007-1014.	0.4	282
98	The Replication Factor C Clamp Loader Requires Arginine Finger Sensors to Drive DNA Binding and Proliferating Cell Nuclear Antigen Loading. <i>Journal of Biological Chemistry</i> , 2006, 281, 35531-35543.	1.6	67
99	High yield bacterial expression of active c-Abl and c-Src tyrosine kinases. <i>Protein Science</i> , 2005, 14, 3135-3139.	3.1	206
100	Mapping the interaction of DNA with the Escherichia coli DNA polymerase clamp loader complex. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 183-190.	3.6	46
101	Out-of-plane motions in open sliding clamps: Molecular dynamics simulations of eukaryotic and archaeal proliferating cell nuclear antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13801-13806.	3.3	65
102	Structure of the Autoinhibited Kinase Domain of CaMKII and SAXS Analysis of the Holoenzyme. <i>Cell</i> , 2005, 123, 849-860.	13.5	293
103	DNA polymerase clamp loaders and DNA recognition. <i>FEBS Letters</i> , 2005, 579, 863-867.	1.3	68
104	Structural analysis of a eukaryotic sliding DNA clamp-clamp loader complex. <i>Nature</i> , 2004, 429, 724-730.	13.7	422
105	Structural Analysis of Autoinhibition in the Ras Activator Son of Sevenless. <i>Cell</i> , 2004, 119, 393-405.	13.5	251
106	Allostery and Coupled Sequence Variation in Nuclear Hormone Receptors. <i>Cell</i> , 2004, 116, 354-356.	13.5	15
107	Nucleotide-Induced Conformational Changes in an Isolated Escherichia coli DNA Polymerase III Clamp Loader Subunit. <i>Structure</i> , 2003, 11, 253-263.	1.6	29
108	Structural Evidence for Feedback Activation by Ras-GTP of the Ras-Specific Nucleotide Exchange Factor SOS. <i>Cell</i> , 2003, 112, 685-695.	13.5	390

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109	A Myristoyl/Phosphotyrosine Switch Regulates c-Abl. <i>Cell</i> , 2003, 112, 845-857.	13.5	404
110	Structural Basis for the Autoinhibition of c-Abl Tyrosine Kinase. <i>Cell</i> , 2003, 112, 859-871.	13.5	762
111	Crystal Structure of a Tetradecameric Assembly of the Association Domain of Ca <sup>2+</sup> /Calmodulin-Dependent Kinase II. <i>Molecular Cell</i> , 2003, 11, 1241-1251.	4.5	164
112	The Conformational Plasticity of Protein Kinases. <i>Cell</i> , 2002, 109, 275-282.	13.5	1,531
113	Multiple BCR-ABL kinase domain mutations confer polyclonal resistance to the tyrosine kinase inhibitor imatinib (STI571) in chronic phase and blast crisis chronic myeloid leukemia. <i>Cancer Cell</i> , 2002, 2, 117-125.	7.7	1,548
114	Clamp loaders and sliding clamps. <i>Current Opinion in Structural Biology</i> , 2002, 12, 217-224.	2.6	132
115	Crystal structures of the kinase domain of c-Abl in complex with the small molecule inhibitors PD173955 and imatinib (STI-571). <i>Cancer Research</i> , 2002, 62, 4236-43.	0.4	684
116	Dynamic Coupling between the SH2 and SH3 Domains of c-Src and Hck Underlies Their Inactivation by C-Terminal Tyrosine Phosphorylation. <i>Cell</i> , 2001, 105, 115-126.	13.5	366
117	Mechanism of Processivity Clamp Opening by the Delta Subunit Wrench of the Clamp Loader Complex of <i>E. coli</i> DNA Polymerase III. <i>Cell</i> , 2001, 106, 417-428.	13.5	236
118	Crystal Structure of the Processivity Clamp Loader Gamma ( $\hat{\Gamma}$ ) Complex of <i>E. coli</i> DNA Polymerase III. <i>Cell</i> , 2001, 106, 429-441.	13.5	322
119	Reciprocal Regulation of Hck Activity by Phosphorylation of Tyr527 and Tyr416. <i>Journal of Biological Chemistry</i> , 2000, 275, 2721-2726.	1.6	108
120	Crystal structure of the DNA polymerase processivity factor of T4 bacteriophage 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 296, 1215-1223.	2.0	176
121	Structural Mechanism for STI-571 Inhibition of Abelson Tyrosine Kinase. <i>Science</i> , 2000, 289, 1938-1942.	6.0	1,712
122	An SH2 domain in disguise. <i>Nature</i> , 1999, 398, 22-23.	13.7	16
123	Crystal Structure of Hck in Complex with a Src Family Selective Tyrosine Kinase Inhibitor. <i>Molecular Cell</i> , 1999, 3, 639-648.	4.5	406
124	The structural basis of the activation of Ras by Sos. <i>Nature</i> , 1998, 394, 337-343.	13.7	692
125	Structure of the Amino-Terminal Protein Interaction Domain of STAT-4. <i>Science</i> , 1998, 279, 1048-1052.	6.0	246
126	MODULAR PEPTIDE RECOGNITION DOMAINS IN EUKARYOTIC SIGNALING. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997, 26, 259-288.	18.3	524



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127	Crystal Structure of the $\beta^2$ Subunit of the Clamp-Loader Complex of E. coli DNA Polymerase III. Cell, 1997, 91, 335-345.	13.5	268
128	Crystal structure of the Src family tyrosine kinase Hck. Nature, 1997, 385, 602-609.	13.7	1,155
129	Activation of the Sre-family tyrosine kinase Hck by SH3 domain displacement. Nature, 1997, 385, 650-653.	13.7	595
130	Structural Basis for the Autoinhibition of Calcium/Calmodulin-Dependent Protein Kinase I. Cell, 1996, 84, 875-887.	13.5	327
131	Structure of the C-Terminal Region of p21WAF1/CIP1 Complexed with Human PCNA. Cell, 1996, 87, 297-306.	13.5	753
132	Three-dimensional structure of the catalytic subunit of protein serine/threonine phosphatase-1. Nature, 1995, 376, 745-753.	13.7	851
133	Crystal structure of the eukaryotic DNA polymerase processivity factor PCNA. Cell, 1994, 79, 1233-1243.	13.5	881
134	Three-dimensional structure of the $\beta^2$ subunit of E. coli DNA polymerase III holoenzyme: A sliding DNA clamp. Cell, 1992, 69, 425-437.	13.5	766
135	Crystal structure of the phosphotyrosine recognition domain SH2 of v-src complexed with tyrosine-phosphorylated peptides. Nature, 1992, 358, 646-653.	13.7	719
136	DNA recognition, warts and all. Nature, 1992, 359, 476-476.	13.7	2
137	Exploration of disorder in protein structures by X-ray restrained molecular dynamics. Proteins: Structure, Function and Bioinformatics, 1991, 10, 340-358.	1.5	105