Friday (august 4)

	Room A (2nd Floor)	Room B1	Room E1
7:00 a.m.	Shuttles depart Hotels to Convention Center		
7:30 a.m. - 6:00 p.m.	Registration - Hall G		
9:00 a.m. - 10:30 a.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	BOSC SIG
10:30 a.m. - 11:00 a.m.	Coffee Break - Satellite & SIG meetings (available outside meeting rooms)		
11:00 a.m - 12:00 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	BOSC SIG
12:00 p.m. - 1:00 p.m.	Lunch - Satellite and SIG meetings (Hall F)		
1:00 p.m. - 3:30 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	BOSC SIG
3:30 p.m. - 4:00 p.m.	Coffee Break - Satellite & SIG meetings (available outside meeting rooms)		
4:00 p.m. - 6:30 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	BOSC SIG
6:30 p.m.	Shuttles depart Convention Center to Hotels		

saturday (august 5)

	Room A (2nd Floor)	Room B1	Room B2	Room E1
7:00 a.m.	Shuttles depart Hotels to Convention Center			
7:30 a.m. - 6:00 p.m.	Registration - Hall G			
9:00 a.m. - 10:30 a.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
10:30 a.m. - 11:00 a.m.	Coffee Break - Satellite & SIG meetings (available outside meeting rooms)			
11:00 a.m - 12:00 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
12:00 p.m. - 1:00 p.m.	Lunch - Satellite and SIG meetings (Hall F)			
1:00 p.m. - 3:30 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
3:30 p.m. - 4:00 p.m.	Coffee Break - Satellite & SIG meetings (available outside meeting rooms)			
4:00 p.m. - 6:30 p.m.	3Dsig Satellite Meeting	Alternative Splicing SIG	Joint BioLINK & Bio-ontologies SIG	BOSC SIG
6:30 p.m.	Shuttles depart Convention Center to Hotels			
7:30 p.m.	3Dsig Satellite Meeting - Dinner (3Dsig Delegates and ticket holders) - Oasis Hotel (Brazil Room)			

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sunday (august 6)

	Room A (2nd Floor)	Room B1	Room B2	Room B3	Room B5	Room B6	Room E1	Room E2
7:00 a.m.	Shuttles depart Hotels to Convention Center							
7:30 a.m. - 6:00 p.m.	Registration - Hall G							
8:30 a.m. - 10:30 a.m.	Student Council Symposium (SCS2)	Tutorial *AM2:* Genomes, Browsers and Databases: Tools For Automated Data Integration Across Multiple Genomes *Peter Schattner*	Tutorial *AM4:* Chemoinformatics *Pierre Baldi*	Tutorial *AM1:* Biological Literature Mining - From Information Retrieval to Biological Discovery *Lars Juhl Jensen*	Tutorial *AM3:* Python Programming for Life Science Researchers *Sebastián Bassi*	Tutorial *AM7:* Exploring Computational Biology with a Massively Parallel High Performance Computing Environment *Kirk Jordan and Scott Emrich*	Tutorial *AM5:* Computing Biological Function: Bioinformatics Approach to the Analysis and Prediction of Protein Function *Yanay Ofran and Marco Punta*	Tutorial *AM6:* Integration and Analysis of Diverse Genomic Data *Olga Troyanskaya*
10:30 a.m. - 10:45 a.m.	Coffee Break - Tutorials and Student Council Symposium (available outside meeting rooms)							
10:45 a.m. - 12:30 p.m.	SCS2 Continued	Tutorial *AM2* Continued	Tutorial *AM4* Continued	Tutorial *AM1* Continued	Tutorial *AM3* Continued	Tutorial *AM7* Continued	Tutorial *AM5* Continued	Tutorial *AM6* Continued
12:30 p.m. - 2:00 p.m.	Lunch for delegates attending Student Council Symposium, delegates attending 2 tutorials and ticket holders - Hall F							
2:00 p.m. - 4:00 p.m.	SCS2 Continued	Tutorial *PM11:* Computational Biology Of Post-Transcriptional Gene Regulation: At The Interplay Of Genomes, Networks And Evolution *Uwe Ohler and Dirk Holste*	Tutorial *PM13:* Protein-Protein Interactions: Structure and Systems Approaches to Analyze Diverse Genomic Data *Anna Panchenko and Benjamin Shoemaker*		Tutorial *PM10:* Introduction to Computational Proteomics - Open Problems *Jacques Colinge*		Tutorial *PM8:* Bayesian Networks For Bioinformatics: An Introduction To Inference And Learning *Chris Needham and James Bradford*	Tutorial *PM9:* From Pathways Databases to Network Models *Baltazar Aguda and Andrew Goryachev*
4:00 p.m. - 4:15 p.m.	Coffee Break - Tutorials and Student Council Symposium (available outside meeting rooms)							
4:15 p.m. - 6:00 p.m.	SCS2 Continued	Tutorial *PM11* Continued	Tutorial *PM13* Continued		Tutorial *PM10* Continued		Tutorial *PM8* Continued	Tutorial *PM9* Continued
6:00 p.m. - 6:30 p.m.	Shuttles depart Convention Center to Hotels							

monday (august 7)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
7:00 a.m.	Shuttles depart Hotels to Convention Center						
7:30 a.m. - 7:30 p.m.	Registration - Hall G						
8:45 a.m. - 10:05 a.m.	Opening Welcome and Introduction of Keynote 1 - Main Auditorium (Hall D) Keynote 1: Robert Huber - Molecular machines for protein degradation						
9:00 a.m. - 9:00 p.m.	Posters on Display - Hall G - 9:00 a.m. - 9:00 p.m.						
10:05 a.m. - 10:30 a.m.	Coffee Break with Exhibitors - Hall C						
10:30 a.m. - 10:55 a.m.	Structural Bioinformatics *Paper 1:* ZPRED: Predicting the distance to the membrane center for residues in alpha-helical membrane proteins *Erik Granseth, Håkan Viklund, Arne Elofsson*	Database and Data Integration *Paper 2:* An experimental metagenome data management and analysis system *Victor Markowitz, Natalia Ivanova, Krishna Palaniappan Ernest Szeto, Frank Korzeniewski, Athanasios Lykidis, Iain Anderson, Konstantinos Mavrommatis, Victor Kunin, Hector Garcia Martin, Inna Dubchak, Phil Hugenholtz, Nikos Kyrpides*	Systems Biology *Paper 3:* Create and assess protein networks through molecular characteristics of individual proteins *Yanay Ofran, Guy Yachdav, Eyal Mozes, Ta-tsen Soong, Rajesh Nair, Burkhard Rost*	Software Demo ArrayExpress	Software Demo Integrated Microbial Genomes (IMG) System	Software Demo SSAHA2	Software Demo GINsim: a software for the qualitative
10:55 a.m. - 11:20 a.m.	Structural Bioinformatics *Paper 4:* A combinatorial pattern discovery approach for the prediction of membrane dipping (re-entrant) loops *Gorka Lasso, John Antoniw, Jonathan Mullins*	Database and Data Integration *Paper 5:* Distance based algorithms for small biomolecule classification and structural similarity search *Emre Karakoc, Artem Cherkasov, S. Cenk Sahinalp*	Systems Biology *Paper 6:* Dense subgraph computation via stochastic search: application to detect transcriptional modules *Logan Everett, Li-San Wang, Sridhar Hannenhalli*				
11:20 a.m. - 11:45 a.m.	Structural Bioinformatics *Paper 7:* Comparative footprinting of DNA-binding proteins *Bruno Contreras-Moreira, Julio Collado-Vides*	Database and Data Integration *Paper 8:* springScape: Visualisation of microarray and contextual bioinformatic data using spring embedding and an information landscape *Timothy Ebbels, Bernard Buxton, David Jones*	Systems Biology *Paper 9:* A decompositional approach to parameter estimation in pathway modeling: A case study of the Akt and MAPK pathways and their crosstalk *Geoffrey Koh, Huey Fern Carol Teong, Marie-Veronique Clement, David Hsu, P S Thiagarajan*				

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monday (august 7)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
11:45 a.m. - 12:10 p.m.	Structural Bioinformatics *Paper 10:* The iRMSD: A local measure of sequence alignment accuracy using structural information *Fabrice Armougom, Sebastien Moretti, Vladimir Keduas, Cedric Notredame*	Database and Data Integration *Paper 11:* SNP Function Portal: a web database for exploring the function implication of SNP alleles *Pinglang Wang, Manhong Dai, Weijian Xuan, Richard C McEachin, Anne U Jackson, Laura J Scott, Brian Athey, Stanley J. Watson, Fan Meng*	Systems Biology *Paper 12:* Bistable Switching and Excitable Behaviour in the Activation of Src at Mitosis *Hendrik Fuß, Werner Dubitzky, Stephen Downes, Mary Jo Kurth*	Software Demo Web Services at the European Bioinformatics Institute	Software Demo HP/Synamatix: Enhancement and Acceleration of Genome Assembly using Novel Pattern Indexing and Retrieval Application	Software Demo Pygr, the Python Graph Database Framework for Bioinfomatics	
12:10 p.m. - 12:35 p.m.	Structural Bioinformatics *Paper 13:* Improved pruning algorithms and divide-and-conquer strategies for dead-end elimination, with application to protein design *Ivelin Georgiev, Ryan Lilien, Bruce Donald*	Database and Data Integration *Paper 14:* Integrating structured biological data by kernel Maximum Mean Discrepancy *Karsten Borgwardt, Arthur Gretton, Malte Rasch, Hans-Peter Kriegel, Bernhard Schoelkopf, Alex Smola*	Systems Biology *Paper 15:* Identification of metabolic units induced by environmental signals *Jose Nacher, Jean-Marc Schwartz, Minoru Kanehisa, Tatsuya Akutsu*				
12:35 p.m. - 2:00 p.m.	Lunch - Hall F		ISCB Open Business Meeting (12:45 p.m.- 1:45 p.m)	Birds of a Feather Flock Together	Birds of a Feather Flock Together	Birds of a Feather Flock Together	Birds of a Feather Flock Together
2:00 p.m. - 2:25 p.m.	Structural Bioinformatics *Paper 16:* Modelling sequential protein folding under kinetic control using hp lattice models *Fabien Huard, Charlotte Deane, Graham Wood*	Human Health *Paper 17:* Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks *Olivier Gevaert, Frank De Smet, Dirk Timmerman, Yves Moreau, Bart De Moor*	Systems Biology *Paper 18:* Inferring functional pathways from multi-perturbation data *Nir Yosef, Alon Kaufman, Eytan Ruppin*				
2:25 p.m. - 2:50 p.m.	Structural Bioinformatics *Paper 19:* A probabilistic approach to protein backbone tracing in electron density maps *Frank DiMaio, Jude Shavlik, George Phillips*	Human Health *Paper 20:* ACIAP, Autonomous hierarchical agglomerative Cluster Analysis based Protocol to partition conformational datasets *Giovanni Bottegoni, Walter Rocchia, Maurizio Recanatini, Andrea Cavalli*	Systems Biology *Paper 21:* Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle *Adrien Fauré, Aurélien Naldi, Claudine Chaouiya, Denis Thieffry*	Software Demo EBI: Text Mining	Software Demo TreeDomViewer: A tool for the visualization of phylogeny and protein domain structure	Software Demo PATIKAweb	Software Demo BioModels Database
2:50 p.m. - 3:15 p.m.	Structural Bioinformatics *Paper 22:* Learning MHC binding *Nebojsa Jojic, M. Reyes-Gomez, D. Heckerman, C. Kadie, O. Furman-Schueler*	Human Health *Paper 23:* Integrating copy number polymorphisms into array CGH analysis using a robust HMM *Sohrab Shah, Xiang Xuan, Ron DeLeeuw, Mehrnoush Khojasteh, Wan Lam, Raymond Ng, Kevin Murphy*	Systems Biology *Paper 24:* Computational inference of the molecular logic for synaptic connectivity in C. elegans *Vinay Varadan, David Miller III, Dimitris Anastassiou*				

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
3:15 p.m. - 3:40 p.m.	Coffee Break with Exhibitors - Hall C						
3:40 p.m. - 4:05 p.m.	New Frontiers Panel Introduction and Session Chair: *Goran Neshich, Embrapa/CNPTIA* Key Challenges in exploiting biomolecular data for Medicine and Agriculture *Janet Thornton, European Bioinformatics Institute, Wellcome Trust* Conceptual questions and key challenges in computational biology *Chris Sander, Memorial Sloan-Kettering Cancer Center*	Human Health *Papaer 25:* Decoding non-unique oligonucleotide hybridization experiments of targets related by a phylogenetic tree *Alexander Schliep, Sven Rahmann*	Systems Biology *Paper 26:* An integrative approach for causal gene identification and gene regulatory pathway inference *Zhidong Tu, Li Wang, Michelle Arbeitman, Ting Chen, Fengzhu Sun*	Software Demo Genome Expression Pathway Analysis Tool (GEPAT)	Software Demo PIRSF Protein Classification System (PCS)	Software Demo GenePro	
4:05 p.m. - 4:30 p.m.		*PLoS Track 1:* Knowledge-Based Analysis of Genome-Wide SNP Scanning Data *Fan Meng*	Systems Biology *Paper 27:* An equilibrium partitioning model connecting gene expression and cis-motif content *Joe Mellor, Charles DeLisi*				
4:30 p.m. - 4:55 p.m.	New Frontiers Session Continued	*PLoS Track 2:* Datamining the Fourth Dimension from Crystal Structures: Function-Structure-Entropy Relationships in Membrane Proteins *Ilan Samish*	*PLoS Panel:* BioTermNet: a system for biomedical text mining *(Asako Koike)* Imitating manual curation of text-mined facts in biomedicine *(Raul Rodriguez-Esteban)* SherLoc: Comprehensive Prediction of Protein Subcellular Localization by Integrating Clues from Sequence Data and the Literature *(Hagit Shatkay)*				
4:55 p.m. - 5:50 p.m.	Introduction of Keynote 2 - Main Auditorium (Hall D) Keynote 2: Tom Blundell - Structural biology, informatics and the discovery of new medicines						
6:00 p.m. - 9:00 p.m.	Poster Session with Authors (Odd Numbers) & Reception - Hall G						
9:30 p.m.	Shuttles depart Convention Center to Hotels						

tuesday (august 8)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
7:00 a.m.	Shuttles depart Hotels to Convention Center						
7:30 a.m. - 7:30 p.m.	Registration - Hall G						
8:45 a.m. - 9:55 a.m.	Morning Welcome, Promotion - ISMB/ECCB 2007 - Introduction of Keynote 3 - Main Auditorium (Hall D) Keynote 3: Kurt Wüthrich - Computational Aspects of NMR Studies with Proteins in Solution						
9:00 a.m. - 9:00 p.m.	Posters on Display - Hall G - 9:00 a.m. - 9:00 p.m.						
9:55 a.m. - 10:20 a.m.	New Frontiers Session Continued The future of the funding for biomolecular data and knowledge infrastructures: proposition for a "Fortaleza declaration" *Amos Bairoch, Swiss Institute of Bioinformatics*	Sequence Analysis *Paper 28:* Indel seeds for homology search *Denise Mak, Yevgeniy Gelfand, Gary Benson*	Molecular and Supramolecular Dynamics *Paper 29:* DynaPred: A structure and sequence based method for the prediction of MHC class I binding peptide sequences and conformations *Iris Antes, Shirley Siu, Thomas Lengauer*				
10:20 a.m. - 10:50 a.m.	Coffee Break with Exhibitors - Hall C						
10:50 a.m. - 11:15 a.m.	New Frontiers Session Continued The changing face of scientific dissemination as it applies to computational biology *Phil Bourne, University of California*	Sequence Analysis *Paper 30:* Interpreting anonymous DNA samples from mass disasters --- probabilistic forensic inference using genetic markers *Tien-ho Lin, Eugene W. Myers, Eric P. Xing*	Text Mining & Information Extraction *Paper 31:* Accessing Images in Bioscience Literature through User-Interface Designs and Natural Language Processing *Hong Yu, Minsuk Lee*	Software Demo OpenMS - A Software Platform for Shotgun Proteomics	Software Demo IBM: Inferring Common Origins	Software Demo Biological Concept Diagram Editor (BCDE)	Software Demo myGrid and ToolBus/PathPort Interoperability
11:15 a.m. - 11:40 a.m.		Sequence Analysis *Paper 32:* BaCelLo: a balanced subcellular localization predictor *Andrea Pierleoni, Pier Luigi Martelli Piero Fariselli, Rita Casadio*	Text Mining & Information Extraction *Paper 33:* Finding the evidences for protein-protein interactions from PubMed abstracts *Hyunchul Jang, Jaesoo Lim, Joon-Ho Lim, Soo-Jun Park, Kyu-Chul Lee, Seon-Hee Park*				

tuesday (august 8)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
11:40 a.m. - 12:05 p.m.	New Frontiers Session Continued	Sequence Analysis *Paper 34:* On counting position weight matrix matches in a sequence, with application to discriminative motif finding *Saurabh Sinha*	Text Mining & Information Extraction *Paper 35:* Novel unsupervised feature filtering of biological data *Roy Varshavsky, Assaf Gottlieb, Michal Linial, David Horn*				
12:05 p.m. - 12:30 p.m.		Sequence Analysis *Paper 36:* Finding regulatory motifs with maximum density subgraph *Eugene Fratkin, Brian Naughton, Douglas Brutlag, Serafim Botzoglou*	Text Mining & Information Extraction *Paper 37:* Integrating image data into biomedical text categorization *Hagit Shatkay, Nawei Chen, Dorothea Blostein*				
12:30 p.m. - 2:00 p.m.	Lunch - Hall F		EBI User's Forum	ISCB Student Council Open Meeting	Birds of a Feather Flock Together Cancer Biomedical Informatics Grid (caBIG), *Peter Covitz*	Birds of a Feather Flock Together Semantic types: towards a common annotation schema for biomedical literature, *D. Rebholz-Schuhman*	Birds of a Feather Flock Together Bioinformatics Core Facilities, *Fran Lewitter*
2:00 p.m. - 2:25 p.m.	Transcriptomics *Paper 38:* Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE *Barrett Foat, Alexandre Morozov, Harmen Bussemaker*	Sequence Analysis *Paper 39:* Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone *Patrick Ng, Niranjan Nagarajan, Neil Jones, Uri Keich*	*PLoS Track 3:* Gene Expression Trees in Blood Cell Development *Ivan Costa*	Software Demo STING_RDB	Software Demo Extend Your Bioinformatics with Accelrys: Integration of new tools in a common workflow environment expands capabilities and biological context	Software Demo GeneChip Analysis System (WGAS)	Software Demo GNARE
2:25 p.m. - 2:50 p.m.	Transcriptomics *Paper 40:* Quantification of transcription factor expression from arabidopsis images *Daniel Mace, Ji-Young Lee, Richard Twigg, Juliette Colinas, Philip Benfey, Uwe Ohler*	Sequence Analysis *Paper 41:* CONTRAfold: RNA secondary structure prediction without physics-based models *Chuong Do, Daniel Woods, Serafim Batzoglou*	*PLoS Track 4:* Pervasive unproductive splicing of SR proteins associated with ultraconserved elements *Steven Brenner*				

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tuesday (august 8)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
2:50 p.m. - 3:15 p.m.	Transcriptomics *Paper 42:* Identifying cycling genes by combining sequence homology and expression data *Yong Lu, Roni Rosenfeld, Ziv Bar-Joseph*	Sequence Analysis *Paper 43:* Context-specific independence mixture modeling for positional weight matrices *Benjamin Georgi, Alexander Schliep*	*PLoS Track 5:* Population Sequencing from Chromatogram Data *Nebojsa Jojic*		Software Demo Genetic Marker Search Engine for Medline	Software Demo GObase	
3:15 p.m. - 3:40 p.m.	Transcriptomics *Paper 44:* Analysis of sample set enrichment scores: assaying the enrichment of sets of genes for individual samples in genome-wide expression profiles *Elena Edelman, Alessandro Porrello, Justin Guinney, Bala Balakumaran, Andrea Bild, Phillip Febbo, Sayan Mukherjee*	Sequence Analysis *Paper 45:* ARTS: Accurate recognition of transcription starts in human *Soeren Sonnenburg, Alexander Zien, Gunnar Raetsch*	*PLoS Track 6:* Sm/lsm genes: a glimpse into early Eukaryotic evolution *Stella Veretnik*				
3:40 p.m. - 4:05 p.m.	Coffee Break with Exhibitors - Hall C						
4:05 p.m. - 4:30 p.m.	Transcriptomics *Paper 46:* Efficient identification of DNA binding partners in a sequence database *Tobias Mann, William Noble*	Sequence Analysis *Paper 47:* Informative priors based on transcription factor structural class improve de novo motif discovery *Leelavati Narlikar, Raluca Gordan, Uwe Ohler, Alexander Hartemink*	*PLoS Track 7:* Comparative analysis of the complete transcriptome of the ENCODE regions in chimpanzees and humans *Philipp Khaitovich*	Software Demo PRIDE and the Ontology Lookup Service	Software Demo Talk to Sun about Life Sciences	Software Demo BlueStar STING - A multiplatform environment for protein structure analysis	Software Demo HARLEM (Hamiltonians to Research LargE Molecules)
4:30 p.m. - 4:55 p.m.	Transcriptomics *Paper 48:* Semi-supervised analysis of gene expression profiles for lineage-specific development in the Caenorhabditis elegans embryo *Yuan Qi, Patrycja Missiuro, Ashish Kapoor, Craig Hunter, Tommi Jaakkola, David Gifford, Hui Ge*	Sequence Analysis *Paper 49:* ProfilePSTMM: capturing tree-structure motifs in carbohydrate sugar chains *Kiyoko Aoki-Kinoshita, Nobuhisa Ueda, Hiroshi Mamitsuka, Minoru Kanehisa*	*PLoS Track 8:* The strength of selection on ultraconserved elements *Christina Chen*				
4:55 p.m. - 5:50 p.m.	Introduction of Keynote 4 - Main Auditorium (Hall D) Keynote 4: Overton Award: Mathieu Blanchette - What mammalian genomes tell us about our ancestors, and vice-versa						
6:00 p.m. - 9:00 p.m.	Poster Session with Authors (Even Numbers) & Reception - Hall G						
9:30 p.m.	Shuttles depart Convention Center to Hotels						

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wednesday (august 9)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
7:30 a.m. - 1:30 p.m.	Registration - Hall G						
7:45 a.m.	Shuttles depart Hotels to Convention Center						
8:45 a.m. - 9:50 a.m.	Morning Welcome and Introduction of Keynote 5 - Main Auditorium (Hall D) Keynote 5: Elena Conti - Molecular mechanisms in RNA degradation						
9:00 a.m. - 1:00 p.m.	Posters on Display - Hall G - 9:00 a.m. - 2:00 p.m.						
9:50 a.m. - 10:15 a.m.	**Evolution & Phylogeny** *Paper 50:* Constructing near-perfect phylogenies with multiple homoplasy events *Ravi Vijaya Satya, Amar Mukherjee, Gabriela Alexe, Laxmi Parida, Gyan Bhanot*	**Ontologies** *Paper 51:* A top-level ontology of functions and its application in the Open Biomedical Ontologies *Patryk Burek, Robert Hoehndorf, Frank Loebe, Johann Visagie, Heinrich Herre, Janet Kelso*	*PLoS Track 9:* Automated Cell Biology in Drug Discovery: Extracting Biological Information from Images of Cell *Eugeni Vaisberg*	**Software Demo** The BioMAZE System	**Software Demo** IMG/M: An Experimental Metagenome Data Management and Analysis System	**Software Demo** MARSMotif: Deciphering Transcriptional Subnetworks from Microarray Expression Data using Regression Splines	**Software Demo** STRING database
10:15 a.m. - 10:40 a.m.	**Evolution & Phylogeny** *Paper 52:* BNTagger: Improved tagging snp selection using bayesian networks *Phil Hyoun Lee, Hagit Shatkay*	**Ontologies** *Paper 53:* An ontology for a robot scientist *Larisa Soldatova, Amanda Clare, Andrew Sparkes, Ross King*	*PLoS Track 10:* Predicting Biological Networks from Diverse Data: a New Role for the Hsp90 Complex *Chad Myers*				
10:40 a.m. - 11:05 a.m.	**Evolution & Phylogeny** *Paper 54:* Mutation parameters from sequence data using graph theoretic measures on lineage trees *Reuma Magori Cohen, Yoram Louzoun, Steven Kleinstein*	**Ontologies** *Paper 55:* Protein classification using ontology classification *Katherine Wolstencroft, Phillip Lord, Lydia Tabernero Andy Brass, Robert Stevens*	*PLoS Track 11:* Gene Expression of C. elegans Neurons Carries Significant Information on *Their Synaptic Connectivity* *Alon Kaufman*				
11:05 a.m. - 11:35 a.m.	Coffee Break with Exhibitors - Hall C						
11:35 a.m. - 12:30 p.m.	Introduction of Keynote 6 - Main Auditorium (Hall D) Keynote 6: Charles DeLisi - New Approaches to Biomarker Discovery						
12:30 p.m.	Shuttles depart for Hotels and/or Beach Park for Delegates and off-site event ticket holders - 1:15 p.m. Last Departure						
6:30 p.m.	Shuttles depart to hotels from Beach Parkt						

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thursday (august 10)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
7:30 a.m. - 5:30 p.m.	Registration - Hall G						
7:45 a.m.	Shuttles depart Hotels to Convention Center						
8:30 a.m. - 4:00 p.m.	Posters on Display - Hall G						
8:45 a.m. - 9:50 a.m.	Morning Welcome and Introduction of Keynote 7 - Main Auditorium (Hall D) Keynote 7: Rich Roberts - The need of Bioinformatics for experimental biologists						
9:50 a.m. - 10:15 a.m.	Proteomics *Paper 56:* Semi-Supervised LC/MS alignment for differential proteomics *Bernd Fischer, Jonas Grossmann, Volker Roth, Wilhelm Gruissem, Sacha Baginsky, Joachim M. Buhmann*	Comparative Genomics *Paper 57:* Hairpins in a haystack: recognizing microrna precursors in comparative genomics data *Jana Hertel, Peter F. Stadler*	*PLoS Track 12:* Splice Form Prediction using Machine Learning *Gunnar Rätsch*	Latin American BioInformatics Introduction Session	Software Demo Pathway Knowledge Management System (PKMS)	Software Demo UniProtKB and InterPro	Software Demo The PANTHER Classification System
10:15 a.m. - 10:40 a.m.	Proteomics *Paper 58:* Annotating proteins by mining protein interaction networks *Mustafa Kirac, Gultekin Ozsoyoglu, Jiong Yang*	Comparative Genomics *Paper 59:* Comparative genomics reveals unusually long motifs in mammalian genomes *Neil Jones, Pavel Pevzner*	*PLoS Track 13:* The consequences of alternative splicing on biological pathways *Melissa Cline*				
10:40 a.m. - 11:10 a.m.	Coffee Break with Exhibitors - Hall C						
11:10 a.m. - 11:35 a.m.	Proteomics *Paper 60:* A model-based approach for mining membrane protein crystallization trials *Sitaram Asur, Srinivasan Parthasarathy, Pichai Raman, Matthew Eric Otey*	Comparative Genomics *Paper 61:* Relative contributions of structural designability and functional diversity in fixation of gene duplicates *Boris Shakhnovich*	*PLoS Track 14:* Analysis of pleiotropy during C. elegans development and interpretation with interactome networks *Hui Ge*	Latin American BioInformatics Session Continued	Software Demo IntAct - an extensible open source framework for molecular interactions	Software Demo CEP: Conformational epitope prediction server	
11:35 a.m. - 12:00 p.m.	Proteomics *Paper 62:* Peptide sequence tag-based blind identification of post-translational modification with point process model *Chunmei Liu, Bo Yan, Yinglei Song, Ying Xu, Liming Cai*	Comparative Genomics *Paper 63:* Automatic clustering of orthologs and inparalogs shared by multiple proteomes *Andrey Alexeyenko, Ivica Tamas, Gang Liu, Erik Sonnhammer*	*PLoS Track 15:* Integrative Analysis of NCI-60 Panel Reveals Candidate Key Genetic Regulators Affected by Genomic Alterations *Doron Lipson*				

thursday (august 10)

	Main Auditorium (Hall D)	Room E1	Room E2	Room A (2nd Floor)	Room B1	Room B2	Room B3
12:00 p.m. - 1:45 p.m.	Lunch Reception & Late Breaking Poster Session with Authors - Hall G / Lunch with Exhibitors - Hall C						
1:45 p.m. - 2:10 p.m.	Proteomics *Paper 64:* Rapid knot detection and application to protein structure prediction *Firas Khatib, Matt Weirauch, Carol Rohl*	Comparative Genomics *Paper 65:* A Sequence-based filtering method for ncRNA identification and its application to searching for Riboswitch Elements *Shaojie Zhang, Ilya Borovok, Yair Aharonowitz, Roded Sharan, Vineet Bafna*	*PLoS Track 16:* Integration of FRAP experiments and 3D simulations of diffusion in the lumen and surface of Endoplasmic Reticulum *Petros Koumoutsakos*	Latin American BioInformatics Session Continued	Software Demo VisANT	Software Demo Swiss-Prot Protein Knowledgebase: ready for the future	
2:10 p.m. - 2:35 p.m.	Proteomics *Paper 66:* A computational approach toward label-free protein quantification using predicted peptide detectability *Haixu Tang, Randy Arnold, Pedro Alves, Zhiyin Xun, David Clemmer, Milos Novotny, James Reilly, Predrag Radivojac*	Comparative Genomics *Paper 67:* Finding novel genes in bacterial communities isolated from the environment *Lutz Krause, Naryttza N. Diaz, Daniela Bartels, Robert A. Edwards, Alfred Pühler, Forest Rohwer, Folker Meyer, Jens Stoye*	*PLoS Track 17:* Comparison of Alternative Splicing Structures in Eukaryotes *Michael Sammeth*				
2:35 p.m. - 3:00 p.m.	*PLoS Track 18:* Comparative Genomics of GPCRs: ET-Guided Annotation and Re-design of Aminergic Receptors *Olivier Lichtarge*	*PLoS Track 19:* DOE Hanford Site Metagenome: A multiple extreme environment that hosts wide diversity of microbes and radiotolerant bacteria *Mustafa Syed, Natalia Maltsev*	*PLoS Track 20:* Probabilistic Genetic Networks analysis of three Plasmodium falciparum strains from dynamical expression signals *Hernando del Portillo and Roberto Cesar Junior Barrera*	Latin American BioInformatics Session Continued			
3:00 p.m. - 3:25 p.m.	*PLoS Track 21:* Recursive Top-Down Quantum Clustering of Biological Data *Michal Linial*	*PLoS Track 22:* Simplified Models of Evolution lead to Improved Prediction of Functional Linkage from Correlated Gain and Loss of Genes among Eukaryotes *Daniel Barker*	*PLoS Track 23:* A Probabilistic Functional Gene Network of Worm: An Extensive and Accurate Systemic Model of a Multi-cellular Organism *Insuk Lee*				
3:25 p.m. - 3:55 p.m.	Coffee with Exhibitors - Hall C						
3:55 p.m. - 4:50 p.m.	Introduction of Keynote 8 - Main Auditorium (Hall D) Keynote 8: Sr. Scientist Accomplishment Award: Michael Waterman - Whole Genome Optical Mapping						
4:50 p.m. - 5:15 p.m.	Conference Awards and Closing						
5:15 p.m.	Shuttles depart Convention Center to Hotels						