

Axel T Brunger

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251
papers

29,752
citations

90
h-index

168
g-index

301
ext. papers

32,215
ext. citations

10.7
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7.37
L-index

| # | Paper | IF | Citations |
|-----|--|-------|-----------|
| 251 | Free R value: a novel statistical quantity for assessing the accuracy of crystal structures. <i>Nature</i> , 1992 , 355, 472-5 | 50.4 | 3703 |
| 250 | Crystal structure of a SNARE complex involved in synaptic exocytosis at 2.4 Å resolution. <i>Nature</i> , 1998 , 395, 347-53 | 50.4 | 1929 |
| 249 | Version 1.2 of the Crystallography and NMR system. <i>Nature Protocols</i> , 2007 , 2, 2728-33 | 18.8 | 1143 |
| 248 | Stochastic boundary conditions for molecular dynamics simulations of ST2 water. <i>Chemical Physics Letters</i> , 1984 , 105, 495-500 | 2.5 | 484 |
| 247 | Polar hydrogen positions in proteins: empirical energy placement and neutron diffraction comparison. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988 , 4, 148-56 | 4.2 | 467 |
| 246 | Determination of three-dimensional structures of proteins by simulated annealing with interproton distance restraints. Application to crambin, potato carboxypeptidase inhibitor and barley serine proteinase inhibitor 2. <i>Protein Engineering, Design and Selection</i> , 1988 , 2, 27-38 | 1.9 | 467 |
| 245 | Crystallographic refinement by simulated annealing. Application to a 2.8 Å resolution structure of aspartate aminotransferase. <i>Journal of Molecular Biology</i> , 1988 , 203, 803-16 | 6.5 | 379 |
| 244 | Checking your imagination: applications of the free R value. <i>Structure</i> , 1996 , 4, 897-904 | 5.2 | 360 |
| 243 | Torsion angle dynamics: reduced variable conformational sampling enhances crystallographic structure refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 277-90 | 4.2 | 345 |
| 242 | ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes. <i>Nature</i> , 2015 , 520, 563-6 | 50.4 | 339 |
| 241 | A new generation of crystallographic validation tools for the protein data bank. <i>Structure</i> , 2011 , 19, 1395-412 | 5.412 | 335 |
| 240 | Protein hydration observed by X-ray diffraction. Solvation properties of penicillopepsin and neuraminidase crystal structures. <i>Journal of Molecular Biology</i> , 1994 , 243, 100-15 | 6.5 | 331 |
| 239 | Active site dynamics in protein molecules: a stochastic boundary molecular-dynamics approach. <i>Biopolymers</i> , 1985 , 24, 843-65 | 2.2 | 323 |
| 238 | Transglutaminase 2 undergoes a large conformational change upon activation. <i>PLoS Biology</i> , 2007 , 5, e327 | 9.7 | 318 |
| 237 | Structural basis of Rab effector specificity: crystal structure of the small G protein Rab3A complexed with the effector domain of rabphilin-3A. <i>Cell</i> , 1999 , 96, 363-74 | 56.2 | 306 |
| 236 | Complete structure of p97/valosin-containing protein reveals communication between nucleotide domains. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 856-63 | 17.6 | 301 |
| 235 | Torsion-angle molecular dynamics as a new efficient tool for NMR structure calculation. <i>Journal of Magnetic Resonance</i> , 1997 , 124, 154-64 | 3 | 284 |

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| 234 | A dimerization motif for transmembrane alpha-helices. <i>Nature Structural Biology</i> , 1994 , 1, 157-63 | | 278 |
| 233 | Substrate recognition strategy for botulinum neurotoxin serotype A. <i>Nature</i> , 2004 , 432, 925-9 | 50.4 | 277 |
| 232 | Structural changes are associated with soluble N-ethylmaleimide-sensitive fusion protein attachment protein receptor complex formation. <i>Journal of Biological Chemistry</i> , 1997 , 272, 28036-41 | 5.4 | 269 |
| 231 | Application of molecular dynamics with interproton distance restraints to three-dimensional protein structure determination. A model study of crambin. <i>Journal of Molecular Biology</i> , 1986 , 191, 523-57 | 6.5 | 265 |
| 230 | The 1.0 Å crystal structure of Ca(2+)-bound calmodulin: an analysis of disorder and implications for functionally relevant plasticity. <i>Journal of Molecular Biology</i> , 2000 , 301, 1237-56 | 6.5 | 263 |
| 229 | Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016 , 540, 453-457 | 50.4 | 260 |
| 228 | Super-resolution biomolecular crystallography with low-resolution data. <i>Nature</i> , 2010 , 464, 1218-22 | 50.4 | 243 |
| 227 | A novel evolutionarily conserved domain of cell-adhesion GPCRs mediates autoproteolysis. <i>EMBO Journal</i> , 2012 , 31, 1364-78 | 13 | 243 |
| 226 | Free R value: cross-validation in crystallography. <i>Methods in Enzymology</i> , 1997 , 277, 366-96 | 1.7 | 228 |
| 225 | Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of <i>Escherichia coli</i> . Combined use of ¹ H nuclear magnetic resonance and restrained molecular dynamics. <i>Journal of Molecular Biology</i> , 1985 , 186, 435-55 | 6.5 | 224 |
| 224 | Folding intermediates of SNARE complex assembly. <i>Nature Structural Biology</i> , 1999 , 6, 117-23 | | 217 |
| 223 | Structure of the ATP-dependent oligomerization domain of N-ethylmaleimide sensitive factor complexed with ATP. <i>Nature Structural Biology</i> , 1998 , 5, 803-11 | | 215 |
| 222 | Interhelical hydrogen bonding drives strong interactions in membrane proteins. <i>Nature Structural Biology</i> , 2000 , 7, 154-60 | | 212 |
| 221 | Native β -synuclein induces clustering of synaptic-vesicle mimics via binding to phospholipids and synaptobrevin-2/VAMP2. <i>ELife</i> , 2013 , 2, e00592 | 8.9 | 211 |
| 220 | Identification of a minimal core of the synaptic SNARE complex sufficient for reversible assembly and disassembly. <i>Biochemistry</i> , 1998 , 37, 10354-62 | 3.2 | 210 |
| 219 | The three-dimensional structure of β -purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>EMBO Journal</i> , 1986 , 5, 2729-2735 | 13 | 208 |
| 218 | Properties of native brain β -synuclein. <i>Nature</i> , 2013 , 498, E4-6; discussion E6-7 | 50.4 | 207 |
| 217 | Conformational variability in the refined structure of the chaperonin GroEL at 2.8 Å resolution. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 1083-94 | 17.6 | 207 |

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| 216 | Structure and function of SNARE and SNARE-interacting proteins. <i>Quarterly Reviews of Biophysics</i> , 2005 , 38, 1-47 | 7 | 204 |
| 215 | Botulinum neurotoxin B recognizes its protein receptor with high affinity and specificity. <i>Nature</i> , 2006 , 444, 1092-5 | 50.4 | 193 |
| 214 | Architecture of the synaptotagmin-SNARE machinery for neuronal exocytosis. <i>Nature</i> , 2015 , 525, 62-7 | 50.4 | 192 |
| 213 | Sampling and efficiency of metric matrix distance geometry: a novel partial metrization algorithm. <i>Journal of Biomolecular NMR</i> , 1992 , 2, 33-56 | 3 | 192 |
| 212 | Refinement of the influenza virus hemagglutinin by simulated annealing. <i>Journal of Molecular Biology</i> , 1990 , 212, 737-61 | 6.5 | 188 |
| 211 | Combining efficient conformational sampling with a deformable elastic network model facilitates structure refinement at low resolution. <i>Structure</i> , 2007 , 15, 1630-41 | 5.2 | 187 |
| 210 | Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 154-62 | 17.6 | 186 |
| 209 | New applications of simulated annealing in X-ray crystallography and solution NMR. <i>Structure</i> , 1997 , 5, 325-36 | 5.2 | 183 |
| 208 | Structural basis of FFAT motif-mediated ER targeting. <i>Structure</i> , 2005 , 13, 1035-45 | 5.2 | 182 |
| 207 | A ubiquitin ligase transfers preformed polyubiquitin chains from a conjugating enzyme to a substrate. <i>Nature</i> , 2007 , 446, 333-7 | 50.4 | 175 |
| 206 | Conformational changes of the multifunction p97 AAA ATPase during its ATPase cycle. <i>Nature Structural Biology</i> , 2002 , 9, 950-7 | | 174 |
| 205 | Central pore residues mediate the p97/VCP activity required for ERAD. <i>Molecular Cell</i> , 2006 , 22, 451-62 | 17.6 | 172 |
| 204 | Mechanistic insights into the recycling machine of the SNARE complex. <i>Nature</i> , 2015 , 518, 61-7 | 50.4 | 167 |
| 203 | Improved structures of full-length p97, an AAA ATPase: implications for mechanisms of nucleotide-dependent conformational change. <i>Structure</i> , 2008 , 16, 715-26 | 5.2 | 167 |
| 202 | The glycoporphin A transmembrane domain dimer: sequence-specific propensity for a right-handed supercoil of helices. <i>Biochemistry</i> , 1992 , 31, 12726-32 | 3.2 | 166 |
| 201 | Single-molecule FRET-derived model of the synaptotagmin 1-SNARE fusion complex. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 318-24 | 17.6 | 157 |
| 200 | Structures of neuroligin-1 and the neuroligin-1/neurexin-1 beta complex reveal specific protein-protein and protein-Ca ²⁺ interactions. <i>Neuron</i> , 2007 , 56, 992-1003 | 13.9 | 157 |
| 199 | Crystal structure of the cytosolic C2A-C2B domains of synaptotagmin III. Implications for Ca ²⁺ -independent snare complex interaction. <i>Journal of Cell Biology</i> , 1999 , 147, 589-98 | 7.3 | 157 |

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| 198 | Statistical analysis of predicted transmembrane alpha-helices. <i>BBA - Proteins and Proteomics</i> , 1998 , 1429, 113-28 | | 156 |
| 197 | Epsin 1 undergoes nucleocytoplasmic shuttling and its eps15 interactor NH(2)-terminal homology (ENTH) domain, structurally similar to Armadillo and HEAT repeats, interacts with the transcription factor promyelocytic leukemia Zn(2)+ finger protein (PLZF). <i>Journal of Cell Biology</i> , 2000 , 149, 537-46 | 7.3 | 152 |
| 196 | Crystal structure of the hCASK PDZ domain reveals the structural basis of class II PDZ domain target recognition. <i>Nature Structural Biology</i> , 1998 , 5, 317-25 | | 149 |
| 195 | Algorithmic Challenges in Computational Molecular Biophysics. <i>Journal of Computational Physics</i> , 1999 , 151, 9-48 | 4.1 | 148 |
| 194 | Nucleotide dependent motion and mechanism of action of p97/VCP. <i>Journal of Molecular Biology</i> , 2005 , 347, 437-52 | 6.5 | 145 |
| 193 | Computational challenges for macromolecular structure determination by X-ray crystallography and solution NMR-spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 1993 , 26, 49-125 | 7 | 143 |
| 192 | Improved prediction for the structure of the dimeric transmembrane domain of glycoporphin A obtained through global searching. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 257-61 | 4.2 | 141 |
| 191 | Structural characterization of the intramolecular interaction between the SH3 and guanylate kinase domains of PSD-95. <i>Molecular Cell</i> , 2001 , 8, 1313-25 | 17.6 | 140 |
| 190 | Rab and Arl GTPase family members cooperate in the localization of the golgin GCC185. <i>Cell</i> , 2008 , 132, 286-98 | 56.2 | 138 |
| 189 | Single molecule observation of liposome-bilayer fusion thermally induced by soluble N-ethyl maleimide sensitive-factor attachment protein receptors (SNAREs). <i>Biophysical Journal</i> , 2004 , 87, 3569-84 ⁹ | 24.9 | 138 |
| 188 | A structural change occurs upon binding of syntaxin to SNAP-25. <i>Journal of Biological Chemistry</i> , 1997 , 272, 4582-90 | 5.4 | 137 |
| 187 | Refractive index-based determination of detergent concentration and its application to the study of membrane proteins. <i>Protein Science</i> , 2005 , 14, 2207-11 | 6.3 | 136 |
| 186 | Experimentally based orientational refinement of membrane protein models: A structure for the Influenza A M2 H+ channel. <i>Journal of Molecular Biology</i> , 1999 , 286, 951-62 | 6.5 | 136 |
| 185 | The primed SNARE-complexin-synaptotagmin complex for neuronal exocytosis. <i>Nature</i> , 2017 , 548, 420-425 | 35.4 | 134 |
| 184 | Accessory proteins stabilize the acceptor complex for synaptobrevin, the 1:1 syntaxin/SNAP-25 complex. <i>Structure</i> , 2008 , 16, 308-20 | 5.2 | 131 |
| 183 | Structural and functional comparisons of nucleotide pyrophosphatase/phosphodiesterase and alkaline phosphatase: implications for mechanism and evolution. <i>Biochemistry</i> , 2006 , 45, 9788-803 | 3.2 | 131 |
| 182 | Structure refinement of oligonucleotides by molecular dynamics with nuclear Overhauser effect interproton distance restraints: application to 5Pd(C-G-T-A-C-G)2. <i>Journal of Molecular Biology</i> , 1986 , 188, 455-75 | 6.5 | 131 |
| 181 | Synaptic proteins promote calcium-triggered fast transition from point contact to full fusion. <i>ELife</i> , 2012 , 1, e00109 | 8.9 | 128 |

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| 180 | In vitro system capable of differentiating fast Ca ²⁺ -triggered content mixing from lipid exchange for mechanistic studies of neurotransmitter release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E304-13 | 11.5 | 127 |
| 179 | Neuronal SNAREs do not trigger fusion between synthetic membranes but do promote PEG-mediated membrane fusion. <i>Biophysical Journal</i> , 2006 , 90, 1661-75 | 2.9 | 125 |
| 178 | Ensemble molecular dynamics yields submillisecond kinetics and intermediates of membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 11916-21 | 11.5 | 124 |
| 177 | Neurexins physically and functionally interact with GABA(A) receptors. <i>Neuron</i> , 2010 , 66, 403-16 | 13.9 | 121 |
| 176 | Exo84 and Sec5 are competitive regulatory Sec6/8 effectors to the RalA GTPase. <i>EMBO Journal</i> , 2005 , 24, 2064-74 | 13 | 121 |
| 175 | Conformational variability of solution nuclear magnetic resonance structures. <i>Journal of Molecular Biology</i> , 1995 , 250, 80-93 | 6.5 | 117 |
| 174 | The ENTH domain. <i>FEBS Letters</i> , 2002 , 513, 11-8 | 3.8 | 115 |
| 173 | Molecular Mechanisms of Synaptic Vesicle Priming by Munc13 and Munc18. <i>Neuron</i> , 2017 , 95, 591-607.e10 | 10.9 | 114 |
| 172 | Role of the gamma-phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. <i>EMBO Journal</i> , 2003 , 22, 4877-87 | 13 | 110 |
| 171 | Single-molecule studies of SNARE complex assembly reveal parallel and antiparallel configurations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 14800-5 | 11.5 | 109 |
| 170 | Goniometer-based femtosecond crystallography with X-ray free electron lasers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17122-7 | 11.5 | 105 |
| 169 | NSF N-terminal domain crystal structure: models of NSF function. <i>Molecular Cell</i> , 1999 , 4, 97-107 | 17.6 | 104 |
| 168 | Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography. <i>ELife</i> , 2015 , 4, | 8.9 | 100 |
| 167 | Neurologin-1 performs neurexin-dependent and neurexin-independent functions in synapse validation. <i>EMBO Journal</i> , 2009 , 28, 3244-55 | 13 | 99 |
| 166 | Crystal structure of the vesicular transport protein Sec17: implications for SNAP function in SNARE complex disassembly. <i>Molecular Cell</i> , 1999 , 4, 85-95 | 17.6 | 98 |
| 165 | Studying calcium-triggered vesicle fusion in a single vesicle-vesicle content and lipid-mixing system. <i>Nature Protocols</i> , 2013 , 8, 1-16 | 18.8 | 96 |
| 164 | Structural basis of the interaction between RalA and Sec5, a subunit of the sec6/8 complex. <i>EMBO Journal</i> , 2003 , 22, 3267-78 | 13 | 94 |
| 163 | Single-wavelength anomalous diffraction phasing revisited. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1413-20 | | 94 |

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| 162 | Crystal structures of a Rab protein in its inactive and active conformations. <i>Journal of Molecular Biology</i> , 2000 , 304, 585-98 | 6.5 | 91 |
| 161 | Inhibition of metalloprotease botulinum serotype A from a pseudo-peptide binding mode to a small molecule that is active in primary neurons. <i>Journal of Biological Chemistry</i> , 2007 , 282, 5004-5014 | 5.4 | 90 |
| 160 | Exploration of disorder in protein structures by X-ray restrained molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 340-58 | 4.2 | 90 |
| 159 | Exploring the structural dynamics of the E.coli chaperonin GroEL using translation-libration-screw crystallographic refinement of intermediate states. <i>Journal of Molecular Biology</i> , 2004 , 342, 229-45 | 6.5 | 88 |
| 158 | Enabling X-ray free electron laser crystallography for challenging biological systems from a limited number of crystals. <i>ELife</i> , 2015 , 4, | 8.9 | 88 |
| 157 | Single-molecule studies of the neuronal SNARE fusion machinery. <i>Annual Review of Biochemistry</i> , 2009 , 78, 903-28 | 29.1 | 87 |
| 156 | Crystallographic refinement by simulated annealing: methods and applications. <i>Methods in Enzymology</i> , 1997 , 277, 243-69 | 1.7 | 86 |
| 155 | Single-molecule studies of synaptotagmin and complexin binding to the SNARE complex. <i>Biophysical Journal</i> , 2005 , 89, 690-702 | 2.9 | 86 |
| 154 | Amino-acid substitutions in a surface turn modulate protein stability. <i>Nature Structural Biology</i> , 1996 , 3, 54-8 | | 86 |
| 153 | Analysis of a yeast SNARE complex reveals remarkable similarity to the neuronal SNARE complex and a novel function for the C terminus of the SNAP-25 homolog, Sec9. <i>Journal of Biological Chemistry</i> , 1997 , 272, 16610-7 | 5.4 | 85 |
| 152 | Automated modeling of coiled coils: application to the GCN4 dimerization region. <i>Protein Engineering, Design and Selection</i> , 1991 , 4, 649-59 | 1.9 | 85 |
| 151 | Ultrahigh-resolution imaging reveals formation of neuronal SNARE/Munc18 complexes in situ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E2812-20 | 11.5 | 84 |
| 150 | Three-dimensional molecular modeling with single molecule FRET. <i>Journal of Structural Biology</i> , 2011 , 173, 497-505 | 3.4 | 84 |
| 149 | Structure of a human A-type potassium channel interacting protein DPPX, a member of the dipeptidyl aminopeptidase family. <i>Journal of Molecular Biology</i> , 2004 , 343, 1055-65 | 6.5 | 83 |
| 148 | Receptor and substrate interactions of clostridial neurotoxins. <i>Toxicon</i> , 2009 , 54, 550-60 | 2.8 | 82 |
| 147 | Recent developments for the efficient crystallographic refinement of macromolecular structures. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 606-11 | 8.1 | 80 |
| 146 | X-ray scattering from unilamellar lipid vesicles. <i>Journal of Applied Crystallography</i> , 2005 , 38, 126-131 | 3.8 | 79 |
| 145 | Mechanistic insights into active site-associated polyubiquitination by the ubiquitin-conjugating enzyme Ube2g2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 3722-7 | 11.5 | 78 |

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| 144 | Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems. <i>Annual Review of Biophysics</i> , 2013 , 42, 265-87 | 21.1 | 76 |
| 143 | Molecular mechanism of the synaptotagmin-SNARE interaction in Ca ²⁺ -triggered vesicle fusion. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 325-31 | 17.6 | 76 |
| 142 | Structural insights into the molecular mechanism of Ca(2+)-dependent exocytosis. <i>Current Opinion in Neurobiology</i> , 2000 , 10, 293-302 | 7.6 | 76 |
| 141 | Botulinum neurotoxin heavy chain belt as an intramolecular chaperone for the light chain. <i>PLoS Pathogens</i> , 2007 , 3, 1191-4 | 7.6 | 74 |
| 140 | A revised model for the oligomeric state of the N-ethylmaleimide-sensitive fusion protein, NSF. <i>Journal of Biological Chemistry</i> , 1998 , 273, 15675-81 | 5.4 | 74 |
| 139 | Transmembrane signal transduction of the alpha(IIb)beta(3) integrin. <i>Protein Science</i> , 2002 , 11, 1800-12 | 6.3 | 73 |
| 138 | De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016 , 539, 43-47 | 50.4 | 73 |
| 137 | Molecular Mechanisms of Fast Neurotransmitter Release. <i>Annual Review of Biophysics</i> , 2018 , 47, 469-497 | 21.1 | 70 |
| 136 | Site-Directed Dichroism As a Method for Obtaining Rotational and Orientational Constraints for Oriented Polymers. <i>Journal of the American Chemical Society</i> , 1997 , 119, 8973-8980 | 16.4 | 68 |
| 135 | Complexin inhibits spontaneous release and synchronizes Ca ²⁺ -triggered synaptic vesicle fusion by distinct mechanisms. <i>ELife</i> , 2014 , 3, e03756 | 8.9 | 68 |
| 134 | Human ornithine aminotransferase complexed with L-canaline and gabaculine: structural basis for substrate recognition. <i>Structure</i> , 1997 , 5, 1067-75 | 5.2 | 67 |
| 133 | New insights into clostridial neurotoxin-SNARE interactions. <i>Trends in Molecular Medicine</i> , 2005 , 11, 377-81 | 5.5 | 67 |
| 132 | Successful prediction of the coiled coil geometry of the GCN4 leucine zipper domain by simulated annealing: comparison to the X-ray structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 133-46 | 4.2 | 66 |
| 131 | Do NOE distances contain enough information to assess the relative populations of multi-conformer structures?. <i>Journal of Biomolecular NMR</i> , 1996 , 7, 72-6 | 3 | 65 |
| 130 | Structural perspectives of phospholamban, a helical transmembrane pentamer. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997 , 26, 157-79 | | 64 |
| 129 | High resolution structure, stability, and synaptotagmin binding of a truncated neuronal SNARE complex. <i>Journal of Biological Chemistry</i> , 2003 , 278, 8630-6 | 5.4 | 64 |
| 128 | NSF and p97/VCP: similar at first, different at last. <i>FEBS Letters</i> , 2003 , 555, 126-33 | 3.8 | 64 |
| 127 | Conformation of the synaptobrevin transmembrane domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8378-83 | 11.5 | 63 |

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| 126 | Considerations for the refinement of low-resolution crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 923-32 | | 62 |
| 125 | Thermodynamics of protein-peptide interactions in the ribonuclease-S system studied by molecular dynamics and free energy calculations. <i>Biochemistry</i> , 1992 , 31, 8661-74 | 3.2 | 60 |
| 124 | A high-transparency, micro-patternable chip for X-ray diffraction analysis of microcrystals under native growth conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1987-97 | | 59 |
| 123 | Structural insights into the molecular mechanism of calcium-dependent vesicle-membrane fusion. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 163-73 | 8.1 | 59 |
| 122 | Molecular dynamics applied to X-ray structure refinement. <i>Accounts of Chemical Research</i> , 2002 , 35, 404-123 | 4.3 | 58 |
| 121 | Solution conformations of human growth hormone releasing factor: comparison of the restrained molecular dynamics and distance geometry methods for a system without long-range distance data. <i>Protein Engineering, Design and Selection</i> , 1987 , 1, 399-406 | 1.9 | 57 |
| 120 | A potent peptidomimetic inhibitor of botulinum neurotoxin serotype A has a very different conformation than SNAP-25 substrate. <i>Structure</i> , 2008 , 16, 1588-97 | 5.2 | 54 |
| 119 | Protein dynamics and distance determination by NOE measurements. <i>FEBS Letters</i> , 1988 , 236, 71-6 | 3.8 | 54 |
| 118 | High-density grids for efficient data collection from multiple crystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 2-11 | 5.5 | 52 |
| 117 | Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 928-40 | | 51 |
| 116 | Formation of a yeast SNARE complex is accompanied by significant structural changes. <i>FEBS Letters</i> , 1997 , 415, 49-55 | 3.8 | 51 |
| 115 | Structure of proteins involved in synaptic vesicle fusion in neurons. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001 , 30, 157-71 | | 51 |
| 114 | Expression of C1ql3 in Discrete Neuronal Populations Controls Efferent Synapse Numbers and Diverse Behaviors. <i>Neuron</i> , 2016 , 91, 1034-1051 | 13.9 | 50 |
| 113 | Thermal Motion and Conformational Disorder in Protein Crystal Structures: Comparison of Multi-Conformer and Time-Averaging Models. <i>Israel Journal of Chemistry</i> , 1994 , 34, 165-175 | 3.4 | 50 |
| 112 | Conformational substrates and uncertainty in macromolecular free energy calculations. <i>The Journal of Physical Chemistry</i> , 1993 , 97, 3409-3417 | | 49 |
| 111 | Helix packing in proteins: prediction and energetic analysis of dimeric, trimeric, and tetrameric GCN4 coiled coil structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 20, 105-23 | 4.2 | 49 |
| 110 | Conformational change of syntaxin linker region induced by Munc13s initiates SNARE complex formation in synaptic exocytosis. <i>EMBO Journal</i> , 2017 , 36, 816-829 | 13 | 47 |
| 109 | Structure and function of the yeast U-box-containing ubiquitin ligase Ufd2p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 15599-606 | 11.5 | 47 |

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| 108 | Electron cryomicroscopy structure of N-ethyl maleimide sensitive factor at 11 Å resolution. <i>EMBO Journal</i> , 2003 , 22, 4365-74 | 13 | 47 |
| 107 | Simulation analysis of structures on the reaction pathway of RNase A. <i>Journal of the American Chemical Society</i> , 1990 , 112, 3826-3831 | 16.4 | 47 |
| 106 | X-ray structure determination at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 128-33 | | 45 |
| 105 | Structural and biochemical studies of botulinum neurotoxin serotype C1 light chain protease: implications for dual substrate specificity. <i>Biochemistry</i> , 2007 , 46, 10685-93 | 3.2 | 45 |
| 104 | The 1.8 Å crystal structure of a statically disordered 17 base-pair RNA duplex: principles of RNA crystal packing and its effect on nucleic acid structure. <i>Journal of Molecular Biology</i> , 1999 , 285, 1577-88 | 6.5 | 45 |
| 103 | Structural principles of SNARE complex recognition by the AAA+ protein NSF. <i>ELife</i> , 2018 , 7, | 8.9 | 45 |
| 102 | 2.3 Å crystal structure of tetanus neurotoxin light chain. <i>Biochemistry</i> , 2005 , 44, 7450-7 | 3.2 | 43 |
| 101 | Mutational analysis of synaptobrevin transmembrane domain oligomerization. <i>Biochemistry</i> , 2002 , 41, 15861-6 | 3.2 | 43 |
| 100 | Towards reconstitution of membrane fusion mediated by SNAREs and other synaptic proteins. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015 , 50, 231-41 | 8.7 | 42 |
| 99 | Polarizable atomic multipole X-ray refinement: application to peptide crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 952-65 | | 41 |
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