



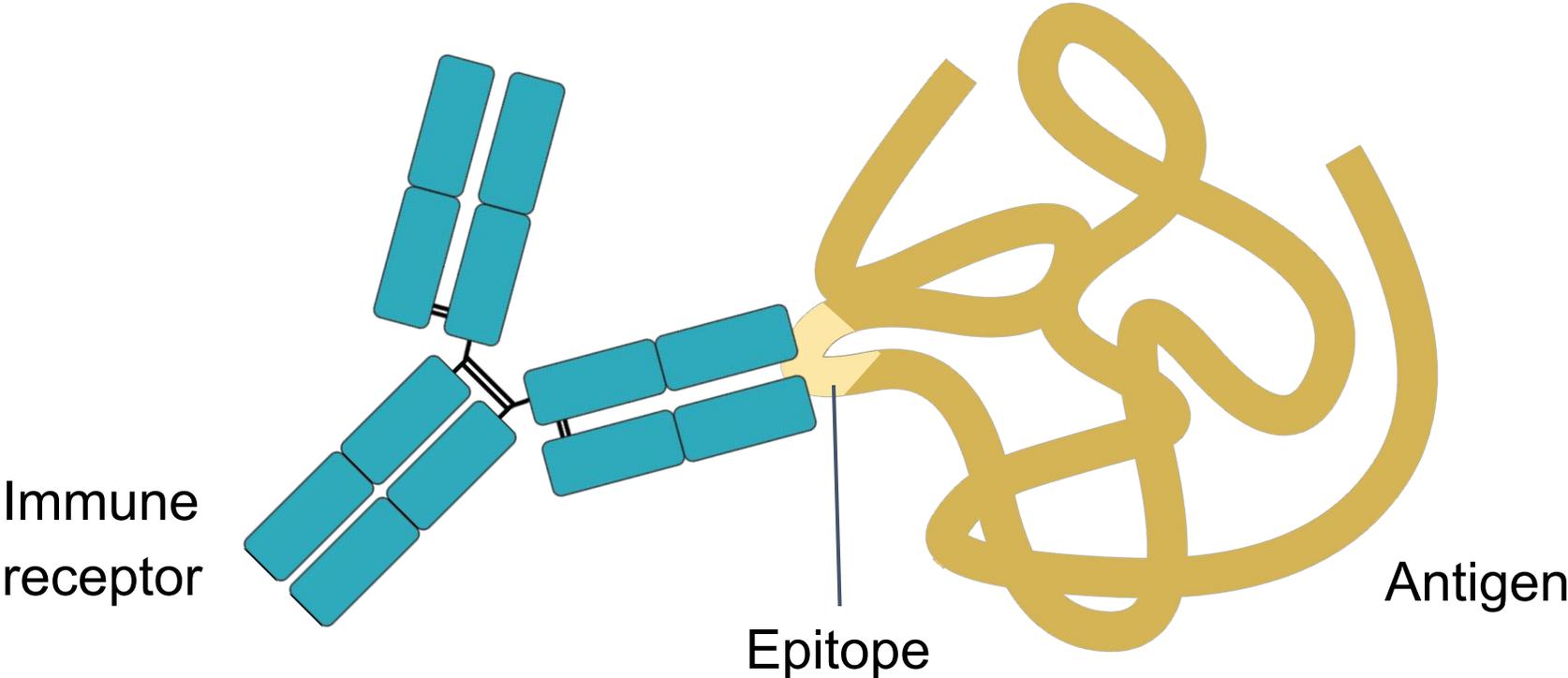
IEDB
Immune Epitope Database & Tools

Receptor Data in the IEDB

iedb.org

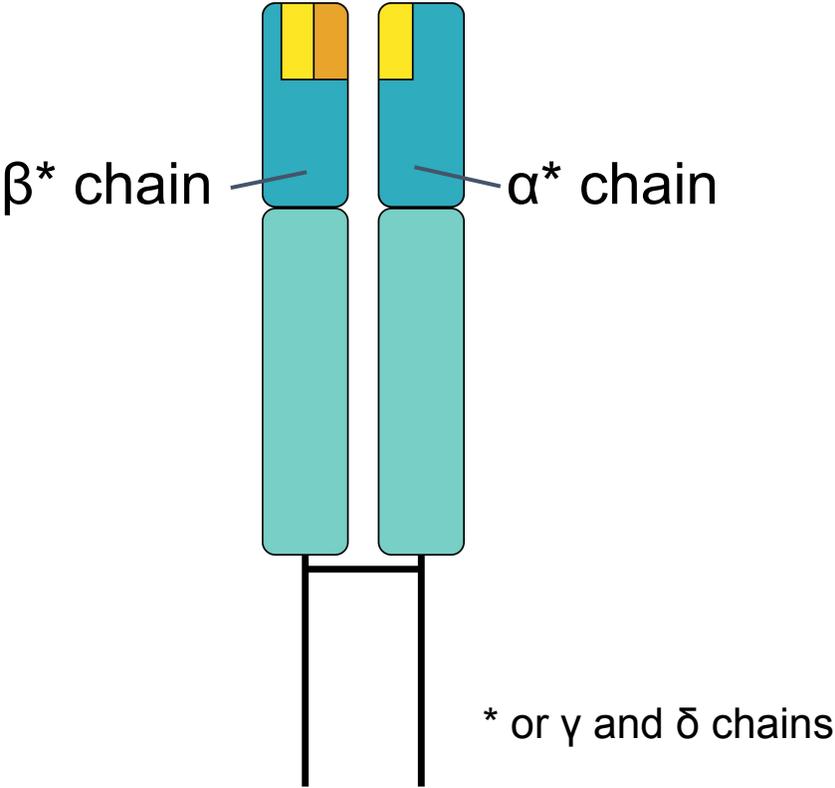
Presented by: Lonneke Scheffer, Bioinformatics Postdoctoral Fellow

Adaptive Immune Receptors Bind Antigen Epitopes

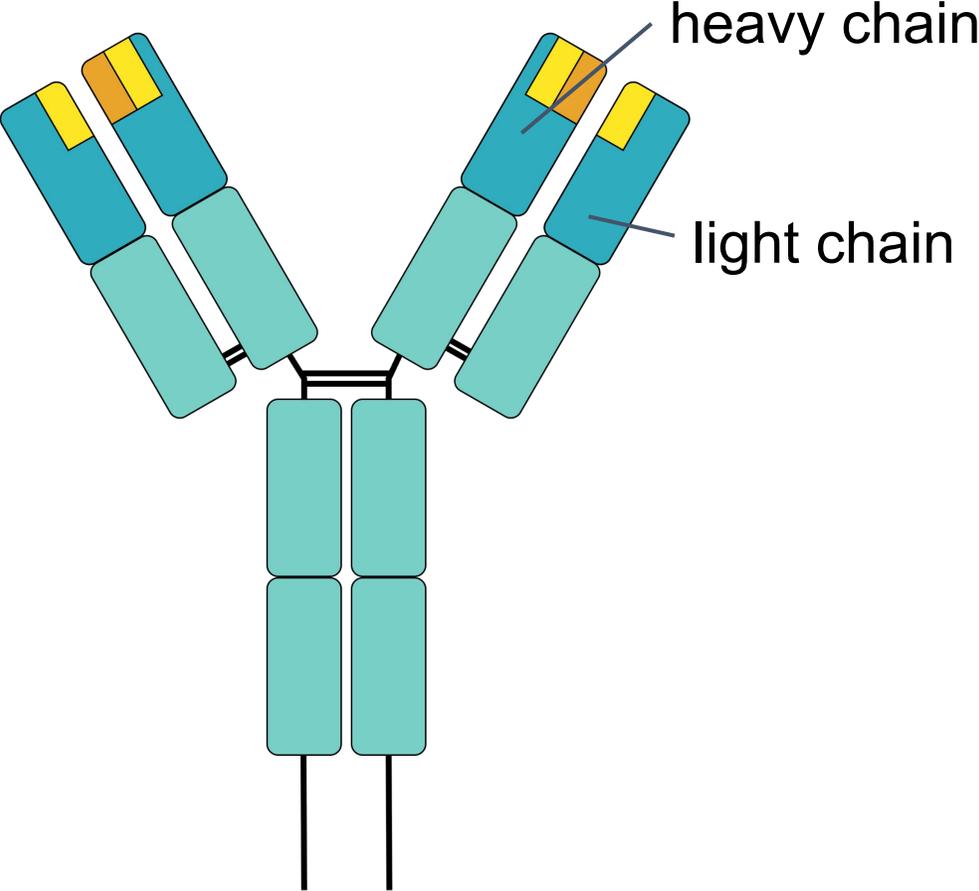


Adaptive Immune Receptors

T cell receptor (TCR)

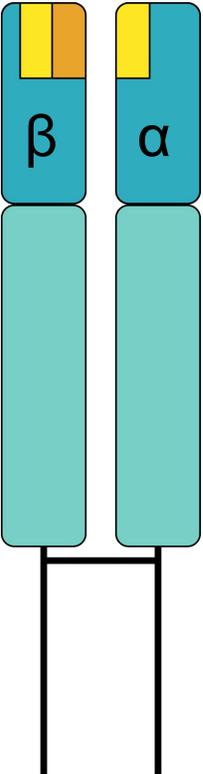


B cell receptor (BCR)

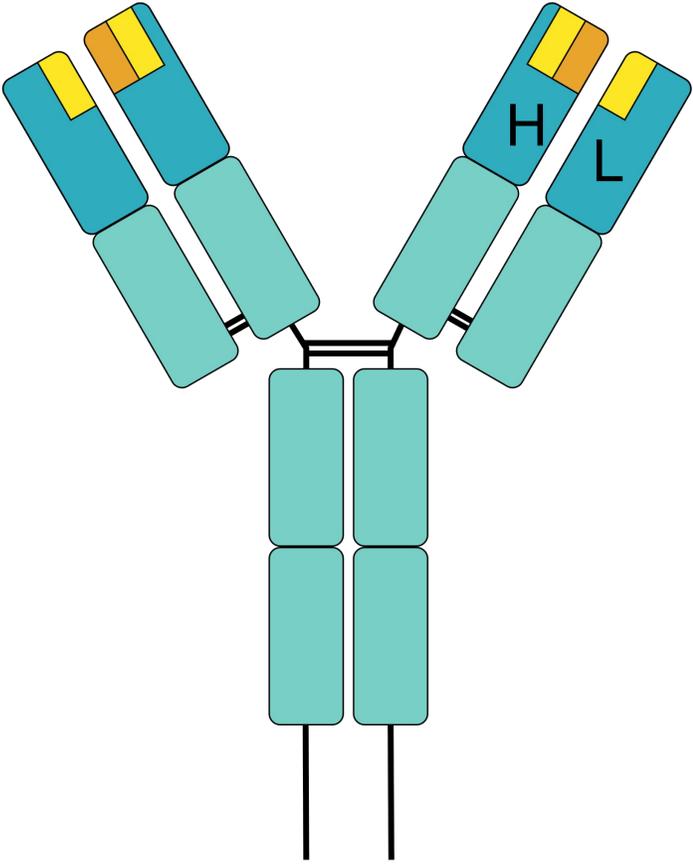


Adaptive Immune Receptors

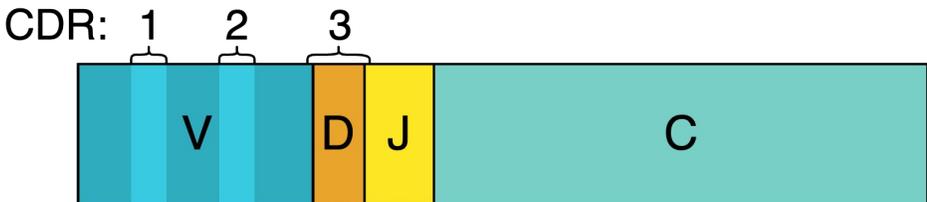
TCR



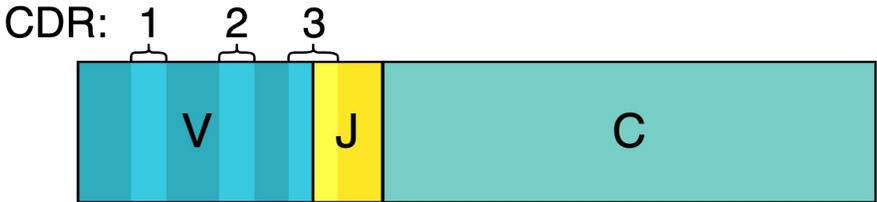
BCR



BCR heavy / TCR β

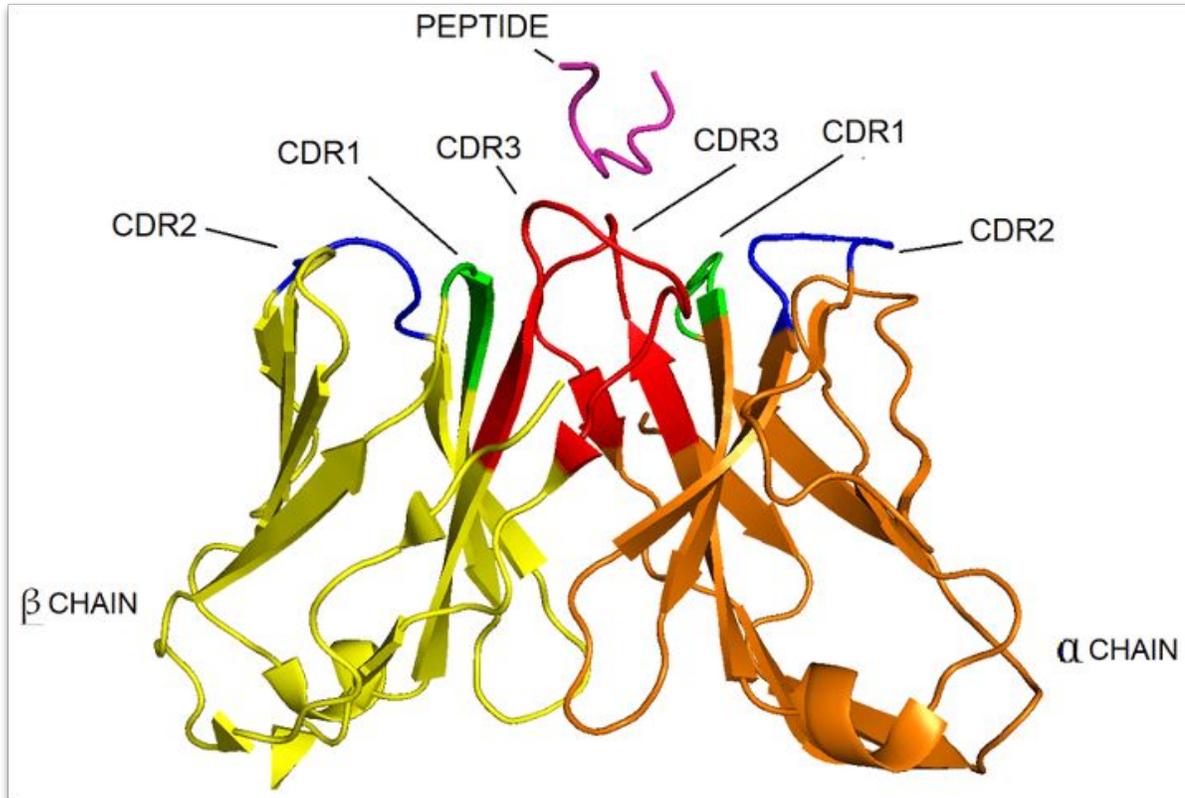


BCR light / TCR α



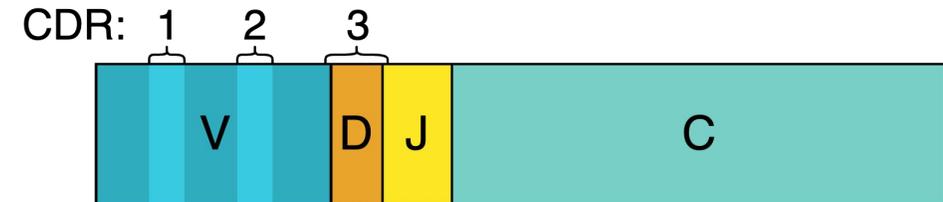
Adaptive Immune Receptors

Complementarity determining regions (**CDRs**), especially **CDR3 β /heavy**, are most important for antigen binding

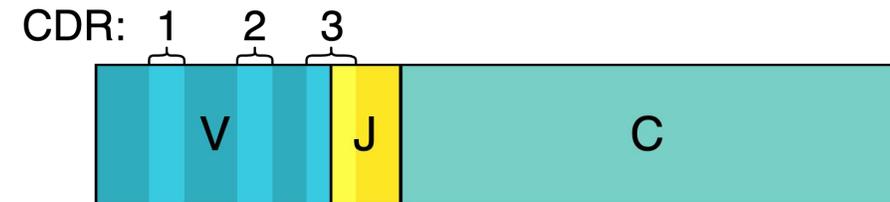


Cinelli, Mattia. (2018). Analysis of murine CDR3 β repertoires using machine learning techniques.

BCR heavy / TCR β



BCR light / TCR α



Receptor Data Currently in the IEDB

IEDB
Immune Epitope Database & Tools

Home | Specialized Searches | Analysis Resource | Support | More IEDB

Current Filters: Include Positive Assays TCR sequence available: Set Antibody sequence available: Set

Epitopes (7795) | Antigens (1589) | Assays (24477) | **Receptors (194768)** | References (3300)

T Cell Receptors (189978) | B Cell Receptors (4790)

Go To Records Starting At 1200 Export Results

189978 Records Found Per Page

Group ID	Species	Type	Chain 1 CDR3	Chain 2 CDR3
47	Homo sapiens (human)	αβ	IVVRSNTGKLI	ASSQDRDTQY
49	Mus musculus (mouse)	αβ	AASANSPTYQR	ASGDAGGGYEQY
50	Mus musculus C57BL/6	αβ	AAS	ASSL
57	Homo sapiens (human)	αβ	AALIQGAQKLV	ASTYHGTGY
94	Homo sapiens (human)	αβ	AVRPLLDGTYIPT	ASSYLGN TGELF
102	Mus musculus (mouse)	αβ	ALSENYGNEKIT	ASGDASGAETLY
103	Mus musculus (mouse)	αβ	ALSENYGNEKIT	ASGDASGGNTLY
104	Mus musculus (mouse)	αβ	AANSPTYQR	ASGDFWGD TLY
109	Homo sapiens (human)	αβ	IVWGGYQKVT	ASRYRDDS YNEQF
110	Homo sapiens (human)	αβ	AVTTDSWGK LQ	ASRPGLAG GRPEQY
111	Homo sapiens (human)	αβ	AVTTDSWGK LQ	ASRPGLMS AQPEQY
114	Mus musculus (mouse)	αβ	AVSDPPPLT	ASGGGGTLY
115	Mus musculus (mouse)	αβ	AVSLERP YLT	ASGGGGTLY
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPLAGEYEQY
117	Homo sapiens (human)	αβ	AVRPTSGGSYIPT	ASSYVGN TGELF

Filter Options

Filter Options

Epitope

Any

Linear peptide

Length

Sequence

Discontinuous

Non-peptidic

3D structure assays

Amino acid modification

Epitope Source

Organism

Ex: influenza, peanut

Antigen

Ex: core, capsid, myosin

Include related structure

Receptor Data Currently in the IEDB

IEDB
Immune Epitope Database & Tools

Home | Specialized Searches | Analysis Resource | Support | More IEDB

Current Filters: Include Positive Assays TCR sequence available: Set Antibody sequence available: Set

Epitopes (7795) | Antigens (1589) | Assays (24477) | **Receptors (194768)** | References (3300)

T Cell Receptors (189978) | B Cell Receptors (4790)

189,978 TCRs (+915 negative)

4,790 BCRs (+77 negative)

978 Records Found

Export Results [↗](#)

25 Per Page

Epitope ID	Species	Chain 1	Chain 2 CDR3
47	Homo sapiens (human)	αβ	IVVRSNTGKLI
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110	Homo sapiens (human)	αβ	AVTTDSWGKLV
111	Homo sapiens (human)	αβ	AVTTDSWGKLV
114	Mus musculus (mouse)	αβ	AVSDPPPLLT
115	Mus musculus (mouse)	αβ	AVSLERPPLYT
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI
117	Homo sapiens (human)	αβ	AVRPTSGGSYIPT

Filter Options: Any, Linear peptide, Length, Sequence, Discontinuous, Non-peptidic, 3D structure assays, Amino acid modification

Epitope Source: Organism (Ex: influenza, peanut), Antigen (Ex: core, capsid, myosin), Include related structure

Receptor Data Currently in the IEDB

IEDB
Immune Epitope Database & Tools

Home | Specialized Searches | Analysis Resource | Support | More IEDB

Current Filters: Include Positive Assays TCR sequence available: Set Antibody sequence available: Set

Epitopes (7795) | Antigens (1589) | Assays (24477) | Receptors (194768) | References (3300)

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189,978 TCRs (+915 negative)

4,790 BCRs (+77 negative)

3,300 references

978 Records Found

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Receptor Data Currently in the IEDB

IEDB
Immune Epitope Database & Tools

Home | Specialized Searches | Analysis Resource | Support | More IEDB

Current Filters: Include Positive Assays TCR sequence available: Set Antibody sequence available: Set

Epitopes (7795) | Antigens (1589) | Assays (24477) | **Receptors (194768)** | References (3300)

T Cell Receptors (189978) | B Cell Receptors (4790)

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189978 Records Found Per Page

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110	Homo sapiens (human)	αβ	AVTTDSWGKIQ	ASRPGLAGGRPEYQ
111	Homo sapiens (human)	αβ	AVTTDSWGKIQ	ASRPGLMSAQPEYQ
114	Mus musculus (mouse)	αβ	AVSDPPPLLT	ASGGGGTLY
115	Mus musculus (mouse)	αβ	AVSLERPPLYT	ASGGGGTLY
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117	Homo sapiens (human)	αβ	AVRPTSGGSYIPT	ASSYVNTGELF

Filter Options
Default

Epitope
 Any
 Linear peptide
 Length
 Sequence
 Discontinuous
 Non-peptidic
 3D structure assays
 Amino acid modification

Epitope Source
 Organism
 Ex: influenza, peanut
 Antigen
 Ex: core, capsid, myosin
 Include related structure

Receptor Data Currently in the IEDB



IEDB
Immune Epitope Database & Tools

Home

Specialized Searches

Analysis Resource

Support

More IEDB

T cell receptor (receptor group ID 94)

Alpha beta TCR with alpha chain CDR3 of AVRPLLDGTYIPT and beta chain CDR3 of ASSYLGNTGELF was reported in Homo sapiens (human). This TCR has accessions for alpha chain [2P5E_D](#), [2P5W_D](#), [2PYE_D](#) and beta chain [2P5E_E](#), [2P5W_E](#), [2PYE_E](#) and was shown in 3D Structures [2P5E](#), [2P5W](#) and [2PYE](#).

Receptor group: these receptors share the same CDR3s

alpha		beta		Epitopes (# assays)
Gene usage	CDR sequences	Gene usage	CDR sequences	
V:TRAV21*01 D: J:TRAJ6*01	CDR1:DSAIYN CDR2:ITPWQRE CDR3:AVRPLLDGTYIPT	V:TRBV6-5*01 D: J:TRBJ2-2*01	CDR1:MNHEY CDR2:SVAIQT CDR3:ASSYLGNTGELF	SLLMWITQC (2)
V Domain: KQEVTTQIPAALSVPEGENLVLNCSFTDSAI...		V Domain: GVTQTPKFKQVLKGTQSMTLQCAQDMNHEY...		
V:TRAV21*01 D: J:TRAJ6*01	CDR1:DSAIYN CDR2:ITPWQRE CDR3:AVRPLLDGTYIPT	V:TRBV6-5*01 D: J:TRBJ2-2*01	CDR1:MNHEY CDR2:SVSVGM CDR3:ASSYLGNTGELF	SLLMWITQC (2)
V Domain: KQQVTQIPAALSVPEGENLVLNCSFTDSAI...		V Domain: GVTQTPKFKQVLKGTQSMTLQCAQDMNHEY...		
V:TRAV21*01 D: J:TRAJ6*01	CDR1:DSAIYN CDR2:IQSSQRE CDR3:AVRPLLDGTYIPT	V:TRBV6-5*01 D: J:TRBJ2-2*01	CDR1:MNHEY CDR2:SVGAGT CDR3:ASSYLGNTGELF	SLLMWITQC (2)
V Domain: KQEVTTQIPAALSVPEGENLVLNCSFTDSAI...		V Domain: GVTQTPKFKQVLKGTQSMTLQCAQDMNHEY...		

Epitope summary

This TCR was studied for the following epitope SLLMWITQC studied as part of Cancer/testis antigen 1 (UniProt:P78358) from Homo sapiens (human) (epitope ID [59278](#), 1 publication, 6 assays).

IEDB Receptor Data Updates

Web Interface Updates

- Home page
- Receptor results tab
- AIRR-format data export

Data Standardization

- New standardization pipeline
- Old vs new receptor data
- Re-curation

Collaborative Projects

- IMMREP2025
- AIRR Knowledge Commons

Web Interface Updates: Receptor Search Panel



Home
Specialized Searches
Analysis Resource
Support
More CEDAR

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 peptidic epitopes primarily studied in humans and non-human primates 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

CEDAR Virtual Short Course July 16, 2025
* [recordings here](#)

AACR Special Conference Talk Sep 26, 2025

Immunogenicity Summit Short Course Oct 7, 2025

AACR 2026 Exhibitor Booth Apr 17-22, 2026

Summary Metrics

Peptidic Epitopes	1,318,913
Non-Peptidic Epitopes	84
T Cell Assays	149,284
B Cell Assays	141,557
MHC Ligand Assays	4,143,073
Epitope Source Organisms	1,722
Restricting MHC Alleles	665
References	5,993

START YOUR SEARCH HERE

Epitope ?

Any
 Linear peptide
 Discontinuous

Exact Matc Ex: AAGIGILTV

Assay ?

T Cell
 B Cell
 MHC Ligand

Ex: Cytotoxicity

Outcome: Positive Negative

Epitope Source ?

Antigen

Cancer-associated antigens:

Neoantigen Mutation:

Viral antigen

Germline/Self/Host antigen

Other antigens from same reference

Receptor (TCR/BCR) ?

Has sequence TCR BCR

Chain CDR3

Host ?

Any
 Human
 Mouse
 Non-human primate

MHC Restriction ?

Any Class I Class II

Cancer ?

Type

Stage

Exposure

Any
 Naturally occurring disease
 Animal model of cancer
 Vaccination

Epitope Analysis Resource

Mutated Peptide Generator. This tool takes a VCF file as input and extracts coding variants to generate corresponding neo-peptides along with their matched wild-type peptides, enabling downstream analysis of potential neoantigens.

Peptide binding to MHC class I molecules. This tool processes amino acid sequences to predict each subsequence's ability to bind to a specific MHC class I molecule. It accepts paired wild-type and mutant peptides, generating side-by-side binding affinity predictions to facilitate comparative analysis.

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) enhances MHC peptide prediction by incorporating the abundance levels of source antigens.

pepX. The Peptide eXpression annotator (pepX) estimates peptide abundance based on RNA-Seq data from selected public databases, providing expression-based insights for a given peptide input.

TCRmatch. TCRMatch compares input CDR3β sequences against curated CDR3β sequences in IEDB and CEDAR, identifying matches that are predicted to share epitope specificity.

[Submit Help/Feedback](#) | [Support](#)
Last Updated: August 22, 2025

Web Interface Updates: Receptor Search Panel

Amino acid modification

Epitope Source ?

Organism
Ex: influenza, peanut

Antigen
Ex: core, capsid, myosin

Cancer-associated antigens:
 Neoantigen Mutation Ex: R24L
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

Receptor ?

Has sequence TCR BCR

Type Any Type Name Ex: DMF5

Paired chains only

Chain Any Type Region CDR3

Sequence Exact Matches Ex: CARNTGNQFYF

Assay ?

Outcome: Positive

T Cell
 B Cell
 MHC Ligand

MHC Restriction ?

Any

16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3 (UniProt:P12977)	Human herpesvirus 4 (Epstein Barr virus)	15	101
59278	SLLMWITQC	Cancer/testis antigen 1 (UniProt:P78358)	Homo sapiens (human)	15	144
65748	TPRVTGGGAM	65 kDa phosphoprotein (UniProt:P06725)	Human herpesvirus 5 (Human cytomegalovirus)	15	17
155	AAGIGILTV	Melanoma antigen recognized by T-cells 1 (UniProt:Q16655)	Homo sapiens (human)	11	28
28061	IPSINVHHY	65 kDa phosphoprotein (UniProt:P06725)	Human herpesvirus 5 (Human cytomegalovirus)	11	27
		Epstein-Barr nuclear antigen 3 (UniProt:P12977)	Human herpesvirus 4 (Epstein Barr virus)	9	18
		Melanoma antigen recognized by T-cells 1 (UniProt:Q16655)	Homo sapiens (human)	8	18
		Lytic switch protein BZLF1 (UniProt:P03206)	Human herpesvirus 4 (Epstein Barr virus)	8	10
51371	QLINTNGSW HIN	Genome polyprotein (UniProt:P27958)	Hepatitis C virus	7	57
76333	YVLDHLIVV	Replication and transcription activator (UniProt:P03209)	Human herpesvirus 4 (Epstein Barr virus)	7	9
6568	CLGGLTMV	Latent membrane protein 2 (UniProt:P13285)	Human herpesvirus 4 (Epstein Barr virus)	6	15

Detailed receptor search side panel: already available on CEDAR & IEDB

Receptor ?

Has sequence TCR BCR

Type Any Type Name Ex: DMF5

Paired chains only

Chain Any Type Region CDR3

Sequence Exact Matches Ex: CARNTGNQFYF

Web Interface Updates: Epitope Column

The screenshot shows the CEDAR web interface. The top navigation bar includes Home, Specialized Searches, Analysis Resource, Support, and More CEDAR. The main content area is titled "NO FILTERS SET" and displays a table of 54,177 records. The table has columns for Group ID, Host, Type, Chain 1 CDR3, Chain 2 CDR3, and Epitope. The Epitope column is highlighted with a red box. The table also includes filter options on the left and pagination controls at the top.

Group ID	Host	Type	Chain 1 CDR3	Chain 2 CDR3	Epitope
57	Homo sapiens (human)	αβ	AALIQGAQKLV	ASTYHGTTY	GELIGTLNAAKVPAD triosephosphate isomerase 1 (23-37) Homo sapiens (human)
94	Homo sapiens (human)	αβ	AVRPLLDGTYIPT	ASSYLGNTGELF	SLLMWITQC Cancer/testis antigen 1 (157-165) Homo sapiens (human)
109	Homo sapiens (human)	αβ	IVWGGYQKVT	ASRYRDDSNEQF	EENLLDFVRF Epstein-Barr nuclear antigen 6 (281-290) Human herpesvirus 4 (Epstein Barr virus)
110	Homo sapiens (human)	αβ	AVTTDSWGK LQ	ASRPGLAGGRPEQY	LGYG FVNYI ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) (87-95) Homo sapiens (human)
110	Homo sapiens (human)	αβ	AVTTDSWGK LQ	ASRPGLAGGRPEQY	LLFGYPVYV transcriptional activator Tax (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
111	Homo sapiens (human)	αβ	AVTTDSWGK LQ	ASRPGLMSAQPEQY	LLFGYPVYV Protein Tax-1 (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPLGAGEYEQY	APQPAPENAY Lytic switch protein BZLF1 (77-86) Human herpesvirus 4 (Epstein Barr virus)

Soon on
IEDB &
CEDAR

Web Interface Updates: Epitope Column

CEDAR
Cancer Epitope Database and Analysis Resource

Home | Specialized Searches | Analysis Resource | Support | More CEDAR

PENDING FILTERS

Search [Reset]

Filter Options ?
Default

Epitope ?

- Any
- Linear peptide
 - Length
 - Sequence
- Discontinuous

3D structure assays
 Amino acid modification

Epitope Source ?

Organism
Ex: influenza, peanut

Antigen
Ex: core, capsid, myosin

Cancer-associated antigens:

- Neoantigen Mutation Ex: R24L
- Viral antigen
- Germline/Self/Host antigen
- Other antigens from same reference

NO FILTERS SET

Epitopes (388871) | Antigens (15334) | Assays (1267765) | **Receptors (54741)** | References (5910)

T Cell Receptors (54177) | B Cell Receptors (564)

54177 Records Found | 25 Per Page | Export Results

Group ID	Host	Type	Chain 1 CDR3	Chain 2 CDR3	Epitope
57	Homo sapiens (human)	αβ	AALIQGAQKLV	ASTYHGTGY	GELIGTLNAAKVPAD triosephosphate isomerase 1 (23-37) Homo sapiens (human)
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Note: multiple rows per "Receptor group"

The AIRR Data Standard for Immune Receptors

- We are adding AIRR export format to IEDB/CEDAR
- The Adaptive Immune Receptor Repertoire (AIRR) Community has developed a standard for immune receptor and repertoire data

AIRR Community Standardized Representations for Annotated Immune Repertoires

[Jason Anthony Vander Heiden](#)^{1,†}, [Susanna Marquez](#)², [Nishanth Marthandan](#)³, [Syed Ahmad Chan Bukhari](#)², [Christian E Busse](#)⁴,
[Brian Corrie](#)⁵, [Uri Hershberg](#)^{6,7,8}, [Steven H Kleinstein](#)^{2,9}, [Frederick A Matsen IV](#)¹⁰, [Duncan K Ralph](#)¹⁰, [Aaron M Rosenfeld](#)⁶,
[Chaim A Schramm](#)¹¹, The AIRR Community[‡], [Scott Christley](#)^{12,*}, [Uri Laserson](#)^{13,*}

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PMCID: PMC6173121 PMID: [30323809](#)

doi: 10.3389/fimmu.2018.02206

More Info: docs.airr-community.org



Web Interface Updates: AIRR Export



CEDAR
Cancer Epitope Database and Analysis Resource

[Home](#)
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[Analysis Resource](#)
[Support](#)
[More CEDAR](#)

PENDING FILTERS

Search Reset

Filter Options ?

Default ▾

Epitope ?

Any

Linear peptide

Length

Sequence

Discontinuous

3D structure assays

Amino acid modification

Epitope Source ?

Organism

Ex: influenza, peanut

Antigen

Ex: core, capsid, myosin

Cancer-associated antigens:

Neoantigen Mutation Ex: R24L

Viral antigen

Germline/Self/Host antigen

Other antigens from same reference

CURRENT FILTERS: x Include Positive Assays

Epitopes (343140)	Antigens (6970)	Assays (1154795)	Receptors (54709)	References (5834)
----------------------	--------------------	---------------------	----------------------	----------------------

T Cell Receptors
(54145)

B Cell Receptors
(564)

Page 1 of 2166

54145 Records Found

25 Per Page

Export Results

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110	Homo sapiens (human)	αβ	AVTTDSWGKLV	ASRPGLAGGRPEQY	LGYGFVNYI ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) (87-95) Homo sapiens (human)
110	Homo sapiens (human)	αβ	AVTTDSWGKLV	ASRPGLAGGRPEQY	LLFGYPVYV transcriptional activator Tax (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
111	Homo sapiens (human)	αβ	AVTTDSWGKLV	ASRPGLMSAQPEQY	LLFGYPVYV Protein Tax-1 (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPLAGEYEQY	APQPAPENAY Lytic switch protein BZLF1 (77-86) Human herpesvirus 4 (Epstein Barr virus)

Web Interface Updates: AIRR Export

EXPORT TO FILE

File Format: **.XLSX**

Header Row Format: **Double Headers**

Export Type: **Full, all data columns**

Columns to Include:

- Receptor
- Reference
- Epitope
- Assay
- Chain 1
- Chain 2

Export

CEDAR
Cancer Epitope Database and Analysis Resource

PENDING FILTERS

Search [] Reset []

Filter Options

Default []

Epitope

Any

Linear peptide

Length []

Sequence []

Discontinuous

3D structure assays

Amino acid modification []

Epitope Source

Organism []
Ex: influenza, peanut

Antigen []
Ex: core, capsid, myosin

Cancer-associated antigens:

Neoantigen Mutation Ex: R24L

Viral antigen

Germline/Self/Host antigen

Other antigens from same reference

CURRENT FILTERS:

Epitopes (343140)

T Cell Receptors (54145)

Page 1 of 21

Group ID	Host	Chain 1	Chain 2	Reference
57	Homo sapiens			
94	Homo sapiens			
109	Homo sapiens			
110	Homo sapiens			
110	Homo sapiens			
111	Homo sapiens			
116	Homo sapiens (human)	$\alpha\beta$	ALSGFYNTDKLI	ASPLGAGEYEQY

References (5834)

25 Per Page | Export Results

Epitope

GELIGTLNAAKVPAD triosephosphate isomerase 1 (23-37) Homo sapiens (human)
SLLMWITQC Cancer/testis antigen 1 (157-165) Homo sapiens (human)
EENLLDFVRF Epstein-Barr nuclear antigen 6 (281-290) Human herpesvirus 4 (Epstein Barr virus)
LGYGFVNYI ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) (87-95) Homo sapiens (human)
LLFGYPVYV transcriptional activator Tax (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
LLFGYPVYV Protein Tax-1 (11-19) Human T-cell leukemia virus type I (Human T cell leukemia virus type 1)
APOQAPENAY Lytic switch protein BZLF1 (77-86) Human herpesvirus 4 (Epstein Barr virus)

Web Interface Updates: AIRR Export

The screenshot displays the CEDAR (Cancer Epitope Database and Analysis Resource) web interface. The main navigation bar includes 'Home' and 'Search'. The left sidebar contains 'PENDING FILTERS' with a search bar and 'Filter Options' set to 'Default'. Below this are sections for 'Epitope' (radio buttons for 'Any', 'Linear peptide', 'Discontinuous') and 'Epitope Source' (checkboxes for '3D structure assays', 'Amino acid modification', 'Organism', 'Antigen', and 'Cancer-associated antigens'). The central area shows 'CURRENT FILTERS' for 'Epitopes (343140)' and 'T Cell Receptors (54145)', with a table listing items by Group ID and Host. An 'EXPORT TO FILE' dropdown menu is open, showing options: 'File Format: .XLSX', 'Header Row Format: Double Headers', 'Export Type: Full, all data columns', 'Columns to export: Default', 'AIRR' (highlighted in blue and marked with a red arrow and the text 'new!'), 'CEDAR Website Displayed', and 'Custom Export'. The background table shows columns for 'Group ID', 'Host', and 'Epitope' with various protein sequences and their sources.

Web Interface Updates: AIRR Export

EXPORT TO FILE

File Format: .TSV
Header Row Format: Single Header
Export Type: AIRR
Columns to Include:

- AIRR
 - cell_id
 - sequence
 - sequence_id
 - reactivity_ref
 - iedb_epitope_id
 - iedb_epitope_name
 - sequence_aa
 - rev_comp
 - productive
 - locus
 - locus_species
 - v_call
 - d_call
 - j_call
 - sequence_alignment
 - germline_alignment

Export

CEDAR
Cancer Epitope Database and Analysis Resource

Home Sp DAR

PENDING FILTERS

Search Reset

Filter Options ?
Default

Epitope ?

Any
 Linear peptide
Length
Sequence
 Discontinuous

3D structure assays
Amino acid modification

Epitope Source ?

Organism
Ex: influenza, peanut

Antigen
Ex: core, capsid, myosin

Cancer-associated antigens:
 Neoantigen Mutation Ex: R24L
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

PENDING FILTERS

Epitopes
(343140)

T Cell Receptors
(54145)

Page 1 of 21

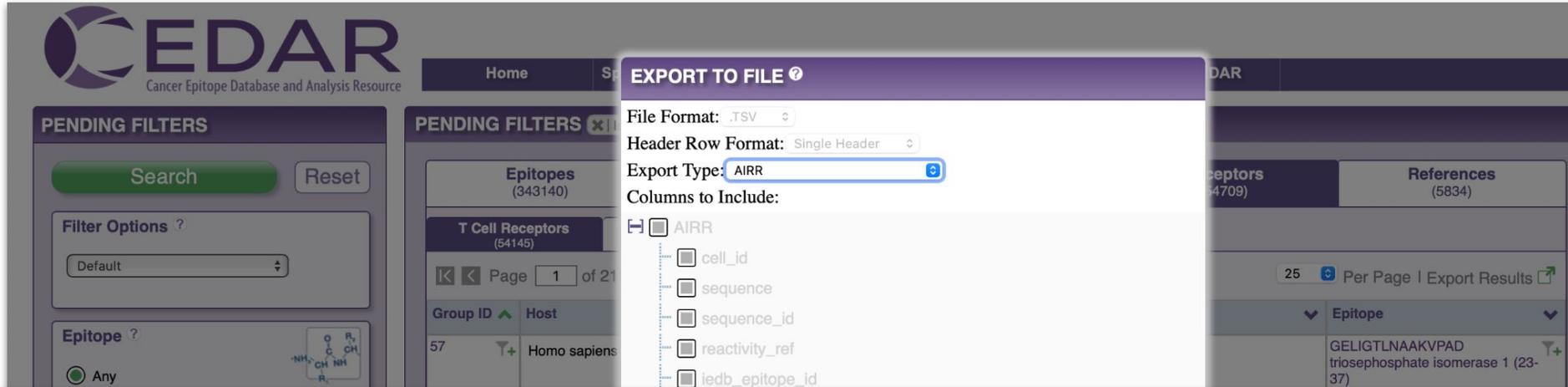
Group ID	Host
57	Homo sapiens
94	Homo sapiens
109	Homo sapiens
110	Homo sapiens
110	Homo sapiens
111	Homo sapiens
116	Homo sapiens (human)

25 Per Page | Export Results

Epitope

GELIGTLNAAKVPAD triosephosphate isomerase 1 (23-37) Homo sapiens (human)
SLLMWITQC Cancer/testis antigen 1 (157-165) Homo sapiens (human)
EENLLDFVRF Epstein-Barr nuclear antigen 6 (281-290) Human herpesvirus 4 (Epstein Barr virus)
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APOQAPENAY Lytic switch protein BZLF1 (77-86) Human herpesvirus 4 (Epstein Barr virus)

Web Interface Updates: AIRR Export



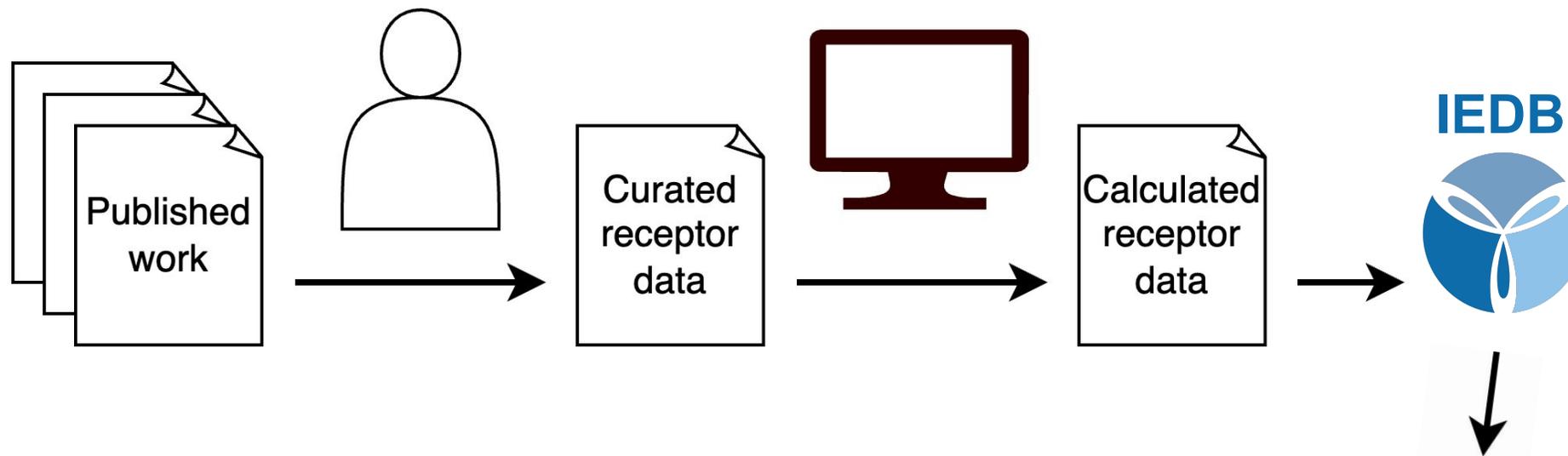
AIRR format download:

cell_id	reactivity_ref	iedb_epitope_id	iedb_epitope_name	iedb_host_specie	locus	v_call	d_call	j_call	cdr1_aa	cdr2_aa	cdr3_aa	junction_aa	sequence_aa
1023_530809	IEDB_RECEPTOR:802	IEDB_EPITOPE:530809	ALEPGPVTA	NCBITAXON:9606	TRA	TRAV21*01		TRAJ53*01	DSAIN	IQSSQRE	AVLSSGGSNYKLT	CAVLSSGGSNYKLT	MKQEVTVIPAALSVPEGE
1023_530809	IEDB_RECEPTOR:802	IEDB_EPITOPE:530809	ALEPGPVTA	NCBITAXON:9606	TRB	TRBV7-3*01		TRBJ2-3*01	SGHTA	FQGTGA	ASSFIGGTDQY	CASSFIGGTDQYF	GAGVSQTPSNKVTEKQK
9144_16878	IEDB_RECEPTOR:1950	IEDB_EPITOPE:16878	FLRGRAYGL	NCBITAXON:9606	TRA	TRAV14/DV4*01		TRAJ49*01			AMREDTGNQFY	CAMREDTGNQFYF	KITQTQPGMFVQEKEAVT
9144_16878	IEDB_RECEPTOR:1950	IEDB_EPITOPE:16878	FLRGRAYGL	NCBITAXON:9606	TRB	TRBV11-2*01		TRBJ2-3*01	SGHAT	FQNGV	ASSFTWTSGGATDQY	CASSFTWTSGGATDQY	MGVAQSPRYKIIKQRQSV
9152_44920	IEDB_RECEPTOR:824	IEDB_EPITOPE:44920	NLVPMVATV	NCBITAXON:9606	TRA	TRAV26-2*01		TRAJ43*01	TISGTDY	GLTSN	ILDNNNDMR	CILDNNNDMRF	MDAKTTQPNSMESNEE
9152_44920	IEDB_RECEPTOR:824	IEDB_EPITOPE:44920	NLVPMVATV	NCBITAXON:9606	TRB	TRBV7-6*01		TRBJ1-4*01	SGHVS	FNYEAQ	ASSLAPGTTNEKLF	CASSLAPGTTNEKLF	MGAGVSQSPRYKVTKRC
9160_16878	IEDB_RECEPTOR:1412	IEDB_EPITOPE:16878	FLRGRAYGL	NCBITAXON:9606	TRA	TRAV26-2*01		TRAJ52*01					
9160_16878	IEDB_RECEPTOR:1412	IEDB_EPITOPE:16878	FLRGRAYGL	NCBITAXON:9606	TRB	TRBV7-8*01	TRBD1*01	TRBJ2-7*01	SGHVS	FQNEAQ	ASSLGQAYEQY	CASSLGQAYEQYF	MGVSQSPRYKVAKRGQI

- Neoantigen Mutation Ex: R24L
- Viral antigen
- Germline/Self/Host antigen
- Other antigens from same reference

116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPLGAGEYEQY	I (Human T cell leukemia virus type 1) AQQPAPENAY Lytic switch protein BZLF1 (77-86) Human herpesvirus 4 (Epstein Barr virus)
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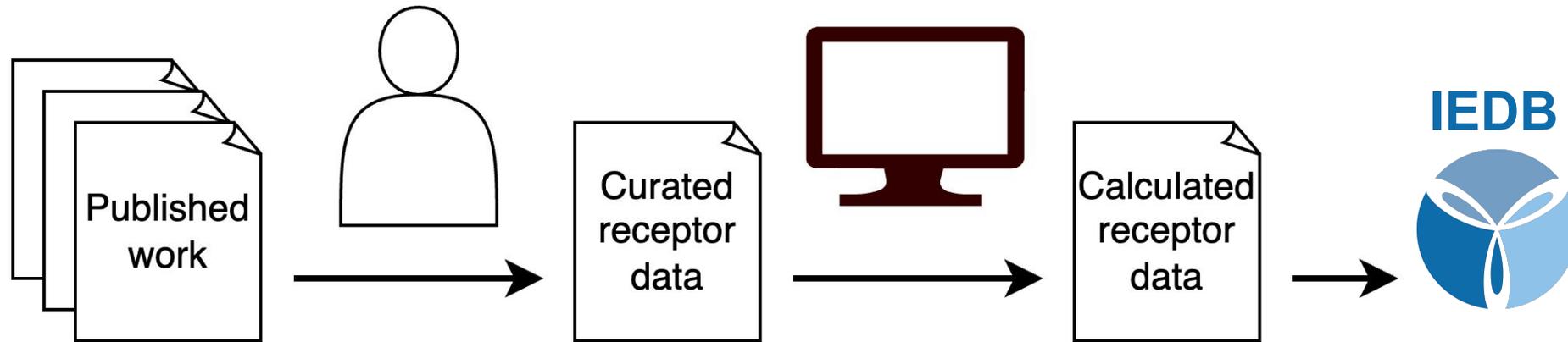
Curated versus Calculated IEDB Receptor Data



Chain 1	Chain 1	Chain 1	Chain 1	Chain 1	Chain 1	Chain 1
Protein Sequence	CDR3 Curated	CDR3 Calculated	CDR3 Start Curated	CDR3 End Curated	CDR3 Start Calculated	CDR3 End Calculated
KTTQPPSMDCAEGRAAN		IVVRSNTGKLI			87	98
KTTQPPSMDCAEGRAAN		IVVRSNTGKLI			87	98

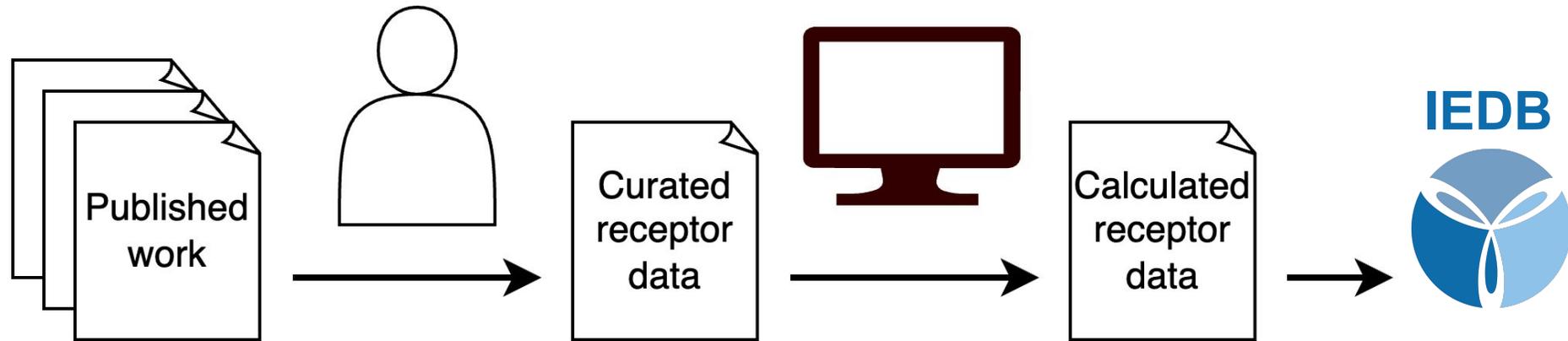
Chain 1	Chain 1	Chain 1	Chain 1	Chain 1	Chain 1
Curated V Gene	Calculated V Gene	Curated D Gene	Calculated D Gene	Curated J Gene	Calculated J Gene
	TRAV26-1*01				TRAJ37*01
TRAV26-1*01	TRAV26-1*01			TRAJ37*01	TRAJ37*01

Curated versus Calculated IEDB Receptor Data



- **Curated** fields are heterogeneous, reported as published
- **Calculated** fields provide data in standardized, computer-readable format

Curated versus Calculated IEDB Receptor Data



- **Curated** fields are heterogeneous, reported as published
- **Calculated** fields provide data in standardized, computer-readable format

We are revising the data to ensure all *calculated* fields are complete and ready-to-use

Available *Curated* Data for all Receptors in the IEDB

	TCR	BCR
Total receptors (receptor groups expanded)	225,983	8,639
Chain 1 has full nt	97	87
Chain 2 has full nt	717	89
Chain 1 has full aa	1,557	6,208
Chain 2 has full aa	1,661	5,300
Chain 1 has curated CDR3 and/or V/J (no full nt/aa)	62,894	2,291
Chain 2 has curated CDR3 and/or V/J (no full nt/aa)	192,326	1,366

Available *Curated* Data for all Receptors in the IEDB

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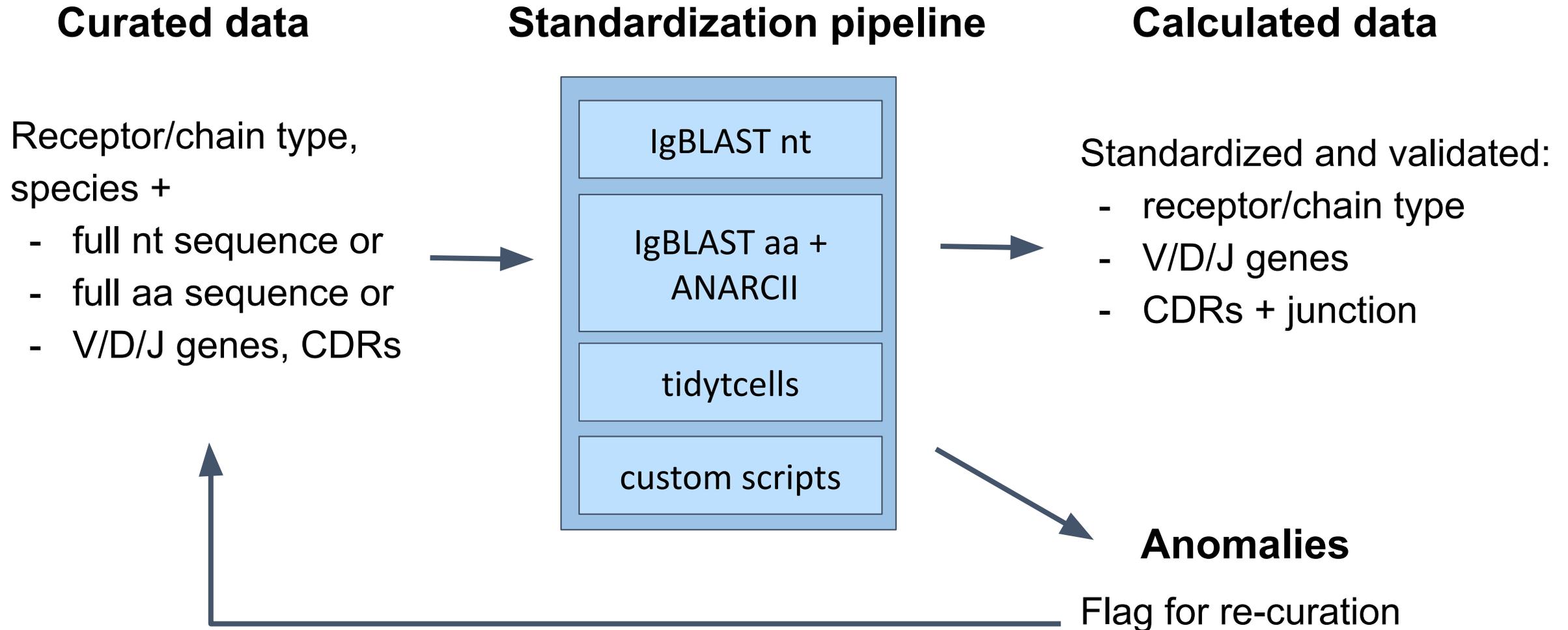
mostly full aa
sequence
(often from PDB
3D structure)

Available *Curated* Data for all Receptors in the IEDB

	TCR	BCR
Total receptors (receptor groups expanded)	225,983	8,639
Chain 1 has full nt	97	87
Chain 2 has full nt	717	89
Chain 1 has full aa	1,557	6,208
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Chain 1 has curated CDR3 and/or V/J (no full nt/aa)	62,894	2,291
Chain 2 has curated CDR3 and/or V/J (no full nt/aa)	192,326	1,366

mostly CDR3
+ gene names

Updated *Calculated* Data Standardization Pipeline



V/D/J Gene Name Standardization Examples

Full sequence data → recalculate (IgBLAST nt/aa)

Automated standardization (tidytcells*):

TCRAV1-2 → TRAV1-2
TCRAJ52-01*01 → TRAJ52*01
TRAV29-01 → TRAV29/DV5

*Support for BCR genes was added as part of this project, see github.com/yutanagano/tidytcells

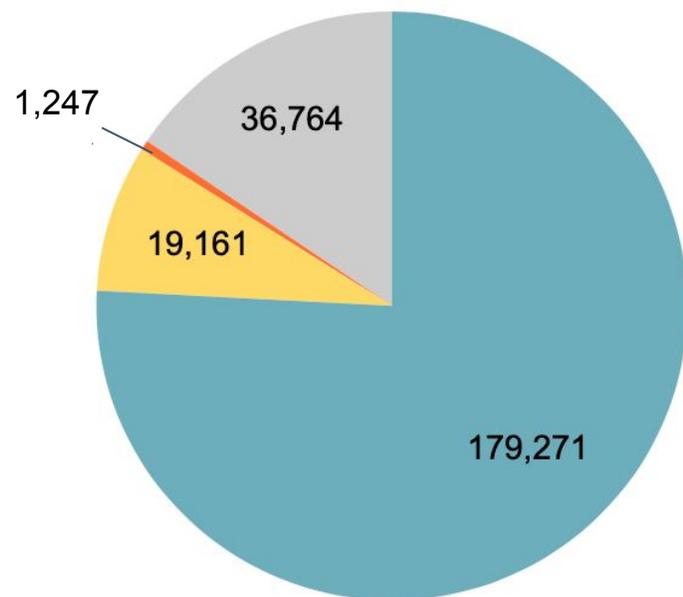
Unable to standardize, human re-curation:

1-1 → TRAV1-1
TRVB12 → TRBV12
05-07*01 → TRBV5-7*01

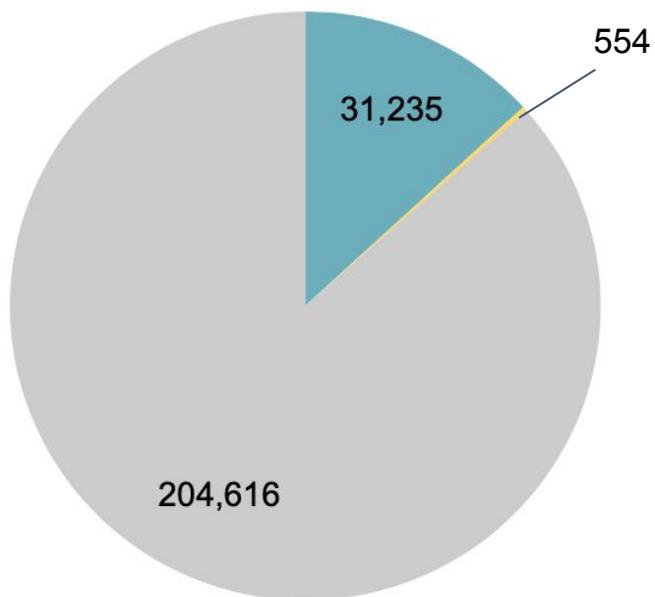
nonexistent gene name/wrong species

TCR Gene Updates Per Chain

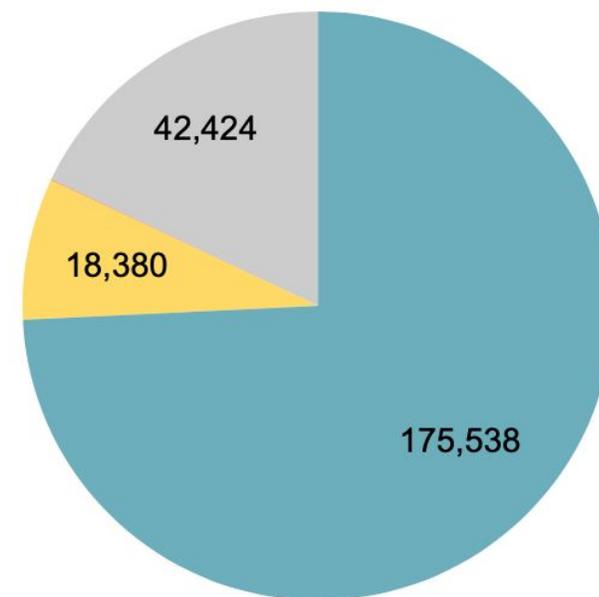
TCRV



TCRD



TCRJ

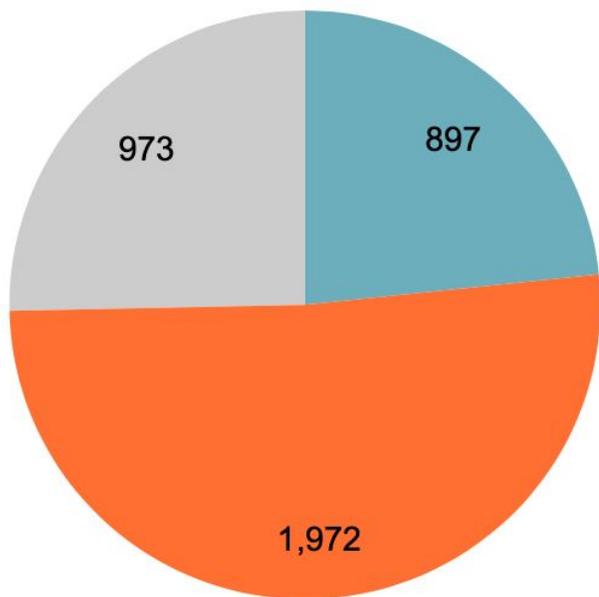


- Gene name stayed the same (tidytcells validated)
- Gene name formatting was corrected (tidytcells)
- Gene was (re-)calculated from full sequence (IgBLAST nt/aa)
- No gene available

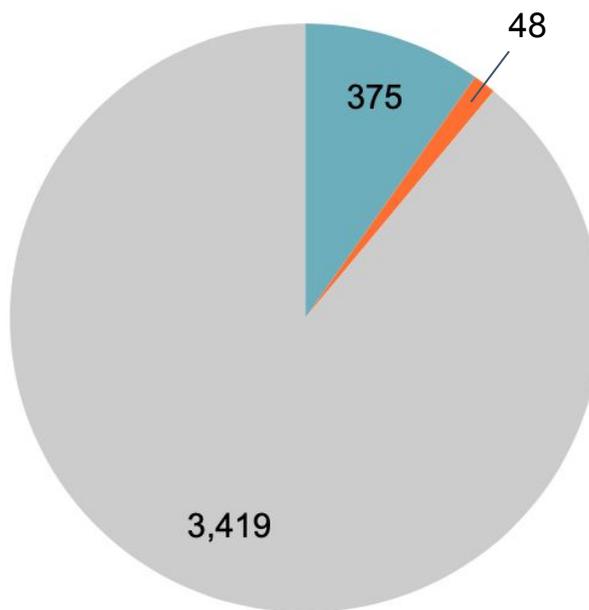
*human data only

BCR Gene Updates Per Chain

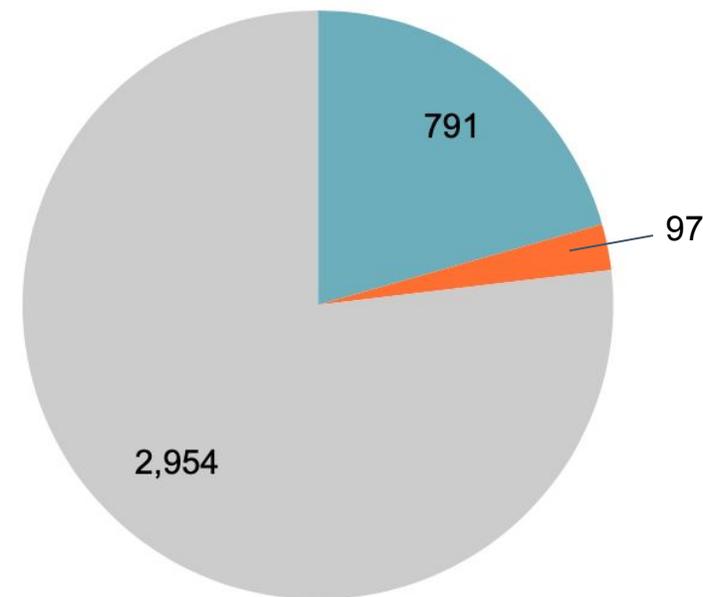
BCRV



BCRD



BCRJ



- Gene name stayed the same (tidytcels validated)
- Gene was (re-)calculated from full sequence (IgBLAST nt/aa)
- No gene available

*human data only

CDR3/Junction Standardization Examples

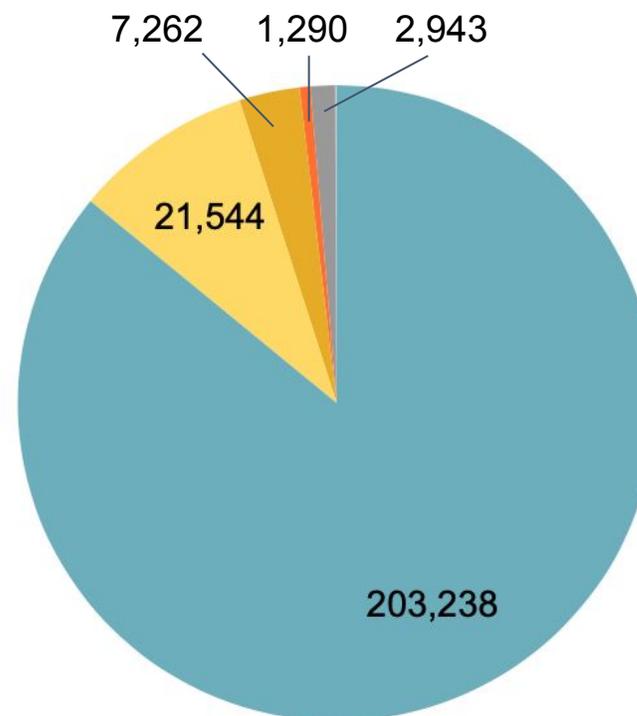
Full sequence data → recalculate (IgBLAST nt / ANARCI)

Curated CDR3		Calculated junction*		Calculated CDR3
CAVLNTGGFKTIF	→	CAVLNTGGFKTIF		
AVLNTGGFKTI	→	C AVLNTGGFKT I F		
AVLNTGG	→	C AVLNTGG F K T I F	→	AVLNTGGFKTI
ASYL CAVLNTGGFKTIF G	→	CAVLNTGGFKTIF		
S AVLNTGGFKTIF	→	C AVLNTGGFKTIF		
DASTGA	→	re-curate/omit		

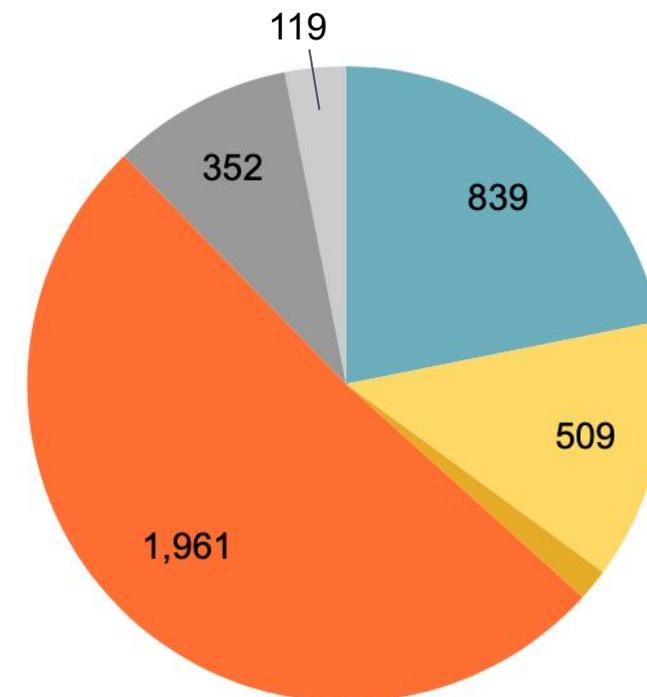
*V/J gene names inform junction standardization, soon available in tidytcels v3

CDR3/Junction Updates per Chain

TCR



BCR



- Curated CDR3 is junction (tidytcalls validated)
- Curated CDR3 is CDR3, recover junction (tidytcalls)
- Non-trivial correction of curated CDR3 (tidytcalls)
- (Re)calculated from full sequence (IgBLAST nt/ANARCI)
- Invalid CDR3, could not be standardized
- No CDR3 information available

*human data only

Anomalous Receptors Flagged for Re-Curation



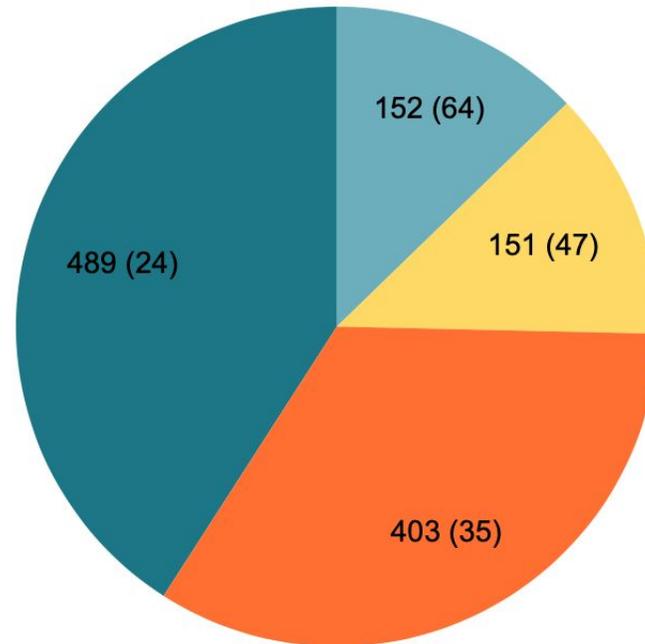
Receptor re-curation
by Dr. Laura Zarebski

- V/D/J gene name errors
- CDR3 sequence errors
- Receptor/chain type errors
- Full sequence/accession errors

Number of receptors (number of studies)

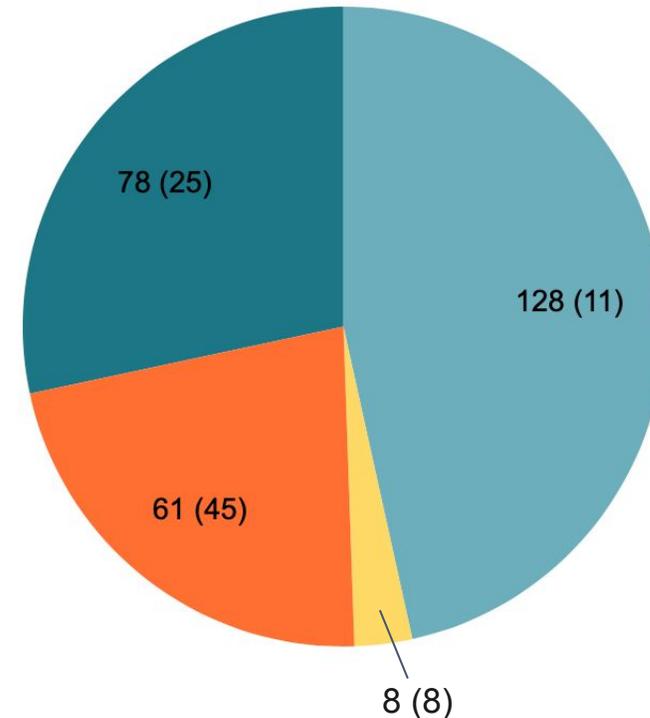
TCR

Total: 1,195 (170)



BCR

Total: 275 (89)



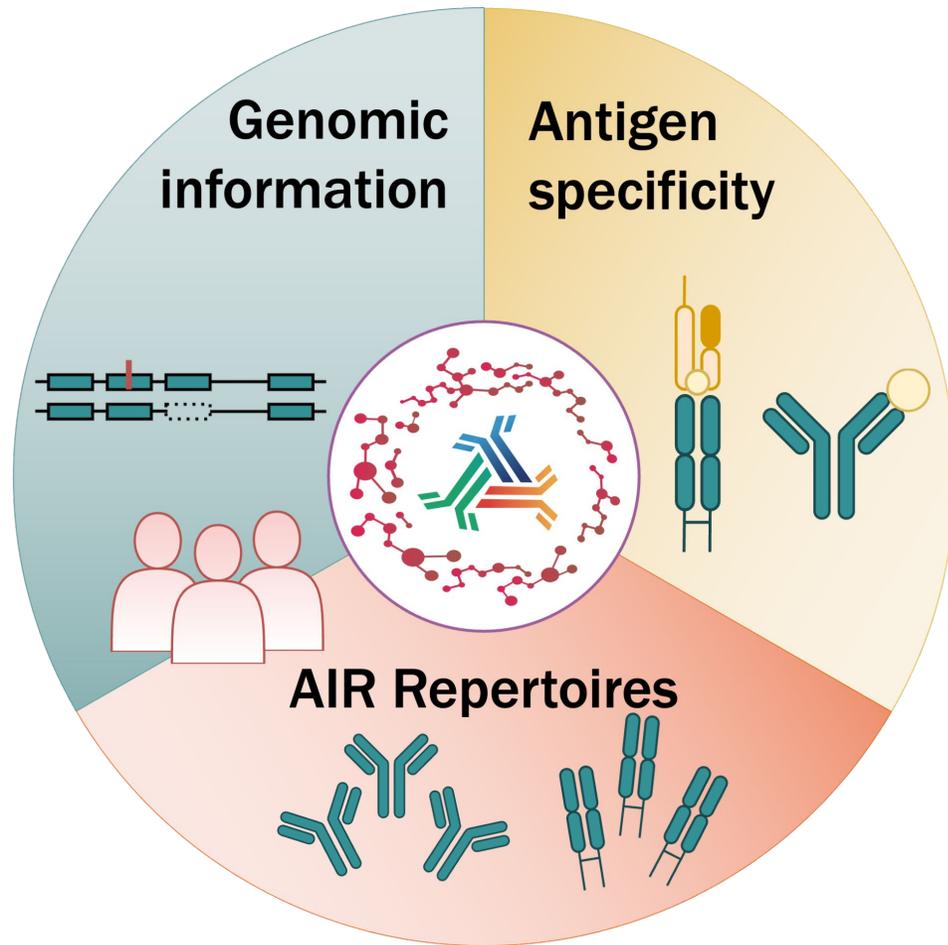
IMMREP25: TCR Specificity Prediction Challenge

The screenshot shows the Kaggle website interface for the IMMREP25 competition. At the top, there is a search bar and navigation links for 'Sign In' and 'Register'. The competition title 'IMMREP25: TCR Specificity Prediction Challenge' is prominently displayed, along with a brief description: 'Competitors will make predictions on previously unpublished TCR-epitope binding data in order to benchmark prediction methods.' Below the title, there are tabs for 'Overview', 'Data', 'Code', 'Models', 'Discussion', 'Leaderboard', and 'Rules'. The 'Overview' section is active, showing the competition dates (March 3rd to March 23rd, 2025) and a progress bar. On the right side, there is a 'Competition Host' section for Justin Barton, a 'Prizes & Awards' section stating 'Does not award Points or Medals', and a 'Participation' section with the following statistics: 242 Entrants, 134 Participants, 126 Teams, and 496 Submissions.

Training data provided by IEDB and VDJdb

IEDB data preprocessing by Dr. Eve Richardson

Integration into the AIRR Knowledge Commons (AKC)



Component repositories:



Publication:

COMMENTARY · Volume 16, Issue 9, 101401, September 17, 2025

[Download Full Issue](#)

The Adaptive Immune Receptor Repertoire Knowledge Commons:
An invitation to the community

[Lindsay G. Cowell](#)^{1,2} · [Scott Christley](#)¹ · [Felix Breden](#)³ · [Kevin A. Burns](#)^{4,5} · [Brian D. Corrie](#)³ · [William D. Lees](#)⁶ · [James A. Overton](#)⁷ · [Bjoern Peters](#)⁸ · [Eve Richardson](#)⁸ · [Krishna M. Roskin](#)^{4,5} · [Lonke Scheffer](#)⁸ · [Randi Vita](#)⁸ · [Corey T. Watson](#)⁹ · [Gur Yaari](#)¹⁰ [Show less](#)

more info: airr-knowledge.org

Acknowledgements

IEDB

Bjoern Peters

Eve Richardson

Randi Vita

Laura Zarebski

Nina Blazeska

Swapnil Mahajan

Daniel Wheeler (LEIDOS)

Jason Cantrell (LEIDOS)

AKC

Scott Christley (UTSW)

Lindsay Cowell (UTSW)

Brian Corrie (SFU)

William Lees (Clareo Biosciences)

James Overton (Knocean)

tidytcalls

Yuta Nagano (UCL)

Thank you!