Sunday, June 21

19:00-20:30 **Dinner**

20:30 **Informal gathering**

Monday, June 22

7:00-8:45 am **Breakfast**

Session 1 (chair Harmen Bussemaker):

8:45-9:00 **Welcome and Introduction**

9:00-9:30 Wilma Olson “DNA topology confers sequence specificity to nonspecific architectural proteins”

9:30-10:00 Robert Kaptein “DNA recognition and target location by the E. coli Lac Repressor”

10:00-10:30 Francisco Melo “Development of new structural bioinformatics tools to advance our understanding of protein-DNA recognition”

10:30-11:00 Phil Bradley “Prediction and design of protein-DNA interactions”

11:00-11:30 **Coffee break**

Session 2 (chair Wilma Olson):

11:30-12:00 Héctor Viadiu “Target gene specificity in the p53 family of transcription factors”

12:00-12:30 Remo Rohs “Quantitative modeling of transcription factor binding specificities using DNA shape”

12:30-13:00 Alberto Perez “Improved force fields, solvents and sampling for nucleic-acid protein complexes”

13:30-15:00 **Lunch**

Session 3 (chair Remo Rohs):

15:00-15:30 Trevor Siggers “Adaptation and Allostery”

15:30-16:00 Sebastiaan Meijsing “How do transcriptional factors "know" where to go in the genome?”

16:00-16:30 Chuck Vinson “The ETS-CRE 16-mer (CCGGAAGTGACGTCAC) on microarrays”

16:30-17:00 **Coffee/Tea break**

Session 4 (chair Trevor Siggers):

17:00-17:30 Raluca Gordan “Assessing direct versus tethered recruitment of transcription factors to the genome”

17:30-18:00 Tom Tullius “Nucleotide-resolution structural maps of DNA and DNA-protein complexes, in vitro and in vivo”

19:00-21:00 **Dinner**

<u>Tuesday, June 23</u>

7:00-9:00 **Breakfast**

Session 5 (chair Héctor Viadiu):

9:00-9:30 Gary Stormo “New methods for determining specificity and cooperativity”

9:30-10:00 Matt Weirauch “Approaches for Understanding Combinatoric Transcription Factor Interactions”

10:00-10:30 Todd Riley “Hidden Markov model analysis reveals complex binding modes for the transcription factor Gcn4”

10:30-11:00 Martha Bulyk “Context Influences on TALE-DNA Binding Revealed by Quantitative Profiling”

11:00-11:30 **Coffee break**

Session 6 (chair Gary Stormo):

11:30-12:00 Marcus Noyes “Advances in the omega-based B1H system for the comparative analysis of protein-DNA interactions”

12:00-12:30 Mona Singh “Exploring variation in Cys2His2 transcription factors”

12:30-13:00 Tim Hughes “Kaleidoscopic evolution of C2H2 zinc finger sequence specificity”

13:30-15:00 **Lunch**

Session 7 (chair Trevor Siggers):

15:00-15:30 Jussi Taipale “Genome-wide analysis of protein-DNA interactions”

15:30-16:00 Harmen Bussemaker “New algorithms for learning feature-based recognition models”

16:00-16:30 Miles Pufall “The Androgen and Glucocorticoid receptors use the same interface to bind DNA with different specificity”

16:30-17:00 **Coffee/Tea break**

Session 8 (chair Miles Pufall):

17:00-17:30 Matt Slattery “Stoichiometric and switch-like regulatory strategies in the ancient response to oxidative stress”

17:30-18:00 Polly Fordyce “Developing and deploying microfluidic tools for understanding transcription factor specificities”

19:00-21:00 **Dinner**

Wednesday, June 24

7:00-9:00 Breakfast

Session 9 (chair Matt Slattery):

9:00-9:30 Michal Levo “Unraveling determinants of transcription factor binding outside the core binding site”

9:30-10:00 Yaron Orenstein “Computational inference of binding site models from high-throughput SELEX data”

Session 10 (20-min student talks, chair Bill Noble):

10:00-10:20 Lin Yang “Dissecting the role of DNA shape readout for different transcription factor families”

10:20-10:40 Carolina Dantas “From DNA base pairs to protein residues: unraveling protein-DNA binding determinants”

10:40-11:00 **Coffee/Tea break**

11:00-11:20 Chaitanya Rastogi “Methods for Inferring Transcription Factor Specificity from SELEX-seq Data”

11:20-11:40 Judith Kribelbauer “Characterizing orientation and spacer preferences of Hox transcription factor complexes using SELEX-seq”

11:40-12:00 Ning Shen “Determination of differential DNA binding specificity between closely related transcription factors”

13:30-14:00 **Quick Lunch**

14:00-18:00 **Excursion to Mount Alban**

19:00-21:00 **Dinner**

Thursday, June 25

8:00-9:00 Breakfast

Session 11 (chair Remo Rohs):

9:00-9:30 Zhiping Weng “Predicting Transcription Factor Binding Sites by Combining Chromatin and Sequence Features”

9:30-10:00 John Stamatoyannopoulos “Decoding TF Occupancy and Function”

10:00-10:30 Cliff Meyer “Modeling Histone Acetylation Maps: from Transcription Factor binding to Gene Expression”

10:30-11:00 Christina Leslie “Learning the recognition code for transcription factor and RNA-binding protein families from high-throughput binding assays”

11:00-11:30 **Coffee break**

Session 12 (chair Polly Fordyce):

11:30-12:00 Roger Pique-Regi “Identifying genetic variants and cellular environments affecting regulation of gene transcription”

12:00-12:30 Alex Morozov “Genome-wide profiling of chromatin structure and accessibility in D. Melanogaster”

12:30-13:00 Bill Noble “Gene regulation in 3D”

13:30-15:00 **Lunch**

Session 13 (chair Matt Slattery):

15:00-15:30 Wyeth Wasserman “Detection of altered TFBS in applied genome analysis

15:30-16:00 Aseem Ansari “Non-obvious "Emergent" cognate sites and "Specificity Locks" revealed by Differential Specificity and Binding Energy Landscapes (DiSELs)”

16:00-16:30 Barak Cohen “Why don't transcription factors get lost? Specificity and cis-regulatory interactions in large genomes”

16:30-17:00 **Coffee break**

Session 14 (chair Harmen Bussemaker):

17:00-17:30 Mark Biggin “Protein/DNA interactions in vivo: Predicting DNA occupancy and function”

17:30-18:00 Dirk Schuebeler “Competition between DNA methylation and transcription factor binding

19:00-21:00 **Dinner**

Friday, June 26

7:00-9:00	**Breakfast**
9:00	Informal discussion / Free time to visit the city of Oaxaca / Departure