

# **BIBLIOGRAPHY**

**Anfinsen, C.B.** (1973). Principles that govern the folding of protein chains. *Science*. **181**, 223-230.

**Anfinsen, C.B., Scheraga, H.A.** (1975). Experimental and theoretical aspects of protein folding. *Adv. Protein Chem.* **29**, 205-300.

**Arnason, T. and Ellison, M.J.** (1994). Stress resistance in *Saccharomyces cerevisiae* is strongly correlated with assembly of a novel type of multiubiquitin chain. *Mol. Cell. Biol.* **14**, 7876-7883.

**Arnheim N., Erlich H.** (1992). Polymerase chain reaction strategy. *Annu. Rev. Biochem.* **61**, 131-156.

**Baboshina, O.V., Haas, A.L.** (1996). Novel multiubiquitin chain linkages catalyzed by the conjugating enzymes E2EPF and RAD6 are recognized by 26S proteasome subunit. *J. Biol. Chem.* **271**, 2823-2831.

**Bachmair, A., and Varshavsky, A.** (1989). The degradation signal in a short lived protein. *Cell*. **56**, 1019-1032.

**Bachmair, A., Finley, D., and Varshavsky, A.** (1986). In vivo half-life of a protein is a function of its amino-terminal residue. *Science*. **234**, 179-186.

**Bachmair, A., Varshavsky, A.** (1989). The degradation signal in a short-lived protein. *Cell*. **56**, 1019-1032.

**Bartel, B., Wüning, I., and Varshavsky, A.** (1990). The recognition component of the N-end rule pathway. *The EMBO Journal*. **9**, 3179-3189.

**Bashford, D., Karplus, M. and Weaver, D.L.** (1990). Protein folding, American Association for the advancement of science. *Ed Gierasch, L M and King*, 283-290.

**Basharov, M.A.** (2000). The posttranslational concept of protein folding: how valid is it? *Biochemistry*. **65**, 1184-91.

**Baumeister, W., Walz, J., Zuhl, F., and Seemuller, E. (1998).** The proteasome: Paradigm of a self-compartmentalizing protease. *Cell*. **92**, 367-380.

**Baumeister, W., Walz, J., Zuhl, F. and Seemuller, E. (1998).** The proteasome: paradigm of a self-compartmentalizing protease. *Cell*. **92**, 367-380.

**Bowerman, B., Kurz, T. (2006).** Degrade to create: developmental requirements for ubiquitin-mediated proteolysis during early *C. elegans* embryogenesis. *Development*. **133**, 773-784.

**Briggs, M.S. and Roder, H. (1992).** Early Hydrogen-Bonding Events in the Folding Reaction of ubiquitin. *Proc. Nat. Acad. Sci.* **89**, 2017-2021.

**Bruster, B., Bruschweiler, R., Ernst, R.R. (1997).** Backbone Dynamics and Structural Characterization of the Partially Folded A State of Ubiquitin by  $^1\text{H}$ ,  $^{13}\text{C}$ , and  $^{15}\text{N}$  Nuclear Magnetic Resonance Spectroscopy. *Biochemistry*. **36**, 13043-13053.

**Bryngelson J.D., Wolynes P.G. (1987).** Spin glasses and the statistical mechanics of protein folding. *Proc. Natl. Acad. Sci.* **84**, 7524-7528.

**Burkhardt, D. (2007).** Role of proteasomes in disease. *BMC Biochemistry*. 1471-2091-2098.

**Catic, A. and Ploegh, H.L. (2005).** Ubiquitin - conserved protein or selfish gene? *TRENDS in Biochemical Sciences*. **30**, 11, 600-604.

**Chan, A.W.E, Hutchinson, E.G., Harris, D. and Thornton, J.M. (1993).** Identification, classification, and analysis of beta-bulges in proteins. *Protein Science*. **2**, 1574-1590.

**Chan, H.S. and Dill, K.A. (1990).** Origins of structure in globular proteins. *Proc. Natl. Acad. Sci.* **87**, 6388-6392.

**Chan, V.J., Tobias, A., Bachmair, D., Marriott, D.J., Ecker, D.K., Gonda, and Varshavsky, A. (1989).** A multiubiquitin chain is confined to a specific lysine in a targeted short-lived protein. *Science*. **243**, 1576-1583.

**Chau, V., Tobias, J.W., Bachmair, A., Marriott, D., Ecker, D.J., Gonda, D.K., and Varshavsky, A. (1989).** A multiubiquitin chain is confined to specific lysine in a targeted short-lived protein. *Science*. **243**, 1576-1583.

**Chen, P.Y., Gopalacushina, B.G., Yang, C.C., Chan, S.I. and Evans, P.A. (2001).** The role of a  $\beta$ -bulge in the folding of the  $\beta$ -hairpin structure in ubiquitin. *Protein science*. **10**, 2063-2074.

**Chyan, C.L., Lin, F.C., Peng, H., Yuan, J.M., Chang, C.H., Lin, S.H. and Yang, G. (2004).** Reversible mechanical unfolding of single ubiquitin molecules. *Biophysical J.* **87**, 3995-4006.

**Ciechanover A. and Iwai K. (2004).** The ubiquitin system: from basic mechanisms to the patient bed. *IUBMB Life*. **56**, 193-201.

**Ciechanover, A., Elias, S., Heller, H., and Hershko, A. (1982).** "Covalentaffinity" purification of ubiquitin-activating enzyme. *J. Biol. Chem.* **257**, 2537-2542.

**Ciechanover, A., Finley, D., Varshavsky, A. (1984).** Ubiquitin dependence of selective protein degradation demonstrated in the mammalian cell cycle mutant ts85. *Cell*. **37**, 57-66.

**Ciechanover, A., Heller, H., Elias, S., Haas, A.L., and Hershko, A. (1980).** ATP-dependent conjugation of reticulocyte proteins with the polypeptide required for protein degradation. *Proc. Natl. Acad. Sci.* **77**, 1365-1368.

**Ciechanover, A., Hod, Y., and Hershko, A. (1978).** A heat-stable polypeptide component of an ATP-dependent proteolytic system from reticulocytes. *Biochem. Biophys. Res. Commun.* **81**, 1100-1105.

**Cox, J.P.L., Evans, P.A., Packman, L.C., Williams, D.H. and Wolfson, D.N. (1993).** Dissecting the structure of a partially folded protein. Circular dichroism and nuclear magnetic resonance studies of peptides from ubiquitin. *J. Mol. Biol.* **234**, 483-492.

**Cyrus Chothia, Alexei V. Finkelstein. (1990).** The Classification and origins of Protein folding patterns. *Annu. Rev. Biochem.* **59**, 1007-1039.

**David Botstein and Gerald R. Fink** (1998). Yeast: An Experimental Organism for Modern Biology. *Science*. **240**, 1439-1443.

**David J. Ecker, Tauseef R. Butt, Jon Marsh, Edmund J. Sternberg, Neil Margolis, Brett P. Monia, Sobhanaditya, J., Muhammad, I.K., Paul L. Weber, Lucian, M., and Stanley T.C.** (1987). Gene synthesis, expression, structures, and functional activities of site-specific mutants of ubiquitin. *J. Biol. Chem.* **262**, 14213-14221.

**David L. Nelson and Michael M. Cox** (2005). *Lehninger Principles of Biochemistry*, Ed. 4<sup>th</sup>., W. H. Freeman and Company, New York.

**David, E.O. Lori, V.C., Raymond, C.S., Julian Adams, Kunio Nagashima and Ulrich Schubert** (2000). Equine infectious anemia virus and the ubiquitin-proteasome system. *Virology*. **278**, 111-121.

**De Alba, E., Rico, M., and Jiménez, M.A.** (1999). The turn sequence directs  $\beta$ -strand alignment in designed  $\beta$ -hairpins. *Protein Science*. **8**, 2234-2244.

**Dieter H.W. and Wolfgang H.** (2004). The proteasome: a proteolytic nanomachine of cell regulation and waste disposal. *Biochimica. Biophysica. Acta*. **1695**, 19-31.

**Dill, K.A.** (1985). Theory for the folding and stability of globular proteins. *Biochemistry*. **24**, 1501-1509.

**Dyson<sup>a</sup>, H.J., Rance, M., Houghten, R.A., Lerner, R.A. and Wright, P.E.** (1988). Folding of immunogenic peptide fragments of proteins in water solution. I. Sequence requirements for the formation of a reverse turn. *J. Mol. Biol.* **201**, 161-200.

**Dyson<sup>b</sup>, H.J., Rance, M., Houghten, R.A., Lerner, R.A. and Wright, P.E.** (1988). Folding of immunogenic peptide fragments of proteins in water solution. II. The nascent helix. *J. Mol. Biol.* **201**, 201-217.

**Feiser, T.M., Tainer, J.A., Geyson, H.M., Houghten, R.A. and Lerner, R.A.** (1987). Influence of protein flexibility and peptide conformation on reactivity of monoclonal anti-peptide antibodies with a protein alpha-helix. *Proc. Natl. Acad. Sci.* **84**, 8568-8572.

- Ferraro, D.M., Hope, E.K., Robertson, A.D. (2005). Site-specific reflex response of ubiquitin to loop insertions. *J. Mol. Biol.* **352**, 575-584.
- Finley, D., Ozkaynak, E., and Varshavsky, A. (1987). The yeast polyubiquitine gene is essential for resistance to high temperatures, starvation, and other stresses. *Cell*. **48**, 1035-1046.
- Finley, D., Sadis, S., Monia, B.P., Boucher, P., Ecker, D.J., Crooke, S.T., and Chau, V. (1994). Inhibition of proteolysis and cell cycle progression in a multiubiquitination-deficient yeast mutant. *Mol. Cell. Biol.* **14**, 5501-5509.
- Galan, J.M. and R. Haguenauer-Tsapis (1997). Ubiquitin Lys63 is involved in ubiquitination of a yeast plasma membrane protein. *The EMBO Journal*. **16**, 5847-5854.
- Galan, J.M., Moreau, V., Andre, B., Volland, C., and Haguenauer-Tsapis, R. (1996). Ubiquitination mediated by the Npi1p/Rsp5p ubiquitin-protein ligase is required for endocytosis of the yeast uracil permease. *J. Biol. Chem.* **271**, 10946-10952.
- Garvey, E.P., Swank, J. and Matthews, C.R. (1989). Protein structure, function and genetics. **6**, 259-266.
- Gavilanes, J.G., De Buitrago, G.G., Perez Castells, R. and Rodrigues, R. (1982). Isolation, characterization and amino acid sequence of a ubiquitin like protein from insect eggs. *J. Biol. Chem.* **257**, 10267-10270.
- Glickman, M.H., Rubin, D.M., Coux, O., Wefes, I., Pfeifer, G., Cjeka, Z., Baumeister, W., Fried, V.A., Finley, D. (1998). A subcomplex of the proteasome regulatory particle required for ubiquitin-conjugate degradation and related to the COP9-signalosome and eIF3. *Cell*. **94**, 615-623.
- Goebel, M.G., Yochem, J., Jentsch, S., McGrath, J.P., Varshavsky, A., and Byers, B. (1988). The yeast cell cycle gene CDC34 encodes a ubiquitin conjugating enzyme. *Science*. **241**, 1331-1335.

- Gonda, D.K., Bachmair, A., Wunning, I., Tobias, J.W., Lane, W.S., and Varshavsky, A.** (1989). Universality and structure of the N-end rule. *J. Biol. Chem.* **264**, 16700-16712.
- Groll, M. and Huber, R.** (2004). Inhibitors of the eukaryotic 20S proteasome core particle: A structural approach. *Biochim. Biophys. Acta.* **1695**, 33-44.
- Guarino, L.A.** (1990) Identification of a Viral Gene Encoding a Ubiquitin-Like Protein, *Proc. Nat Acad. Sci. USA.* **87**, 409-413.
- Haas, A.L. and Rose, I.A.** (1982). The Mechanism of Ubiquitin activating enzyme. *J. Bio. Chem.* **257**, 10329-10337.
- Hagen, S.J.** (2007). Probe-dependent and nonexponential relaxation kinetics: unreliable signatures of downhill protein folding. *Proteins.* **68**, 205-217.
- Haque, T.S. and Gellman, S.H.** (1997). Insights on beta-hairpin stability in aqueous solution from peptides with enforced type I' and type II' beta-turns. *J Am. Chem. Soc.* **119**, 2303-2304.
- Harding, M.M., Williams, D.H. and Woolfson, D.N.** (1991). Characterization of a partially denatured state of a protein by two-dimensional NMR: reduction of the hydrophobic interactions in ubiquitin. *Biochemistry.* **30**, 3120-3128.
- Hanna, J., Leggett, D.S. and Finley D.** (2003). Ubiquitin depletion as a key mediator of toxicity by translation inhibitor. *Mol. Cell. Bio.* **23**, 9251-9261.
- Heather M. Went and Sophie E. Jackson** (2004). Is an intermediate state populated on the folding pathway of Ubiquitin? *FEBS letters.* **567**, 333-338.
- Hershko A., Hiller H.** (1985). Occurrence of a polyubiquitin structure in ubiquitin-protein conjugates. *Biochem. Biophys. Res. Comm.* **128**, 1079-1086.
- Hershko, A. and Ciechanover, A.** (1998). The ubiquitin system. *Annu. Rev. Biochem.* **67**, 425-479.

- Hershko, A., Ciechanover, A., and Varshavsky, A. (2000).** The ubiquitin system. *Nat. Med.* **10**, 1073-1081.
- Hershko, A., Ciechanover, A., Heller, H., Haas, A.L., and Rose, I.A. (1980).** Proposed role of ATP in protein breakdown: conjugation of proteins with multiple chains of the polypeptide of ATP-dependent proteolysis. *Proc. Natl. Acad. Sci.* **77**, 1783-1786.
- Hershko, A., Ganoth, D., Pehrson, J., Palazzo, R.E., and Cohen, L.H. (1991).** Methylated ubiquitin inhibits cyclin degradation in clam embryo extracts. *J. Biol. Chem.* **266**, 16376-16379.
- Hershko, A., Heller, H., Elias, S., and Ciechanover, A. (1983).** Components of ubiquitin-protein ligase system. *J. Biol. Chem.* **258**, 8206- 8214.
- Hershko, A., Leshinsky, E., Ganoth, D., and Heller, H. (1984).** ATP-dependent degradation of ubiquitin-protein conjugates. *Proc. Natl. Acad. Sci.* **81**, 1619-1623.
- Hicke L. (1999).** Getting down with ubiquitin: turning off cell-surface receptors, transporters and channels. *Trends Cell. Biol.* **9**, 107-112.
- Hicke, L. and Riezman, H. (1996).** Ubiquitination of a yeast plasma membrane receptor signals its ligand-stimulated endocytosis. *Cell.* **84**, 277-287.
- Hicke, L., Dunn, R. (2003).** Regulation of membrane protein transport by ubiquitin and ubiquitin-binding proteins. *Annu. Rev. Cell. Dev. Biol.* **19**, 141-172.
- Hobler, S.C., Williams, A., Fischer, D., Wang, J.J., Sun, X., Fischer, J.E., Monaco, J.J., Hasselgren P-O. (1999).** Activity and expression of the 20S proteasome are increased in skeletal muscle during sepsis. *Am. J. Physiol.* **277**, 434-440.
- Hochstrasser, M., and Varshavsky, A. (1990).** In vivo degradation of a transcriptional regulator: The yeast Mata2 repressor. *Cell.* **61**, 697-708.



**Hochstrasser, M., Ellison, M.J., Chau, V., and Varshavsky, A.** (1991). The short lived MATa2 transcriptional regulator is ubiquitinated in vivo. *Proc. Natl. Acad. Sci.* **88**, 4606-4610.

**Hofmann, R.M. and Cecile M. Pickart** (2001). In Vitro Assembly and Recognition of Lys-63 Polyubiquitin Chains. *J. Bio. Chem.* **276**, 27936-27943.

**Jaenicke, R.** (1991). Protein folding: local structures, domains, subunits, and assemblies. *Biochemistry.* **30**, 3147-3161.

**Jentsch, S. and Pyrowolakis, G.** (2000). Ubiquitin and its kin: how close are the family ties? *Trends Cell. Biol.* **10**, 335-342.

**Jentsch, S., McGrath, J.P., and Varshavsky, A.** (1987). The yeast DNA repair gene RAD6 encodes a ubiquitin-conjugating enzyme. *Nature.* **329**, 131-134.

**Joanna R.M., and Ellen Solomon** (2004). BRCA1: BARD1 induces the formation of conjugated ubiquitin structures, dependent on K6 of ubiquitin, in cells during DNA replication and repair. *Hum. Mol. Genet.* **13**, 807-817.

**Johnson, E.S., Ma, P.C.M., Ota, I.M., Varshavsky, A.** (1995). A proteolytic pathway that recognizes ubiquitin as a degradation signal. *J. Biol. Chem.* **270**, 17442-17456.

**Johnson, E. S., Bartel, B., Seufert W., & Varshavsky, A.** (1992). Ubiquitin as a degradation signal: *The EMBO. Journal.* **11**, 497-505.

**Johnson, E.S., Gonda, D.K., Varshavsky, A.,** (1990). Cis-trans recognition and subunit-specific degradation of short-lived proteins. *Nature.* **346**, 287-291.

**Judith Frydman.** (2001). Folding of newly translated proteins in vivo: The role of molecular chaperones. *Annu. Rev. Biochem.* **70**, 603-649.

**Karin M and Ben-Neriah, Y.** (2000). Phosphorylation meets ubiquitination: the control of NF-(kappa)B activity. *Annu. Rev. Immunol.* **18**, 621-663.

- Karplus, M. and Weaver, D.L.** (1976). Protein-folding dynamics. *Nature*. **260**, 404-406.
- Keck S., Nitsch R., Grune T., Ullrich O.** (2003). Proteasome inhibition by paired helical filament-tau in brains of patients with Alzheimer's disease. *J. Neurochem.* **85**, 115-122.
- Khorasanizadeh S., Peters L.D., Butt T.R. and Roder H.** (1993). Folding and stability of a tryptophan containing mutant of ubiquitin. *Biochemistry*. **32**, 7054-7063.
- Kim, P.S. and Baldwin, R.L.** (1982). Specific intermediates in the folding reactions of small proteins and the mechanism of protein folding. *Annu. Rev. Biochem.* **51**, 459-489.
- Kloetzel P.M.** (2004). The proteasome and MHC class I antigen processing. *Biochim. Biophys. Acta*. **1695**, 225-233.
- Kyte J, Doolittle R.F.** (1982). A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* **157**, 105-132.
- Lee, D.H. and Goldberg, A.L.** (1998). Proteasome inhibitors: Valuable new tools for cell biologists. *Trends Cell. Biol.* **8**, 397-403.
- Loladze, V.V. and Makhatadze, G.I.** (2002). Removal of surface charge-charge interactions from ubiquitin leaves the protein folded and very stable. *Protein Science*. **11**, 174-177.
- Loladze, V.V., Eemolenko, D.N. and Makhatadze, G.I.** (2001). Heat capacity changes upon burial of polar and nonpolar groups in proteins. *Protein Science*. **10**, 343-1352.
- Makhatadze, G.I., Loladze, V.V., Ermolenko, D.N., Chen, X.F. and Thomas, S.T.** (2003). Contribution of surface salt bridges to protein stability: guidelines for protein engineering. *J.Mol. Biol.* **327**, 1135-1148.
- Mark Hochstrasser** (1996). Ubiquitin-dependent protein degradation. *Annu. Rev. Genet.* **30**, 405-439.

- McLeish, M.J., Neilsen, K.J., Wade, J.D. and Craik, D.J.** (1993). A peptide corresponding to the N-terminal 13 residues of T4 lysozyme forms an  $\alpha$ -helix. *FEBS Letters*. **315**, 323-328.
- McNaught, K.S.P., Jenner, P.** (2001). Proteasomal function is impaired insubstantia nigra in Parkinson's disease. *Neurosci. Lett.* **297**, 191-194.
- Milner-White, E.J. and Poet, R.** (1987). Loops, bulges, turns and hairpins in proteins. *Trends Biochem. Sci.* **12**, 189-192.
- Monia, B.P., Ecker, D.J. and Crooke, S.T.** (1990) New Perspectives on the Structure and Function of Ubiquitin. *Biotechnology*. **8**, 209-215.
- Montelione, G.T. and Scheraga, H.A.** (1989). Formation of local structures in protein folding. *Acc. Chem. Res.* **22**, 70-75.
- Murakami, Y., Matsufuji, S., Kameji, T., Hayashi, S., Igarashi, K., Tamura, T., Tanaka, K., Ichihara, A.** (1992). Ornithine decarboxylase is degraded by the 26S proteasome without ubiquitination. *Nature*. **360**, 597-599.
- Murray A.W.,** (2004). Recycling the cell cycle: cyclins revisited. *Cell*. **116**, 221-234.
- Nandi, D., Tahiliani, P., Kumar, A. and Chandu, D.** (2006). The Ubiquitin-proteasome system. *J. Bio. sci.* **31**, 137-155.
- Nishikawa, H., Oooka, S., Sato, K., Arima, K., Okamoto, J., Klevit, R.E., Fukuda, M., Ohta, T.** (2004). Mass spectrophotometric and mutational analyses reveal Lys-6-linked polyubiquitin chains catalyzed by BRCA1-BARD1 ubiquitin ligase. *J. Biol. Chem.* **279**, 3916-3924.
- Ozakanak Engin, Daniel Finley, Mark J. Solomon and Alexander V.** (1987). The yeast ubiquitin genes: a family of natural gene fusions. *The EMBO Journal*. **6**, 1429-1439.
- Ozkaynak, E., Finley, D., and Varshavsky, A.** (1984). The yeast ubiquitine gene: Head-to-tail repeats encoding a polyubiquitin precursor protein. *Nature*. **312**, 663-666.

**Pauling, L.** (1960). *The Nature of the Chemical Bond. Ed. 3<sup>rd</sup>.*, Cornell University Press.

**Pauling, L. and Corey, R.B.** (1951). Configurations of polypeptide chains with favored orientations of the polypeptide around single bonds: Two pleated sheets. *Proc. Natl. Acad. Sci.* **37**, 729-740.

**Pauling, L., Corey, R.B. and Branson, H.R.** (1951). The Structure of Proteins: Two hydrogen-bonded helical configurations of the polypeptide chain. *Proc. Nat. Acad. Sci.* **37**, 205-211.

**Peter S. Kim, Robert L. Baldwin** (1990). Intermediates in the folding reactions of small proteins. *Annu. Rev. Biochem.* **59**, 631-60.

**Pickart M Cecile** (2004). Back to the future with ubiquitin. *Cell.* **116**, 181-190.

**Pickart M Cecile, and David Fushman** (2004). Polyubiquitin chains: polymeric protein signals. *Current Opinion in Chemical Biology.* **8**, 610-616.

**Pickart, C. and Cohen, R.E.** (2004). Proteasomes and their kin: Proteases in the machine age. *Nat. Rev. Mol. Cell. Biol.* **5**, 177-187.

**Pickart, C.M.** (2000). Ubiquitin in chains. *Trends Biochem. Sci.* **25**, 544-548.

**Ramachandran G.N., Ramakrishnan C. and Sasisekharan V.** (1963). Stereochemistry of polypeptide chain configurations. *J. Mol. Biol.* **7**, 95-99.

**Ratna Prabha C. and Mohan Rao, Ch.** (2004). Oxidative refolding of lysozyme in trifluoroethanol (TFE) and ethylene glycol; interfering role of preexisting alpha helical structure and intermolecular hydrophobic interactions. *FEBS letters* **357**, 67-72.

**Rechsteiner, M.** (1998). The 26S proteasome. In Ubiquitin and the biology of the cell. *Plenum Press, New York.* 147-189.

**Rechsteiner, M. and Hill, C.P.** (2005). Mobilizing the proteolytic machine: Cell biological roles of proteasome activators and inhibitors. *Trends Cell Biol.* **15**, 27-33.

**Recksteiner, M.** (1998). The 26S proteasome in ubiquitin and the biology of the cell. *Ed. Plenum Press, New York*, 147-189.

**Reckstener, M.** (1998). Ubiquitin. *Ed. plenum, New York*. **346**, 787-788.

**Reed, S.I., Ratchets and clocks** (2003). The cell cycle, ubiquitylation and protein turnover. *Nat. Rev. Mol. Cell Biol.* **4**, 855-864.

**Richardson, J.S., Getzoff, E.D., and Richardson, D.C.** (1978). The bulge: A common small unit of non-repetitive protein structure. *Proc. Natl. Acad. Sci.* **75**, 2574-2578.

**Robert, L. B. and George, D.** (1999). Rose. Is Protein folding hierarchic? Local structure and peptide folding. *TIBS* **24**, 26-33.

**Roder, H., Elove, G.A. and Englander, S.W.** (1988). Structural Characterization of fplding intermediates in cytochrome c by H-exchange labeling and proton NMR. *Nature.* **335**, 700-704.

**Rogers S., Wells R., Rechsteiner M.** (1986). Amino acid sequences common to rapidly degraded proteins: the PEST hypothesis. *Science.* **234**, 364-368.

**Russell, N. S., and Wilkinson, K.D.** (2004). Identification of a novel 29-linked polyubiquitin binding protein, Ufd3, using polyubiquitin chain analogues. *Biochemistry.* **43**, 4844-4854.

**Sambrook and Russel** (2001). Molecular Cloning: A Laboratory Manual. *Ed. 3<sup>rd</sup>. Cold Spring Harbor Laboratory Press.*

**Santiveri, C.M., Rico, M. and Jimenez, M.A.** (2000). Position effect of cross-strand side-chain interactions on [beta]-hairpin formation. *Protein Science.* **9**, 2152-2160.

**Schlesinger, D.H. and Goldstein, G.** (1975). Molecular conservation of 74 amino acid sequence of ubiquitin between cattle and man. *Nature.* **255**, 423-424.

**Schlesinger, D.H., Goldstein, G. and Nail, H.D.** (1975). Complete amino acid sequence of ubiquitin, an adenylate cyclase stimulating polypeptide probably universal in living cells. *Biochemistry*. **14**, 2214-2218.

**Searle, M.S., Williams, D.H. and Packman, L.C.** (1995). Folding of a short linear peptide into a water-stable  $\beta$ -hairpin: non-native structure in a peptide derived from the N-terminal sequence of ubiquitin. *Nature Struct. Biol.* **2**, 999-1006.

**Serrano, L., Matouschek, A. and Fersht, A.R.** (1992). The Folding of an Enzyme VI. *J. Mol. Biol.* **224**, 847-859.

**Spence, J., Gali, R.R., Dittmar, G., Sherman, F., Karin, M., Finley, D.** (2000). Cell cycle-regulated modification of the ribosome by a variant multiubiquitin chain. *Cell*. **102**, 67-76.

**Spence, J., Sadis, S., Haas, A.L. and Finley, D.** (1995). Ubiquitin mutant with specific defects in DNA repair and multiubiquitination. *Mol. Cell. Biol.* **15**, 1265-1273.

**Spence, J., Sadis, S., Haas, A.L., Finley, D.** (1995). A ubiquitin mutant with specific defects in DNA repair and multiubiquitination. *Mol. Cell. Biol.* **15**, 1265-1273.

**Stockman, B.J., Euvard, A. and Scahill, T.A.** (1993). Heteronuclear three-dimensional NMR spectroscopy of a partially denatured protein: the A-state of human ubiquitin. *J. Biomol. NMR*. **3**, 285-396.

**Sun, L., Chen, Z.J.** (2004). The novel functions of ubiquitination in signaling. *Curr. Opin. Cell. Biol.* **16**, 119-126.

**Sundd, M. and Robertson, A.D.** (2003). Rearrangement of charge-charge interactions in variant ubiquitins as detected by double-mutant cycles and NMR. *J. Mol. Biol.* **332**, 927-936.

**Sundd, M., Iverson, N., Ibarra Molero B., Sanchez-Ruiz, J. M., and Robertson, A.D.** (2002). Electrostatic interactions in ubiquitin: stabilization of carboxylates by lysine amino groups. *Biochemistry*. **41**, 7586-7596.

**Thomas, S.T. and Makhatadze, G.I.** (2000). Contribution of the 30/36 hydrophobic contact at the C-terminus of the alpha-helix to the stability of the ubiquitin molecule. *Biochemistry*. **39**, 10275–10283.

**Thrower, J.S., Hoffman, L., Rechsteiner, M. and Pickart, C.M.** (2000). Recognition of the polyubiquitin proteolytic signal. *The EMBO Journal*. **19**, 94-102.

**Ulrich, H.D.** (2002). Degradation or maintenance: actions of the ubiquitin system on eukaryotic chromatin. *Eukaryot. Cell*. **1**, 1-10.

**Varshavsky, A.** (1996). The N-end rule: Functions, mysteries, uses. *Proc. Natl. Acad. Sci.* **93**, 12142-12149.

**Varshavsky, A.** (1997). The ubiquitin system. *Trends in Biochem. Sci.* **22**, 383-387.

**Verma, R. and Deshaies, R.** (2000). A proteasome howdunit: the case of the missing signal. *Cell*. **101**, 341-344.

**Vierstra, R.D., Langan, S.M. and Schaller, G.E.** (1986). Complete amino acid sequence of ubiquitin from the higher plant *Avena sativa*. *Biochemistry*. **25**, 3105-3108.

**Vijay-kumar, S., Bugg, C.E. and Cook, W.J.** (1987). Structure of ubiquitin refined at 1.8 Å resolutions. *J. Mol. Biol.* **194**, 513-544.

**Vijay-kumar, S., Bugg, C.E., Wilkinson, K.D., Vierstra, R.D., Hatfield, P.M., and Cook, W.J.** (1987). Comparison of the three dimensional structures of Human, Yeast and Oat Ubiquitin. *J. Biol. Chem.* **262**, 6396-6399.

**Waltho, J.P., Fehrer, V.A., Lerner, R.A., Wright, P.E.** (1989). Conformation of a T cell stimulating peptide in aqueous solution. *FEBS Letters*. **250**, 400-404.

**Watson, D.C., Leavy, W.B. and Dixon, G.H.** (1978). Free ubiquitin is a non-histone protein of trout testis chromatin. *Nature*. **276**, 196-198.

**Weissmann, A.M.** (1997). Regulating protein degradation by ubiquitination. *Immunology Today*. **18**, 189-196.

**Wilkinson, K.D., Cox, M.J., O' Connors, B.B. and Shapira, R.** (1986). Structure and activities of a variant ubiquitin sequence from bakers' yeast. *Biochemistry*. **25**, 4999-5004.

**Wilkinson, K.D., Urban, M.K., and Haas, A.L.** (1980). Ubiquitin is the ATP-dependent proteolytic factor of rabbit reticulocytes. *J. Biol. Chem.* **255**, 7529-7532.

**Wilmot, C.M. and Thornton J.M.** (1988). Analysis and prediction of the different types of beta-turn in proteins. *J. Mol. Biol.* **203**, 221-232.

**Whitby, F.G., Xia, G., Pickart, C.M. and Hill, C.P.** (1998) crystal structure of the human ubiquitin-like protein NEDD8 and interactions with ubiquitin pathway enzymes. *J. Biol. Chem.* **273**, 34983-34991.

**Wolf, D.H. and Hilt, W.** (2004). The proteasome: A proteolytic nanomachine of cell regulation and waste disposal. *Biochim. Biophys. Acta*. **1695**, 19-31.

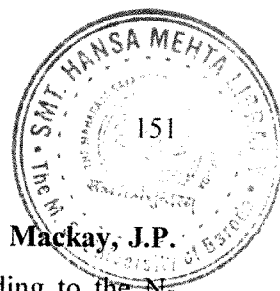
**Wright, P.E., Dyson, H.J. and Lerner, R.A.** (1988). Conformation of peptide fragments of proteins in aqueous solution: implications for initiation of protein folding. *Biochemistry*. **27**, 7167-7175.

**Wu, L.C., Laub, P.B., Elove, G.A., Carvey, J. and Roder, H.** (1993). A non-covalent peptide complex as a model for an early folding intermediate of cytochrome c. *Biochemistry*. **32**, 10271-10276.

**Wu-Baer, F., Lagazon, K., Yuan, W., Baer, R.** (2003). The BRCA1/BARD1 Heterodimer Assembles Polyubiquitin Chains through an Unconventional Linkage Involving Lysine Residue K6 of Ubiquitin. *J. Biol. Chem.* **278**, 34743-34746.

**Zerella, R., Chen, P.Y., Evans, P.A., Raine, A., and Williams, D.H.** (2000). Structural characterization of mutant peptides derived from ubiquitin and implications for protein folding. *Protein Science*. **9**, 2142-2150.





**Zerella, R., Evans, P.A., Ionides, J.M.C., Packman, L.C., Trotter, B.W., Mackay, J.P. and Williams, D.H.** (1999). Autonomous folding of a peptide corresponding to the N-terminal beta-hairpin from ubiquitin. *Protein Science*. **8**, 1320-1331.

**Zhou, H., Cao, F., Wang, Z., Yu, Z.X., Nguyen, H.P., Evans, J., Li, S.H., Li, X.J.** (2003). Huntingtin forms toxic NH<sub>2</sub>-terminal fragment complexes that are promoted by the age-dependent decrease in proteasome activity. *J. Cell. Biol.* **163**, 109-118.