Sunday, June 21
19:00-20:30 Dinner
20:30 Informal gathering

Monday, June 22
7:00-8:45 am Breakfast

Session 1 (chair Harman 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

**Tuesday, June 23**

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 Kriebelbauer “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