

Bibliography

A.S. Mildvan, D.J. Weber, A. Kulipulos. (1992). Quantitative interpretations of double mutations of enzymes. *Arch. Biochem. Biophys.* **294**, 327–340.

A.S. Mildvan. (2004). Inverse thinking about double mutants of enzymes. *Biochemistry.* **43** 14517–14520.

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

Aydin Haririnia, Rati Verma, Nisha Purohit, Michael Z Twarog, Raymond J Deshaies, Dan Bolon, David Fushman. (2008). Mutations in the hydrophobic core of ubiquitin differentially affect its recognition by receptor proteins. *J Mol Biol.* **375**(4), 979-96.

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.

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

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.

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.

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

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.
- 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 PY, Gopalacushina BG, Yang CC, Chan SI, Evans PA.** (2001). The role of a beta-bulge in the folding of the beta-hairpin structure in ubiquitin. *Protein Sci.* **10**(10), 2063-2074.
- Chen, J., Sun, J. Nonproteolytic Functions of Ubiquitin in Cell Signaling** (2009). *Cell*.
- Chen, P.Y., Gopalacushina, B.G., Yang, C.C., Chan, S.I. and Evans, P.A.** (2001). The role of a β -bulge in the folding of the β -hairpin structure in ubiquitin. *Protein science*. **10**, 2063-2074.
- Ciechanover A. and Iwai K.** (2004). The ubiquitin system: from basic mechanisms to the patient bed. *IUBMB Life*. **56**, 193-201.
- 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.

- David Botstein and Gerald R. Fink** (1998). Yeast: An Experimental Organism for Modern Biology. *Science*. **240**, 1439-1443.
- de Alba E, Jiménez MA, Rico M, Nieto JL.** (1996). Conformational investigation of designed short linear peptides able to fold into beta-hairpin structures in aqueous solution. *Fold Des*. **1**(2), 133-44.
- De Alba, E., Rico, M., and Jiménez, M.A.** (1999). The turn sequence directs β -strand alignment in designed β -hairpins. *Protein Science*. **8**, 2234-2244.
- Dill, K.A.** (1985). Theory for the folding and stability of globular proteins. *Biochemistry*. **24**, 1501-1509.
- Dyson^a, 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^b, 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.
- 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.
- Garvey, E.P., Swank, J. and Matthews, C.R.** (1989). Protein structure, function and genetics. **6**, 259-266.
- 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.
- Groll, M. and Huber, R.** (2004). Inhibitors of the eukaryotic 20S proteasome core particle: A structural approach. *Biochim. Biophys. Acta*. **1695**, 33-44.

- 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.
- Hanna, J., Leggett, D.S. and Finley D.** (2003). Ubiquitin depletion as a key mediator of toxicity by translation inhibitors. *Mol. Cell. Bio.* **23**, 9251-9261.
- 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.
- 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., 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. 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.,** (1996). Ubiquitin-dependent Protein Degradation. *Annual Reviews Genetics.* **30**:405-39.
- 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.
- Jaenicke, R.** (1991). Protein folding: local structures, domains, subunits, and assemblies. *Biochemistry.* **30**, 3147-3161.
- Jentsch, S., McGrath, J.P., and Varshavsky, A.** (1987). The yeast DNA repair gene RAD6 encodes a ubiquitin-conjugating enzyme. *Nature.* **329**, 131-134.
- Johnson, E. S., Bartel, B., Seufert W., & Varshavsky, A.** (1992). Ubiquitin as a degradation signal. *The EMBO. Journal.* **11**, 497-505.
- 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.
- 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.
- 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.
- Lee SY, Pullen L, Virgil DJ, et al.** (2014). Alanine scan of core positions in ubiquitin reveals links between dynamics, stability, and function. *J Mol Biol.* **426**(7), 1377-1389.
- 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.

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 α -helix. *FEBS Letters*. **315**, 323-328.

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.

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 ubiquitin gene: Head-to-tail repeats encoding a polyubiquitin precursor protein. *Nature*. **312**, 663-666.

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., (2001) Mechanisms Underlying Ubiquitination. *Annual Reviews Biochemistry*. **70**:503-33.

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

R Beal, Q Deveraux, G Xia, M Rechsteiner, C Pickart. (1996). Surface hydrophobic residues of multiubiquitin chains essential for proteolytic targeting. *Proc Natl Acad Sci.* **93**(2), 861-6.

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

Rechsteiner, M. (1988). Ubiquitin. *Springer*.

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.

- Reed, S.I., Ratchets and clocks** (2003). The cell cycle, ubiquitylation and protein turnover. *Nat. Rev. Mol. Cell Biol.* **4**, 855-864.
- Riemen AJ, Waters ML.** (2008) Stabilization of the N-terminal beta-hairpin of ubiquitin by a terminal hydrophobic cluster. *Biopolymers.* **90**(3), 394-8.
- Roder, H., Elove, G.A. and Englander, S.W.** (1988). Structural Characterization of folding intermediates in cytochrome c by H-exchange labeling and proton NMR. *Nature.* **335**, 700-704.
- Roscoe BP, Thayer KM, Zeldovich KB, Fushman D, Bolon DN.** (2013). Analyses of the effects of all ubiquitin point mutants on yeast growth rate. *J Mol Biol.* **425**, 1363–77.
- 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 MS, Williams DH, Packman LC.** (1995). A short linear peptide derived from the N-terminal sequence of ubiquitin folds into a water-stable non-native beta-hairpin. *Nat Struct Biol.* **2**(11), 999-1006.
- Searle, M.S., Williams, D.H. and Packman, L.C.** (1995). Folding of a short linear peptide into a water-stable β -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.
- Sloper-Mould KE, Jemc JC, Pickart CM, Hicke L.** (2001). Distinct functional surface regions on ubiquitin. *J Biol Chem.* **276**, 30483–9.
- 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.

- 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., 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.
- Varshavsky, A.** (2005). Regulated Protein Degradation. *Trends in Biochem. Sci.* **30**(6):283-6.
- 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.
- Wilkinson, K.D.** (1997). Regulation of Ubiquitin-Dependent Processes by Deubiquitinating Enzymes. *FASEB J.* **11**(14), 1245-56.
- 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.
- 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.
- 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 NH₂-terminal fragment complexes that are promoted by the age-dependent decrease in proteasome activity. *J. Cell. Biol.* **163**, 109-118.