האוניברסיטה העברית בירושלים

סילבוס

מבנה ותפקיד של חלבונים-מעבדה - 81821

תאריך עדכון אחרון 26-10-2015

נקודות זכות באוניברסיטה העברית: 3

תואר: מוסמך

היחידה האקדמית שאחראית על הקורס: מדעים ביורפואיים

השנה הראשונה בתואר בה ניתן ללמוד את הקורס: 0

סמסטר: סמסטר א'

שפת ההוראה: עברית

קמפוס: עין כרם

מורה אחראי על הקורס (רכז): פרופ אורה פורמן-שולר

דוא"ל של המורה האחראי על הקורס: oraf@ekmd.huji.ac.il

שעות קבלה של רכז הקורס: יום ג 14:00-15:00

מורי הקורס:

גב אריאלה וינברג-שוקרון
מר רועי גרניט
גב טטיאנה שסטקין
פרופ חנה מרגלית

<u>תאור כללי של הקורס:</u>
הקורס עוסק במבנה ותפקיד של חלבונים, תוך התייחסות לקשר רצף-מבנה-תפקיד. עקרונות המשמשים
לקיפול חלבונים. השפעת מוטציות על מבנה החלבון. אפיון משפחות חלבונים. אספקטים אבולוציונים הנגזרים
ורמציה גנומית. אספקטים מבניים בתהליכי הכרה בין מולקולות. התרגיל יתקיים בכיתת המחשבים ובו שיטות ממוחשבות להצגה וניתוח של מבנים תלת מימדיים, ניבוי מבני על סמך אינפורמצית רצף, זיהוי ים אופיניים ושיוך רצף למשפחת חלבונים ידועה.

<u>מטרות הקורס:</u>
מטרת הקורס הינה להקנות לסטודנט
רקע על הבסיס המבני של חלבונים.

חלק זה מכיל את התרגילים.

התרגילים מלוות בהרצאות)קורס מס 81817(

<u>תוצרי למידה</u>
<u>בסיומו של קורס זה, סטודנטים יהיו מסוגלים:</u>
איפיון חלבון על בסיס המבנה שלו

הבנת הבסיס המבני של יציבות ופעילות
חלבונים

<u>דרישות נוכחות (%):</u>
80

<u>שיטת ההוראה בקורס:</u> הרצאות (81817#) ותרגילים

<u>רשימת נושאים / תכנית הלימודים בקורס:</u>
Ex1:
• Databases of protein sequence and structure (uniprot; pdb)
• Structural visualization: introduction to Pymol
• Pymol example: HLA-peptide binding

• Databases for structure classification (SCOP & CATH)

Sequence → structure
Ex2: Helices & sheets
Ex3: Evolutionary conservation of protein structure: the hemoglobin family
Ex4:
• Measure of similarity and quality of protein structures: RMSD; NMR vs. xray
• Prediction of effect of mutation on protein stability
Protein structure prediction & design
Ex5:
• Basics of sequence-based structure prediction: PSSM & PSIBLAST
• Secondary structure prediction
Ex6:
• Fold recognition + Comparative modeling
Ex7:
• Prediction of effect of mutations in human proteins on protein stability and function
Ex8: Protein design
Ex9: Adaptation to extremes
Structure → function
Ex10: The structural basis of function
Specific examples: Protein-DNA interactions; Transmembrane proteins
Ex11: DNA-protein interactions
• DNA
• Zn Fingers
DNA-protein interactions, cont.
• HTH
• Bzip

<u>חומר חובה לקריאה:</u>
none

<u>חומר לקריאה נוספת:</u>
References Lecture 1: Introduction
• Levitt, M. (2001). The birth of computational structural biology. Nature Structural Biology 8:392–393
Protein basics:
Book Chapters:
** Chapter 1 in Branden & Tooze*
** Chapter 1.1-1.3 in Proteins (Creighton)*
Forces that determine protein structure
Book Chapters:

** Panel 2-3 in Molecular Biology of the Cell, 4th ed. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid&eq;mboc4.box.198 * Chapter 4.1 in Proteins (Creighton)*

Lecture 2: Protein Secondary Structure & Protein Classification

Book Chapters:

** Chapter 2-5 in Branden & Tooze*

** Chapter 5.1, 5.3 in Proteins (Creighton)*

Databases of protein structure classification

(1) SCOP: http://scop.mrc-lmb.cam.ac.uk/scop/; http://scop.berkeley.edu

• Murzin AG, Brenner SE, Hubbard T, Chothia C. (1995). SCOP: a structural classification of proteins database for the investigation of sequences and structures. J Mol Biol. 247:536-40.

• Andreeva A, Howorth D, Chandonia JM, Brenner SE, Hubbard TJ, Chothia C, Murzin AG. (2008). Data growth and its impact on the SCOP database: new developments. Nucleic Acids Research 36:D419-25.

• Andreeva A, Howorth D, Chothia C, Kulesha E, Murzin, AG. (2014). SCOP2 prototype: a new approach to protein structure mining. Nucleic Acids Research 42:D310–4.

(2) CATH: http://www.cathdb.info/

• Orengo CA, Michie AD, Jones DT, Swindells MB, Thornton JM. (1997). CATH: A Hierarchic Classification of Protein Domain Structures. Structure 5:1093-1108

• Sillitoe I, Cuff AL, Dessailly BH, Dawson NL, Furnham N, Lee D, Lees JG, Lewis TE, Studer RA, Rentzsch R, Yeats C, Thornton JM, Orengo CA. (2012). New functional families (FunFams) in CATH to improve the mapping of conserved functional sites to 3D structures. Nucleic Acids Research 41:D490-498.

(3) ECOD: http://prodata.swmed.edu/ECOD/ Grishin Lab, to be published Lecture 3:

Anfinsen's principle: Sequence determines structure

• Anfinsen (1973). Principles that govern the folding of protein chains Science 181:223-30.

Determinants of secondary structure;

• Pace N and Scholtz M. (1998). A helix propensity scale based on experimental studies of peptides and proteins. Biophysical Journal 75:422-427

• Munoz V and Serrano L. (1995). Helix design, prediction and stability. Curr Opin Biotechnol 6:382-386

- • Smith CK, Withka JM and Regan L. (1994) A thermodynamic scale for the beta sheet forming tendencies of the amino acids. Biochemistry 33:5510-7

• West MW and Hecht MH (1995). Binary patterning of polar and nonpolar amino acids in the sequences and structures of native proteins. Protein Sci. 4:2032-2039

• Xiong H, Buckwalter BL, Shieh HM, and Hecht MH (1995). Periodicity of polar and -nonpolar amino acids is the major determinant of secondary structure in self assembling oligomeric peptides. PNAS 92:6349

• Kabsch and Sander (1983). Dictionary of protein secondary structure: Pattern recognition of hydrogen-bonded and geometrical features. FEBS letters 22:2577-2637.

• Minor and Kim (1996). Context-dependent secondary structure formation of a designed protein sequence. Nature 380:730-4.
• Pace N and Scholtz M. (1998). A helix propensity scale based on experimental studies of peptides and proteins. Biophysical journal 75:422-427
• Munoz V and Serrano L. (1995). Helix design, prediction and stability. Curr Opin Biotechnol 6:382-386
- • Smith CK, Withka JM and Regan L. (1994) A thermodynamic scale for the beta sheet forming tendencies of the amino acids. Biochemistry 33:5510-7
• West MW and Hecht MH (1995). Binary patterning of polar and nonpolar amino acids in the sequences and structures of native proteins. Protein Sci. 4:2032-2039
• Xiong H, Buckwalter BL, Shieh HM, and Hecht MH (1995). Periodicity of polar and -nonpolar amino acids is the major determinant of secondary structure in self assembling oligomeric peptides. Proceedings of the National Academy of Sciences 92:6349
• Minor and Kim (1996). Context-dependent secondary structure formation of a designed protein sequence. Nature 380:730-4.
• Kabsch and Sander (1983). Dictionary of protein secondary structure: Pattern recognition of hydrogen-bonded and geometrical features. FEBS letters 22:2577-2637.
Lecture 4: Sequence-Structure relationship: Evolution and mutational analysis
Evolutionary conservation in the globin family
• Lesk and Chothia (1980). How different amino acid sequences determine similar protein structures: the structure and evolutionary dynamics of the globins J Mol Biol 136:225-70.

Effect of mutations on protein structure
Suppressor trna assays
• Rennell, Bouvier, Hardy and Poteete (1991). Systematic mutation of bacteriophage T4 lysozyme J Mol Biol 222:67-88.
• Suckow, Markiewicz, Kleina, Miller, Kisters-Woike and Muller-Hill (1996). Genetic studies of the Lac repressor. XV: 4000 single amino acid substitutions and analysis of the resulting phenotypes on the basis of the protein structure J Mol Biol 261:509-23.
Targeted mutation + measure of protein stability
• Matthews. (1996). Structural and genetic analysis of the folding and function of T4 lysozyme. The FASEB Journal: 10:35-41
• He, Wood, Baase, Xiao and Matthews (2004). Alanine-scanning mutagenesis of the β-sheet region of phage T4 lysozyme suggests that tertiary context has a dominant effect on β-sheet formation. Protein Sci. 13:2716-2724
• Lim and Sauer (1989). Alternative packing arrangements in the hydrophobic core of λ repressor. Nature 339:31-36
• Lim, Hodel, Sauer and Richards (1994). The crystal structure of a mutant protein with altered but improved hydrophobic core packing. Proc Natl Acad Sci USA 91:423-427
Deep mutational sequencing
- • Fowler, Araya, Fleishman, Kellogg, Stephany, Baker and Fields (2010). High

resolution mapping of protein sequence-function relationships. Nat Methods 7:741-746.

• Araya & Fowler (2011). Deep mutational scanning: assessing protein function on a massive scale. Trends in biotechnology 29:9.

Lecture 5: Protein Folding

Book Chapters:

** Chapter 6 in Branden & Tooze*

** A good description of Phi analysis and chevron plots can be found in the wikipedia*

http://en.wikipedia.org/wiki/Phi_value_analysis

http://en.wikipedia.org/wiki/Chevron_plot

Reviews:

• Dill and Chan (1997). From Levinthal to pathways to funnels Nat Struct Biol 4:10-9.

• Phi analysis: Fersht (1997). Nucleation mechanisms in protein folding Curr Opin Struct Biol 7:3-9.

• Sosnick & Barrick (2011). The folding of single domain proteins — have we reached a consensus? Curr Opin Struct Biol 21:12-24.

• Horwich, A. L. (2011). Protein folding in the cell: an inside story. Nature Medicine 17:1211– 1216.

Research Papers:

• Levinthal (1969). How to fold graciously Mossbauer Spectroscopy in Biological Systems: Monticello, Illinois 22-24.

• Zwanzig (1995). Simple model of protein folding kinetics. PNAS 92:9801-4.

• Go (1983). Theoretical studies of protein folding Annu Rev Biophys Bioeng 12:183-210.

• Kim and Baldwin (1982). Specific intermediates in the folding reactions of small proteins and the mechanism of protein folding Annu Rev Biochem 51:459-89.

• Myers and Oas (2002). Mechanism of fast protein folding Annu Rev Biochem 71:783-815.

• Arai and Kuwajima (2000). Role of the molten globule state in protein folding Adv Protein Chem 53:209-82.

• Lindorff-Larsen, Piana, Dror and Shaw (2011). How Fast-Folding Proteins Fold. Science 334:517-520.

Lecture 6: Secondary structure prediction

Good short introduction to Artificial Neural Networks: ANN

Krogh (2008). What are artificial neural networks? Nat Biotechnol 26:195-7.

Initial approaches for secondary structure prediction

Chou PY, Fasman GD (1974). Conformational parameters for amino acids in helical, beta-sheet, and random coil regions calculated from proteins. Biochemistry 13, 211-222.

Garnier J, Osguthorpe DJ, Robson B (1978). Analysis of the accuracy and implications of simple methods for predicting the secondary structure of globular

proteins. J Mol Biol 120, 97-120.
Levin JM, Pascarella S, Argos P, Garnier J (1993). □□Quantification of secondary structure prediction improvement using multiple alignments. Protein Eng 6, 849-854
Kabsch and Sander (1983). How good are predictions of protein secondary structure? FEBS Lett 155:179-82.
PHD & PredictProtein PHD
Rost & Sander (1993). Prediction of protein secondary structure at better than 70% accuracy. J Mol Biol 232:584-99.
PROFsec
Rost (2001). Review: Protein secondary structure prediction continues to rise. J Struct Biol 134: 204-18.
PredictProtein
Yachdav, Kloppmann, Kajan, Hecht, Goldberg, Hamp,..., Rost (2014). PredictProtein—an open resource for online prediction of protein structural and functional features. Nucleic Acids Research 42:W337–43.
https://www.predictprotein.org

PSIPRED
Jones (1999). Protein secondary structure prediction based on position-specific scoring matrices J Mol Biol 292:195-202.
Bryson K, McGuffin LJ, Marsden RL, Ward JJ, Sodhi JS. & Jones DT. (2005) Protein structure prediction servers at University College London. Nucl. Acids Res. 33: W36-38
Conformational Switches
Young, Kirshenbaum, Dill and Highsmith (1999). Predicting conformational switches in proteins Protein Sci 8:1752-64.
Lecture 7: Template-based modeling of protein structure
Sequence and structural similarities
Sander and Schneider (1991). Database of homology-derived protein structures and the structural meaning of sequence alignment. Proteins: Structure, Function and Genetics 9:56-68
Fold recognition
Jones, Taylor and Thornton (1992). A new approach to protein fold recognition Nature 358:86-9. RAPTORX: Peng & Xu (2011). Raptorx: Exploiting structure information for protein alignment
by statistical inference. Proteins 79:161–171.
GENTHREADER: Jones (1999). GenTHREADER: an efficient and reliable protein fold recognition method for genomic sequences J Mol Biol 287:797-815.
HHSEARCH & HHPRED: Söding (2005). Protein homology detection by HMM-HMM comparison. Bioinformatics 21:951-960.
Homology modeling
Marti-Renom, Stuart, Fiser, Sanchez, Melo and Sali (2000). Comparative protein structure modeling of genes and genomes Annu Rev Biophys Biomol Struct 29:291-325.
Fiser and Sali (2003). Modeller: generation and refinement of homology-based protein structure models. Methods Enzymol 374:461-91.

Pieper et al. (2013). ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research 42: D336–D346.
Biasini, Bienert, Waterhouse, ... & Schwede (2014). SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. Nucleic Acids Research 42:W252–8.
Wallner and Elofsson (2005). All are not equal: a benchmark of different homology modeling programs. Protein Sci 14:1315-27.
Loop modeling
Canutescu and Dunbrack (2003). Cyclic coordinate descent: A robotics algorithm for protein loop closure. Protein Sci 12:963-72.
Coutsias et al. (2004) A kinematic view of loop closure. Journal of computational chemistry 25:510-28

Mandell et al. (2009). Sub-angstrom accuracy in protein loop reconstruction by robotics-inspired conformational sampling. Nat Methods. 6:551-2
Rotamer libraries
Dunbrack (2002). Rotamer Libraries in the 21st Century. Current Opinion in Structural Biology: 12:431–440.
Lecture 8: Ab initio modeling, CASP, structural genomics and "phenomics"
Rosetta
Rohl, C. A., Strauss, C. E. M., Misura, K. M. S., & Baker, D. (2004). Protein structure prediction using Rosetta. Methods in Enzymology, 383, 66–93.
Das, R., & Baker, D. (2008). Macromolecular modeling with rosetta. Annual review of biochemistry, 77, 363–382.
Bradley, P., Misura, K. M. S., & Baker, D. (2005). Toward high-resolution de novo structure prediction for small proteins. Science, 309, 1868–1871.
Kim, D. E., Blum, B., Bradley, P., & Baker, D. (2009). Sampling bottlenecks in de novo protein structure prediction Journal of molecular biology, 393, 249–260.
Cooper, S., Khatib, F., Treuille, A., Barbero, J., Lee, J., Beenen, M., Leaver-Fay, A., et al. (2010). Predicting protein structures with a multiplayer online game Nature, 466, 756–760.
Khatib, F., DiMaio, F., Foldit Contenders Group, Foldit Void Crushers Group, Cooper, S., Kazmierczyk, M., et al. (2011). Crystal structure of a monomeric retroviral protease solved by protein folding game players. Nature Structural & Molecular Biology, 18, 1175–1177.
I-Tasser
Zhang, Y. & Skolnick, J. (2004). Automated structure prediction of weakly homologous proteins on a genomic scale. PNAS 101(20), 7594–7599.
Wu, S., Skolnick, J., & Zhang, Y. (2007). Ab initio modeling of small proteins by iterative TASSER simulations BMC biology, 5, 17.
Roy, A., Kucukural, A., & Zhang, Y. (2010). I-TASSER: a unified platform for automated protein structure and function prediction. Nature protocols, 5, 725–738.
CASP
Casp 9 issue: Proteins special issue vol:79, S10
Kryshtafovych, A., Fidelis, K., & Moult, J. (2011). CASP9 results compared to those of previous

casp experiments. Proteins, 79, 196–207.
Casp 10 issue: Proteins special issue vol:82, S2
http://www.predictioncenter.org/casp10/meeting/talks.html
Structural genomics
Chandonia, J.-M., & Brenner, S. E. (2006). The impact of structural genomics: expectations and outcomes Science 311:347–351
Khafizov, K., Madrid-Aliste, C., Almo, S. C., & Fiser, A. (2014). Trends in structural coverage of the protein universe and the impact of the Protein Structure Initiative. PNAS 111:3733–3738.

Drew, K., Winters, P., Butterfoss, G. L., Berstis, V., Uplinger, K., Armstrong, J., Riffle, M., et al. (2011). The Proteome Folding Project: proteome-scale prediction of structure and function Genome research 21: 1981–1994.
Lewis, T. E., Sillitoe, I., Andreeva, A., Blundell, T. L., Buchan, D. W. A., Chothia, C., et al. (2014). Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research. doi:10.1093/nar/gku973
Large-scale mapping of disease associated mutations (snps)
Katsonis, P., Koire, A., Wilson, S. J., Hsu, T.-K., Lua, R. C., Wilkins, A. D., & Lichtarge, O. (2014). Single nucleotide variations: Biological impact and theoretical interpretation. Protein Science 23:1650–1666.
Adzhubei, I. A., Schmidt, S., Peshkin, L., Ramensky, V. E., Gerasimova, A., Bork, P., et al. (2010). A method and server for predicting damaging missense mutations. Nature Methods 7:248– 249.
Lecture 9: Protein Design
Kamtekar, S., Schiffer, J. M., Xiong, H., Babik, J. M., & Hecht, M. H. (1993). Protein design by binary patterning of polar and nonpolar amino acids. Science, 262, 1680–1685.
Rojas, N. R., Kamtekar, S., Simons, C. T., McLean, J. E., Vogel, K. M., Spiro, T. G., Farid, R. S., et al. (1997). De novo heme proteins from designed combinatorial libraries. Protein Science:6,2512–2524.
Dahiyat, B. I., & Mayo, S. L. (1997). De novo protein design: fully automated sequence selection. Science, 278, 82–87.
Kuhlman, B., & Baker, D. (2000). Native protein sequences are close to optimal for their structures. PNAS, 97, 10383–10388.
Harbury, P. B., Plecs, J. J., Tidor, B., Alber, T., & Kim, P. S. (1998). High-resolution protein design with backbone freedom. Science, 282, 1462–1467.
Design of a novel globular protein fold with atomic-level accuracy. (2003). Design of a novel globular protein fold with atomic-level accuracy. Science, 302, 1364–1368.
Watters, A., Deka, P., Corrent, C., Callender, D., Varani, G., Sosnick, T., & Baker, D. (2007). The highly cooperative folding of small naturally occurring proteins is likely the result of natural selection. Cell, 128, 613–624.
Koga, N., Tatsumi-Koga, R., Liu, G., Xiao, R., Acton, T. B., Montelione, G. T., & Baker, D. (2012). Principles for designing ideal protein structures. Nature, 491, 222–227.
Röthlisberger, D., Khersonsky, O., Wollacott, A. M., Jiang, L., DeChancie, J., Betker,

J., Gallaher, J. L., et al. (2008). Kemp elimination catalysts by computational enzyme design. Nature, 453, 190–195.
Jiang, L., Althoff, E., Clemente, F., Doyle, L., Rothlisberger, D., Zanghellini, A., Gallaher, J., et al. (2008). De novo computational design of retro-aldol enzymes. Science, 319, 1387.
Havranek, J. J., & Harbury, P. B. (2003). Automated design of specificity in molecular recognition Nature structural biology, 10, 45–52.

Ambroggio, X., & Kuhlman, B. (2006). Design of protein conformational switches. Current opinion in structural biology, 16, 525–530.
Levskaya, A., Weiner, O. D., Lim, W. A., & Voigt, C. A. (2009). Spatiotemporal control of cell signalling using a light-switchable protein interaction. Nature, 461, 997–1001.
Lecture 10: Protein Function
Gene Ontology
Ashburner, M., Ball, C. A., Blake, J. A., Botstein, D., Butler, H., Cherry, J. M., et al. (2000). Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nature Genetics 25:25–29
Moonlighting Proteins
Jeffery, C. (1999). Moonlighting proteins. Trends in Biochemical Sciences 24:8–11.
Jeffery, C. J. (2009). Moonlighting proteins--an update. Molecular bioSystems 5:345–350
Jeffery, C. J. (2004). Molecular mechanisms for multitasking: recent crystal structures of moonlighting proteins. Current Opinion in Structural Biology 14: 663–668
Tompa, P., Szász, C., & Buday, L. (2005). Structural disorder throws new light on moonlighting. Trends in Biochemical Sciences 30:484–489
In vitro evolution of new functions
Khersonsky, O., Roodveldt, C., & Tawfik, D. S. (2006). Enzyme promiscuity: evolutionary and mechanistic aspects. Current Opinion in Chemical Biology 10: 498–508
Khersonsky, O., & Tawfik, D. S. (2010). Enzyme promiscuity: a mechanistic and evolutionary perspective. Annual Review of Biochemistry 79:471–505
Griffiths, A. D., & Tawfik, D. S. (2006). Miniaturising the laboratory in emulsion droplets. Trends in Biotechnology 24:395–402
Lecture 11: Prediction of Protein Function
Xin, F., & Radivojac, P. (2011). Computational methods for identification of functional residues in protein structures. Current Protein & Peptide Science, 12: 456–469.
Cheng, G., Qian, B., Samudrala, R., & Baker, D. (2005). Improvement in protein functional site prediction by distinguishing structural and functional constraints on protein family evolution using computational design. Nucleic Acids Research, 33: 5861–5867.
Elcock, A. (2001). Prediction of functionally important residues based solely on the computed energetics of protein structure. JMB 312:885-896.
Amitai, G., Shemesh, A., Sitbon, E., Shklar, M., Netanely, D., Venger, I., &

Pietrokovski, S. (2004). Network analysis of protein structures identifies functional residues. Journal of Molecular Biology 344:1135–1146.
Ben-Shimon, A., & Eisenstein, M. (2005). Looking at Enzymes from the Inside out: The Proximity of Catalytic Residues to the Molecular Centroid can be used for Detection of Active Sites and Enzyme–Ligand Interfaces. Journal of Molecular Biology, 351:309–326.

Lichtarge, O., & Sowa, M. E. (2002). Evolutionary predictions of binding surfaces and interactions. Current Opinion in Structural Biology, 12:21–27.
Pazos, F. & Sternberg, M. J. E. (2004). Automated prediction of protein function and detection of functional sites from structure. PNAS 101:14754–14759.
Wass, M. N., & Sternberg, M. J. E. (2008). ConFunc--functional annotation in the twilight zone. Bioinformatics 24:798–806.
Laskowski, R. A., Watson, J. D., & Thornton, J. M. (2005). ProFunc: a server for predicting protein function from 3D structure. Nucleic Acids Research, 33:W89–W93.
Watson, J. D., Sanderson, S., Ezersky, A., Savchenko, A., Edwards, A., Orengo, C., et al. (2007). Towards fully automated structure-based function prediction in structural genomics: a case study. Journal of Molecular Biology 367:1511–1522.
Radivojac, P., Clark, W. T., Oron, T. R., Schnoes, A. M., Wittkop, T., Sokolov, A., et al. (2013). A large-scale evaluation of computational protein function prediction. Nature Methods 10:221-227
Lecture 12: Protein-DNA recognition and binding DNA Structure
** Chapter 7 in Branden & Tooze*
** Review:*
Seeman, Rosenberg and Rich (1976). "Sequence-specific recognition of double helical nucleic acids by proteins". Proc Natl Acad Sci U S A 73:804-8.
Helix-Turn-Helix
** Chapter 8 in Branden & Tooze*
** Research Papers:*
Wharton, R. P., Brown, E. L., & Ptashne, M. (1984). Substituting an alpha-helix switches the sequence-specific DNA interactions of a repressor. Cell 38:361–369
Wharton, R. P., & Ptashne, M. (1985). Changing the binding specificity of a repressor by redesigning an alpha-helix. Nature 316:601–605.
Zinc Fingers
** Chapter 10 in Branden & Tooze*
Research Papers:
Pavletich NP1, Pabo CO. (1991) Zinc finger-DNA recognition: crystal structure of a Zif268-DNA complex at 2.1 A. Science 10:809-17.
Leucine Zippers
** Chapter 10 in Branden & Tooze Reviews:*
** Ellenberger (1994). "Getting a grip on DNA recognition: structures of the basic region leucine zipper, and the basic region helix-loop-helix DNA-binding domains". Curr Opin Struct Biol 4:12- 21.*

Research Papers:
** Landschulz, Johnson and McKnight (1988). The leucine zipper: a hypothetical*

structure common to a new class of DNA binding proteins. Science 240:1759-64.
** Landschulz, Johnson and McKnight (1989). The DNA binding domain of the rat liver nuclear protein C/EBP is bipartite. Science 243:1681-8.*
** Agre, Johnson and McKnight (1989). Cognate DNA binding specificity retained after leucine zipper exchange between GCN4 and C/EBP. Science 246:922-6.*
** Sellers and Struhl (1989). Changing fos oncoprotein to a jun-independent DNA binding protein with GCN4 dimerization specificity by swapping "leucine zippers". Nature 341:74-6.*
** O'Shea, Klemm, Kim and Alber (1991). X-ray structure of the GCN4 leucine zipper, a two- stranded, parallel coiled coil. Science 254:539-44.*
** O'Shea, Rutkowski and Kim (1992). Mechanism of specificity in the Fos-Jun oncoprotein heterodimer. Cell 68:699-708.*
** Ellenberger, Brandl, Struhl and Harrison (1992). The GCN4 basic region leucine zipper binds DNA as a dimer of uninterrupted alpha helices: crystal structure of the protein-DNA complex. Cell 71:1223-37.*
** Konig and Richmond (1993). The X-ray structure of the GCN4-bZIP bound to ATF/CREB site DNA shows the complex depends on DNA flexibility. J Mol Biol 233:139-54.*
Design of specific Leucine Zippers
Grigoryan, G., Reinke, A. W., & Keating, A. E. (2009). Design of protein-interaction specificity gives selective bZIP-binding peptides. Nature 458:859–864
TAL effectors
Review:
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