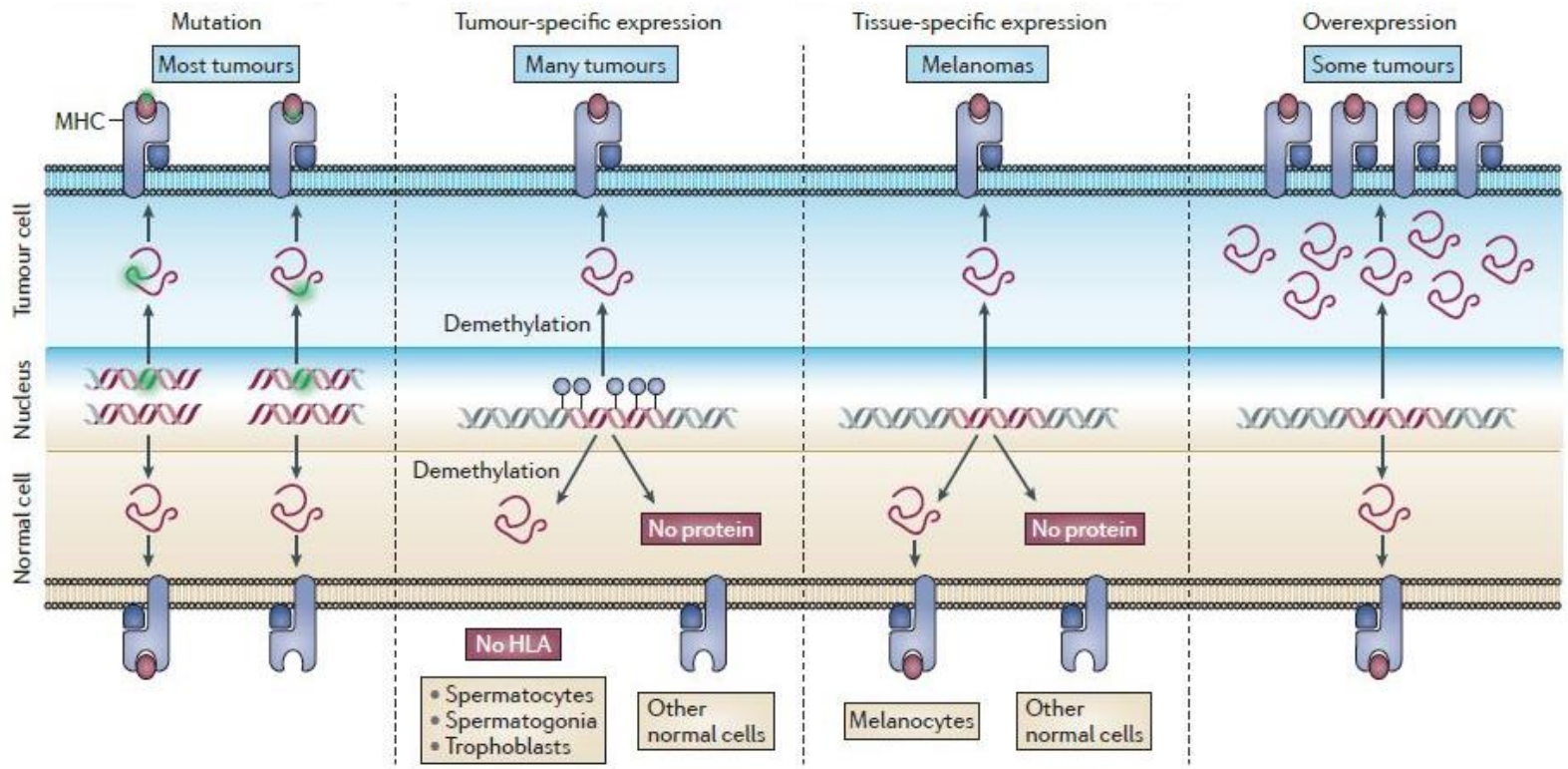
IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Cancer Epitope Database and Analysis Resource (CEDAR)

Presented by: Zeynep Koşaloğlu-Yalçın, Instructor

Cancer Antigens



Coulie et al, Nat Rev Cancer. 2014 Feb

Motivation for the CEDAR Project

1

IMPORTANCE

- Cancer epitopes play a key role in cancer immunology and immunotherapy
- They are important in understanding the biological mechanisms associated with treatment efficacy and developing more effective therapeutic approaches

2

COMMUNITY NEED

- Several resources attempted to catalog cancer epitopes (e.g. TANTIGEN, CAPED, NEPdb, dbPepNEO, etc.)
  - Existing resources do not capture all epitope data in a granular fashion linked to the biological, immunological, and clinical contexts
  - All resources only provide limited computational prediction and analysis tools

We developed The Cancer Epitope Database and Analysis Resource to fill these gaps

Motivation for the CEDAR Project

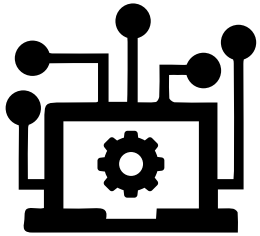
- IEDB hosts epitope data for
  - Allergy
  - Infectious diseases
  - Autoimmune diseases
  - Transplantation / Alloantigens
  - But **NOT** Cancer

We received funding from the NCI to develop a resource for cancer epitopes

NIH NATIONAL CANCER INSTITUTE

Informatics Technology for Cancer Research (ITCR)

Cancer Epitope Database and Analysis Resource (CEDAR)



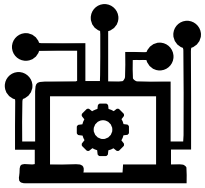
Database

Analysis Resource

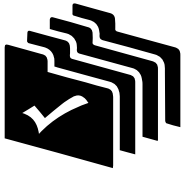
Comprehensively cataloging all cancer epitope-related data linked to the biological, immunological, and clinical contexts

Computational epitope prediction and analysis tools providing researchers access to predictive strategies and objective evaluations of their performance

Specific Aims of the CEDAR Project



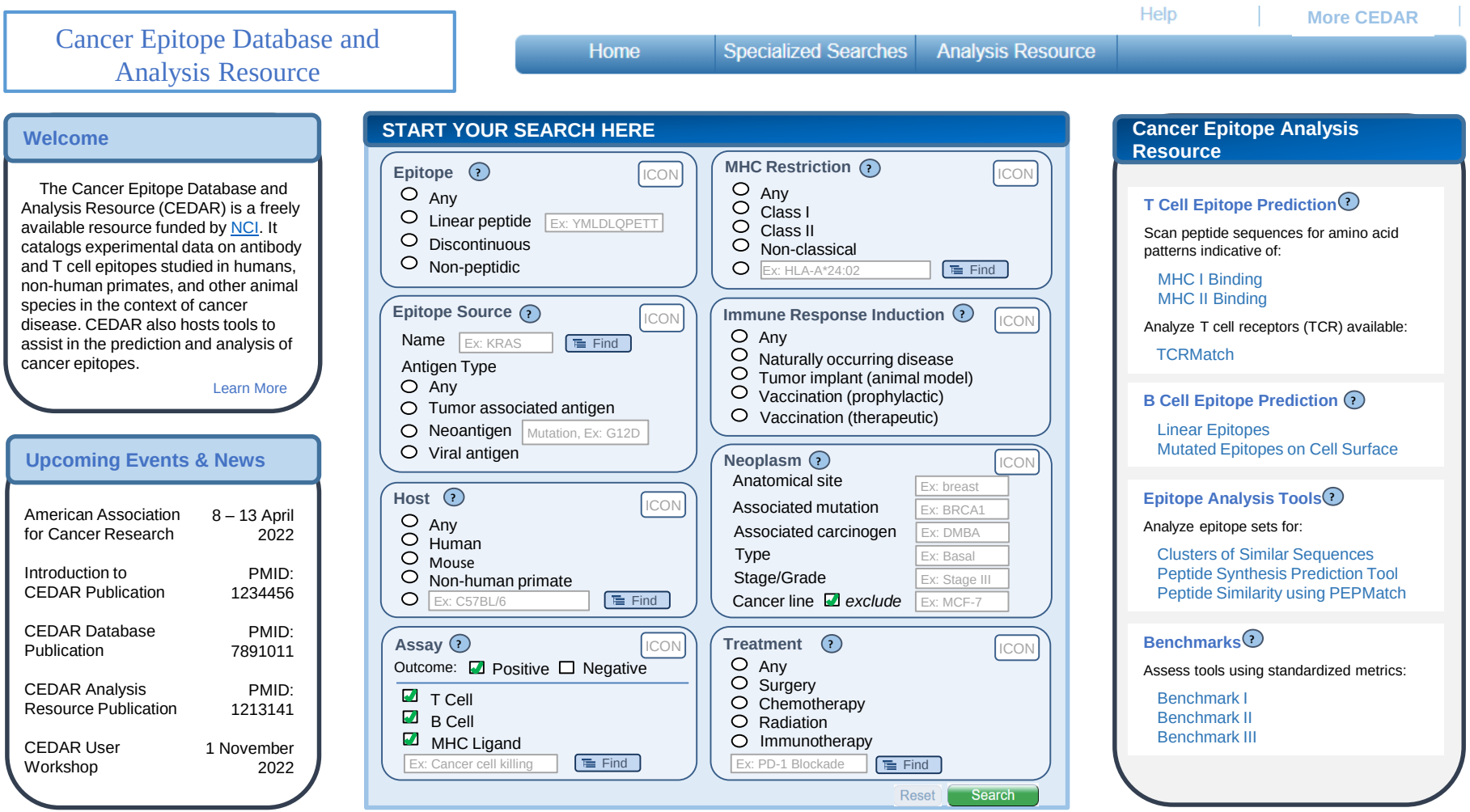
1) Establish the CEDAR database, ontology, and query and reporting functionality



2) Curate literature epitope data, relevant to cancer immunology

3) Provide a validated set of cancer epitope prediction and analysis tools

4) Implement a multifaceted outreach program to engage the cancer research community


Cancer Epitope Database and Analysis Resource
Help
More CEDAR
Home
Specialized Searches
Analysis Resource
Welcome
The Cancer Epitope Database and Analysis Resource (CEDAR) is a freely available resource funded by NCI. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of cancer disease. CEDAR also hosts tools to assist in the prediction and analysis of cancer epitopes.
Learn More
Upcoming Events & News
American Association for Cancer Research 8 – 13 April 2022
Introduction to CEDAR Publication PMID: 1234456
CEDAR Database Publication PMID: 7891011
CEDAR Analysis Resource Publication PMID: 1213141
CEDAR User Workshop 1 November 2022
START YOUR SEARCH HERE
Epitope
ICON
Any
Linear peptide
Ex: YMLDLQPETT
Discontinuous
Non-peptidic
MHC Restriction
ICON
Any
Class I
Class II
Non-classical
Ex: HLA-A*24:02
Find
Epitope Source
ICON
Name
Ex: KRAS
Find
Antigen Type
Any
Tumor associated antigen
Neoantigen
Mutation, Ex: G12D
Viral antigen
Immune Response Induction
ICON
Any
Naturally occurring disease
Tumor implant (animal model)
Vaccination (prophylactic)
Vaccination (therapeutic)
Host
ICON
Any
Human
Mouse
Non-human primate
Ex: C57BL/6
Find
Neoplasm
ICON
Anatomical site
Ex: breast
Associated mutation
Ex: BRCA1
Associated carcinogen
Ex: DMBA
Type
Ex: Basal
Stage/Grade
Ex: Stage III
Cancer line
exclude
Ex: MCF-7
Assay
ICON
Outcome:
Positive
Negative
T Cell
B Cell
MHC Ligand
Ex: Cancer cell killing
Find
Treatment
ICON
Any
Surgery
Chemotherapy
Radiation
Immunotherapy
Ex: PD-1 Blockade
Find
Reset
Search
Cancer Epitope Analysis Resource
T Cell Epitope Prediction
Scan peptide sequences for amino acid patterns indicative of:
MHC I Binding
MHC II Binding
Analyze T cell receptors (TCR) available:
TCRMatch
B Cell Epitope Prediction
Linear Epitopes
Mutated Epitopes on Cell Surface
Epitope Analysis Tools
Analyze epitope sets for:
Clusters of Similar Sequences
Peptide Synthesis Prediction Tool
Peptide Similarity using PEPMatch
Benchmarks
Assess tools using standardized metrics:
Benchmark I
Benchmark II
Benchmark III
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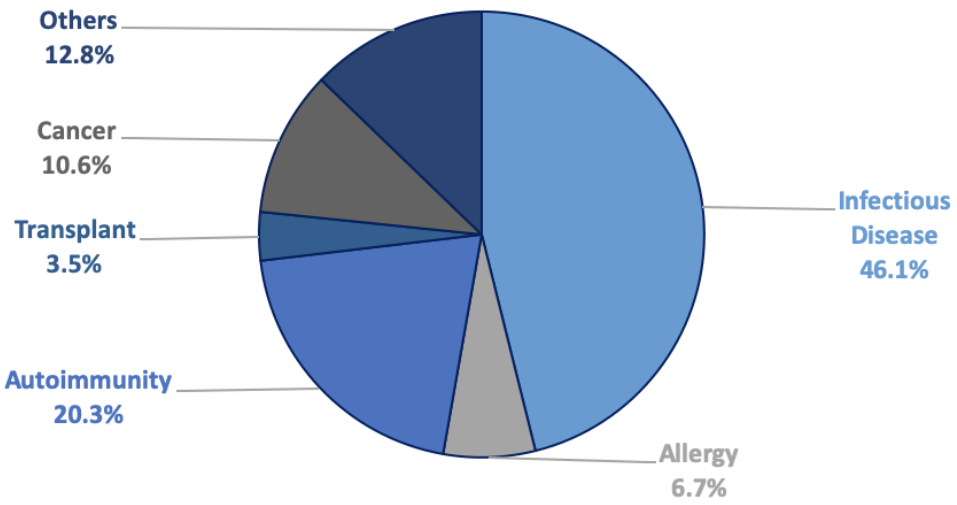
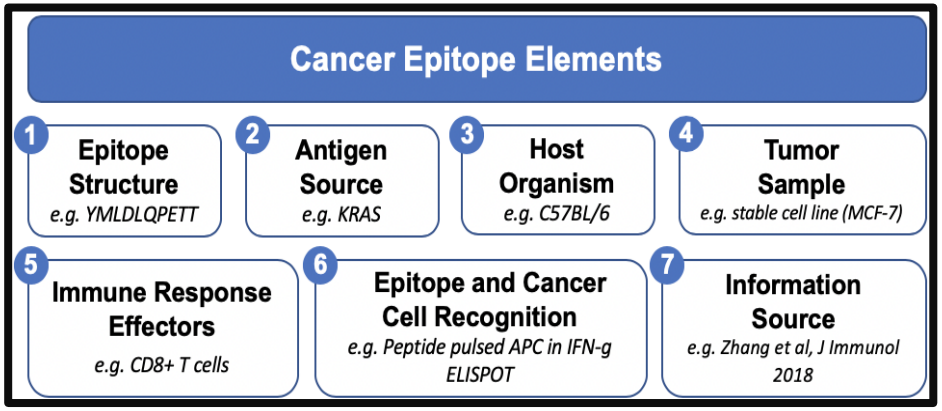
Supported by a grant from the National Cancer Institute, a component of the National Institutes of Health
Last Updated: July 04, 2021

Curation of cancer-related epitope data

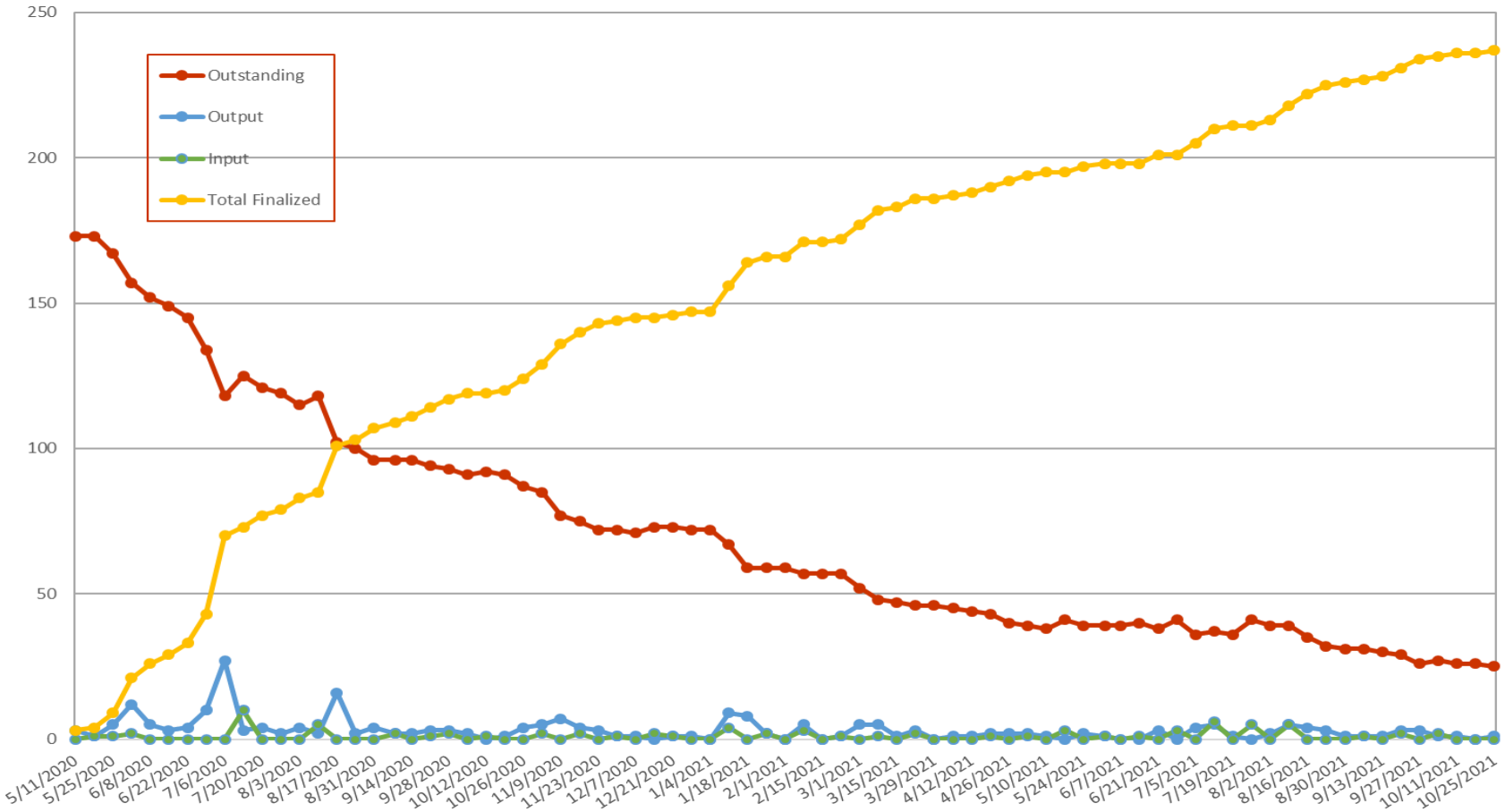


3,543 papers identified as cancer relevant

- internal que for curation: started with neoepitopes and prostate antigens
- Updated curation rules

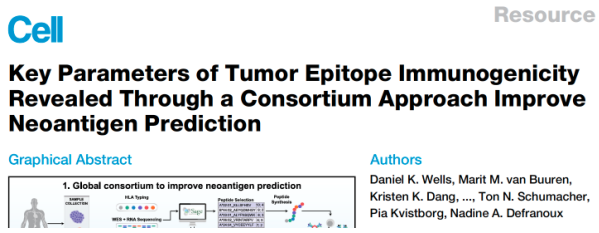


During the last year we have started a pilot curation of neoepitope cancer papers



Provide web-implementations for published but hard to access cancer-epitope related tools in CEDAR

- Curate published tools and pipelines (functionality offered, frequency of re-use / citation, ease of implementation, licensing requirements)
- Prioritize tools to implement in CEDAR based on cost-benefit analysis
- Provide web-accessible implementations in the CEDAR Analysis Resource


Cell

Resource

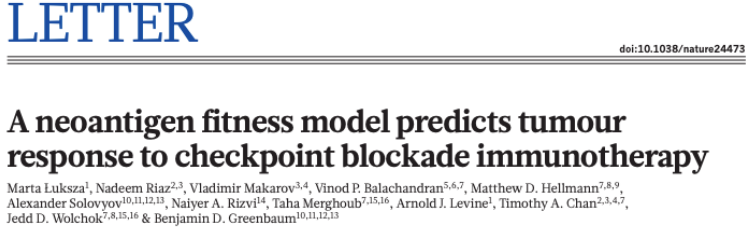
Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction

Graphical Abstract

1. Global consortium to improve neoantigen prediction

Authors

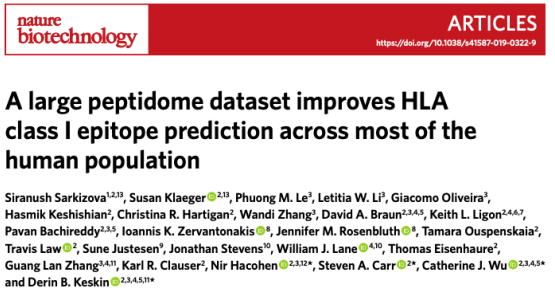
Daniel K. Wells, Marit M. van Buuren, Kristen K. Dang, ..., Ton N. Schumacher, Pia Kvistborg, Nadine A. Defranoux


LETTER

doi:10.1038/nature24473

A neoantigen fitness model predicts tumour response to checkpoint blockade immunotherapy

Marta Łuksza[1], Nadeem Riaz[2,3], Vladimir Makarov[3,4], Vinod P. Balachandran[5,6,7], Matthew D. Hellmann[7,8,9], Alexander Solovyov[10,11,12,13], Naiyer A. Rizvi[14], Taha Merghoub[7,15,16], Arnold J. Levine[1], Timothy A. Chan[2,3,4,7], Jedd D. Wolchok[7,8,15,16] & Benjamin D. Greenbaum[10,11,12,13]


nature biotechnology

ARTICLES

https://doi.org/10.1038/s41587-019-0322-9

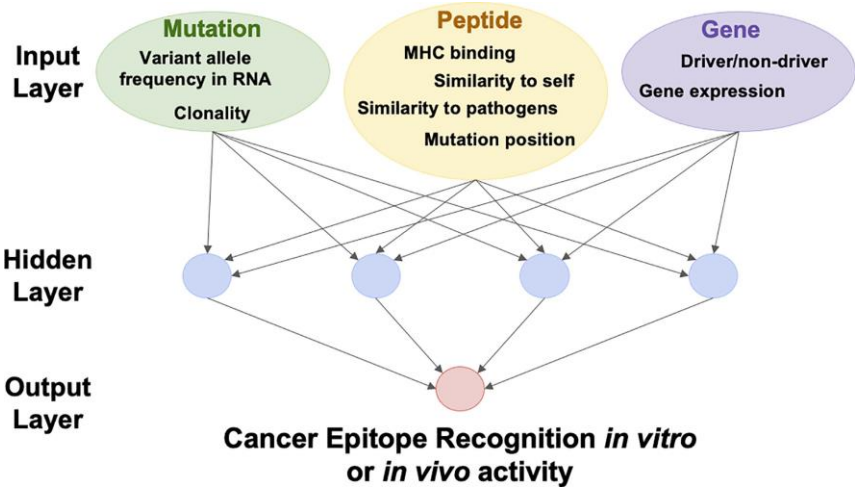
A large peptidome dataset improves HLA class I epitope prediction across most of the human population

Siranush Sarkizova[1,2,13], Susan Klaeger[2,13], Phuong M. Le[3], Letitia W. Li[3], Giacomo Oliveira[3], Hasmik Keshishian[2], Christina R. Hartigan[2], Wandi Zhang[3], David A. Braun[2,3,4,5], Keith L. Ligon[2,4,6,7], Pavan Bachireddy[2,3,5], Ioannis K. Zervantonakis[8], Jennifer M. Rosenbluth[8], Tamara Ouspenskaia[2], Travis Law[2], Sune Justesen[9], Jonathan Stevens[10], William J. Lane[4,10], Thomas Eisenhaure[2], Guang Lan Zhang[3,4,11], Karl R. Clauser[2], Nir Hacohen[2,3,12*], Steven A. Carr[2*], Catherine J. Wu[2,3,4,5*] and Derin B. Keskin[2,3,4,5,11*]

Develop and provide access to new cancer epitope analysis and prediction tools

- **Provide prediction tools <u>tailored to the needs of cancer immunologists</u>**
  - what neoepitopes are generated by a given mutation?
  - side-by-side predictions for mutant and wild-type peptides

- **Develop <u>novel prediction tools</u> for cancer epitopes**
  - combined assessment of expression and binding
  - include additional features when predicting epitopes



Use curated cancer epitope datasets to benchmark epitope prediction tools

- Assemble comprehensive sets of cancer epitope data and make available in simple format for bioinformaticians for tool training and testing
- Conduct benchmarks of prediction tools on cancer epitope datasets
- Manual compile and run benchmarks (initially)
- Automated benchmarks of all tools implemented in CEDAR, using newly curated data

Examples of benchmark targets for prediction tools

- What peptides in a tumor sample are processed and presented on MHC
- What neo-epitopes are recognized by T cells from a cancer patient?

Summary

- CEDAR will be an extension of IEDB, containing cancer-related epitope data and tools
- Exiting tools will be adapted to the needs of cancer researchers and novel cancer-specific tools will be developed
- First release planned in second quarter of 2022