

	Name of presenter		Title
1	Orit	Adato	Pan cancer analysis of differential expression of HOX genes compared with correlated healthy tissues
2	Ariel	Afek	High-throughput investigation of DNA deformability in protein recognition using mispairs
3	Rotem	Aharoni	Dynamical comparison between Myoglobin and Hemoglobin
4	Leon	Anavy	Improved DNA based storage capacity and fidelity using composite DNA letters
5	Shimshi	Atar	Designing and modeling the fitness of hundreds of synthetic Porcine circovirus variants
6	Oren	Avram	M1CR0B1AL1Z3R - A user-friendly webserver for the analysis of microbial genomics data
7	Shir	Bahiri Elitzur	The interactions between the rRNA and the mRNA in prokaryotes shape the entire transcripts
8	Anna	Bakhman	Structure-based computational dissection of Receptor Tyrosine Kinase-Ligand interactions
9	Eran	Barash	BacPaCS – Bacterial Pathogenicity Classification via Sparse-SVM
10	Lia	Baron	Computational deciphering and modeling of the regulatory information encoded in the PCV genome
11	Ruth	Barshir	Disease interpretation of non-coding RNA genes
12	Ilan	Ben-Bassat	A Deep Neural Network Approach for Learning Intrinsic Protein-RNA Binding Preferences
13	Rina	Ben-El	Studying the functional relationship between transcription factors and non-coding RNAs
14	Shaked	Bergman	Computational modeling of miRNA-mRNA interaction gives insight to post-transcriptional regulation
15	Evgeni	Bolotin	Patterns of bacterial gene content variation recapitulate across diverse environments
16	Noa	Bossel Ben-Moshe	scRNA-seq based dynamic deconvolution to dissect human infection
17	Nadav	Brandes	Learning Cancer Genes through Mutation Impact
18	Gon	Carmi	Protein-Protein Interactions of Stress-Response Genes are Conserved in Subterranean and Fossorial An
19	Dan	Coster	A model for early detection of cancer risk based on routine check-up data
20	Rajesh	Detroja	Pedigree analysis to uncover biomarkers in complex diseases using liquid biopsy
21	Alon	Diament	cMapApp: unsupervised coding sequence optimization in any given organism

22	Gal	Dinstag	Personalized prioritization of cancer driver mutations
23	Vadim	Dubinsky	Dynamics Of Antibiotic Resistance in the human gut microbiome revealed by longitudinal metagenomics
24	Jonathan	Engel	Gene cluster discovery under functional constraints and its applications to microbial genomes
25	Hila	Failayev	Computational Study of Coronaviruses Protein-Protein Interaction with the Host Cell
26	Simon	Fishilevich	GeneHancer – the integrated database of enhancers, promoters and their gene targets
27	Shani Talia	Gal-Oz	Sexual dimorphism in the immune system transcriptome
28	Noa	Gil	Production of spliced long noncoding RNAs specifies regions with increased enhancer activity
29	Ilia	Goland	Inferring protein-DNA binding preferences from microarray data using deep learning
30	Nir	Gonen	Coupling between amino acid biosynthesis and gene expression demands under ER stress
31	Roni Tom	Haas	A-to-I RNA editing affects gene expression after heat shock
32	Aharon	Hait	Cell type specific enhancer-promoter network inference based on single omic data
33	Keren	Halabi	A codon model for associating phenotypic traits with altered selective patterns of sequence evolution
34	Maayan	Hassidim	Cluster Switches in Gene Expression Data
35	Sabreen	Higazy	Structural elements in G-alpha subunits determine interaction specificity towards RGS proteins
36	Sabrin	Hilau	The effect of genetic variation on growth and death parameters of laboratory and natural E. coli
37	Naama	Hurwitz	Pep-Whisperer: Evolution Guided Design of Inhibitory Peptides
38	Ran	Israeli	RGS6 and RGS7 discriminate between the highly similar Gαo and Gαi via a unique structural motif
39	Guy	Kelman	Single Cell Resolution of Craniofacial Enhancers In Vivo
40	Alisa	Khramushin	The challenges of blind protein-peptide docking
41	Eli	Kopel	Decreased A-to-I RNA editing as a source of keratinocytes' dsRNA in psoriasis
42	Shoval	Lagziel	Inferring cancer dependencies on metabolic genes from large-scale genetic screens
43	Dena	Leshkowitz	UTAP: User-friendly Transcriptome Analysis Pipeline

44	Doron	Levin	Discrete whole cell model of translation enables connecting the genotype to the phenotype
45	Michal	Lipschuetz	Choosing the Optimal Timing of Epidural Analgesia in Primiparas and Multiparas
46	Rosalie	Lipsh	Design of catalytic repertoires
47	Zohar Carlos	Manber	Identification of cancer driver mutations in the noncoding genome
48	Andres	Maya Aguirre	Interaction between PDI and Integrin $\alpha\beta 3$; a Docking and Molecular Dynamics Study
49	Shay	Meiri	Functional exploration of changes in exon number of orthologous genes across the phylogenetic tree
50	Naama	Messika Gold	Tel Aviv university
51	Shoval	Miyara	Gene expression characterization of the hunger hormone ghrelin and estimation of its role in chicken
52	Amitai	Mordechai	Differential miRNA Editing in Cerebellum and Prefrontal Cortex in Autistic and Neurotypical Brains
53	Joshua	Moss	Comprehensive Human Cell-Type Methylation Atlas allows Identification of Origins of Circulating Cell
54	Hadas	Ner-Gaon	Identifying differentially spliced genes in the mouse immune system
55	Dvir	Netanely	Integrative analysis of multi-omic cancer data using PROMO
56	Moran	Neuhof	Decoding the Genome of the Dead Sea Scrolls
57	Gal	Novich	Bacterial phenotype prediction using genome sequence features
58	Arup	Panda	Exploring evidences of selection for local intrinsic disorder in proteins across the tree of life
59	Michael	Peeri	High resolution analysis of the selection on local mRNA folding strength across the tree of life
60	David	Pellow	Exploring sequence properties in plasmid assemblies
61	Michal	Perach	mRNA sequences evolved to control protein folding via ribosome pausing
62	Tom	Rabinowitz	Hoobari: Bayesian-based noninvasive prenatal diagnosis of single-gene disorders
63	Nimrod (Shalom)	Rappoport	NEMO: Cancer Subtyping by Multi-Omics Integration
64	Hillel	Roth	A Computational Tool for the Measurement of Low Density RNA Editing
65	Mark	Rozanov	AAAnchor: CNN guided detection of anchor amino acids in high resolution cryo-EM density maps

66	Omer	Sabary	Quality Control Tool for Synthetic DNA Libraries
67	Niv	Sabath	Stress-induced transcriptional readthrough
68	Renana	Sabi Salman	Novel Insights into Gene Expression Regulation during Meiosis Revealed by Translation Elongation Dyn
69	Ayelet	Minkov	Studying speciation genomics using ARGweaver
70	Moran	Sharon	Computational analysis offering tissue context to molecular pathways
71	Tair	Shauli	Human Specific Amino Acid Substitution Matrix Reveals Functional and Clinical Signatures
72	Eldad	Shulman	Exploration of alternative polyadenylation using single-cell RNA sequencing
73	Eyal	Simonovsky	Large-scale analysis associates expression variability of drug targets with drug effectiveness
74	Judith	Somekh	Batch correction evaluation framework using a-priori gene-gene associations
75	Doron	Stupp	Phylogenetic profiling for predicting PPI and interaction context using local co-evolution
76	Eliya	Sultan	Computational characterization of tumor infiltrating immune cells
77	Dina	Svetlitsky	CSBFinder: Discovery of colinear syntenic blocks across thousands of prokaryotic genomes
78	Michal	Twik	The MalaCards database: comprehensive infrastructure for human genomic disease decipherment.
79	Kerem	Wainer Katsir	Identifying cell doublets from single cell sequencing using allele-specific expression
80	Adi	Watzman	Evolution and transmission in the human gut microbiota
81	Iddo	Weiner	Solving the riddle of the evolution of Shine-Dalgarno based translation in chloroplasts
82	Zohar	Zafrir	Attenuation of RNA Viruses based on a computational rational design
83	Eyal	Zajfman	Computational design of single domain antibodies
84	Yoram	Zarai	Evolutionary Selection for Under-Represented Nucleotide Sub-Sequences in Viruses and Related Hosts
85	Ron	Zeira	Sorting cancer karyotypes using double-cut-and-joins, duplications and deletions
86	Binyamin	Zuckerman	NXF1 availability regulates export of inefficiently spliced, long and intronless RNAs
87	Tania	Dubovik	Architecture of a multi-cellular polygenic network governing immune cellular homeostasis

- 88 Mayan Levy **High Resolution Longitudinal Immune Profiling Reveals a Clinically Meaningful Metric from Dynamics of Healthy Immune-Aging Towards an Older Adult Homeostasis**
- 89 Karen Chait **Global architecture of the neuro-immune network in the periphery reveals a richer alphabet vocabulary of immune regulation**

