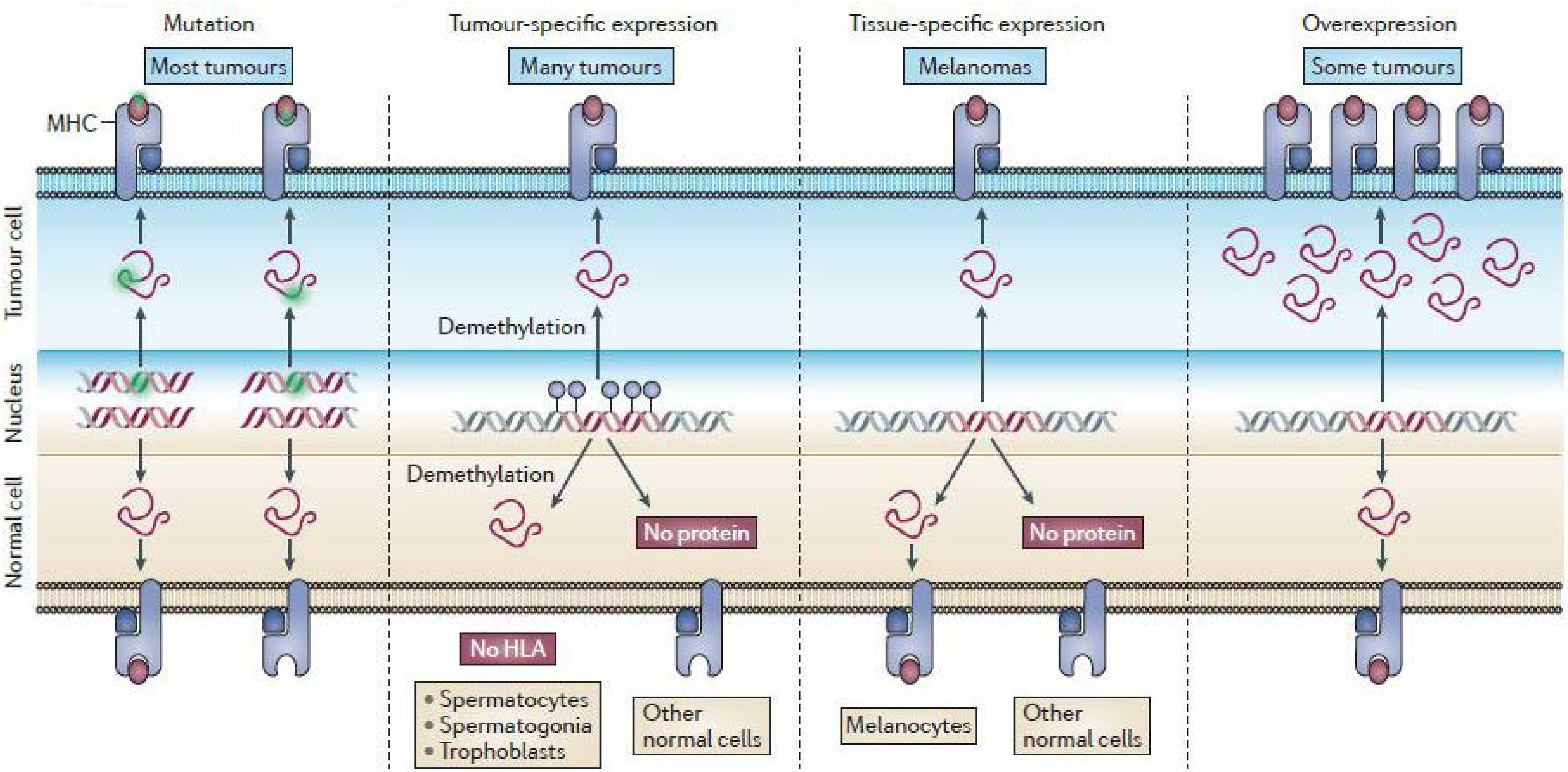
Cancer Epitope Database and Analysis Resource (CEDAR)

Presented by: Zeynep Koşaloğlu-Yalçin, Instructor Cancer Bioinformatics

Cancer Epitopes are Derived from Cancer Antigens



Coulie et al, Nat Rev Cancer. 2014 Feb

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 **National Cancer Institute** 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

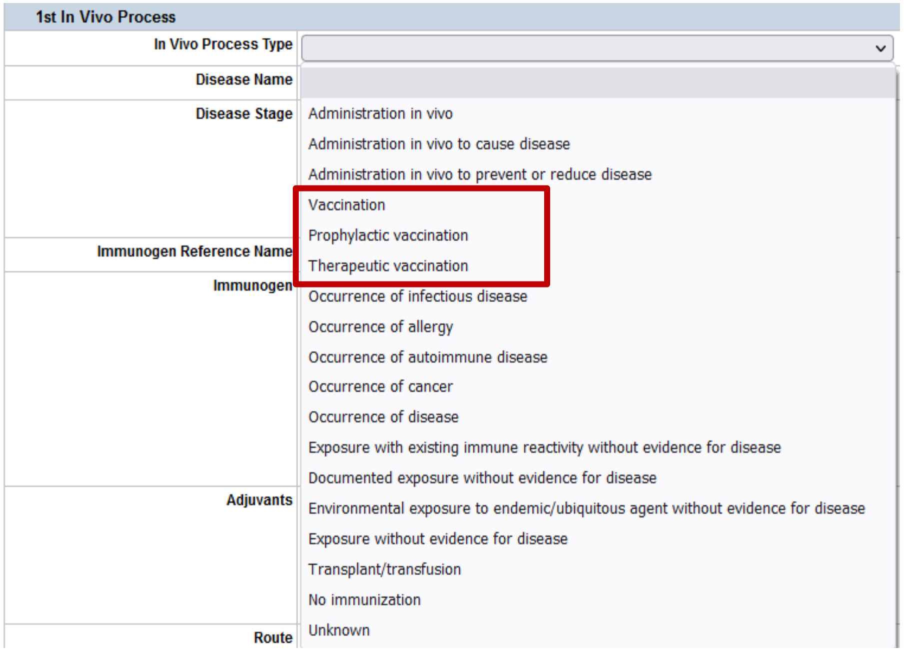
Comprehensively cataloging all cancer epitope-related data linked to the biological, immunological, and clinical contexts

Analysis Resource

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

CEDAR Database Design Process

- **Reached Out to Experts:** Interviewed cancer experts to identify important search fields for cancer research
- **Prototyped User Interfaces:** Designed database query interface wireframes
- **Introduced Cancer Curation Rules**, for example:
  i. Captured cancer types in more detail
  ii. Distinguished vaccination types (prophylactic / therapeutic)
  iii. Distinguished between allo- and xeno-adoptive transfer.



Curation of Cancer-related Epitope Data

Utilizing the IEDB curation process:

PubMed / PDB
- Complex query
- Bi-weekly

→

Classifier
- Content based categories
- Retrained annually

→

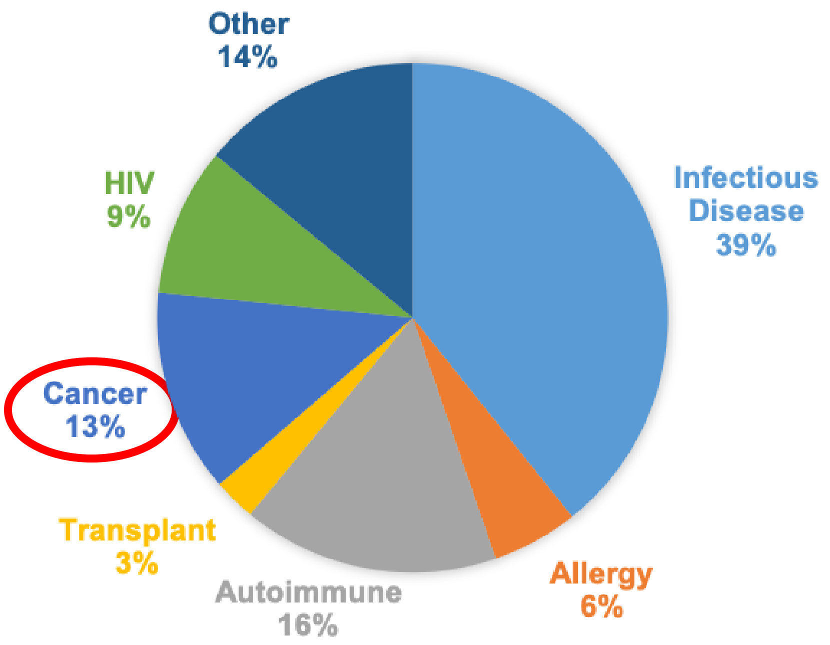
Abstract Review
- Manual scan
- Confirmation of classification

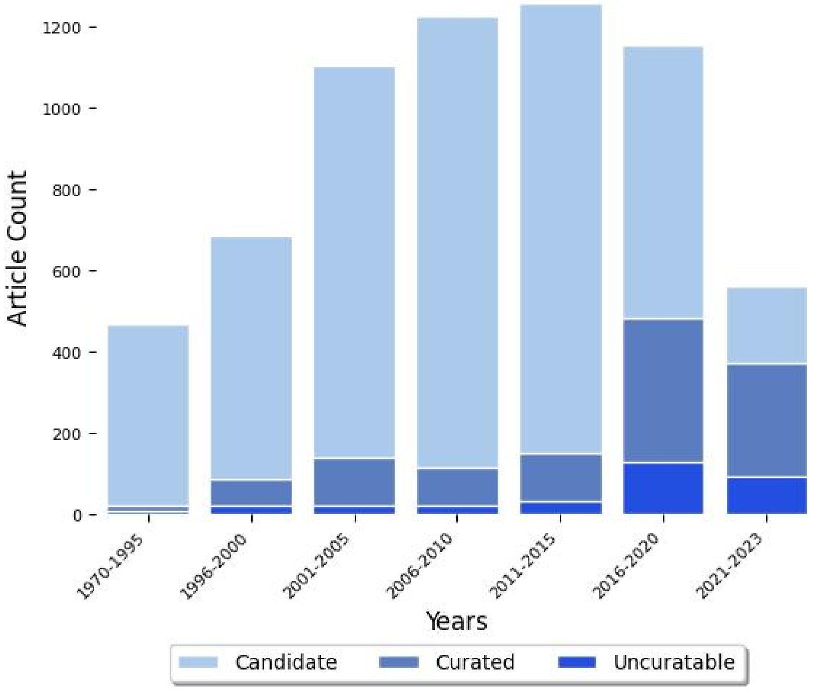
→

Manual Curation
- Assigned to curators
- Peer review

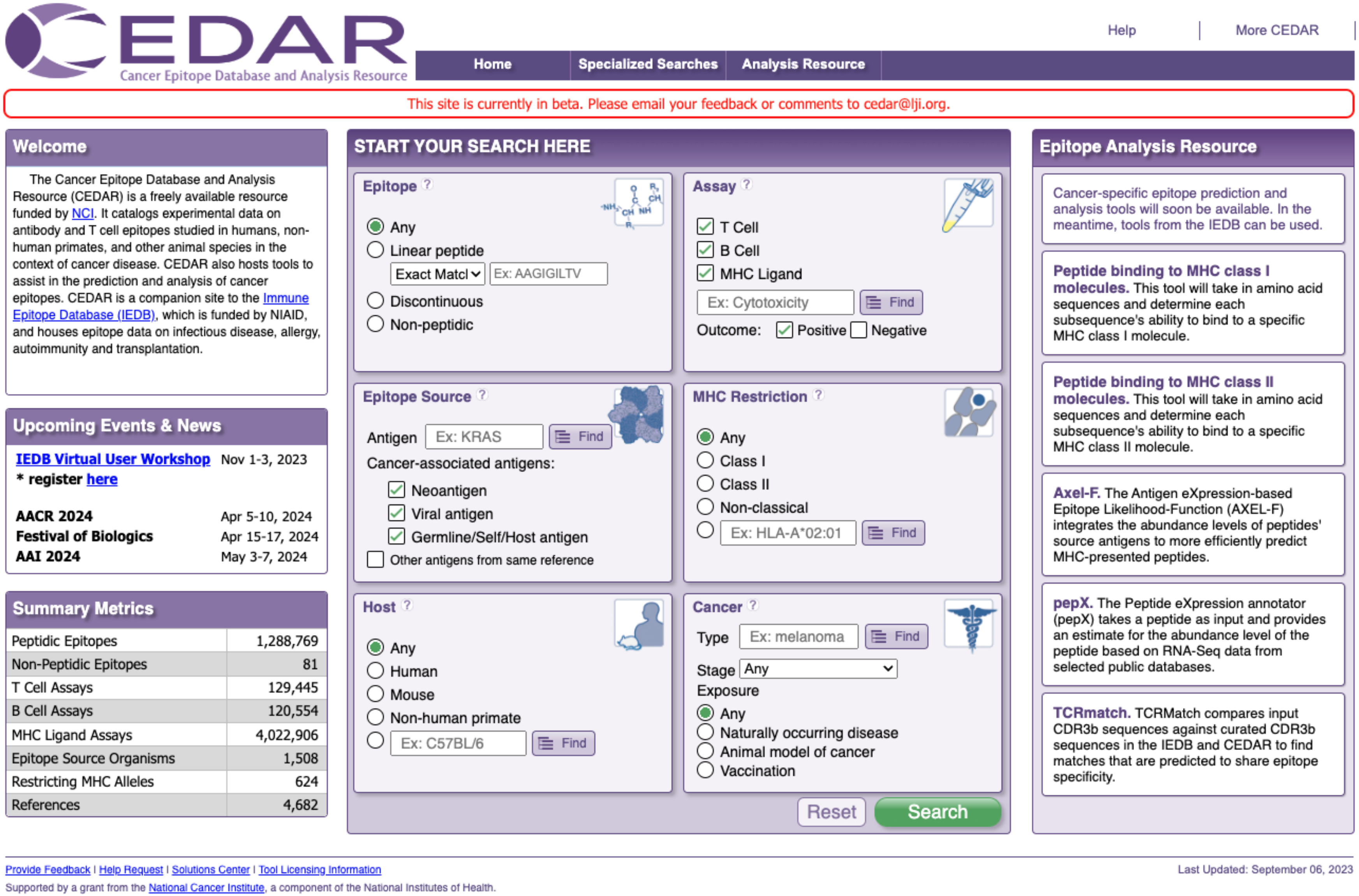
Cancer Curated Category	% Complete	No. of Papers
Prostate Cancer	99%	235
Neoepitope category	96%	450
Published papers in 2023	85%	57
Published papers in 2022	97%	110
Published papers in 2021	97%	83
Published papers in 2020	95%	109
Published papers in 2019	83%	92

Breakdown of Classified and Curatable References





cedar.iedb.org



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Summary Metrics

Peptidic Epitopes	1,288,769
Non-Peptidic Epitopes	81
T Cell Assays	129,445
B Cell Assays	120,554
MHC Ligand Assays	4,022,906
Epitope Source Organisms	1,508
Restricting MHC Alleles	624
References	4,682

START YOUR SEARCH HERE

Epitope ?
- ● Any
- ○ Linear peptide
  - Exact Match | Ex: AAGIGILTV
- ○ Discontinuous
- ○ Non-peptidic

Assay ?
- ☑ T Cell
- ☑ B Cell
- ☑ MHC Ligand
- Ex: Cytotoxicity | Find
- Outcome: ☑ Positive ☐ Negative

Epitope Source ?
- Antigen: Ex: KRAS | Find
- Cancer-associated antigens:
  - ☑ Neoantigen
  - ☑ Viral antigen
  - ☑ Germline/Self/Host antigen
- ☐ Other antigens from same reference

MHC Restriction ?
- ● Any
- ○ Class I
- ○ Class II
- ○ Non-classical
- ○ Ex: HLA-A*02:01 | Find

Host ?
- ● Any
- ○ Human
- ○ Mouse
- ○ Non-human primate
- ○ Ex: C57BL/6 | Find

Cancer ?
- Type: Ex: melanoma | Find
- Stage: Any
- Exposure
  - ● Any
  - ○ Naturally occurring disease
  - ○ Animal model of cancer
  - ○ Vaccination

Reset | Search

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Provide Feedback | Help Request | Solutions Center | Tool Licensing Information

Last Updated: September 06, 2023

Supported by a grant from the National Cancer Institute, a component of the National Institutes of Health.

Data in CEDAR

- 77,557 T cell Assays
  - 37,056 unique epitopes from 10,941 antigens
- 46,321 B Cell Assays
  - 19,815 unique epitopes from 862 antigens
- 705,286 Ligand Elution Assays
  - 214,905 unique epitopes from 3,651 antigens

T Cell Data in CEDAR

Most epitopes are from common cancer types

Disease Type	# epitopes
melanoma	8,172
healthy	7,084
colorectal cancer	6,577
lung non-small cell carcinoma	2,445
hepatocellular carcinoma	1,071
bile duct cancer	876
skin melanoma	788
pancreatic ductal adenocarcinoma	668
glioblastoma	611
pancreatic cancer	431

Antigen	# epitopes
MAGEA10	173
TP53	149
KRAS	70
MLANA	65
GRPR	60
NRAS	53
TTN	53
EGFR	45
MUC16	31
PIK3CA	23

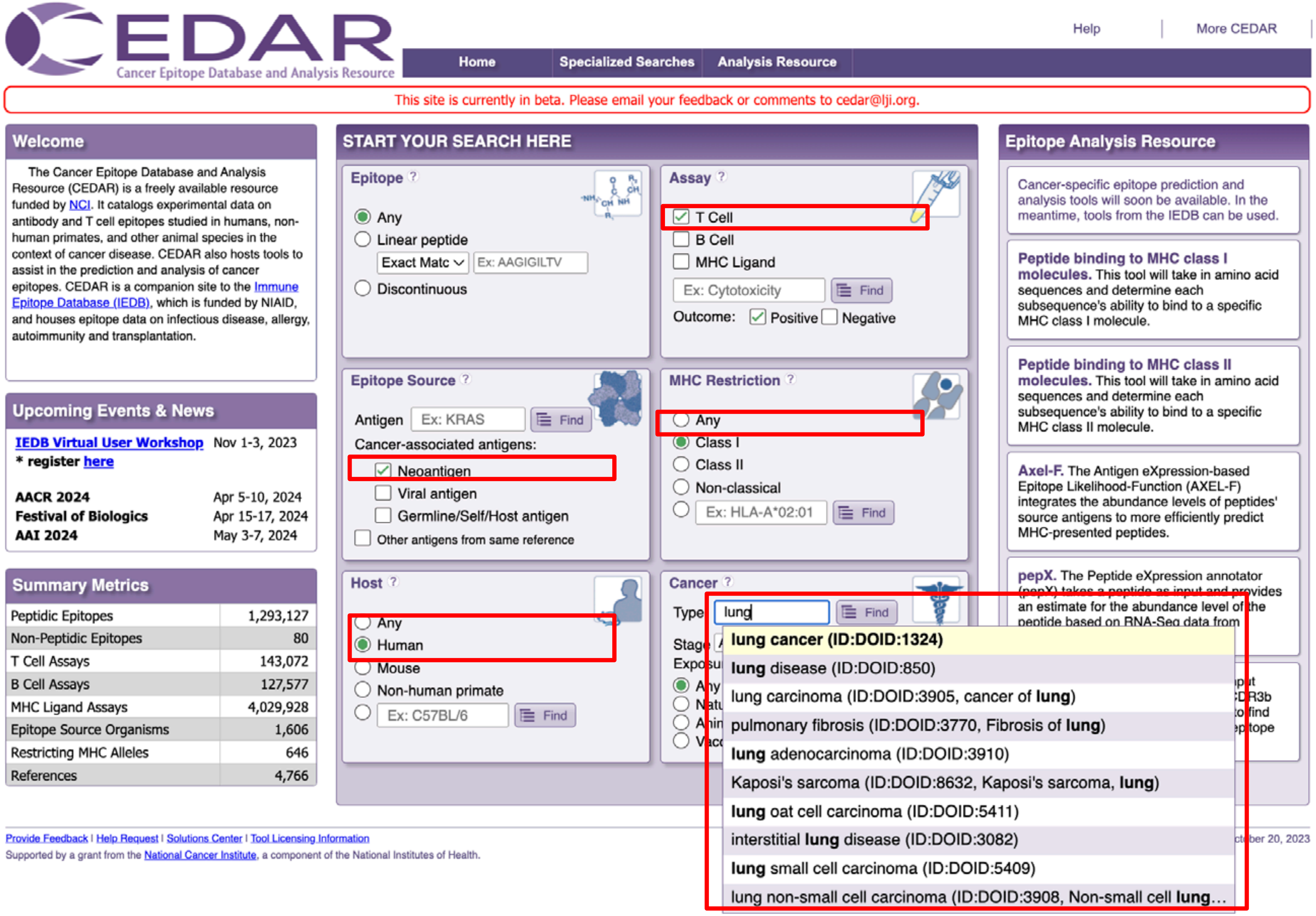
Neoantigens in CEDAR

- 21,610 neoantigens with T cell assays currently in CEDAR
- 3,397 neoantigens with positive T cell assay outcomes

➔ meta-analysis of these neoantigens ongoing

Example Query: Neoantigens in Lung Cancer

Positive data for Neoantigen T cell assay outcomes with MHC Class I restriction in human host



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○ Ex: HLA-A*02:01 Find

Host ?

○ Any
● Human
○ Mouse
○ Non-human primate
○ Ex: C57BL/6 Find

Cancer ?

Type lung Find
Stage
Exposu
● Any
○ Natu
○ Anin
○ Vacc

- **lung cancer (ID:DOID:1324)**
- **lung** disease (ID:DOID:850)
- lung carcinoma (ID:DOID:3905, cancer of **lung**)
- pulmonary fibrosis (ID:DOID:3770, Fibrosis of **lung**)
- **lung** adenocarcinoma (ID:DOID:3910)
- Kaposi's sarcoma (ID:DOID:8632, Kaposi's sarcoma, **lung**)
- **lung** oat cell carcinoma (ID:DOID:5411)
- interstitial **lung** disease (ID:DOID:3082)
- **lung** small cell carcinoma (ID:DOID:5409)
- lung non-small cell carcinoma (ID:DOID:3908, Non-small cell **lung**…

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o find
pitope

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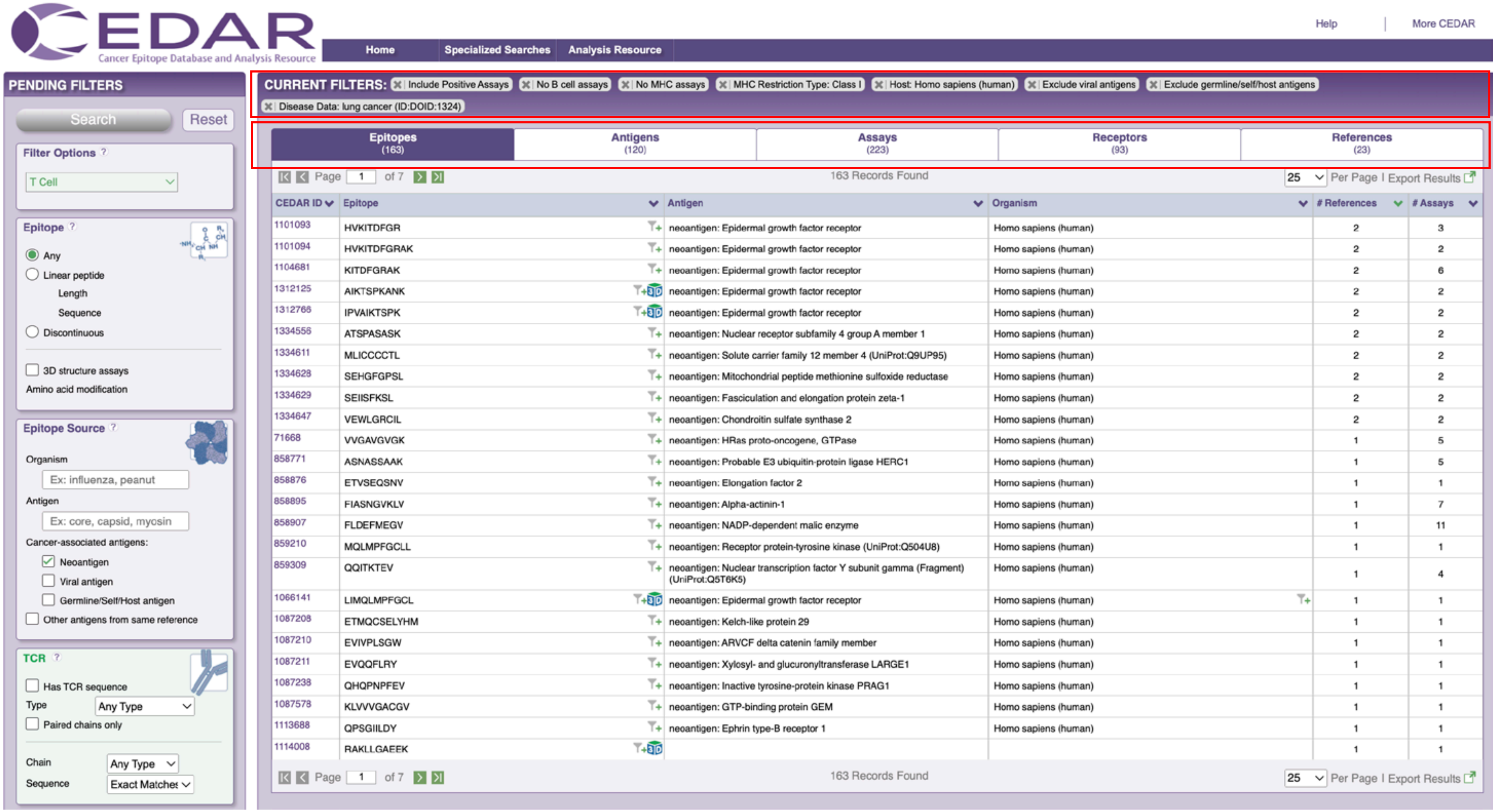
Supported by a grant from the National Cancer Institute, a component of the National Institutes of Health.
ctober 20, 2023

Example Results: Neoantigens in Lung Cancer

Positive data for Neoantigen T cell assay outcomes with MHC Class I restriction in human host



CURRENT FILTERS: Include Positive Assays | No B cell assays | No MHC assays | MHC Restriction Type: Class I | Host: Homo sapiens (human) | Exclude viral antigens | Exclude germline/self/host antigens | Disease Data: lung cancer (ID:DOID:1324)

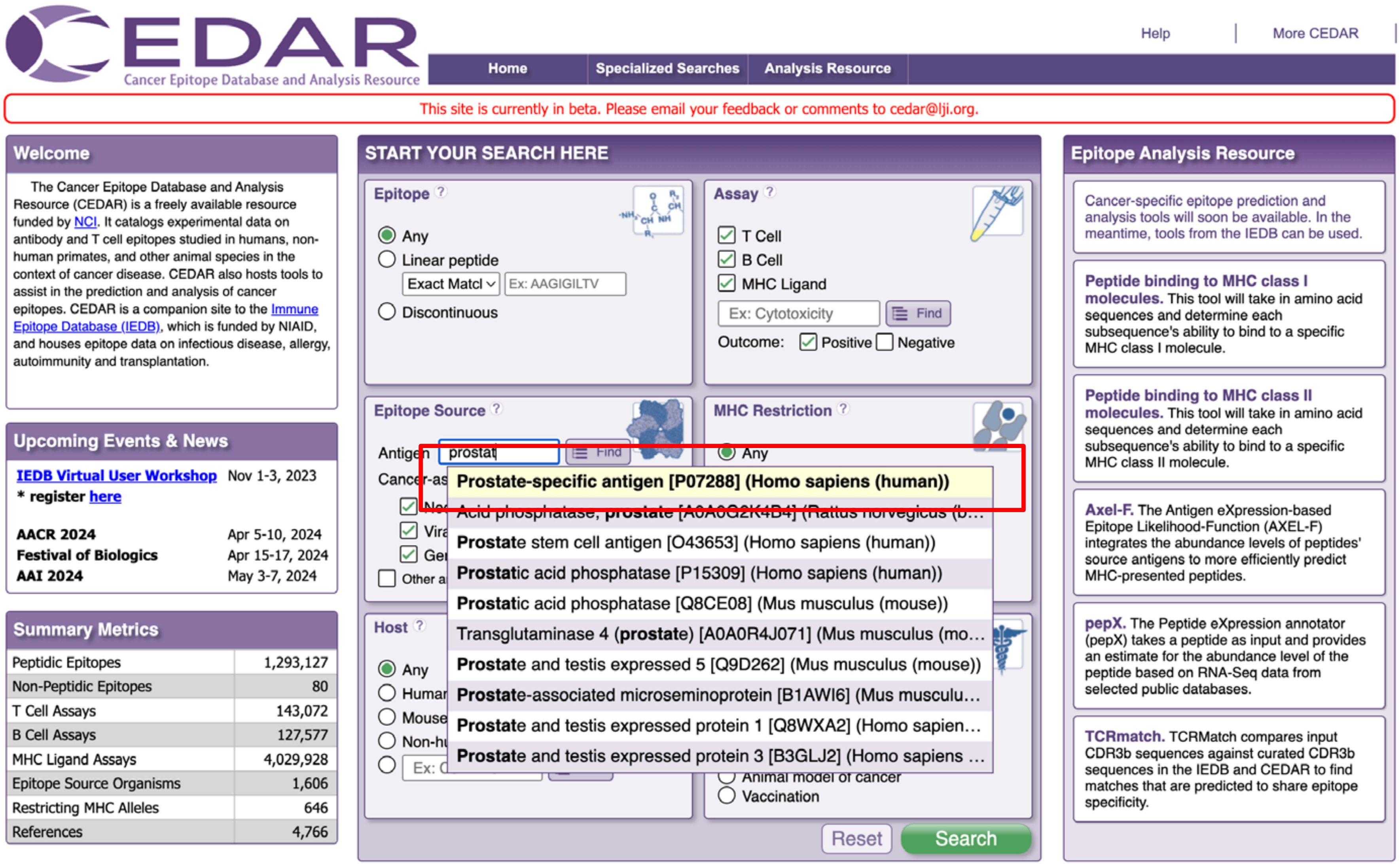
Epitopes (163)	Antigens (120)	Assays (223)	Receptors (93)	References (23)

Page 1 of 7 — 163 Records Found — 25 Per Page | Export Results

CEDAR ID	Epitope	Antigen	Organism	# References	# Assays
1101093	HVKITDFGR	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	2	3
1101094	HVKITDFGRAK	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	2	2
1104681	KITDFGRAK	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	2	6
1312125	AIKTSPKANK	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	2	2
1312768	IPVAIKTSPK	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	2	2
1334556	ATSPASASK	neoantigen: Nuclear receptor subfamily 4 group A member 1	Homo sapiens (human)	2	2
1334611	MLICCCCTL	neoantigen: Solute carrier family 12 member 4 (UniProt:Q9UP95)	Homo sapiens (human)	2	2
1334628	SEHGFGPSL	neoantigen: Mitochondrial peptide methionine sulfoxide reductase	Homo sapiens (human)	2	2
1334629	SEIISFKSL	neoantigen: Fasciculation and elongation protein zeta-1	Homo sapiens (human)	2	2
1334647	VEWLGRCIL	neoantigen: Chondroitin sulfate synthase 2	Homo sapiens (human)	2	2
71668	VVGAVGVGK	neoantigen: HRas proto-oncogene, GTPase	Homo sapiens (human)	1	5
858771	ASNASSAAK	neoantigen: Probable E3 ubiquitin-protein ligase HERC1	Homo sapiens (human)	1	5
858876	ETVSEQSNV	neoantigen: Elongation factor 2	Homo sapiens (human)	1	1
858895	FIASNGVKLV	neoantigen: Alpha-actinin-1	Homo sapiens (human)	1	7
858907	FLDEFMEGV	neoantigen: NADP-dependent malic enzyme	Homo sapiens (human)	1	11
859210	MQLMPFGCLL	neoantigen: Receptor protein-tyrosine kinase (UniProt:Q504U8)	Homo sapiens (human)	1	1
859309	QQITKTEV	neoantigen: Nuclear transcription factor Y subunit gamma (Fragment) (UniProt:Q5T6K5)	Homo sapiens (human)	1	4
1066141	LIMQLMPFGCL	neoantigen: Epidermal growth factor receptor	Homo sapiens (human)	1	1
1087208	ETMQCSELYHM	neoantigen: Kelch-like protein 29	Homo sapiens (human)	1	1
1087210	EVIVPLSGW	neoantigen: ARVCF delta catenin family member	Homo sapiens (human)	1	1
1087211	EVQQFLRY	neoantigen: Xylosyl- and glucuronyltransferase LARGE1	Homo sapiens (human)	1	1
1087238	QHQPNPFEV	neoantigen: Inactive tyrosine-protein kinase PRAG1	Homo sapiens (human)	1	1
1087578	KLVVVGACGV	neoantigen: GTP-binding protein GEM	Homo sapiens (human)	1	1
1113688	QPSGIILDY	neoantigen: Ephrin type-B receptor 1	Homo sapiens (human)	1	1
1114008	RAKLLGAEEK			1	1

Page 1 of 7 — 163 Records Found — 25 Per Page | Export Results

Example Query: Prostate-specific Antigen



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Exact Match | Ex: AAGIGILTV
○ Discontinuous

Assay

☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: Cytotoxicity | Find
Outcome: ☑ Positive ☐ Negative

Epitope Source

Antigen: prostat | Find
Cancer-as

☑ Neo
☑ Vira
☑ Ger
☐ Other a

Prostate-specific antigen [P07288] (Homo sapiens (human))
Acid phosphatase, **prostate** [A0A0G2K4B4] (Rattus norvegicus (b…
Prostate stem cell antigen [O43653] (Homo sapiens (human))
Prostatic acid phosphatase [P15309] (Homo sapiens (human))
Prostatic acid phosphatase [Q8CE08] (Mus musculus (mouse))
Transglutaminase 4 (**prostate**) [A0A0R4J071] (Mus musculus (mo…
Prostate and testis expressed 5 [Q9D262] (Mus musculus (mouse))
Prostate-associated microseminoprotein [B1AWI6] (Mus musculu…
Prostate and testis expressed protein 1 [Q8WXA2] (Homo sapien…
Prostate and testis expressed protein 3 [B3GLJ2] (Homo sapiens …

MHC Restriction

● Any

Host

● Any
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○ Non-hu
○ Ex: C

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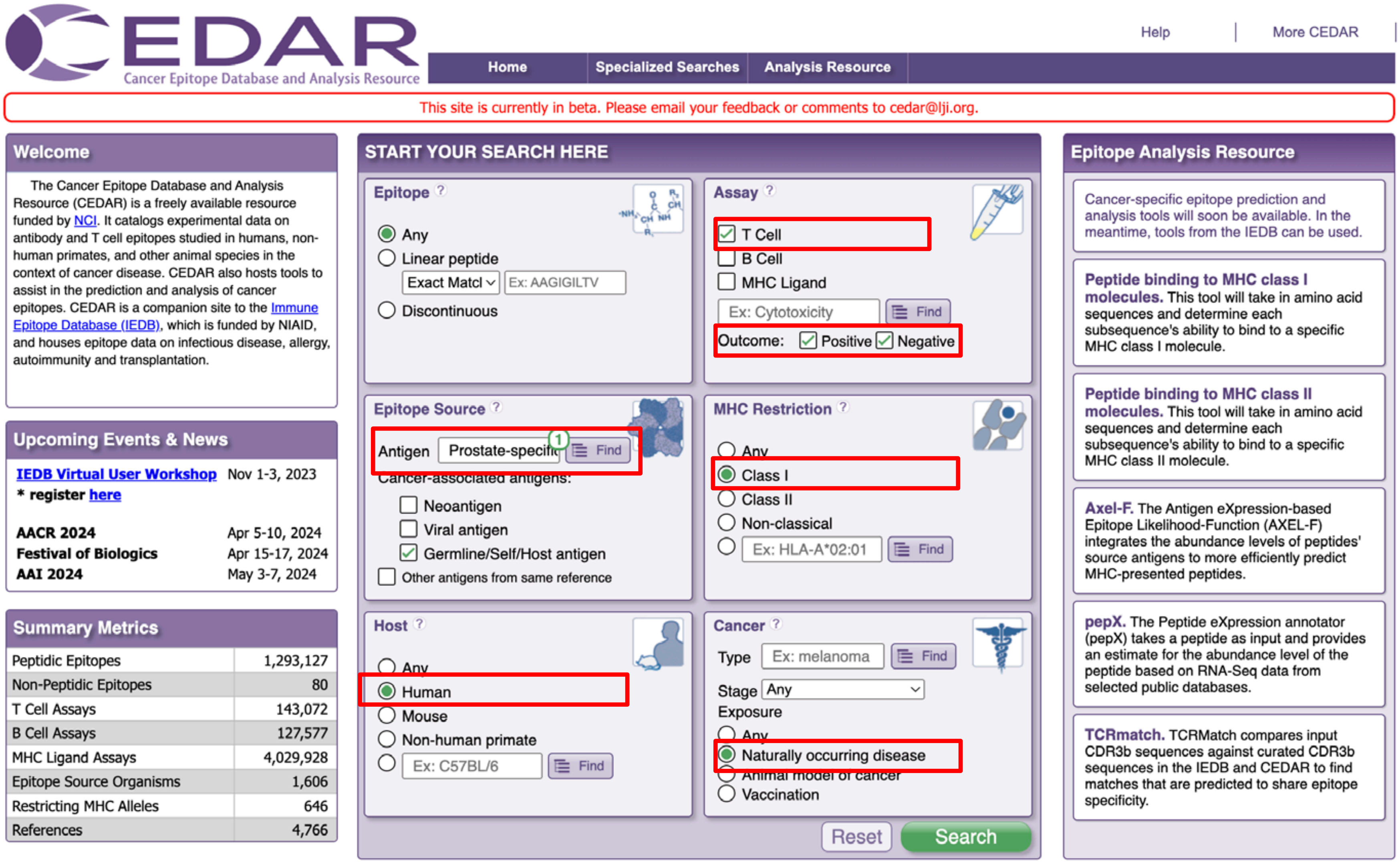

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Epitope Source
- Antigen: Prostate-specific (1) — Find
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MHC Restriction
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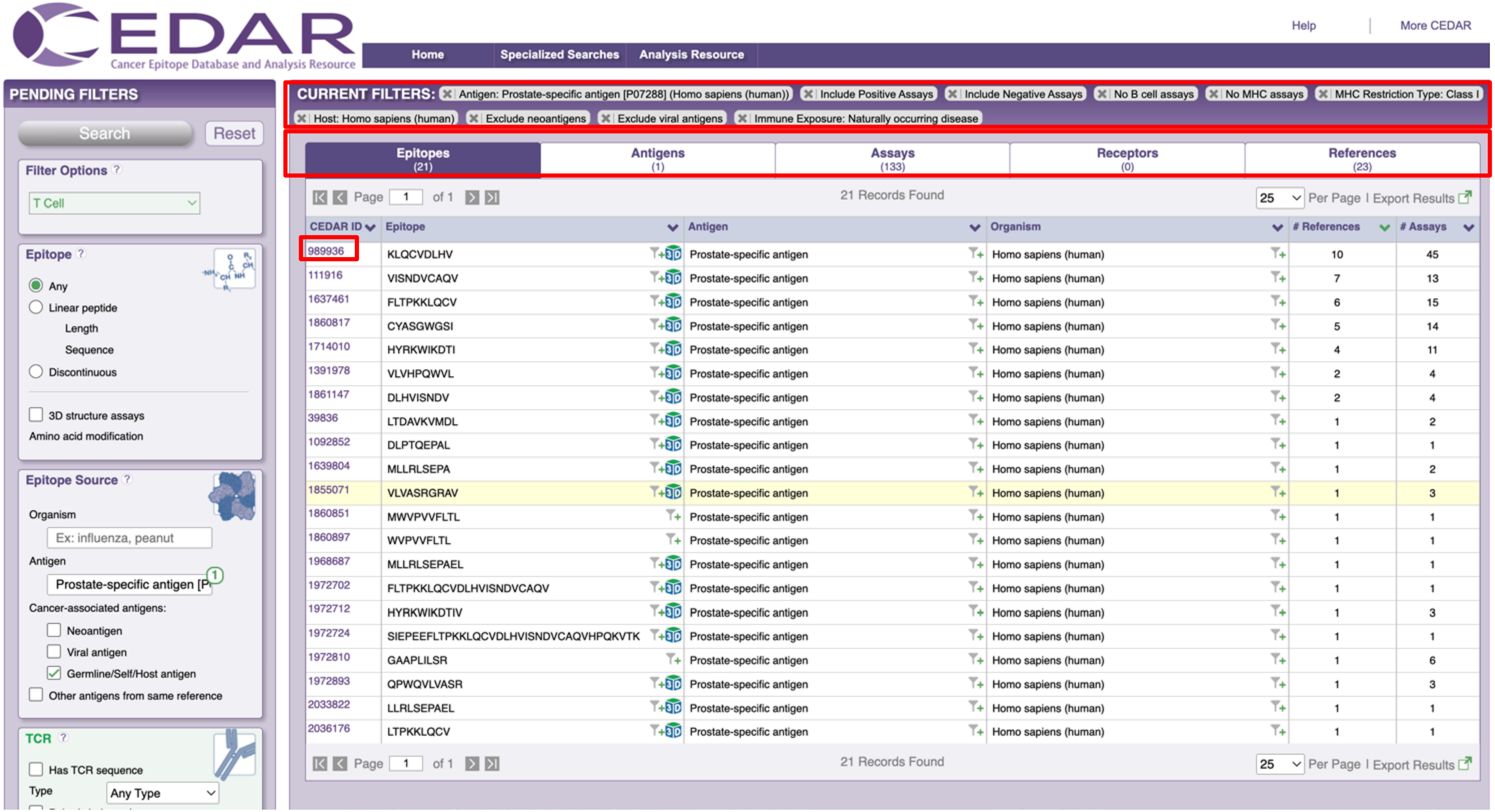

T Cell

Epitope: ● Any ○ Linear peptide (Length, Sequence) ○ Discontinuous

☐ 3D structure assays

Amino acid modification

Organism: Ex: influenza, peanut

Antigen: Prostate-specific antigen [P

Cancer-associated antigens:

☐ Neoantigen

☐ Viral antigen

☑ Germline/Self/Host antigen

☐ Other antigens from same reference

☐ Has TCR sequence

Type: Any Type

CURRENT FILTERS: ✖ Antigen: Prostate-specific antigen [P07288] (Homo sapiens (human)) ✖ Include Positive Assays ✖ Include Negative Assays ✖ No B cell assays ✖ No MHC assays ✖ MHC Restriction Type: Class I ✖ Host: Homo sapiens (human) ✖ Exclude neoantigens ✖ Exclude viral antigens ✖ Immune Exposure: Naturally occurring disease

Epitopes (21) | Antigens (1) | Assays (133) | Receptors (0) | References (23)

Page 1 of 1 — 21 Records Found — 25 Per Page | Export Results

CEDAR ID	Epitope	Antigen	Organism	# References	# Assays
989936	KLQCVDLHV	Prostate-specific antigen	Homo sapiens (human)	10	45
111916	VISNDVCAQV	Prostate-specific antigen	Homo sapiens (human)	7	13
1637461	FLTPKKLQCV	Prostate-specific antigen	Homo sapiens (human)	6	15
1860817	CYASGWGSI	Prostate-specific antigen	Homo sapiens (human)	5	14
1714010	HYRKWIKDTI	Prostate-specific antigen	Homo sapiens (human)	4	11
1391978	VLVHPQWVL	Prostate-specific antigen	Homo sapiens (human)	2	4
1861147	DLHVISNDV	Prostate-specific antigen	Homo sapiens (human)	2	4
39836	LTDAVKVMDL	Prostate-specific antigen	Homo sapiens (human)	1	2
1092852	DLPTQEPAL	Prostate-specific antigen	Homo sapiens (human)	1	1
1639804	MLLRLSEPA	Prostate-specific antigen	Homo sapiens (human)	1	2
1855071	VLVASRGRAV	Prostate-specific antigen	Homo sapiens (human)	1	3
1860851	MWVPVVFLTL	Prostate-specific antigen	Homo sapiens (human)	1	1
1860897	WVPVVFLTL	Prostate-specific antigen	Homo sapiens (human)	1	1
1968687	MLLRLSEPAEL	Prostate-specific antigen	Homo sapiens (human)	1	1
1972702	FLTPKKLQCVDLHVISNDVCAQV	Prostate-specific antigen	Homo sapiens (human)	1	1
1972712	HYRKWIKDTIV	Prostate-specific antigen	Homo sapiens (human)	1	3
1972724	SIEPEEFLTPKKLQCVDLHVISNDVCAQVHPQKVTK	Prostate-specific antigen	Homo sapiens (human)	1	1
1972810	GAAPLILSR	Prostate-specific antigen	Homo sapiens (human)	1	6
1972893	QPWQVLVASR	Prostate-specific antigen	Homo sapiens (human)	1	3
2033822	LLRLSEPAEL	Prostate-specific antigen	Homo sapiens (human)	1	1
2036176	LTPKKLQCV	Prostate-specific antigen	Homo sapiens (human)	1	1

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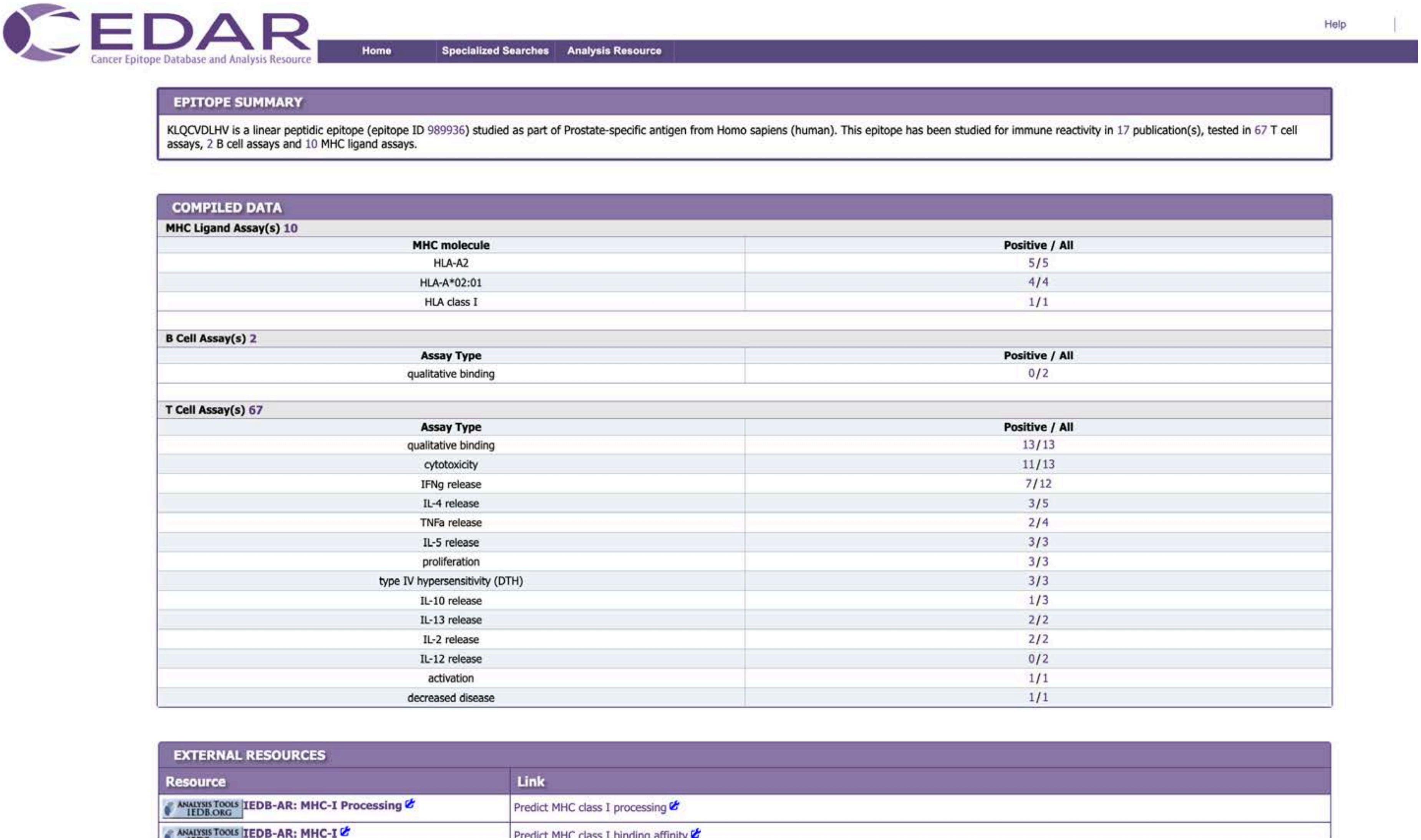
Query can be refined further on the 'Results' page via our 'Filter Options'

Example Results: Prostate-specific Antigen

Epitope details page summarizes all assays and results for epitope



EPITOPE SUMMARY

KLQCVDLHV is a linear peptidic epitope (epitope ID 989936) studied as part of Prostate-specific antigen from Homo sapiens (human). This epitope has been studied for immune reactivity in 17 publication(s), tested in 67 T cell assays, 2 B cell assays and 10 MHC ligand assays.

COMPILED DATA

MHC Ligand Assay(s) 10

MHC molecule	Positive / All
HLA-A2	5/5
HLA-A*02:01	4/4
HLA class I	1/1

B Cell Assay(s) 2

Assay Type	Positive / All
qualitative binding	0/2

T Cell Assay(s) 67

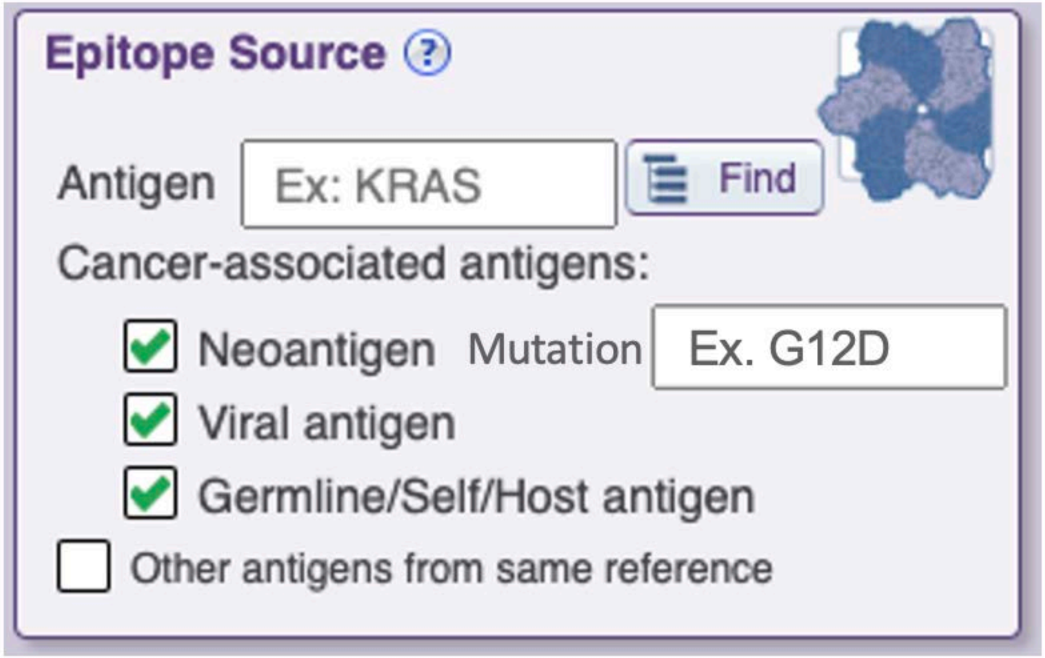
Assay Type	Positive / All
qualitative binding	13/13
cytotoxicity	11/13
IFNg release	7/12
IL-4 release	3/5
TNFa release	2/4
IL-5 release	3/3
proliferation	3/3
type IV hypersensitivity (DTH)	3/3
IL-10 release	1/3
IL-13 release	2/2
IL-2 release	2/2
IL-12 release	0/2
activation	1/1
decreased disease	1/1

EXTERNAL RESOURCES

Resource	Link
ANALYSIS TOOLS IEDB.ORG IEDB-AR: MHC-I Processing	Predict MHC class I processing
ANALYSIS TOOLS IEDB-AR: MHC-I	Predict MHC class I binding affinity

Additional Features Under Development (I)

Enable search for neoantigens derived from a specific amino acid mutation



Epitope Source ?

Antigen: Ex: KRAS

Cancer-associated antigens:

- ☑ Neoantigen Mutation: Ex. G12D
- ☑ Viral antigen
- ☑ Germline/Self/Host antigen

☐ Other antigens from same reference

Additional Features Under Development (II)

Provide information about the mutation underlying the neoantigen

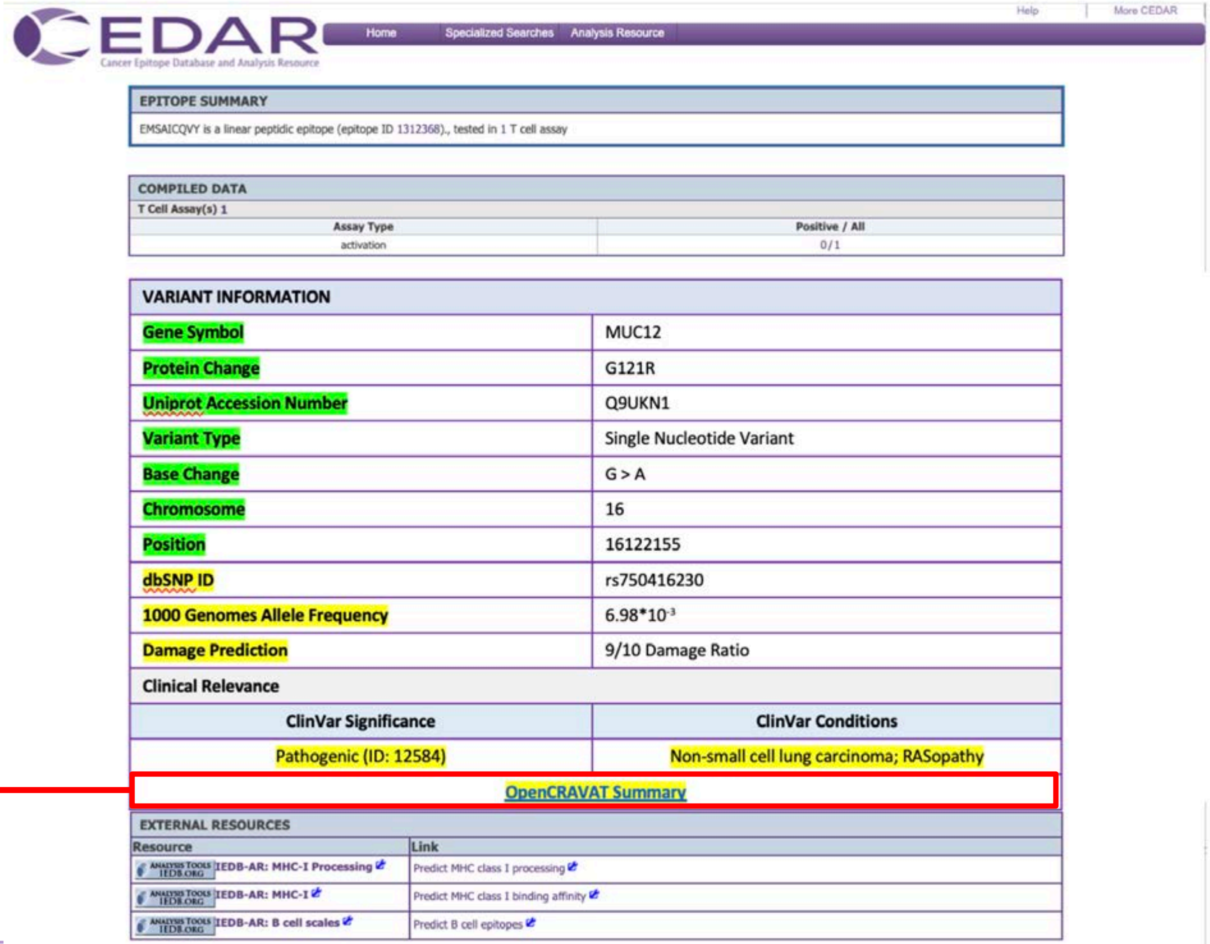
- Collaboration with external tools:

UCSC TransVar for mapping peptides to the genome (amino acid mutation vs DNA mutation)

OpenCRAVAT for retrieving information about the DNA mutation

Additional Features Under Development (II)

Provide information about the mutation underlying the neoantigen



EPITOPE SUMMARY

EMSAICQVY is a linear peptidic epitope (epitope ID 1312368)., tested in 1 T cell assay

COMPILED DATA

T Cell Assay(s) 1

Assay Type	Positive / All
activation	0/1

VARIANT INFORMATION	
Gene Symbol	MUC12
Protein Change	G121R
Uniprot Accession Number	Q9UKN1
Variant Type	Single Nucleotide Variant
Base Change	G > A
Chromosome	16
Position	16122155
dbSNP ID	rs750416230
1000 Genomes Allele Frequency	$6.98*10^{-3}$
Damage Prediction	9/10 Damage Ratio
Clinical Relevance	
ClinVar Significance	**ClinVar Conditions**
Pathogenic (ID: 12584)	Non-small cell lung carcinoma; RASopathy
OpenCRAVAT Summary	

EXTERNAL RESOURCES

Resource	Link
ANALYSIS TOOLS IEDB.ORG IEDB-AR: MHC-I Processing	Predict MHC class I processing
ANALYSIS TOOLS IEDB.ORG IEDB-AR: MHC-I	Predict MHC class I binding affinity
ANALYSIS TOOLS IEDB.ORG IEDB-AR: B cell scales	Predict B cell epitopes

Analysis Resource

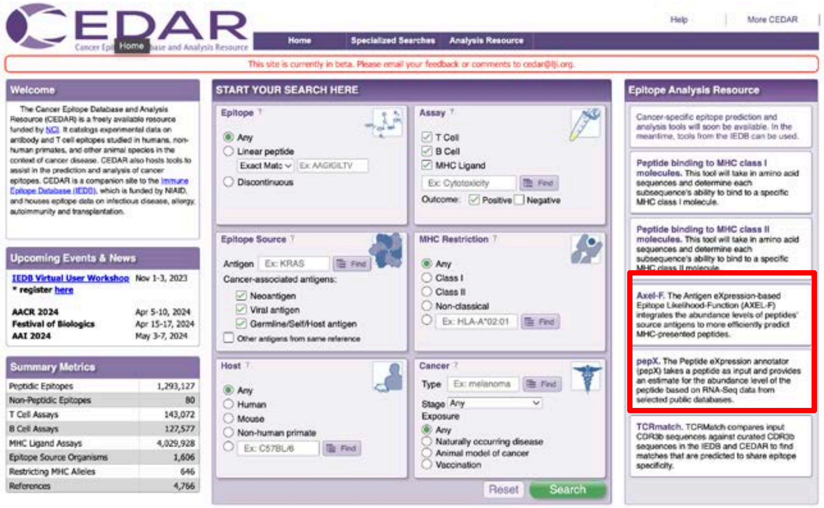
Computational epitope prediction and analysis tools providing researchers access to predictive strategies and objective evaluations of their performance

Overarching Analysis Resource Goals

1. **Provide prediction tools tailored to the needs of cancer immunologists**
2. **Develop novel prediction tools for cancer epitopes**
3. **Provide web-implementations for published but hard to access cancer-epitope related tools in CEDAR**
4. **Use curated cancer epitope datasets to benchmark epitope prediction tools**

Develop Novel Prediction Tools for Cancer Epitopes

- **2 tools published recently**
  - **Axel-F**: combined assessment of antigen expression and MHC binding
  - **pepX**: provides an estimate for the abundance level of the peptide based on RNA-Seq data from selected public databases such as TCGA, CCLE, etc



This site is currently in beta. Please email your feedback or comments to cedar@lji.org.

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. CEDAR is a companion site to the Immune Epitope Database (IEDB), which is funded by NIAID, and houses epitope data on infectious disease, allergy, autoimmunity and transplantation.

Upcoming Events & News

IEDB Virtual User Workshop * register here	Nov 1-3, 2023
AACR 2024	Apr 5-10, 2024
Festival of Biologics	Apr 15-17, 2024
AAI 2024	May 3-7, 2024

Summary Metrics

Peptidic Epitopes	1,293,127
Non-Peptidic Epitopes	80
T Cell Assays	143,072
B Cell Assays	127,577
MHC Ligand Assays	4,029,928
Epitope Source Organisms	1,606
Restricting MHC Alleles	646
References	4,766

START YOUR SEARCH HERE

Epitope
● Any
○ Linear peptide
Exact Matc Ex: AAGIGILTV
○ Discontinuous

Assay
☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: Cytotoxicity
Outcome: ☑ Positive ☐ Negative

Epitope Source
Antigen Ex: KRAS
Cancer-associated antigens:
☑ Neoantigen
☑ Viral antigen
☑ Germline/Self/Host antigen
☐ Other antigens from same reference

MHC Restriction
● Any
○ Class I
○ Class II
○ Non-classical
○ Ex: HLA-A*02:01

Host
● Any
○ Human
○ Mouse
○ Non-human primate
○ Ex: C57BL/6

Cancer
Type Ex: melanoma
Stage Any
Exposure
● Any
○ Naturally occurring disease
○ Animal model of cancer
○ Vaccination

Epitope Analysis Resource

Cancer-specific epitope prediction and analysis tools will soon be available. In the meantime, tools from the IEDB can be used.

Peptide binding to MHC class I molecules. This tool will take in amino acid sequences and determine each subsequence's ability to bind to a specific MHC class I molecule.

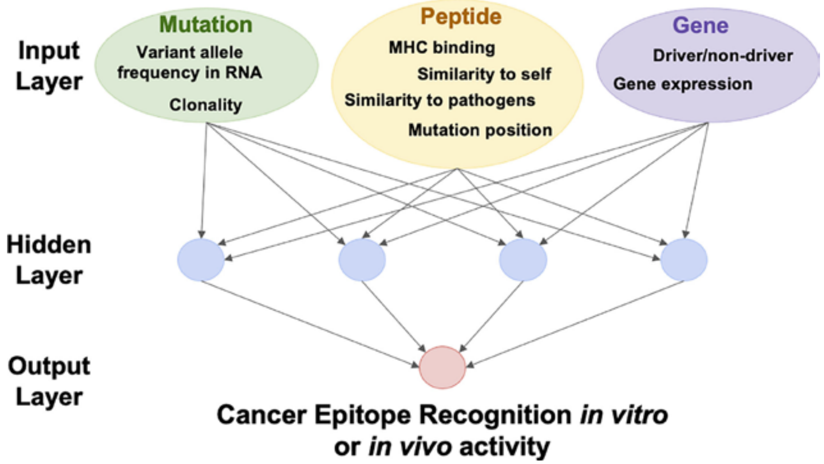
Peptide binding to MHC class II molecules. This tool will take in amino acid sequences and determine each subsequence's ability to bind to a specific MHC class II molecule.

Axel-F. The Antigen eXpression-based Epitope Likelihood-Function (AXEL-F) integrates the abundance levels of peptides' source antigens to more efficiently predict MHC-presented peptides.

pepX. The Peptide eXpression annotator (pepX) takes a peptide as input and provides an estimate for the abundance level of the peptide based on RNA-Seq data from selected public databases.

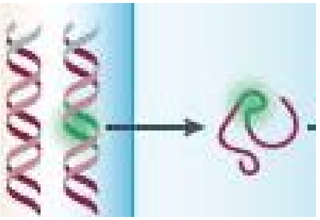
TCRmatch. TCRMatch compares input CDR3b sequences against curated CDR3b sequences in the IEDB and CEDAR to find matches that are predicted to share epitope specificity.

- **Future tool development**
  - include additional features when predicting epitopes

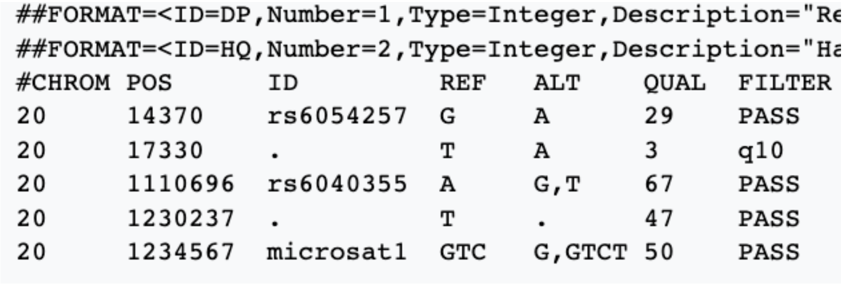


Provide prediction tools tailored to the needs of cancer immunologists (I)

- **What neoepitopes are generated by a given DNA mutation?**



DNA Mutations in VCF format



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20     17330    .         T    A      3     q10
20     1110696  rs6040355 A    G,T    67    PASS
20     1230237  .         T    .      47    PASS
20     1234567  microsat1 GTC  G,GTCT 50    PASS
```

Mutated Peptides

IPDRAPGWTRNSCPAG
KIPDRAPGWTRNSC
RVKIPDRAPGWTR
PDRAPGWTRNS

Provide prediction tools tailored to the needs of cancer immunologists (II)

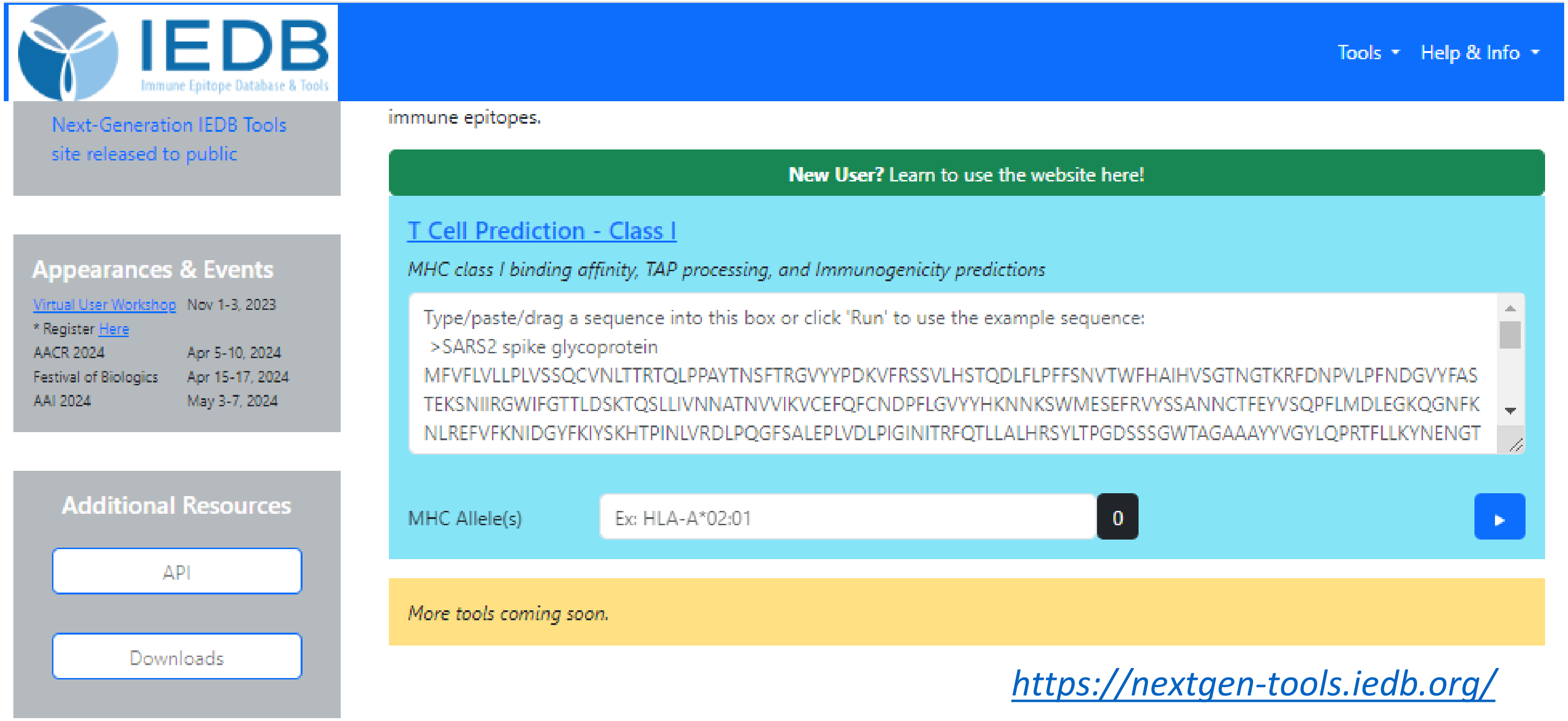
- **Side-by-side predictions for mutant and wild-type peptides**

WT Peptide	MT Peptide	WT IC50	MTIC50	Δ IC50
IPDRA**V**GWTRNSCPAG	IPDRA**P**GWTRNSCPAG	30.63	278.54	247.91
KIPDRA**V**GWTRNSC	KIPDRA**P**GWTRNSC	4569.09	20.45	4548.64
RVKIPDRA**V**GWTR	RVKIPDRA**P**GWTR	789.43	3450.56	2661.13
PDRA**V**GWTRNS	PDRA**P**GWTRNS	7689.34	9870.23	2180.89

CEDAR & the Next-Generation Tools

Planned Releases

- 2.0 - Target March 2024 - Cancer-focused functionality
  - Peptide expression estimator (PepX)
  - Mutated peptide generation
  - Paired wild-type and mutant peptide predictions



Next-Generation IEDB Tools site released to public

immune epitopes.

New User? Learn to use the website here!

Appearances & Events

Virtual User Workshop	Nov 1-3, 2023
* Register Here	
AACR 2024	Apr 5-10, 2024
Festival of Biologics	Apr 15-17, 2024
AAI 2024	May 3-7, 2024

T Cell Prediction - Class I

MHC class I binding affinity, TAP processing, and Immunogenicity predictions

```
Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
 >SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFAS
TEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFK
NLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGT
```

MHC Allele(s): Ex: HLA-A*02:01

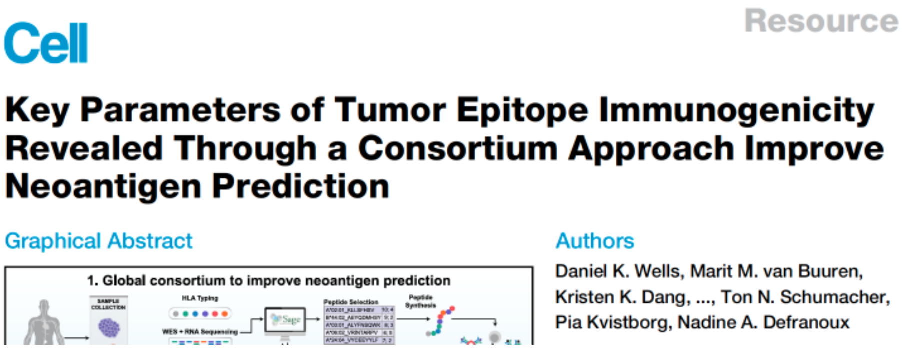
Additional Resources

More tools coming soon.

https://nextgen-tools.iedb.org/

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

- Prioritize tools to implement in CEDAR based on cost-benefit analysis



Cell

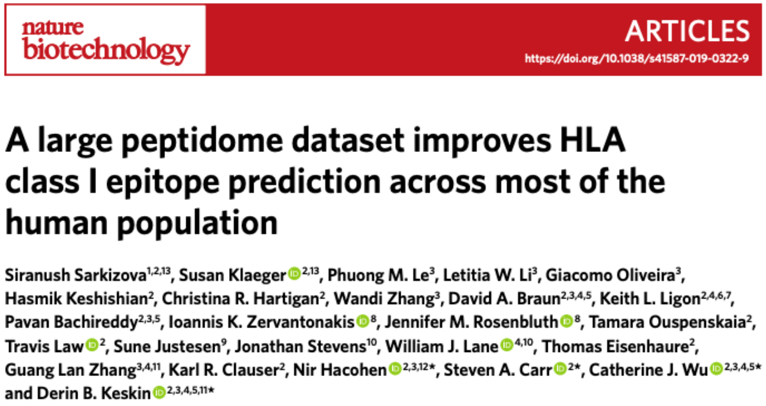
Resource

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

Graphical Abstract

Authors

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



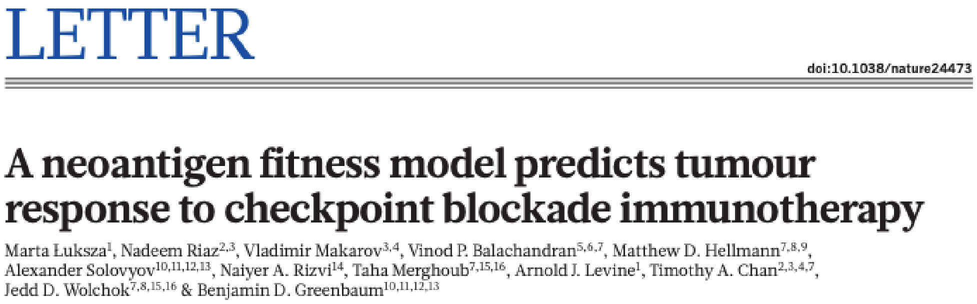
nature biotechnology

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]*



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]

Use curated cancer epitope datasets to benchmark epitope prediction tools

- Assemble comprehensive sets of cancer epitope data
- 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?

CEDAR at AACR 2024 – Booth 3753

Visit our booth!

Citing CEDAR in Research

JOURNAL ARTICLE

The Cancer Epitope Database and Analysis Resource (CEDAR)

Zeynep Koşaloğlu-Yalçın ✉, Nina Blazeska, Randi Vita, Hannah Carter, Morten Nielsen, Stephen Schoenberger, Alessandro Sette, Bjoern Peters

Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D845–D852, https://doi.org/10.1093/nar/gkac902

Published: 17 October 2022 **Article history** ▾

Summary

CEDAR is an extension of the IEDB, containing cancer-related epitope data and tools

1. **cedar.iedb.org is a working cancer epitope database**
2. **Literature curation is moving rapidly**
3. **Existing tools will be adapted to the needs of cancer researchers and novel cancer-specific tools will be developed. Cancer benchmark datasets are being assembled.**
4. **Community engagement has been initiated and will continually increase**