

# Masahiro Kinoshita

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1466001/publications.pdf>

Version: 2024-02-01

146  
papers

3,404  
citations

109137

35  
h-index

174990

52  
g-index

150  
all docs

150  
docs citations

150  
times ranked

1811  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of an Outward Proton Pumping Rhodopsin with a New Record in Thermostability by Means of Amino Acid Mutations. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1004-1015.	1.2	7
2	Controlling the Rigidity of Kinesin-Propelled Microtubules in an <i>In Vitro</i> Gliding Assay Using the Deep-Sea Osmolyte Trimethylamine <i>N</i> -Oxide. <i>ACS Omega</i> , 2022, 7, 3796-3803.	1.6	2
3	On the functioning mechanism of an ATP-driven molecular motor. <i>Biophysics and Physicobiology</i> , 2021, 18, 60-66.	0.5	2
4	Evaluation of the role of the DNA surface for enhancing the activity of scaffolded enzymes. <i>Chemical Communications</i> , 2021, 57, 3925-3928.	2.2	12
5	Appendix 1: Angle-Dependent Integral Equation Theory. <i>Springer Briefs in Molecular Science</i> , 2021, , 71-75.	0.1	0
6	Appendix 2: Morphometric Approach. <i>Springer Briefs in Molecular Science</i> , 2021, , 77-79.	0.1	0
7	A New View on Mechanism of Functional Expression of an ATP-Driven Molecular Motor. <i>Springer Briefs in Molecular Science</i> , 2021, , 5-28.	0.1	0
8	Elucidation of cosolvent effects thermostabilizing water-soluble and membrane proteins. <i>Journal of Molecular Liquids</i> , 2020, 301, 112403.	2.3	7
9	Comparison based on statistical thermodynamics between globule-to-coil transition of poly( <i>N</i> -isopropylacrylamide) and cold denaturation of a protein. <i>Journal of Molecular Liquids</i> , 2020, 317, 114129.	2.3	10
10	Enhanced enzymatic activity exerted by a packed assembly of a single type of enzyme. <i>Chemical Science</i> , 2020, 11, 9088-9100.	3.7	12
11	Accurate and rapid calculation of hydration free energy and its physical implication for biomolecular functions. <i>Biophysical Reviews</i> , 2020, 12, 469-480.	1.5	8
12	Development and structural determination of an anti-PrPC aptamer that blocks pathological conformational conversion of prion protein. <i>Scientific Reports</i> , 2020, 10, 4934.	1.6	13
13	Methodology for Further Thermostabilization of an Intrinsically Thermostable Membrane Protein Using Amino Acid Mutations with Its Original Function Being Retained. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1709-1716.	2.5	5
14	Hydration properties of a protein at low and high pressures: Physics of pressure denaturation. <i>Journal of Chemical Physics</i> , 2020, 152, 065103.	1.2	14
15	How Does a Microbial Rhodopsin RxR Realize Its Exceptionally High Thermostability with the Proton-Pumping Function Being Retained?. <i>Journal of Physical Chemistry B</i> , 2020, 124, 990-1000.	1.2	15
16	Theoretical identification of thermostabilizing amino acid mutations for G-protein-coupled receptors. <i>Biophysical Reviews</i> , 2020, 12, 323-332.	1.5	5
17	An accurate and rapid method for calculating hydration free energies of a variety of solutes including proteins. <i>Journal of Chemical Physics</i> , 2019, 150, 175101.	1.2	20
18	How Does the Recently Discovered Peptide MIP Exhibit Much Higher Binding Affinity than an Anticancer Protein p53 for an Oncoprotein MDM2?. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3533-3544.	2.5	10

#	ARTICLE	IF	CITATIONS
19	Reduced density profile of small particles near a large particle: Results of an integral equation theory with an accurate bridge function and a Monte Carlo simulation. <i>Journal of Chemical Physics</i> , 2019, 151, 044506.	1.2	8
20	Mechanism of globule-to-coil transition of poly(N-isopropylacrylamide) in water: Relevance to cold denaturation of a protein. <i>Journal of Molecular Liquids</i> , 2019, 292, 111374.	2.3	20
21	Analyses based on statistical thermodynamics for large difference between thermophilic rhodopsin and xanthorhodopsin in terms of thermostability. <i>Journal of Chemical Physics</i> , 2019, 150, 055101.	1.2	9
22	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26.	3.9	85
23	Mechanism of protein-RNA recognition: analysis based on the statistical mechanics of hydration. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 9167-9180.	1.3	12
24	Physical Origin of Thermostabilization by a Quadruple Mutation for the Adenosine A <sub>2a</sub> Receptor in the Active State. <i>Journal of Physical Chemistry B</i> , 2018, 122, 4418-4427.	1.2	8
25	Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor. <i>Nature Chemical Biology</i> , 2018, 14, 1150-1158.	3.9	59
26	Statistical thermodynamics for the unexpectedly large difference between disaccharide stereoisomers in terms of solubility in water. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 23684-23693.	1.3	5
27	Universal effects of solvent species on the stabilized structure of a protein. <i>Journal of Chemical Physics</i> , 2018, 149, 045105.	1.2	22
28	Effects of salt or cosolvent addition on solubility of a hydrophobic solute in water: Relevance to those on thermal stability of a protein. <i>Journal of Chemical Physics</i> , 2017, 146, 055102.	1.2	21
29	Unraveling protein folding mechanism by analyzing the hierarchy of models with increasing level of detail. <i>Journal of Chemical Physics</i> , 2017, 147, 125102.	1.2	21
30	Unified elucidation of the entropy-driven and -opposed hydrophobic effects. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 25891-25904.	1.3	16
31	Entropic enrichment of cosolvent near a very large solute immersed in solvent-cosolvent binary mixture: Anomalous dependence on bulk cosolvent concentration. <i>Journal of Molecular Liquids</i> , 2017, 247, 403-410.	2.3	5
32	Hot-Spot Residues to be Mutated Common in G Protein-Coupled Receptors of Class A: Identification of Thermostabilizing Mutations Followed by Determination of Three-Dimensional Structures for Two Example Receptors. <i>Journal of Physical Chemistry B</i> , 2017, 121, 6341-6350.	1.2	29
33	Identification of thermostabilizing mutations for a membrane protein whose three-dimensional structure is unknown. <i>Journal of Computational Chemistry</i> , 2017, 38, 211-223.	1.5	18
34	Molecular Machines. <i>Springer Briefs in Molecular Science</i> , 2016, , 21-61.	0.1	0
35	Physical origins of remarkable thermostabilization by an octuple mutation for the adenosine A <sub>2a</sub> receptor. <i>Chemical Physics Letters</i> , 2016, 657, 119-123.	1.2	12
36	Effects of monohydric alcohols and polyols on the thermal stability of a protein. <i>Journal of Chemical Physics</i> , 2016, 144, 125105.	1.2	16

#	ARTICLE	IF	CITATIONS
37	Dynamics of the entropic insertion of a large sphere into a cylindrical vessel. <i>Journal of Chemical Physics</i> , 2016, 144, 105103.	1.2	4
38	Identification of Thermostabilizing Mutations for Membrane Proteins: Rapid Method Based on Statistical Thermodynamics. <i>Journal of Physical Chemistry B</i> , 2016, 120, 3833-3843.	1.2	25
39	High-Rate Charging of Zinc Anodes Achieved by Tuning Hydration Properties of Zinc Complexes in Water Confined within Nanopores. <i>Journal of Physical Chemistry C</i> , 2016, 120, 24112-24120.	1.5	23
40	Water based on a molecular model behaves like a hard-sphere solvent for a nonpolar solute when the reference interaction site model and related theories are employed. <i>Journal of Physics Condensed Matter</i> , 2016, 28, 344003.	0.7	14
41	Statistical thermodynamics of aromatic-aromatic interactions in aqueous solution. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 32406-32417.	1.3	5
42	Statistical Thermodynamics for Actin-Myosin Binding: The Crucial Importance of Hydration Effects. <i>Biophysical Journal</i> , 2016, 110, 2496-2506.	0.2	14
43	A highly efficient hybrid method for calculating the hydration free energy of a protein. <i>Journal of Computational Chemistry</i> , 2016, 37, 712-723.	1.5	6
44	On the physics of thermal-stability changes upon mutations of a protein. <i>Journal of Chemical Physics</i> , 2015, 143, 125102.	1.2	12
45	Physicochemical origin of high correlation between thermal stability of a protein and its packing efficiency: a theoretical study for staphylococcal nuclease mutants. <i>Biophysics and Physicobiology</i> , 2015, 12, 1-12.	0.5	11
46	Essential roles of protein-solvent many-body correlation in solvent-entropy effect on protein folding and denaturation: Comparison between hard-sphere solvent and water. <i>Journal of Chemical Physics</i> , 2015, 142, 145103.	1.2	53
47	An accurate and efficient computation method of the hydration free energy of a large, complex molecule. <i>Journal of Chemical Physics</i> , 2015, 142, 175101.	1.2	6
48	Mechanism of One-to-Many Molecular Recognition Accompanying Target-Dependent Structure Formation: For the Tumor Suppressor p53 Protein as an Example. <i>Journal of Physical Chemistry B</i> , 2015, 119, 14120-14129.	1.2	20
49	Penetration of Platinum Complex Anions into Porous Silicon: Anomalous Behavior Caused by Surface-Induced Phase Transition. <i>Journal of Physical Chemistry C</i> , 2015, 119, 19105-19116.	1.5	14
50	Effect of cation species on surface-induced phase transition observed for platinum complex anions in platinum electrodeposition using nanoporous silicon. <i>Journal of Chemical Physics</i> , 2014, 141, 074701.	1.2	10
51	Physical origins of the high structural stability of CLN025 with only ten residues. <i>Journal of Chemical Physics</i> , 2014, 141, 105103.	1.2	5
52	Binding of an RNA aptamer and a partial peptide of a prion protein: crucial importance of water entropy in molecular recognition. <i>Nucleic Acids Research</i> , 2014, 42, 6861-6875.	6.5	68
53	Changes in hydrophobic and hydrophilic hydration properties caused by raising the pressure or by lowering the temperature. <i>Chemical Physics Letters</i> , 2014, 610-611, 1-7.	1.2	5
54	2P004 Statistical thermodynamics of one-to-many molecular recognition accompanied by partner-dependent folding : in the case of p53 protein (01A. Protein:Structure,Poster,The 52nd Annual) Tj ETQq0 0 0.0gBT /Overlock 10 T		

#	ARTICLE	IF	CITATIONS
55	On the physics of multidrug efflux through a biomolecular complex. Journal of Chemical Physics, 2013, 139, 205102.	1.2	9
56	Entropic release of a big sphere from a cylindrical vessel. Chemical Physics Letters, 2013, 561-562, 159-165.	1.2	9
57	Effects of sugars on the thermal stability of a protein. Journal of Chemical Physics, 2013, 138, 245101.	1.2	46
58	A new theoretical approach to biological self-assembly. Biophysical Reviews, 2013, 5, 283-293.	1.5	75
59	3P114 Statistical Thermodynamics for Binding of an RNA Aptamer and a Partial Peptide of a Prion Protein(O4. Nucleic acid binding proteins,Poster). Seibutsu Butsuri, 2013, 53, S230.	0.0	0
60	3P109 Theoretical Enhancement of Structural Stability of a Membrane Protein for X-ray Crystallography(O3. Membrane proteins,Poster). Seibutsu Butsuri, 2013, 53, S230.	0.0	0
61	A scoring function based on solvation thermodynamics for protein structure prediction. Biophysics (Nagoya-shi, Japan), 2012, 8, 127-138.	0.4	1
62	1PT154 Structural stability of a protein in aqueous and nonaqueous environments(The 50th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.0	0
63	3PT116 Entropic release of a big sphere from a cylindrical vessel(The 50th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
64	1PT137 Effects of sugars on the thermal stability of proteins(The 50th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	0.0	0
65	Evaluation of protein-ligand binding free energy focused on its entropic components. Journal of Computational Chemistry, 2012, 33, 550-560.	1.5	26
66	Structural stability of proteins in aqueous and nonpolar environments. Journal of Chemical Physics, 2012, 137, 135103.	1.2	30
67	Physical origin of hydrophobicity studied in terms of cold denaturation of proteins: comparison between water and simple fluids. Physical Chemistry Chemical Physics, 2012, 14, 14554.	1.3	42
68	Characterization of Experimentally Determined Native-Structure Models of a Protein Using Energetic and Entropic Components of Free-Energy Function. Journal of Physical Chemistry B, 2012, 116, 7776-7786.	1.2	6
69	Revolutionary Protein Hydration Theory I. Beyond the Asakura-Oosawa Theory. Seibutsu Butsuri, 2012, 52, 203-205.	0.0	0
70	Revolutionary Protein Hydration Theory III. Theoretical Examination. Seibutsu Butsuri, 2012, 52, 300-303.	0.0	0
71	Evolutionary Protein Hydration Theory II. Practical Applications of New Theory. Seibutsu Butsuri, 2012, 52, 250-253.	0.0	0
72	Crucial importance of the water-entropy effect in predicting hot spots in protein-protein complexes. Physical Chemistry Chemical Physics, 2011, 13, 16236.	1.3	20

#	ARTICLE	IF	CITATIONS
73	1L1536 A theoretical analysis on water-entropy change in yeast F <sub>1</sub> -ATPase during 16 degrees rotation of gamma subunit(Molecular motor 1,The 49th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2011, 51, S62.	0.0	0
74	1H1436 Crucial Importance of Water-Entropy Effect for Hot Spots in Protein-Protein Complexes(Protein: Property 2,The 49th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2011, 51, S49.	0.0	0
75	1SG-06 Cooperative Roles of Water and ATP in Functioning of ATP-Driven Proteins(1SG) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Seibutsu Butsuri, 2011, 51, S6.	0.0	0
76	A Simple Theory for Entropic Interaction Induced between Large Spheres in a Binary Mixture of Small and Medium Spheres. Journal of the Physical Society of Japan, 2011, 80, 114802.	0.7	1
77	Morphometric approach to thermodynamic quantities of solvation of complex molecules: Extension to multicomponent solvent. Journal of Chemical Physics, 2011, 135, 045103.	1.2	17
78	Free energy function for discriminating the native fold of a protein from misfolded decoys. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2161-2171.	1.5	28
79	Model of insertion and release of a large solute into and from a biopolymer complex. Chemical Physics Letters, 2011, 504, 221-224.	1.2	11
80	Effects of heme on the thermal stability of mesophilic and thermophilic cytochromes c: Comparison between experimental and theoretical results. Journal of Chemical Physics, 2011, 134, 025101.	1.2	35
81	Potential of mean force between a large solute and a biomolecular complex: A model analysis on protein flux through chaperonin system. Journal of Chemical Physics, 2011, 135, 185101.	1.2	18
82	3P077 Refinement of Modeled Protein Structure by Replica Exchange Molecular Dynamics and Hydration Entropy based Scoring Function(Protein: Property,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 377	0.0	0
83	1P073 Development of a free-energy function toward predicting the native structure of a protein(Protein:Property,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S32.	0.0	0
84	1P049 Import and export of a solute using solvation effects : a study on chaperonin GroEL(Protein:Property,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S27.	0.0	0
85	1P062 Theoretical Prediction of Hot Spots in Protein-Protein Complexes(Protein:Property,The 48th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 377	0.0	0
86	1P111 Effects of heme on the thermal stability of cytochromes c : Comparison between experimental and theoretical results(Heme proteins,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S38-S39.	0.0	0
87	1P186 1YA1115 Crucial importance of translational entropy of water in rotation mechanism of F1-ATPase(Molecular motor,Early Research in Biophysics Award Candidate Presentations,Early) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 377 Seibutsu Butsuri, 2010, 50, S52.	0.0	0
88	Entropic insertion of a big sphere into a cylindrical vessel. Chemical Physics Letters, 2010, 488, 1-6.	1.2	24
89	Effects of side-chain packing on the formation of secondary structures in protein folding. Journal of Chemical Physics, 2010, 132, 065105.	1.2	43
90	Roles of translational motion of water molecules in sustaining life. Frontiers in Bioscience - Landmark, 2009, Volume, 3419.	3.0	68

#	ARTICLE	IF	CITATIONS
91	1P-046 Pressure effect on helix-coil transition of an alanine -based peptide : Statistical-mechanical analysis(Protein:Property, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2009, 49, S70.	0.0	0
92	Pressure effects on structures formed by entropically driven self-assembly: Illustration for denaturation of proteins. Physical Review E, 2009, 79, 011912.	0.8	45
93	Molecular origin of the negative heat capacity of hydrophilic hydration. Journal of Chemical Physics, 2009, 130, 144705.	1.2	39
94	Importance of Translational Entropy of Water in Biological Self-Assembly Processes like Protein Folding. International Journal of Molecular Sciences, 2009, 10, 1064-1080.	1.8	81
95	A statistical-mechanical analysis on the hypermobile water around a large solute with high surface charge density. Journal of Chemical Physics, 2009, 130, 014707.	1.2	33
96	Three-Dimensional Density Profiles of Small and Medium Spheres near a Pair of Large Spheres: Relevance to Entropic Interaction Induced between Large Spheres. Journal of the Physical Society of Japan, 2009, 78, 044801.	0.7	17
97	Free energy function based on an all-atom model for proteins. Proteins: Structure, Function and Bioinformatics, 2009, 77, 950-961.	1.5	32
98	Theoretical analysis on thermal stability of a protein focused on the water entropy. Chemical Physics Letters, 2009, 474, 190-194.	1.2	40
99	2P-055 New computational method for protein-ligand binding affinities focused on water entropy(Protein:Property, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2009, 49, S115.	0.0	0
100	1P-045 A Theoretical Analysis on Characteristics of Protein Structures Induced by Cold Denaturation(Protein:Property, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2009, 49, S70.	0.0	0
101	1P-047 Roles of side-chain packing in the formation of secondary structures of a protein(Protein:Property, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2009, 49, S70.	0.0	0
102	1P-127 Entropic potential field formed for a linear-motor protein near a filament : Simple model calculation I(Molecular motor, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2009, 49, S83.	0.0	0
103	1P-048 Crucial importance of water-entropy effect in thermal stability of proteins(Protein:Property,) Tj ETQq1 1 0.784314 rgBT /Overl	0.0	0
104	Theoretical Analysis on Hyper-mobile Water Around a Solute. Hyomen Kagaku, 2009, 30, 157-161.	0.0	0
105	Thermodynamics of apoplastocyanin folding: Comparison between experimental and theoretical results. Journal of Chemical Physics, 2008, 128, 225104.	1.2	85
106	Molecular mechanism of pressure denaturation of proteins. Journal of Chemical Physics, 2008, 129, 145103.	1.2	74
107	Molecular origin of the hydrophobic effect: Analysis using the angle-dependent integral equation theory. Journal of Chemical Physics, 2008, 128, 024507.	1.2	91
108	1P-011 Parameters related to intramolecular hydrogen bonds characterizing the protein native structure(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2008, 48, S22.	0.0	0

#	ARTICLE	IF	CITATIONS
109	1P-070 Thermodynamics of apoplastocyanin folding : Comparison between experimental and theoretical results(Invited Talk for Early Research in Biophysics Award,Early Research in Biophysics Award)(The TJ ETQq1 1 0.784314 rgBT /Overlock	0.0	0
110	1P-079 Analysis on thermal stability of a protein focused on water entropy(The 46th Annual Meeting of) Tj ETQq0 0.0 rgBT /Overlock 10	0.0	0
111	2P-038 Evaluation of multiphysics methodologies for the calculation of ligand-protein binding free energy(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S81.	0.0	0
112	3P-115 A theoretical analysis on the hyper-mobile water molecules near a solute(The 46th Annual) Tj ETQq0 0.0 rgBT /Overlock 10 Tf 50	0.0	0
113	Theoretical analysis on changes in thermodynamic quantities upon protein folding: Essential role of hydration. Journal of Chemical Physics, 2007, 126, 225102.	1.2	75
114	A theoretical analysis on hydration thermodynamics of proteins. Journal of Chemical Physics, 2006, 125, 024911.	1.2	139
115	Remarkable Solvent Effects on Depletion Interaction in Crowding Media: Analyses Using the Integral Equation Theories. Journal of the Physical Society of Japan, 2006, 75, 064804.	0.7	24
116	Roles of entropic excluded-volume effects in colloidal and biological systems: Analyses using the three-dimensional integral equation theory. Chemical Engineering Science, 2006, 61, 2150-2160.	1.9	48
117	Crucial importance of translational entropy of water in pressure denaturation of proteins. Journal of Chemical Physics, 2006, 125, 024910.	1.2	51
118	Depletion potential between large spheres immersed in a multicomponent mixture of small spheres. Journal of Chemical Physics, 2006, 125, 084910.	1.2	37
119	On the physics of pressure denaturation of proteins. Journal of Physics Condensed Matter, 2006, 18, L107-L113.	0.7	39
120	Pair-correlation entropy of hydrophobic hydration: Decomposition into translational and orientational contributions and analysis of solute-size effects. Journal of Chemical Physics, 2006, 124, 024512.	1.2	38
121	Morphometric Approach to the Solvation Free Energy of Complex Molecules. Physical Review Letters, 2006, 97, 078101.	2.9	143
122	Density and orientational structure of water around a hydrophobic solute: effects due to the solute size. Journal of Molecular Liquids, 2005, 119, 47-54.	2.3	41
123	Potential of Mean Force between Solute Atoms in Salt Solution: Effects Due to Salt Species and Relevance to Conformational Transition of Biomolecules. Bulletin of the Chemical Society of Japan, 2005, 78, 1431-1441.	2.0	34
124	Translational-Entropy Gain of Solvent upon Protein Folding. Biophysical Journal, 2005, 89, 2701-2710.	0.2	138
125	Water Structure and Phase Transition Near a Surface. Journal of Solution Chemistry, 2004, 33, 661-687.	0.6	29
126	Interaction between surfaces with solvophobicity or solvophilicity immersed in solvent: Effects due to addition of solvophobic or solvophilic solute. Journal of Chemical Physics, 2003, 118, 8969-8981.	1.2	49



#	ARTICLE	IF	CITATIONS
127	Partial Molar Volume and Compressibility of Alkali <sup>+</sup> Halide Ions in Aqueous Solution: A Hydration Shell Analysis with an Integral Equation Theory of Molecular Liquids. <i>Journal of Physical Chemistry B</i> , 2002, 106, 7308-7314.	1.2	42
128	Spatial distribution of a depletion potential between a big solute of arbitrary geometry and a big sphere immersed in small spheres. <i>Journal of Chemical Physics</i> , 2002, 116, 3493-3501.	1.2	95
129	Methodology of predicting approximate shapes and size distribution of micelles: Illustration for simple models. <i>Journal of Computational Chemistry</i> , 2002, 23, 1445-1455.	1.5	11
130	Interaction between large spheres immersed in small spheres: remarkable effects due to a trace amount of medium-sized spheres. <i>Chemical Physics Letters</i> , 2002, 353, 259-269.	1.2	24
131	Hydration structure and stability of Met-enkephalin studied by a three-dimensional reference interaction site model with a repulsive bridge correction and a thermodynamic perturbation method. <i>Journal of Chemical Physics</i> , 2000, 113, 9830-9836.	1.2	29
132	Interaction between solute molecules in medium density solvents. <i>Molecular Physics</i> , 2000, 98, 725-736.	0.8	6
133	Peptide Conformations in Alcohol and Water: Analyses by the Reference Interaction Site Model Theory. <i>Journal of the American Chemical Society</i> , 2000, 122, 2773-2779.	6.6	40
134	Solvent Effects on Formation of Tertiary Structure of Protein. <i>Seibutsu Butsuri</i> , 2000, 40, 374-378.	0.0	4
135	Theoretical Analysis on the Metal-Aqueous Electrolyte Solution Interface. <i>Hyomen Kagaku</i> , 1999, 20, 288-294.	0.0	1
136	Calculation of solvation free energy using RISM theory for peptide in salt solution. <i>Journal of Computational Chemistry</i> , 1998, 19, 1724-1735.	1.5	39
137	Analysis on Fractal-Like Behaviour Expected for Migration of Radionuclides in Geologic Sorbing Media. <i>Journal of Nuclear Science and Technology</i> , 1998, 35, 40-48.	0.7	0
138	First-Principle Determination of Peptide Conformations in Solvents: A Combination of Monte Carlo Simulated Annealing and RISM Theory. <i>Journal of the American Chemical Society</i> , 1998, 120, 1855-1863.	6.6	79
139	Analysis of salt effects on solubility of noble gases in water using the reference interaction site model theory. <i>Journal of Chemical Physics</i> , 1997, 106, 5202-5215.	1.2	75
140	Fractal-like behavior of a mass-transport process. <i>AIChE Journal</i> , 1997, 43, 2187-2193.	1.8	9
141	Calculation of hydration free energy for a solute with many atomic sites using the RISM theory: A robust and efficient algorithm. <i>Journal of Chemical Physics</i> , 1997, 106, 1320-1326.		38
142	Interaction between macroparticles in a simple model system of a nonpolar liquid containing trace amounts of water. <i>Journal of Chemical Physics</i> , 1996, 105, 7184-7191.	1.2	13
143	Interaction between macroparticles in Lennard-Jones fluids or in hard-sphere mixtures. <i>Journal of Chemical Physics</i> , 1996, 105, 7177-7183.	1.2	74
144	Interaction between macroparticles in aqueous electrolytes. <i>Journal of Chemical Physics</i> , 1996, 105, 2487-2499.	1.2	61

#	ARTICLE	IF	CITATIONS
145	Fractal-like behavior observed for a mass-transport process. AICHE Journal, 1992, 38, 1667-1670.	1.8	6
146	Percolation Phenomenon for Dissolution of Sodium Borosilicate Glasses in Aqueous Solutions. Journal of the American Ceramic Society, 1991, 74, 783-787.	1.9	23