

Jonathan King

List of Publications by Year in descending order

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148
papers

10,583
citations

20817

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36028

97
g-index

149
all docs

149
docs citations

149
times ranked

4758
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Congressional Budget Responses to the Pandemic: Fund Health Care, Not Warfare. <i>American Journal of Public Health</i> , 2021, 111, 200-201. | 2.7 | 1 |
| 2 | Hydro-epidemiological modelling of bacterial transport and decay in nearshore coastal waters. <i>Water Research</i> , 2021, 196, 117049. | 11.3 | 10 |
| 3 | Cataract. <i>Nature Reviews Disease Primers</i> , 2015, 1, 15014. | 30.5 | 90 |
| 4 | Tyrosine/Cysteine Cluster Sensitizing Human β -Crystallin to Ultraviolet Radiation-Induced Photoaggregation In Vitro. <i>Biochemistry</i> , 2014, 53, 979-990. | 2.5 | 25 |
| 5 | Tryptophan Cluster Protects Human β -Crystallin from Ultraviolet Radiation-Induced Photoaggregation In Vitro. <i>Photochemistry and Photobiology</i> , 2013, 89, 1106-1115. | 2.5 | 49 |
| 6 | The C-terminal cysteine annulus participates in auto-chaperone function for Salmonellaphage P22 tailspike folding and assembly. <i>Bacteriophage</i> , 2012, 2, 36-49. | 1.9 | 3 |
| 7 | Contributions of aromatic pairs to the folding and stability of long-lived human β -crystallin. <i>Protein Science</i> , 2011, 20, 513-528. | 7.6 | 41 |
| 8 | Zernike Phase Contrast Cryo-Electron Microscopy and Tomography for Structure Determination at Nanometer and Subnanometer Resolutions. <i>Structure</i> , 2010, 18, 903-912. | 3.3 | 118 |
| 9 | Ubiquitin Proteasome Pathway-Mediated Degradation of Proteins: Effects Due to Site-Specific Substrate Deamidation. , 2010, 51, 4164. | | 30 |
| 10 | Formation of Amyloid Fibrils In Vitro from Partially Unfolded Intermediates of Human β -Crystallin. , 2010, 51, 672. | | 70 |
| 11 | Partially Folded Aggregation Intermediates of Human β -, β -, and β -Crystallin Are Recognized and Bound by Human I β -Crystallin Chaperone. <i>Journal of Molecular Biology</i> , 2010, 401, 134-152. | 4.2 | 61 |
| 12 | Hydrophobic Core Mutations Associated with Cataract Development in Mice Destabilize Human β -Crystallin. <i>Journal of Biological Chemistry</i> , 2009, 284, 33285-33295. | 3.4 | 50 |
| 13 | Mechanism of the Very Efficient Quenching of Tryptophan Fluorescence in Human β - and β -Crystallins: The β -Crystallin Fold May Have Evolved To Protect Tryptophan Residues from Ultraviolet Photodamage. <i>Biochemistry</i> , 2009, 48, 3708-3716. | 2.5 | 84 |
| 14 | Femtosecond Fluorescence Spectra of Tryptophan in Human β -Crystallin Mutants: Site-Dependent Ultrafast Quenching. <i>Journal of the American Chemical Society</i> , 2009, 131, 16751-16757. | 13.7 | 44 |
| 15 | The Structure of the Cataract-Causing P23T Mutant of Human β -Crystallin Exhibits Distinctive Local Conformational and Dynamic Changes. , <i>Biochemistry</i> , 2009, 48, 2597-2609. | 2.5 | 57 |
| 16 | Backbone structure of the infectious μ 15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008, 451, 1130-1134. | 27.8 | 204 |
| 17 | Mechanism of the Efficient Tryptophan Fluorescence Quenching in Human β -Crystallin Studied by Time-Resolved Fluorescence. <i>Biochemistry</i> , 2008, 47, 10705-10721. | 2.5 | 54 |
| 18 | Human β crystallins form fibrillar amyloid aggregates through a partially unfolded intermediate. <i>FASEB Journal</i> , 2008, 22, 1010.3. | 0.5 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Mutations associated with early cataract development in mice destabilize human gammaD-crySTALLIN. FASEB Journal, 2008, 22, 232-232. | 0.5 | 0 |
| 20 | Formation of amyloid fibrils in vitro by human gammaD-crySTALLIN and its isolated domains. Molecular Vision, 2008, 14, 81-9. | 1.1 | 61 |
| 21 | Genome Sequence, Structural Proteins, and Capsid Organization of the Cyanophage Syn5: A Horned Bacteriophage of Marine Synechococcus. Journal of Molecular Biology, 2007, 368, 966-981. | 4.2 | 92 |
| 22 | Genomic and structural analysis of Syn9, a cyanophage infecting marine Prochlorococcus and Synechococcus. Environmental Microbiology, 2007, 9, 1675-1695. | 3.8 | 158 |
| 23 | Mechanism of the Highly Efficient Quenching of Tryptophan Fluorescence in Human I ³ D-CrySTALLIN. Biochemistry, 2006, 45, 11552-11563. | 2.5 | 86 |
| 24 | Fold recognition and accurate sequence-structure alignment of sequences directing I ² -sheet proteins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 976-985. | 2.6 | 24 |
| 25 | Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. Nature, 2006, 439, 612-616. | 27.8 | 280 |
| 26 | Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. Protein Science, 2006, 15, 102-112. | 7.6 | 42 |
| 27 | Cryo-EM Asymmetric Reconstruction of Bacteriophage P22 Reveals Organization of its DNA Packaging and Infecting Machinery. Structure, 2006, 14, 1073-1082. | 3.3 | 149 |
| 28 | An elongated spine of buried core residues necessary for in vivo folding of the parallel beta-helix of P22 tailspike adhesin. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3575-3580. | 7.1 | 29 |
| 29 | Glutamine Deamidation Destabilizes Human I ³ D-CrySTALLIN and Lowers the Kinetic Barrier to Unfolding. Journal of Biological Chemistry, 2006, 281, 30782-30793. | 3.4 | 108 |
| 30 | Amino Acid Sequence Control of the Folding of the Parallel I ² -Helix, the Simplest I ² -Sheet Fold. Lecture Notes in Computer Science, 2005, , 472-473. | 1.3 | 0 |
| 31 | Interdomain side-chain interactions in human I ³ D crySTALLIN influencing folding and stability. Protein Science, 2005, 14, 2030-2043. | 7.6 | 92 |
| 32 | Aggregation of granulocyte-colony stimulating factor in vitro involves a conformationally altered monomeric state. Protein Science, 2005, 14, 2246-2257. | 7.6 | 102 |
| 33 | Monoclonal Antibody Epitope Mapping Describes Tailspike I ² -Helix Folding and Aggregation Intermediates. Journal of Biological Chemistry, 2005, 280, 23032-23040. | 3.4 | 10 |
| 34 | Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils. Journal of Computational Biology, 2005, 12, 777-795. | 1.6 | 8 |
| 35 | Lattice Transformations and Subunit Conformational Changes in Phage Capsid Maturation. Journal of Theoretical Medicine, 2005, 6, 99-105. | 0.5 | 1 |
| 36 | Stalled Folding Mutants in the Triple I ² -Helix Domain of the Phage P22 Tailspike Adhesin. Journal of Molecular Biology, 2005, 354, 1103-1117. | 4.2 | 6 |

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| 37 | Contributions of hydrophobic domain interface interactions to the folding and stability of human γ D-crystallin. <i>Protein Science</i> , 2005, 14, 569-581. | 7.6 | 93 |
| 38 | Protein Folding Failure Sets High-Temperature Limit on Growth of Phage P22 in <i>Salmonella enterica</i> Serovar Typhimurium. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4840-4847. | 3.1 | 17 |
| 39 | Wrap-and-pack. , 2004, , . | | 2 |
| 40 | Buried hydrophobic side-chains essential for the folding of the parallel β -helix domains of the P22 tailspike. <i>Protein Science</i> , 2004, 13, 2291-2303. | 7.6 | 16 |
| 41 | Probing folding and fluorescence quenching in human γ D crystallin Greek key domains using triple tryptophan mutant proteins. <i>Protein Science</i> , 2004, 13, 2223-2235. | 7.6 | 92 |
| 42 | In vitro unfolding, refolding, and polymerization of human gammaD crystallin, a protein involved in cataract formation. <i>Protein Science</i> , 2003, 12, 480-490. | 7.6 | 156 |
| 43 | Homotrimeric, β -Stranded Viral Adhesins and Tail Proteins. <i>Journal of Bacteriology</i> , 2003, 185, 4022-4030. | 2.2 | 57 |
| 44 | Predicting the Beta-Helix Fold from Protein Sequence Data. <i>Journal of Computational Biology</i> , 2002, 9, 261-276. | 1.6 | 37 |
| 45 | Characterization of the Protrimer Intermediate in the Folding Pathway of the Interdigitated β -Helix Tailspike Protein. <i>Biochemistry</i> , 2002, 41, 5093-5103. | 2.5 | 22 |
| 46 | Cyanobacterial photosynthesis in the oceans: the origins and significance of divergent light-harvesting strategies. <i>Trends in Microbiology</i> , 2002, 10, 134-142. | 7.7 | 305 |
| 47 | The interdigitated beta-helix domain of the P22 tailspike protein acts as a molecular clamp in trimer stabilization. <i>Protein Science</i> , 2002, 11, 820-830. | 7.6 | 32 |
| 48 | Distinct cysteine sulfhydryl environments detected by analysis of Raman S-H markers of Cys ¹¹ Ser mutant proteins. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 307, 899-911. | 4.2 | 90 |
| 49 | Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. <i>Protein Science</i> , 2001, 10, 1023-1031. | 7.6 | 83 |
| 50 | Role for cysteine residues in the in vivo folding and assembly of the phage P22 tailspike. <i>Protein Science</i> , 2001, 10, 397-410. | 7.6 | 28 |
| 51 | A Newly Synthesized, Ribosome-bound Polypeptide Chain Adopts Conformations Dissimilar from Early in Vitro Refolding Intermediates. <i>Journal of Biological Chemistry</i> , 2001, 276, 25411-25420. | 3.4 | 71 |
| 52 | Phycobiliprotein genes of the marine photosynthetic prokaryote <i>Prochlorococcus</i> : evidence for rapid evolution of genetic heterogeneity. <i>Microbiology (United Kingdom)</i> , 2001, 147, 3171-3182. | 1.8 | 33 |
| 53 | β -Helix core packing within the triple-stranded oligomerization domain of the P22 tailspike. <i>Protein Science</i> , 2000, 9, 2338-2343. | 7.6 | 24 |
| 54 | Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. <i>Journal of Molecular Biology</i> , 2000, 297, 615-626. | 4.2 | 68 |

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| 55 | In Vitro Unfolding/Refolding of Wild Type Phage P22 Scaffolding Protein Reveals Capsid-binding Domain. <i>Journal of Biological Chemistry</i> , 1999, 274, 16135-16140. | 3.4 | 19 |
| 56 | Folding and Stability of Mutant Scaffolding Proteins Defective in P22 Capsid Assembly. <i>Journal of Biological Chemistry</i> , 1999, 274, 16141-16146. | 3.4 | 8 |
| 57 | A green light for protein folding. <i>Nature Biotechnology</i> , 1999, 17, 637-638. | 17.5 | 6 |
| 58 | There's a right way and a wrong way: in vivo and in vitro folding, misfolding and subunit assembly of the P22 tailspike. <i>Structure</i> , 1999, 7, R131-R139. | 3.3 | 76 |
| 59 | [22] Detection of early aggregation intermediates by native gel electrophoresis and native Western blotting. <i>Methods in Enzymology</i> , 1999, 309, 333-350. | 1.0 | 21 |
| 60 | Solution X-Ray Scattering-Based Estimation of Electron Cryomicroscopy Imaging Parameters for Reconstruction of Virus Particles. <i>Biophysical Journal</i> , 1999, 76, 2249-2261. | 0.5 | 34 |
| 61 | Effects of Oxygen on Recombinant Protein Expression. <i>Biotechnology Progress</i> , 1998, 14, 393-409. | 2.6 | 73 |
| 62 | Cold rescue of the thermolabile tailspike intermediate at the junction between productive folding and off-pathway aggregation. <i>Protein Science</i> , 1998, 7, 1516-1523. | 7.6 | 36 |
| 63 | Role of the Scaffolding Protein in P22 Procapsid Size Determination Suggested by T=4 and T=7 Procapsid Structures. <i>Biophysical Journal</i> , 1998, 74, 559-568. | 0.5 | 90 |
| 64 | Mutational Effects on Inclusion Body Formation. <i>Advances in Protein Chemistry</i> , 1997, 50, 243-264. | 4.4 | 39 |
| 65 | Prevalence of temperature sensitive folding mutations in the parallel beta coil domain of the phage P22 tailspike endorhamnosidase. <i>Journal of Molecular Biology</i> , 1997, 267, 88-102. | 4.2 | 48 |
| 66 | Monitoring the refolding pathway for a large multimeric protein using capillary zone electrophoresis. <i>Journal of Chromatography A</i> , 1997, 769, 315-323. | 3.7 | 19 |
| 67 | Disulphide-bonded intermediate on the folding and assembly pathway of a non-disulphide bonded protein. <i>Nature Structural Biology</i> , 1997, 4, 450-455. | 9.7 | 57 |
| 68 | Refolding with a piece of the ring. <i>Nature Biotechnology</i> , 1997, 15, 514-515. | 17.5 | 3 |
| 69 | Conformation of P22 tailspike folding and aggregation intermediates probed by monoclonal antibodies. <i>Protein Science</i> , 1997, 6, 99-108. | 7.6 | 65 |
| 70 | Polymerization mechanism of polypeptide chain aggregation. , 1997, 54, 333-343. | | 83 |
| 71 | Polymerization mechanism of polypeptide chain aggregation. <i>Biotechnology and Bioengineering</i> , 1997, 54, 333-343. | 3.3 | 1 |
| 72 | Three-dimensional Structure of Scaffolding-containing Phage P22 Procapsids by Electron Cryo-microscopy. <i>Journal of Molecular Biology</i> , 1996, 260, 85-98. | 4.2 | 97 |

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| 73 | Thermolabile folding intermediates: inclusion body precursors and chaperonin substrates. FASEB Journal, 1996, 10, 57-66. | 0.5 | 151 |
| 74 | Scaffolding Mutants Identifying Domains Required for P22 Procapsid Assembly and Maturation. Virology, 1996, 225, 82-96. | 2.4 | 60 |
| 75 | Unexpected pathways to protein stabilization. Nature Biotechnology, 1996, 14, 436-436. | 17.5 | 2 |
| 76 | Specific aggregation of partially folded polypeptide chains: The molecular basis of inclusion body composition. Nature Biotechnology, 1996, 14, 1283-1287. | 17.5 | 301 |
| 77 | Stability of Wild-type and Temperature-sensitive Protein Subunits of the Phage P22 Capsid. Journal of Biological Chemistry, 1995, 270, 16595-16601. | 3.4 | 27 |
| 78 | In vitro folding of phage P22 coat protein with amino acid substitutions that confer in vivo temperature sensitivity. Biochemistry, 1995, 34, 6815-6826. | 2.5 | 32 |
| 79 | Multimeric intermediates in the pathway to the aggregated inclusion body state for P22 tailspike polypeptide chains. Protein Science, 1995, 4, 900-908. | 7.6 | 81 |
| 80 | Binding of Scaffolding Subunits within the P22 Procapsid Lattice. Virology, 1994, 205, 188-197. | 2.4 | 51 |
| 81 | Three-dimensional Transformation of Capsids Associated with Genome Packaging in a Bacterial Virus. Journal of Molecular Biology, 1993, 231, 65-74. | 4.2 | 163 |
| 82 | Inhibition of viral capsid assembly by 1,1'-bis(4-anilinonaphthalene-5-sulfonic acid). Biochemistry, 1993, 32, 10658-10665. | 2.5 | 66 |
| 83 | Folding of the phage P22 coat protein in vitro. Biochemistry, 1993, 32, 10839-10847. | 2.5 | 57 |
| 84 | Amino Acid Sequence Determinants of Polypeptide Chain Folding and Inclusion Body Formation. ACS Symposium Series, 1993, , 24-37. | 0.5 | 2 |
| 85 | Amino acid substitutions influencing intracellular protein folding pathways. FEBS Letters, 1992, 307, 20-25. | 2.8 | 49 |
| 86 | Folding and assembly of oligomeric proteins in Escherichia coli. Current Opinion in Biotechnology, 1992, 3, 468-473. | 6.6 | 32 |
| 87 | Mechanisms of Inclusion Body Formation. ACS Symposium Series, 1991, , 35-49. | 0.5 | 19 |
| 88 | Thermal unfolding pathway for the thermostable P22 tailspike endorhamnosidase. Biochemistry, 1991, 30, 6260-6269. | 2.5 | 67 |
| 89 | Pathway for the Thermal Unfolding of Wild Type and Mutant Forms of the Thermostable P22 Tailspike Endorhamnosidase. ACS Symposium Series, 1991, , 119-132. | 0.5 | 3 |
| 90 | Mutations Affecting Protein Folding and Misfolding in Vivo. , 1991, , 129-136. | | 1 |

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| 91 | Conformational states of the bacteriophage P22 capsid subunit in relation to self-assembly. <i>Biochemistry</i> , 1990, 29, 5626-5633. | 2.5 | 34 |
| 92 | Conformational stability of P22 tailspike proteins carrying temperature-sensitive folding mutations. <i>Biochemistry</i> , 1990, 29, 4181-4187. | 2.5 | 39 |
| 93 | Novel second-site suppression of a cold-sensitive defect in phage P22 procapsid assembly. <i>Journal of Molecular Biology</i> , 1990, 216, 701-716. | 4.2 | 28 |
| 94 | Genetic Analysis of Polypeptide Chain Folding and Misfolding in Vivo. , 1990, , 59-78. | | 4 |
| 95 | Protein Folding Intermediates and Inclusion Body Formation.. <i>Nature Biotechnology</i> , 1989, 7, 690-697. | 17.5 | 273 |
| 96 | Purification and organization of the gene 1 portal protein required for phage P22 DNA packaging. <i>Biochemistry</i> , 1988, 27, 1849-1856. | 2.5 | 83 |
| 97 | Scaffolding protein regulates the polymerization of P22 coat subunits into icosahedral shells in vitro. <i>Journal of Molecular Biology</i> , 1988, 202, 743-757. | 4.2 | 186 |
| 98 | Initiation of P22 procapsid assembly in vivo. <i>Journal of Molecular Biology</i> , 1988, 202, 77-86. | 4.2 | 76 |
| 99 | Secondary structure and thermostability of the phage P22 tailspike. <i>Journal of Molecular Biology</i> , 1988, 199, 491-502. | 4.2 | 66 |
| 100 | Nature and distribution of sites of temperature-sensitive folding mutations in the gene for the P22 Tailspike polypeptide chain. <i>Journal of Molecular Biology</i> , 1988, 204, 607-619. | 4.2 | 68 |
| 101 | Aggregate formation from thermolabile intermediates in the maturation of the thermostable P22 tailspike. <i>Biochemical Society Transactions</i> , 1988, 16, 105-108. | 3.4 | 4 |
| 102 | Identification of Sites Influencing the Folding and Subunit Assembly of the P22 Tailspike Polypeptide Chain Using Nonsense Mutations. <i>Genetics</i> , 1987, 117, 157-171. | 2.9 | 33 |
| 103 | The DNA Injection Apparatus of Phage P22. <i>Biophysical Journal</i> , 1986, 49, 24-26. | 0.5 | 22 |
| 104 | Identification of the 9-aminoacridine/DNA complex responsible for photodynamic inactivation of P22. <i>Biochemistry</i> , 1986, 25, 5858-5864. | 2.5 | 13 |
| 105 | Genetic Analysis of Protein Folding Pathways. <i>Nature Biotechnology</i> , 1986, 4, 297-303. | 17.5 | 36 |
| 106 | [13]Mutational analysis of protein folding pathways: The P22 tailspike endorhamnosidase. <i>Methods in Enzymology</i> , 1986, 131, 250-266. | 1.0 | 55 |
| 107 | A late gene product of phage P22 affecting virus infectivity. <i>Virology</i> , 1985, 143, 368-379. | 2.4 | 7 |
| 108 | Steps in the stabilization of newly packaged DNA during phage P22 Morphogenesis. <i>Journal of Molecular Biology</i> , 1984, 172, 523-543. | 4.2 | 84 |

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| 109 | DNA injection proteins are targets of acridine-sensitized photoinactivation of bacteriophage P22. <i>Journal of Molecular Biology</i> , 1984, 180, 837-863. | 4.2 | 30 |
| 110 | Genetic and biochemical analysis of in vivo protein folding and subunit assembly. <i>Biopolymers</i> , 1983, 22, 125-129. | 2.4 | 9 |
| 111 | The Use of Salmonella Bacteriophage P22 to Study the Multiple Mechanisms of Acridine-Induced Damage. , 1983, , 79-109. | | 0 |
| 112 | The Legal and Legislative Background. <i>Environment</i> , 1982, 24, 24-36. | 1.4 | 0 |
| 113 | Assembly in vitro of bacteriophage P22 procapsids from purified coat and scaffolding subunits. <i>Journal of Molecular Biology</i> , 1982, 156, 633-665. | 4.2 | 65 |
| 114 | Structural studies of P22 phage, precursor particles, and proteins by laser Raman spectroscopy. <i>Biochemistry</i> , 1982, 21, 3866-3878. | 2.5 | 42 |
| 115 | Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail spike protein. <i>Journal of Molecular Biology</i> , 1981, 145, 633-651. | 4.2 | 117 |
| 116 | Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail spike protein. <i>Journal of Molecular Biology</i> , 1981, 145, 653-676. | 4.2 | 81 |
| 117 | Purification of the coat and scaffolding proteins from procapsids of bacteriophage P22. <i>Virology</i> , 1981, 112, 529-547. | 2.4 | 65 |
| 118 | Introduction: From Genes to Organelles. <i>Quarterly Review of Biology</i> , 1980, 55, 329-333. | 0.1 | 0 |
| 119 | Scaffolding Proteins and the Genetic Control of Virus Shell Assembly. <i>Quarterly Review of Biology</i> , 1980, 55, 369-393. | 0.1 | 20 |
| 120 | Investigation of secondary structures and macromolecular interactions in bacteriophage p22 by laser raman spectroscopy. <i>Biophysical Journal</i> , 1980, 32, 234-237. | 0.5 | 6 |
| 121 | Regulation of Structural Protein Interactions as Revealed in Phage Morphogenesis. , 1980, , 101-132. | | 23 |
| 122 | TEMPERATURE-SENSITIVE MUTANTS BLOCKED IN THE FOLDING OR SUBUNIT ASSMBLY OF THE BACTERIOPHAGE P22 TAILSPIKE PROTEIN. I. FINE-STRUCTURE MAPPING. <i>Genetics</i> , 1980, 96, 331-352. | 2.9 | 68 |
| 123 | Structural studies of bacteriophage lambda heads and proheads by small angle X-ray diffraction. <i>Journal of Molecular Biology</i> , 1979, 134, 575-594. | 4.2 | 36 |
| 124 | Genetic Control of Complex Bacteriophage Assembly. , 1979, , 581-633. | | 15 |
| 125 | Control of the synthesis of phage p22 scaffolding protein is coupled to capsid assembly. <i>Cell</i> , 1978, 15, 551-560. | 28.9 | 57 |
| 126 | Structure of phage P22 coat protein aggregates formed in the absence of the scaffolding protein. <i>Journal of Molecular Biology</i> , 1978, 126, 721-747. | 4.2 | 115 |

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| 127 | The size of the bacteriophage T4 head in solution with comments about the dimension of virus particles as visualized by electron microscopy. <i>Journal of Molecular Biology</i> , 1978, 122, 247-253. | 4.2 | 30 |
| 128 | Isolation and characterization of precursors in T4 baseplate assembly the complex of gene 10 and gene 11 products. <i>Journal of Molecular Biology</i> , 1978, 124, 469-486. | 4.2 | 24 |
| 129 | Antigenic gene products of bacteriophage T4 baseplates. <i>Virology</i> , 1978, 86, 312-328. | 2.4 | 10 |
| 130 | Molecular reorganization in the hexagon to star transition of the baseplate of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1977, 116, 489-523. | 4.2 | 112 |
| 131 | Functions of two new genes in <i>Salmonella</i> phage P22 assembly. <i>Virology</i> , 1977, 76, 725-739. | 2.4 | 93 |
| 132 | Assembly of the tail of bacteriophage T4. <i>Journal of Supramolecular Structure</i> , 1975, 3, 24-38. | 2.3 | 16 |
| 133 | Harvard XYY study. <i>Science</i> , 1975, 187, 298-299. | 12.6 | 10 |
| 134 | Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 645-672. | 4.2 | 123 |
| 135 | Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 673-694. | 4.2 | 98 |
| 136 | Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 695-716. | 4.2 | 142 |
| 137 | Intracellular visualization of precursor capsids in phage P22 mutant infected cells. <i>Virology</i> , 1975, 68, 182-199. | 2.4 | 79 |
| 138 | P22 morphogenesis I: Catalytic scaffolding protein in capsid assembly. <i>Journal of Supramolecular Structure</i> , 1974, 2, 202-224. | 2.3 | 173 |
| 139 | Catalytic head assembling protein in virus morphogenesis. <i>Nature</i> , 1974, 251, 112-119. | 27.8 | 218 |
| 140 | Bacteriophage T4 tail assembly: Structural proteins and their genetic identification. <i>Journal of Molecular Biology</i> , 1973, 75, 315-337. | 4.2 | 97 |
| 141 | Bacteriophage T4 tail assembly: Proteins of the sheath, core and baseplate. <i>Journal of Molecular Biology</i> , 1973, 75, 339-358. | 4.2 | 106 |
| 142 | Mechanism of head assembly and DNA encapsulation in <i>Salmonella</i> phage P22. <i>Journal of Molecular Biology</i> , 1973, 80, 669-695. | 4.2 | 313 |
| 143 | Mechanism of head assembly and DNA encapsulation in <i>Salmonella</i> phage P22. <i>Journal of Molecular Biology</i> , 1973, 80, 697-731. | 4.2 | 236 |
| 144 | Genetic Identification of Amino Acid Sequences Influencing Protein Folding. , 1973, , 275-291. | | 4 |

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| 145 | Polypeptides of the tail fibres of bacteriophage T4. Journal of Molecular Biology, 1971, 62, 465-477. | 4.2 | 970 |
| 146 | Bacteriophage T4 tail assembly: Four steps in core formation. Journal of Molecular Biology, 1971, 58, 693-709. | 4.2 | 92 |
| 147 | Assembly of bacteriophage T4 tail fibers: The sequence of gene product interaction. Journal of Molecular Biology, 1969, 39, 583-601. | 4.2 | 78 |
| 148 | Assembly of the tau of bacteriophage T4. Journal of Molecular Biology, 1968, 32, 231-262. | 4.2 | 283 |