

Jonathan King

List of Publications by Citations

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|--------------------|-------------------------|----------------|-----------------|
| 145 papers | 9,216 citations | 59 h-index | 92 g-index |
| 149 ext. papers | 9,624 ext. citations | 8.4 avg, IF | 5.78 L-index |

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 145 | Polypeptides of the tail fibres of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1971 , 62, 465-77 | 6.5 | 872 |
| 144 | Specific aggregation of partially folded polypeptide chains: the molecular basis of inclusion body composition. <i>Nature Biotechnology</i> , 1996 , 14, 1283-7 | 44.5 | 277 |
| 143 | Cyanobacterial photosynthesis in the oceans: the origins and significance of divergent light-harvesting strategies. <i>Trends in Microbiology</i> , 2002 , 10, 134-42 | 12.4 | 267 |
| 142 | Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. <i>Nature</i> , 2006 , 439, 612-6 | 50.4 | 258 |
| 141 | Mechanism of head assembly and DNA encapsulation in Salmonella phage p22. I. Genes, proteins, structures and DNA maturation. <i>Journal of Molecular Biology</i> , 1973 , 80, 669-95 | 6.5 | 253 |
| 140 | Assembly of the tail of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1968 , 32, 231-62 | 6.5 | 227 |
| 139 | Mechanism of head assembly and DNA encapsulation in Salmonella phage P22. II. Morphogenetic pathway. <i>Journal of Molecular Biology</i> , 1973 , 80, 697-731 | 6.5 | 203 |
| 138 | Protein Folding Intermediates and Inclusion Body Formation.. <i>Nature Biotechnology</i> , 1989 , 7, 690-697 | 44.5 | 196 |
| 137 | Backbone structure of the infectious epsilon15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008 , 451, 1130-4 | 50.4 | 188 |
| 136 | Catalytic head assembling protein in virus morphogenesis. <i>Nature</i> , 1974 , 251, 112-9 | 50.4 | 182 |
| 135 | Scaffolding protein regulates the polymerization of P22 coat subunits into icosahedral shells in vitro. <i>Journal of Molecular Biology</i> , 1988 , 202, 743-57 | 6.5 | 167 |
| 134 | Three-dimensional transformation of capsids associated with genome packaging in a bacterial virus. <i>Journal of Molecular Biology</i> , 1993 , 231, 65-74 | 6.5 | 151 |
| 133 | P22 morphogenesis. I: Catalytic scaffolding protein in capsid assembly. <i>Journal of Supramolecular Structure</i> , 1974 , 2, 202-24 | | 146 |
| 132 | Genomic and structural analysis of Syn9, a cyanophage infecting marine Prochlorococcus and Synechococcus. <i>Environmental Microbiology</i> , 2007 , 9, 1675-95 | 5.2 | 139 |
| 131 | Thermolabile folding intermediates: inclusion body precursors and chaperonin substrates. <i>FASEB Journal</i> , 1996 , 10, 57-66 | 0.9 | 138 |
| 130 | Cryo-EM asymmetric reconstruction of bacteriophage P22 reveals organization of its DNA packaging and infecting machinery. <i>Structure</i> , 2006 , 14, 1073-82 | 5.2 | 136 |
| 129 | In vitro unfolding, refolding, and polymerization of human gammaD crystallin, a protein involved in cataract formation. <i>Protein Science</i> , 2003 , 12, 480-90 | 6.3 | 136 |

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| 128 | Genetic control of bacteriophage T4 baseplate morphogenesis. III. Formation of the central plug and overall assembly pathway. <i>Journal of Molecular Biology</i> , 1975 , 99, 695-716 | 6.5 | 114 |
| 127 | Zernike phase contrast cryo-electron microscopy and tomography for structure determination at nanometer and subnanometer resolutions. <i>Structure</i> , 2010 , 18, 903-12 | 5.2 | 110 |
| 126 | Temperature-sensitive mutants blocked in the folding or subunit of the bacteriophage P22 tail spike protein. II. Active mutant proteins matured at 30 degrees C. <i>Journal of Molecular Biology</i> , 1981 , 145, 633-51 | 6.5 | 101 |
| 125 | Structure of phage P22 coat protein aggregates formed in the absence of the scaffolding protein. <i>Journal of Molecular Biology</i> , 1978 , 126, 721-47 | 6.5 | 101 |
| 124 | Genetic control of bacteriophage T4 baseplate morphogenesis. I. Sequential assembly of the major precursor, in vivo and in vitro. <i>Journal of Molecular Biology</i> , 1975 , 99, 645-72 | 6.5 | 99 |
| 123 | Glutamine deamidation destabilizes human gammaD-crystallin and lowers the kinetic barrier to unfolding. <i>Journal of Biological Chemistry</i> , 2006 , 281, 30782-93 | 5.4 | 97 |
| 122 | Molecular reorganization in the hexagon to star transition of the baseplate of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1977 , 116, 489-523 | 6.5 | 94 |
| 121 | Aggregation of granulocyte-colony stimulating factor in vitro involves a conformationally altered monomeric state. <i>Protein Science</i> , 2005 , 14, 2246-57 | 6.3 | 89 |
| 120 | Three-dimensional structure of scaffolding-containing phage p22 procapsids by electron cryo-microscopy. <i>Journal of Molecular Biology</i> , 1996 , 260, 85-98 | 6.5 | 88 |
| 119 | Probing folding and fluorescence quenching in human gammaD crystallin Greek key domains using triple tryptophan mutant proteins. <i>Protein Science</i> , 2004 , 13, 2223-35 | 6.3 | 87 |
| 118 | Contributions of hydrophobic domain interface interactions to the folding and stability of human gammaD-crystallin. <i>Protein Science</i> , 2005 , 14, 569-81 | 6.3 | 85 |
| 117 | Bacteriophage T4 tail assembly: structural proteins and their genetic identification. <i>Journal of Molecular Biology</i> , 1973 , 75, 315-37 | 6.5 | 82 |
| 116 | Bacteriophage T4 tail assembly: proteins of the sheath, core and baseplate. <i>Journal of Molecular Biology</i> , 1973 , 75, 339-58 | 6.5 | 82 |
| 115 | Mechanism of the highly efficient quenching of tryptophan fluorescence in human gammaD-crystallin. <i>Biochemistry</i> , 2006 , 45, 11552-63 | 3.2 | 81 |
| 114 | Interdomain side-chain interactions in human gammaD crystallin influencing folding and stability. <i>Protein Science</i> , 2005 , 14, 2030-43 | 6.3 | 81 |
| 113 | Distinct cysteine sulfhydryl environments detected by analysis of Raman S-hh markers of Cys-->Ser mutant proteins. <i>Journal of Molecular Biology</i> , 2001 , 307, 899-911 | 6.5 | 81 |
| 112 | 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, 559-68 | 2.9 | 81 |
| 111 | Bacteriophage T4 tail assembly: four steps in core formation. <i>Journal of Molecular Biology</i> , 1971 , 58, 693-709 | 6.9 | 80 |

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| 110 | Steps in the stabilization of newly packaged DNA during phage P22 morphogenesis. <i>Journal of Molecular Biology</i> , 1984 , 172, 523-43 | 6.5 | 79 |
| 109 | Genome sequence, structural proteins, and capsid organization of the cyanophage Syn5: a "horned" bacteriophage of marine synechococcus. <i>Journal of Molecular Biology</i> , 2007 , 368, 966-81 | 6.5 | 78 |
| 108 | Purification and organization of the gene 1 portal protein required for phage P22 DNA packaging. <i>Biochemistry</i> , 1988 , 27, 1849-56 | 3.2 | 78 |
| 107 | Genetic control of bacteriophage T4 baseplate morphogenesis. II. Mutants unable to form the central part of the baseplate. <i>Journal of Molecular Biology</i> , 1975 , 99, 673-94 | 6.5 | 78 |
| 106 | Mechanism of the very efficient quenching of tryptophan fluorescence in human gamma D- and gamma S-crystallins: the gamma-crystallin fold may have evolved to protect tryptophan residues from ultraviolet photodamage. <i>Biochemistry</i> , 2009 , 48, 3708-16 | 3.2 | 77 |
| 105 | Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. <i>Protein Science</i> , 2001 , 10, 1023-31 | 6.3 | 76 |
| 104 | Multimeric intermediates in the pathway to the aggregated inclusion body state for P22 tailspike polypeptide chains. <i>Protein Science</i> , 1995 , 4, 900-8 | 6.3 | 75 |
| 103 | Functions of two new genes in Salmonella phage P22 assembly. <i>Virology</i> , 1977 , 76, 725-39 | 3.6 | 75 |
| 102 | Polymerization mechanism of polypeptide chain aggregation. <i>Biotechnology and Bioengineering</i> , 1997 , 54, 333-43 | 4.9 | 73 |
| 101 | Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail spike protein. III. Intensive polypeptide chains synthesized at 39 degrees C. <i>Journal of Molecular Biology</i> , 1981 , 145, 653-76 | 6.5 | 72 |
| 100 | Assembly of bacteriophage T4 tail fibers: the sequence of gene product interaction. <i>Journal of Molecular Biology</i> , 1969 , 39, 583-601 | 6.5 | 72 |
| 99 | Initiation of P22 procapsid assembly in vivo. <i>Journal of Molecular Biology</i> , 1988 , 202, 77-86 | 6.5 | 69 |
| 98 | Intracellular visualization of precursor capsids in phage P22 mutant infected cells. <i>Virology</i> , 1975 , 68, 182-99 | 3.6 | 67 |
| 97 | 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, R131-9 | 5.2 | 66 |
| 96 | Formation of amyloid fibrils in vitro from partially unfolded intermediates of human gammaC-crystallin 2010 , 51, 672-8 | | 65 |
| 95 | A newly synthesized, ribosome-bound polypeptide chain adopts conformations dissimilar from early in vitro refolding intermediates. <i>Journal of Biological Chemistry</i> , 2001 , 276, 25411-20 | 5.4 | 64 |
| 94 | Inhibition of viral capsid assembly by 1,1'-(4-anilino)naphthalene-5-sulfonic acid). <i>Biochemistry</i> , 1993 , 32, 10658-65 | 3.2 | 63 |
| 93 | Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. <i>Journal of Molecular Biology</i> , 2000 , 297, 615-26 | 6.5 | 62 |

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| 92 | Thermal unfolding pathway for the thermostable P22 tailspike endorhamnosidase. <i>Biochemistry</i> , 1991 , 30, 6260-9 | 3.2 | 62 |
| 91 | Assembly in vitro of bacteriophage P22 procapsids from purified coat and scaffolding subunits. <i>Journal of Molecular Biology</i> , 1982 , 156, 633-65 | 6.5 | 62 |
| 90 | 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, 607-19 | 6.5 | 61 |
| 89 | Purification of the coat and scaffolding proteins from procapsids of bacteriophage P22. <i>Virology</i> , 1981 , 112, 529-47 | 3.6 | 61 |
| 88 | Conformation of P22 tailspike folding and aggregation intermediates probed by monoclonal antibodies. <i>Protein Science</i> , 1997 , 6, 99-108 | 6.3 | 60 |
| 87 | Formation of amyloid fibrils in vitro by human gammaD-crystallin and its isolated domains. <i>Molecular Vision</i> , 2008 , 14, 81-9 | 2.3 | 60 |
| 86 | Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail-spike protein. I. Fine-structure mapping. <i>Genetics</i> , 1980 , 96, 331-52 | 4 | 58 |
| 85 | Effects of oxygen on recombinant protein expression. <i>Biotechnology Progress</i> , 1998 , 14, 393-409 | 2.8 | 56 |
| 84 | Folding of the phage P22 coat protein in vitro. <i>Biochemistry</i> , 1993 , 32, 10839-47 | 3.2 | 56 |
| 83 | Secondary structure and thermostability of the phage P22 tailspike. XX. Analysis by Raman spectroscopy of the wild-type protein and a temperature-sensitive folding mutant. <i>Journal of Molecular Biology</i> , 1988 , 199, 491-502 | 6.5 | 56 |
| 82 | Partially folded aggregation intermediates of human gammaD-, gammaC-, and gammaS-crystallin are recognized and bound by human alphaB-crystallin chaperone. <i>Journal of Molecular Biology</i> , 2010 , 401, 134-52 | 6.5 | 55 |
| 81 | Scaffolding mutants identifying domains required for P22 procapsid assembly and maturation. <i>Virology</i> , 1996 , 225, 82-96 | 3.6 | 55 |
| 80 | Disulphide-bonded intermediate on the folding and assembly pathway of a non-disulphide bonded protein. <i>Nature Structural Biology</i> , 1997 , 4, 450-5 | | 53 |
| 79 | The structure of the cataract-causing P23T mutant of human gammaD-crystallin exhibits distinctive local conformational and dynamic changes. <i>Biochemistry</i> , 2009 , 48, 2597-609 | 3.2 | 51 |
| 78 | Mechanism of the efficient tryptophan fluorescence quenching in human gammaD-crystallin studied by time-resolved fluorescence. <i>Biochemistry</i> , 2008 , 47, 10705-21 | 3.2 | 50 |
| 77 | Control of the synthesis of phage P22 scaffolding protein is coupled to capsid assembly. <i>Cell</i> , 1978 , 15, 551-60 | 56.2 | 49 |
| 76 | Mutational analysis of protein folding pathways: the P22 tailspike endorhamnosidase. <i>Methods in Enzymology</i> , 1986 , 131, 250-66 | 1.7 | 47 |
| 75 | Amino acid substitutions influencing intracellular protein folding pathways. <i>FEBS Letters</i> , 1992 , 307, 20-5.8 | | 45 |

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| 74 | Hydrophobic core mutations associated with cataract development in mice destabilize human gammaD-crystallin. <i>Journal of Biological Chemistry</i> , 2009 , 284, 33285-95 | 5.4 | 44 |
| 73 | Binding of scaffolding subunits within the P22 procapsid lattice. <i>Virology</i> , 1994 , 205, 188-97 | 3.6 | 44 |
| 72 | 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 | 6.5 | 43 |
| 71 | Homotrimeric, beta-stranded viral adhesins and tail proteins. <i>Journal of Bacteriology</i> , 2003 , 185, 4022-30 | 3.5 | 43 |
| 70 | Structural studies of P22 phage, precursor particles, and proteins by laser Raman spectroscopy. <i>Biochemistry</i> , 1982 , 21, 3866-78 | 3.2 | 38 |
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| 68 | Cataract. <i>Nature Reviews Disease Primers</i> , 2015 , 1, 15014 | 51.1 | 36 |
| 67 | Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. <i>Protein Science</i> , 2006 , 15, 102-12 | 6.3 | 36 |
| 66 | Mutational effects on inclusion body formation. <i>Advances in Protein Chemistry</i> , 1997 , 50, 243-64 | | 34 |
| 65 | Cold rescue of the thermolabile tailspike intermediate at the junction between productive folding and off-pathway aggregation. <i>Protein Science</i> , 1998 , 7, 1516-23 | 6.3 | 34 |
| 64 | Tryptophan cluster protects human D-crystallin from ultraviolet radiation-induced photoaggregation in vitro. <i>Photochemistry and Photobiology</i> , 2013 , 89, 1106-15 | 3.6 | 33 |
| 63 | Contributions of aromatic pairs to the folding and stability of long-lived human D-crystallin. <i>Protein Science</i> , 2011 , 20, 513-28 | 6.3 | 32 |
| 62 | Solution x-ray scattering-based estimation of electron cryomicroscopy imaging parameters for reconstruction of virus particles. <i>Biophysical Journal</i> , 1999 , 76, 2249-61 | 2.9 | 32 |
| 61 | Conformational states of the bacteriophage P22 capsid subunit in relation to self-assembly. <i>Biochemistry</i> , 1990 , 29, 5626-33 | 3.2 | 32 |
| 60 | Conformational stability of P22 tailspike proteins carrying temperature-sensitive folding mutations. <i>Biochemistry</i> , 1990 , 29, 4181-7 | 3.2 | 32 |
| 59 | In vitro folding of phage P22 coat protein with amino acid substitutions that confer in vivo temperature sensitivity. <i>Biochemistry</i> , 1995 , 34, 6815-26 | 3.2 | 31 |
| 58 | Folding and assembly of oligomeric proteins in Escherichia coli. <i>Current Opinion in Biotechnology</i> , 1992 , 3, 468-73 | 11.4 | 31 |
| 57 | Structural studies of bacteriophage lambda heads and proheads by small angle X-ray diffraction. <i>Journal of Molecular Biology</i> , 1979 , 134, 575-94 | 6.5 | 31 |

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| 56 | Predicting the beta-helix fold from protein sequence data. <i>Journal of Computational Biology</i> , 2002 , 9, 261-76 | 1.7 | 30 |
| 55 | Phycobiliprotein genes of the marine photosynthetic prokaryote <i>Prochlorococcus</i> : evidence for rapid evolution of genetic heterogeneity. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 3171-82 | 2.9 | 30 |
| 54 | The interdigitated beta-helix domain of the P22 tailspike protein acts as a molecular clamp in trimer stabilization. <i>Protein Science</i> , 2002 , 11, 820-30 | 6.3 | 29 |
| 53 | Role for cysteine residues in the in vivo folding and assembly of the phage P22 tailspike. <i>Protein Science</i> , 2001 , 10, 397-410 | 6.3 | 28 |
| 52 | DNA injection proteins are targets of acridine-sensitized photoinactivation of bacteriophage P22. <i>Journal of Molecular Biology</i> , 1984 , 180, 837-63 | 6.5 | 27 |
| 51 | An elongated spine of buried core residues necessary for in vivo folding of the parallel beta-helix of P22 tailspike adhesin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3575-80 | 11.5 | 26 |
| 50 | Identification of sites influencing the folding and subunit assembly of the P22 tailspike polypeptide chain using nonsense mutations. <i>Genetics</i> , 1987 , 117, 157-71 | 4 | 26 |
| 49 | Stability of wild-type and temperature-sensitive protein subunits of the phage P22 capsid. <i>Journal of Biological Chemistry</i> , 1995 , 270, 16595-601 | 5.4 | 25 |
| 48 | 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, 247-53 | 6.5 | 25 |
| 47 | Novel second-site suppression of a cold-sensitive defect in phage P22 procapsid assembly. <i>Journal of Molecular Biology</i> , 1990 , 216, 701-16 | 6.5 | 24 |
| 46 | Tyrosine/cysteine cluster sensitizing human D-crystallin to ultraviolet radiation-induced photoaggregation in vitro. <i>Biochemistry</i> , 2014 , 53, 979-90 | 3.2 | 22 |
| 45 | Beta-helix core packing within the triple-stranded oligomerization domain of the P22 tailspike. <i>Protein Science</i> , 2000 , 9, 2338-43 | 6.3 | 22 |
| 44 | Ubiquitin proteasome pathway-mediated degradation of proteins: effects due to site-specific substrate deamidation 2010 , 51, 4164-73 | | 21 |
| 43 | Characterization of the protrimer intermediate in the folding pathway of the interdigitated beta-helix tailspike protein. <i>Biochemistry</i> , 2002 , 41, 5093-103 | 3.2 | 21 |
| 42 | Fold recognition and accurate sequence-structure alignment of sequences directing beta-sheet proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 976-85 | 4.2 | 20 |
| 41 | Detection of early aggregation intermediates by native gel electrophoresis and native western blotting. <i>Methods in Enzymology</i> , 1999 , 309, 333-50 | 1.7 | 20 |
| 40 | Genetic Analysis of Protein Folding Pathways. <i>Nature Biotechnology</i> , 1986 , 4, 297-303 | 44.5 | 20 |
| 39 | Monitoring the refolding pathway for a large multimeric protein using capillary zone electrophoresis. <i>Journal of Chromatography A</i> , 1997 , 769, 315-323 | 4.5 | 19 |

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| 38 | The DNA injection apparatus of phage p22. <i>Biophysical Journal</i> , 1986 , 49, 24-6 | 2.9 | 19 |
| 37 | 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, 469-86 | 6.5 | 19 |
| 36 | Mechanisms of Inclusion Body Formation. <i>ACS Symposium Series</i> , 1991 , 35-49 | 0.4 | 18 |
| 35 | Regulation of Structural Protein Interactions as Revealed in Phage Morphogenesis 1980 , 101-132 | | 18 |
| 34 | Scaffolding proteins and the genetic control of virus shell assembly. <i>Quarterly Review of Biology</i> , 1980 , 55, 369-93 | 5.4 | 17 |
| 33 | In vitro unfolding/refolding of wild type phage P22 scaffolding protein reveals capsid-binding domain. <i>Journal of Biological Chemistry</i> , 1999 , 274, 16135-40 | 5.4 | 15 |
| 32 | Assembly of the tail of bacteriophage T4. <i>Journal of Supramolecular Structure</i> , 1975 , 3, 24-38 | | 15 |
| 31 | 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, 4840-7 | 4.8 | 14 |
| 30 | Buried hydrophobic side-chains essential for the folding of the parallel beta-helix domains of the P22 tailspike. <i>Protein Science</i> , 2004 , 13, 2291-303 | 6.3 | 13 |
| 29 | Identification of the 9-aminoacridine/DNA complex responsible for photodynamic inactivation of P22. <i>Biochemistry</i> , 1986 , 25, 5858-64 | 3.2 | 13 |
| 28 | Genetic Control of Complex Bacteriophage Assembly 1979 , 581-633 | | 11 |
| 27 | Monoclonal antibody epitope mapping describes tailspike beta-helix folding and aggregation intermediates. <i>Journal of Biological Chemistry</i> , 2005 , 280, 23032-40 | 5.4 | 9 |
| 26 | Antigenic gene products of bacteriophage T4 baseplates. <i>Virology</i> , 1978 , 86, 312-28 | 3.6 | 9 |
| 25 | Wrap-and-Pack: a new paradigm for beta structural motif recognition with application to recognizing beta trefoils. <i>Journal of Computational Biology</i> , 2005 , 12, 777-95 | 1.7 | 8 |
| 24 | Folding and stability of mutant scaffolding proteins defective in P22 capsid assembly. <i>Journal of Biological Chemistry</i> , 1999 , 274, 16141-6 | 5.4 | 8 |
| 23 | Genetic and biochemical analysis of in vivo protein folding and subunit assembly. <i>Biopolymers</i> , 1983 , 22, 125-9 | 2.2 | 8 |
| 22 | Harvard XYY study. <i>Science</i> , 1975 , 187, 298-9 | 33.3 | 7 |
| 21 | Stalled folding mutants in the triple beta-helix domain of the phage P22 tailspike adhesin. <i>Journal of Molecular Biology</i> , 2005 , 354, 1103-17 | 6.5 | 6 |

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| 20 | A late gene product of phage P22 affecting virus infectivity. <i>Virology</i> , 1985 , 143, 368-79 | 3.6 | 6 |
| 19 | Investigation of secondary structures and macromolecular interactions in bacteriophage p22 by laser Raman spectroscopy. <i>Biophysical Journal</i> , 1980 , 32, 234-7 | 2.9 | 5 |
| 18 | Hydro-epidemiological modelling of bacterial transport and decay in nearshore coastal waters. <i>Water Research</i> , 2021 , 196, 117049 | 12.5 | 5 |
| 17 | Genetic Analysis of Polypeptide Chain Folding and Misfolding in Vivo 1990 , 59-78 | | 4 |
| 16 | The C-terminal cysteine annulus participates in auto-chaperone function for Salmonella phage P22 tailspike folding and assembly. <i>Bacteriophage</i> , 2012 , 2, 36-49 | | 3 |
| 15 | Unexpected pathways to protein stabilization. <i>Nature Biotechnology</i> , 1996 , 14, 436 | 44.5 | 2 |
| 14 | Amino Acid Sequence Determinants of Polypeptide Chain Folding and Inclusion Body Formation. <i>ACS Symposium Series</i> , 1993 , 24-37 | 0.4 | 2 |
| 13 | Pathway for the Thermal Unfolding of Wild Type and Mutant Forms of the Thermostable P22 Tailspike Endorhamnosidase. <i>ACS Symposium Series</i> , 1991 , 119-132 | 0.4 | 2 |
| 12 | Aggregate formation from thermolabile intermediates in the maturation of the thermostable P22 tailspike. <i>Biochemical Society Transactions</i> , 1988 , 16, 105-8 | 5.1 | 2 |
| 11 | Wrap-and-pack 2004 , | | 1 |
| 10 | Lattice Transformations and Subunit Conformational Changes in Phage Capsid Maturation. <i>Journal of Theoretical Medicine</i> , 2005 , 6, 99-105 | | 1 |
| 9 | Polymerization mechanism of polypeptide chain aggregation 1997 , 54, 333 | | 1 |
| 8 | Mutations Affecting Protein Folding and Misfolding in Vivo 1991 , 129-136 | | 1 |
| 7 | Amino Acid Sequence Control of the Folding of the Parallel β -Helix, the Simplest β -Sheet Fold. <i>Lecture Notes in Computer Science</i> , 2005 , 472-473 | 0.9 | |
| 6 | From genes to organelles. <i>Quarterly Review of Biology</i> , 1980 , 55, 329-33 | 5.4 | |
| 5 | The Legal and Legislative Background. <i>Environment</i> , 1982 , 24, 24-36 | 2.8 | |
| 4 | Human Γ -crystallins form fibrillar amyloid aggregates through a partially unfolded intermediate. <i>FASEB Journal</i> , 2008 , 22, 1010.3 | 0.9 | |
| 3 | Mutations associated with early cataract development in mice destabilize human gammaD-crystallin. <i>FASEB Journal</i> , 2008 , 22, 232-232 | 0.9 | |

2 Genetic Identification of Amino Acid Sequences Influencing Protein Folding **1973**, 275-291

1 The Use of Salmonella Bacteriophage P22 to Study the Multiple Mechanisms of Acridine-Induced Damage **1983**, 79-109