

# **BIO 5113 PRINCIPLES OF BIOCHEMISTRY**

**UTSA, Spring, 2016**

Monday & Wednesday, 2:30-3:45 PM, MH 3.02.26

**Instructor:** Dr. Robert Renthal

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Office hours: by appointment

**Course outline and learning objectives:** Topics to be included in the course: structure and function of DNA, RNA, carbohydrates, lipids, and proteins; enzyme activity; regulation and signaling mechanisms. Students will be engaged in critical thinking and problem solving in biochemistry.

**Format:** Class periods will consist of lectures by the instructor and discussion of the assigned reading. The schedule of lecture topics is listed on page 2.

**Exams:** Three midterm exams. If an exam date conflicts with a student's anticipated absence (e.g. for a graduate school interview or paper presentation at a scientific meeting), a make-up exam may be scheduled if the instructor is given written notification at least 1 week before the exam. Make-up exams for emergencies will be considered on an individual basis.

**Reading assignments:** There is no textbook for the course. Journal articles related to the lecture topics will be posted on the Blackboard web site. The articles, numbered 1-39, are listed on pages 3-4, and the article numbers for each lecture are listed on the schedule (p. 2).

**Written work:** Each student will be assigned an additional journal article on a topic related to one of the scheduled lectures. The student will briefly write a paper summarizing the article (2-3 pages) and explain how it relates to the lecture topic. Each paper will be posted on the Blackboard web site. The list of assignments will be distributed in February, with the first paper due in March.

**Grading:** Exams will each count 28% of the final grade; paper will count 16%.

## Schedule

<b>Date</b>	<b>Topic</b>	<b>Reading</b>
Jan 11	Protein properties	1-2
13	Protein folding	3-5
20	Proteomics	6
25	Protein modifications	7
27	Protein association	8-9
Feb 1	Ligand binding	10
3	Fibrous proteins and coiled coils	11-13
8	Domains: protein-protein interactions	14-15
10	Domains: lipid-binding	16
15	<b>Exam I</b> (Jan. 11-Feb.10)	
17	no class	
22	Domains: nucleotide-binding I	17
24	Domains: nucleotide-binding II	18
29	Ubiquitin and protein degradation	19-20
Mar 2	Domains: carbohydrate-binding	21-22
7	Metabolomics and lipidomics	23-24
9	mTOR	25
21	Polynucleotides	26-27
23	Nucleic acid modifications	28-29
28	<b>Exam II</b> (Feb. 17-Mar.23)	
30	Domains: helix-turn-helix	30
Apr 4	Domains: zinc finger, leucine zipper	31-32
6	Chromatin	33-34
11	DNA replication	35
13	RNA polymerase	36
18	Aminoacyl tRNA synthetase	37
20	Ribozymes	38
25	Ribosomes	39
27	<b>Exam III</b> (Mar. 30- Apr. 25)	

## Reading assignments

- 1) "Protein families and their evolution---a structural perspective." Orengo, C.A. & Thornton, J.M., *Annu. Rev. Biochem.* 74: 867-900 (2005)
- 2) "Transitive homology-guided structural studies lead to discovery of Cro proteins with 40% sequence identity but different folds." C. Roessler et al., *Proc. Nat. Acad. Sci. USA* 105: 2343-2348 (2008)
- 3) "The present view of the mechanism of protein folding." D. Daggett & A. Fersht, *Nature Rev. Mol. Cell Biol.* 4: 497-502 (2003)
- 4) "The nature of protein folding pathways." Englander, S.W. & Mayne, L. *Proc. Nat. Acad. Sci. USA* 111: 15873-15880 (2014)
- 5) "The GroEL-GroES chaperonin machine: a nano-cage for protein folding.: M. Hayer-Hartl, A. Bracher, F.U. Hartl. *Trends in Biochem. Sci.* 41: 62-76 (2016)
- 6) "High-throughput proteomics." Z. Ahang, S. Wu, D.L. Stenoien & L. Pasa-Tolic. *Annu. Rev. Analyt. Chem.* 47: 427-454 (2014)
- 7) "Fringe benefits: functional and structural impacts of O-glycosylation on the extracellular domain of Notch receptors." N. Rana & R. Haltiwanger, *Curr. Opin. Struct. Biol.* 21: 583-589 (2011)
- 8) "Principles of assembly reveal a periodic table of protein complexes.: S. Ahnert, J. Marsh, H. Hernandez, C. Robinson, S. Teichmann. *Science* aaa2245 (2015)
- 9) "An empirical framework for binary interactome mapping." K. Venkatesan et al., *Nature Methods* 6: 83-90 (2009)
- 10) "Rapid measurement of binding constants and heats of binding using a new titration calorimeter." T. Wiseman, S. Williston, J. Brants, L-N. Lin. *Analyt. Biochem.* 179: 131-137 (1989)
- 11) "Coiled coil domains: stability, specificity, and biological implications." J.M. Mason & K. M. Arndt, *ChemBioChem* 5: 170- 176 (2004)
- 12) "A quantitative kinetic model for the in vitro assembly of intermediate filaments from tetrameric vimentin " R. Kirmse, S. Portet, N. Mucke, U. Aebi, H. Herrmann & J. Langowski, *J. Biol. Chem.* 282: 18563-18572 (2007)
- 13) "Chemical crosslinking with disuccinimidyl tartrate defines the relative positions of the two antiparallel coiled coils of the desmin protofilament unit." N. Geisler, *FEBS Lett.* 323:63- 67(1993)
- 14) "When protein folding is simplified to protein coiling: the continuum of solenoid protein structures," B. Kobe & A. Kajava, *Trends in Biochem. Sci.* 25:509-515 (2000)
- 15) "WD-repeat proteins: structure characteristics, biological function, and their involvement in human diseases," D. Li & R. Roberts, *Cell. Mol. Life Sci.* 58:2085-2097 (2001)
- 16) "Membrane recognition by phospholipid-binding domains." M. Lemmon, *Nature Rev. Mol. Cell Biol.* 9: 99-111 (2008)
- 17) "Structure-function relationships of the G domain, a canonical switch motif." A. Wittinghofer & I. Vetter, *Annu. Rev. Biochem.* 80:943-971 (2011)
- 18) "High-resolution microtubule structures reveal the structural transitions in  $\alpha\beta$ -tubulin upon GTP hydrolysis." G. Alushin, G. Lander, E. Kellogg, R. Zhang, D. Baker, E. Nogales, *Cell* 157: 1117-1129 (2014)
- 19) "RING domain E3 ubiquitin ligases." R. Deshaies & C. Joazeiro, *Annu. Rev. Biochem.* 78: 399-434 (2009)

- 20) "Recognition and processing of ubiquitin-protein conjugates by the proteasome." D. Finley, *Annu. Rev. Biochem.* 78: 477-513 (2009)
- 21) "Mannose 6-phosphate receptors: news twists in the tale." P. Ghosh, N. Dahms & S. Kornfeld, *Nature Rev. Mol. Cell. Biol.* 4: 202-212 (2003)
- 22) "Glycosylation, galectins and cellular signaling." C. Boscher, J. Dennis & I. Nabi, *Curr. Opin. Cell Biol.* 23: 383-392 (2011)
- 23) "Single-cell metabolomics: analytical and biological perspectives." R. Zenobi, *Science* 342: 1243259 (2013)
- 24) "Lipidomics: analysis of the lipid composition of cells and subcellular organelles by electrospray ionization mass spectrometry." B. Brugger, *Annu. Rev. Biochem.* 83: 79-98 (2014)
- 25) "mTOR signaling in growth control and disease." M. Laplante & D. Sabatini, *Cell* 149: 274-293 (2012)
- 26) "Non-B DNA conformations, genomic rearrangements, and human disease," A. Bacolla & R. D. Wells, *J. Biol. Chem.* 279: 47411-47414 (2004)
- 27) "In vivo genome-wide profiling of RNA secondary structure reveals novel regulatory features." Y. Ding, Y. Tang, C. Kwok, Y. Zhang, P. Bevilacqua & S. Assmann, *Nature* 505: 696-700 (2014)
- 28) "Genome-wide approaches to studying chromatin modifications." D. Schones & K. Zhao, *Nature Rev. Genetics* 9: 179-191 (2008)
- 29) "The RNA modification database, RNAMDB: 2011 update." W. Cantara et al., *Nuc. Acids Res.* 39: D195-D201 (2011)
- 30) "Variation in homeodomain DNA binding revealed by high-resolution analysis of sequence preferences." M. Berger et al., *Cell* 133: 1266-1276 (2008)
- 31) "C2H2 zinc finger proteins greatly expand the human regulatory lexicon." H. Najafabadi et al., *Nature Biotechnology* 33, 555-562 (2015)
- 32) "Structural basis for the diversity of DNA recognition by bZIP transcription factors." Y. Fujii, T. Shimizu, T. Toda, M. Yanagida & T. Hakoshima, *Nature Structural Biol.* 7: 889-893 (2000)
- 33) "Methods for identifying higher-order chromatin structure." S. Sajjan & R.D. Hawkins. *Annu. Rev. Genomics Hum. Genet.* 13: 59082 (2012)
- 34) "Stacked thin layers of metaphase chromatin explain the geometry of chromosome rearrangements and banding." J.-R. Daban, *Scientific Reports* 5: 14891 (2015)
- 35) "Motors, switches, and contacts in the replisome." S. Hamdan & C. Richardson, *Annu. Rev. Biochem.* 78:205-243 (2009)
- 36) "Real-time observation of the initiation of RNA polymerase II transcription." F. Fazal, C. Meng, K. Murakami, R. Kornberg & S. Block, *Nature* 525: 274-277 (2015)
- 37) "Exploring the evolutionary diversity and assembly modes of multi-aminoacyl-tRNA synthetase complexes: lessons from unicellular organisms." D. Laporte et al., *FEBS Letters* 588: 4268-4278 (2014)
- 38) "Structural basis of pre-mRNA splicing." J. Hang, R. Wan, C. Yan & Y. Shi, *Science* 349: 1191-1198 (2015)
- 39) "The structural basis of large ribosomal subunit function," P.B. Moore & T.A. Steitz, *Annu. Rev. Biochem.* 72: 813-850 (2003)