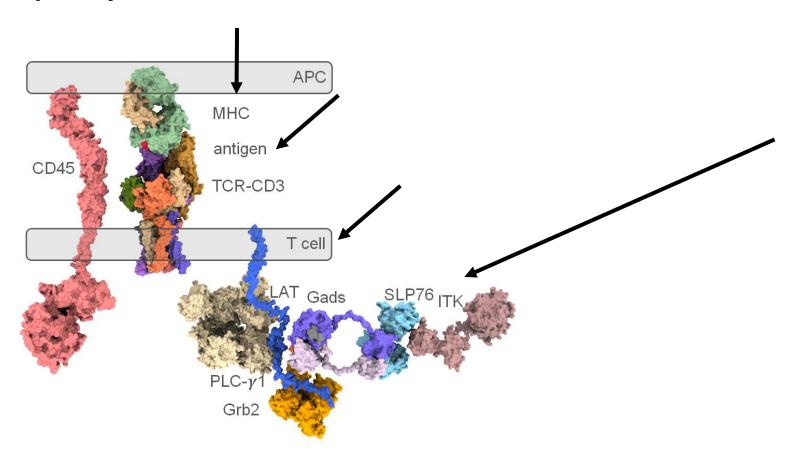
Extracting information for integrative modeling of T-cell activation using NLP approach

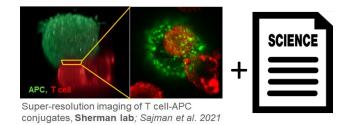
Ofer Feinstein
Dr. Barak Raveh & Dr. Gabi Stanovsky

☐ The immunological synapse by Dr. Dina Schneidman



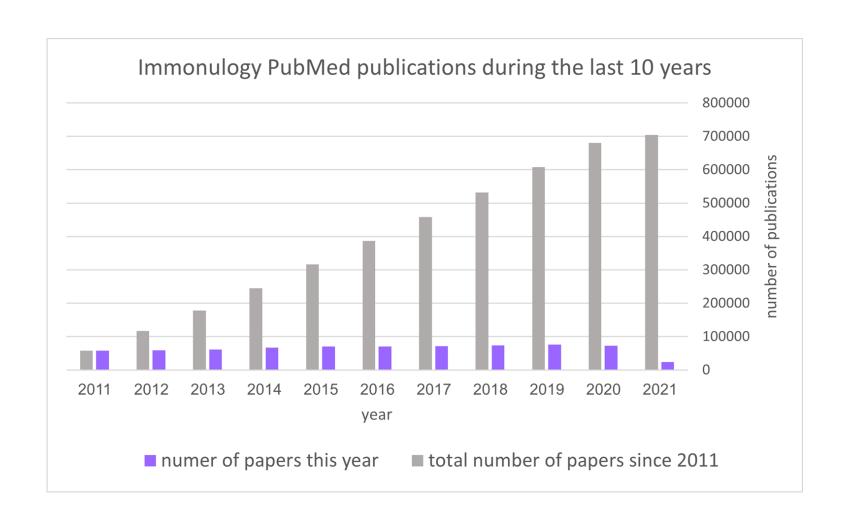
Motivation for integrative modeling

☐ Combining data from multiple sources of information (experimental & literature)



- Biology data is Noisy, Sparse, Ambiguous and inconsistently
- ☐ Combining all sources of information together increases precision & accuracy

Data challenge in integrative modeling



Motivation for using Natural Language Processing (NLP)

- Integrative modeling needs to take into account millions of papers
- This is far beyond what a single person or lab can read in a lifetime!

NLP helps filter this data and find relevant information



Current status of NLP

☐ Highly-dependent on domain

☐ Uses deep learning to find patterns in the data

Works at the sentence level

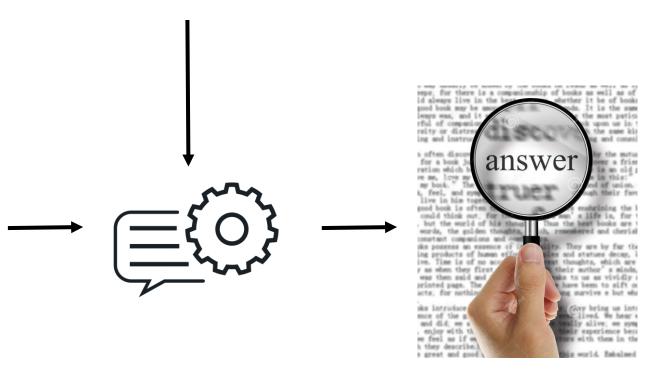


Current status of NLP

- ☐ What are the main molecules participate in the immunological synapse?
- What is known about their binding affinity?
- \blacksquare What is known about the association or dissociation constants between the molecules?
- ☐ What is known about their phosphorylation or dephosphorylation?

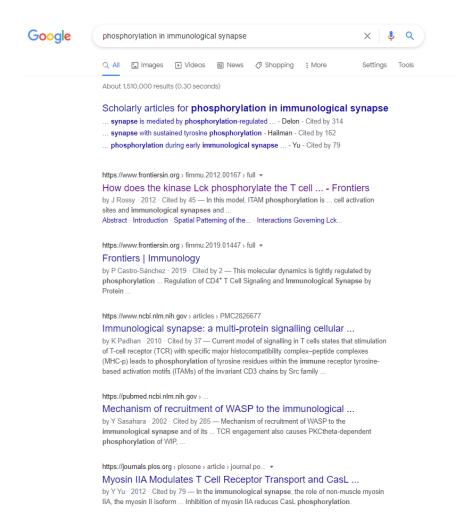
ABSTRACT

The essential function of the T cell receptor (TCR) is to translate the engagement of peptides on the major histocompatibility complex (pMHC) into appropriate intracellular signals through the associated cluster of differentiation 3 (CD3) complex. The spatial organization of the TCR-CD3 complex in the membrane is thought to be a key regulatory element of signal transduction, raising the question of how receptor clustering impacts on TCR triggering. How signal transduction at the TCR-CD3 complex encodes the quality and quantity of pMHC molecules is not fully understood. This question can be approached by reconstituting T cell signaling in model and cell membranes and addressed by single-molecule imaging of endogenous proteins in T cells. We highlight such methods and further discuss how TCR clustering could affect pMHC rebinding rates, the local balance between kinase and phosphatase activity and/or the lipid environment to regulate the signal efficiency of the TCR-CD3 complex. We also examine whether clustering could affect the conformation of cytoplasmic CD3 tails through a biophysical mechanism. Taken together, we highlight how the spatial organization of the TCR-CD3 complex - addressed by reconstitution approaches - has emerged as a key regulatory element in signal transduction of this archetypal immune receptor.



Why not use Google?

What is known about phosphorylation in the immunological synapse?



People also ask	
What is the function of the immunological synapse?	-
The immunological synapse (IS) is an excellent example of cell–cell communication, where signals are exchanged between two cells, resulting in a well-structured line of defense during adaptive immune response.	
https://www.sciencedirect.com > topics > immunological-s	
Immunological Synapse - an overview ScienceDirect Topics	
Search for: What is the function of the immunological synapse?	
How does the kinase LCK phosphorylate the T cell receptor?	`
What is LCK in immunology?	`
What is the function of LCK?	`
Why is the immunological synapse crucial for T cell activation?	`
Where does immunological synapse occur?	`
What activates LCK?	`
How many domains are found in the LCK protein?	`
Is LCK membrane bound?	`
What does CTLA 4 bind to?	`
What is the role of LCK in the TCR signaling cascade?	`
What potential mechanisms may be contributing to the immune dysregulation seen in patients with ZAP70 deficiency?	~

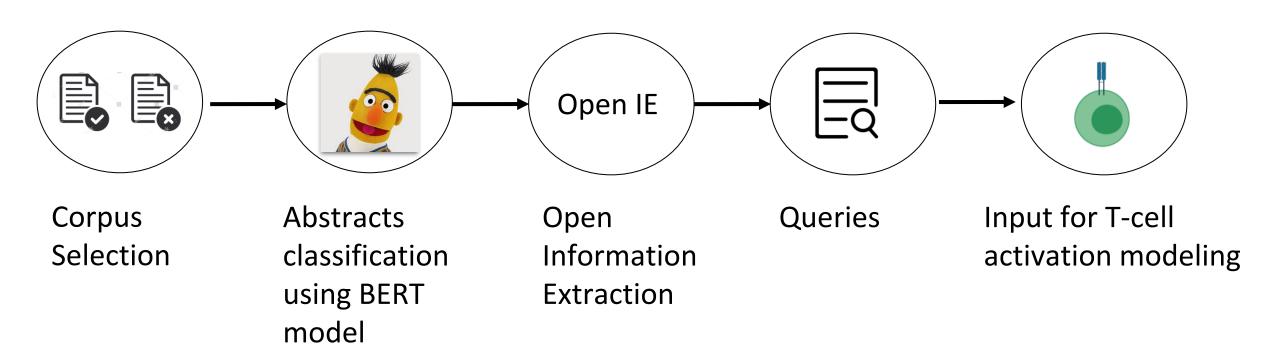
Queries in numbers

☐ Database contains ~16M statements from ~500K papers

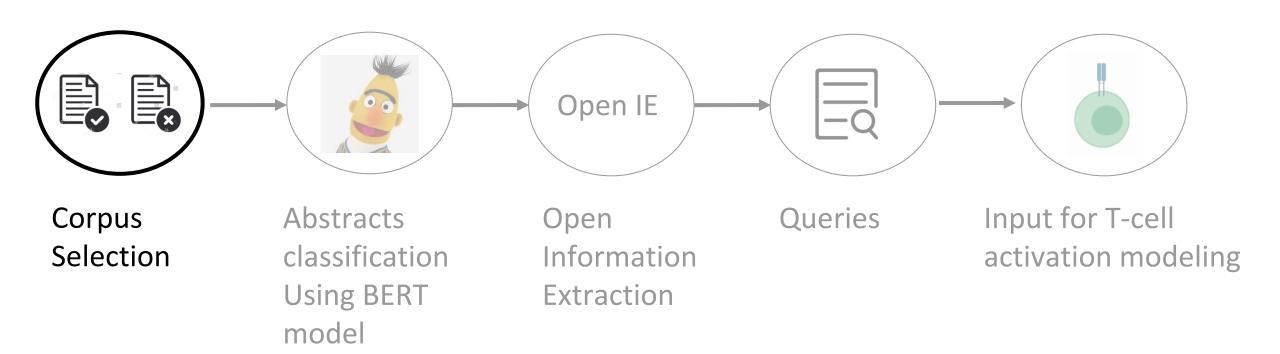
"LAT and Lck tyrosine phosphorylated exclusively following CD38 engagement."

- ☐ ~5000 statements from "phosphorylation" query
- ☐ ~180 statements from "immunological synapse" query
- ☐ ~1000 statements from "dissociation" query

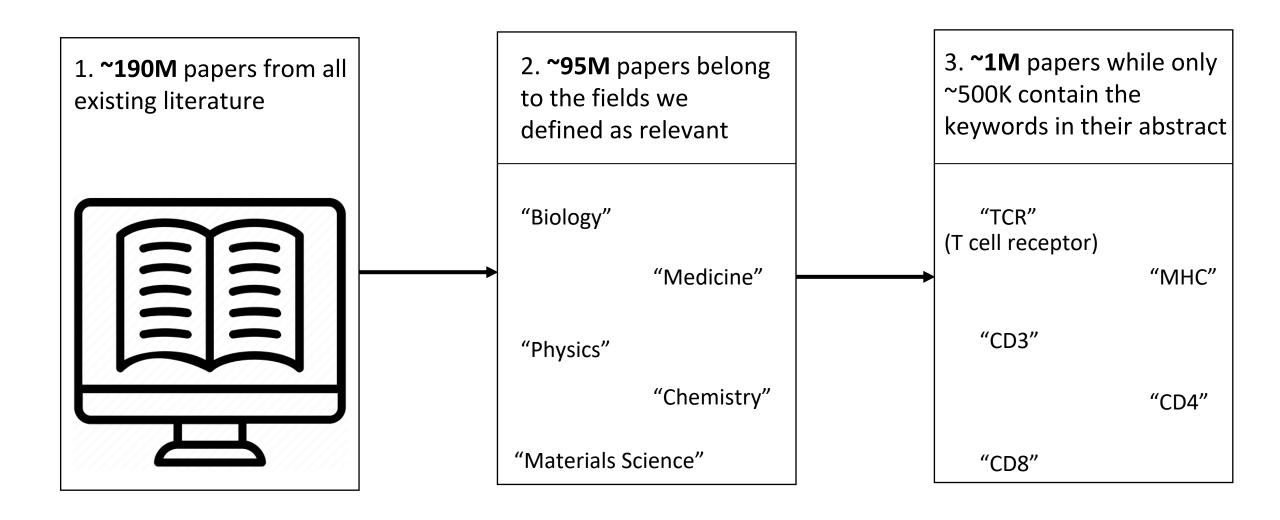
Workflow



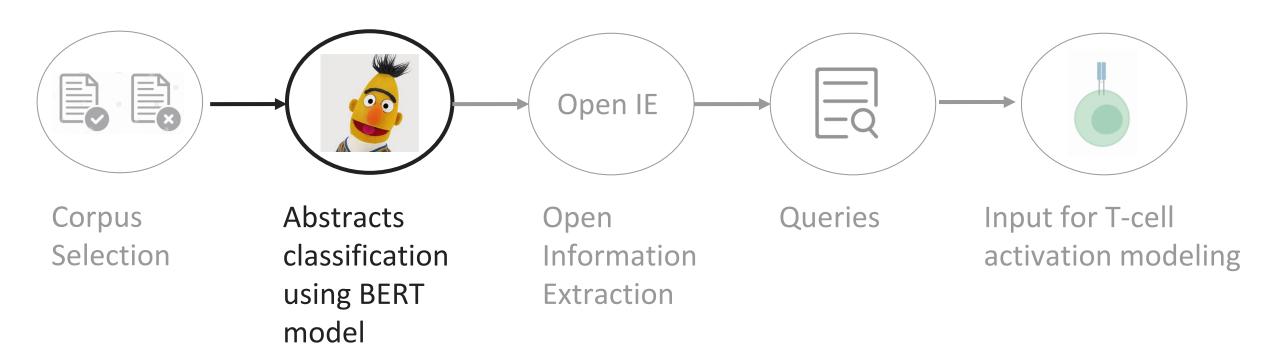
Workflow



Corpus Selection



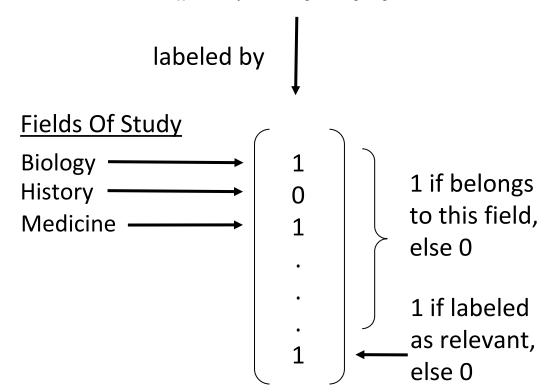
Workflow



Abstracts classification

ABSTRACT

The essential function of the T cell receptor (TCR) is to translate the engagement of peptides on the major histocompatibility complex (pMHC) into appropriate intracellular signals through the associated cluster of differentiation 3 (CD3) complex. The spatial organization of the TCR–CD3 complex in the membrane is thought to be a key regulatory element of signal transduction, raising the question of how receptor clustering impacts on TCR triggering. How signal transduction at the TCR–CD3 complex encodes the quality and quantity of pMHC molecules is not fully understood. This question can be approached by reconstituting T cell signaling in model and

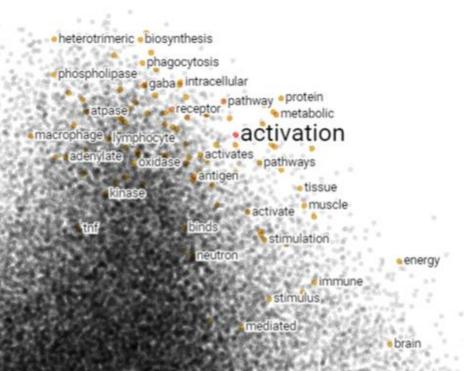


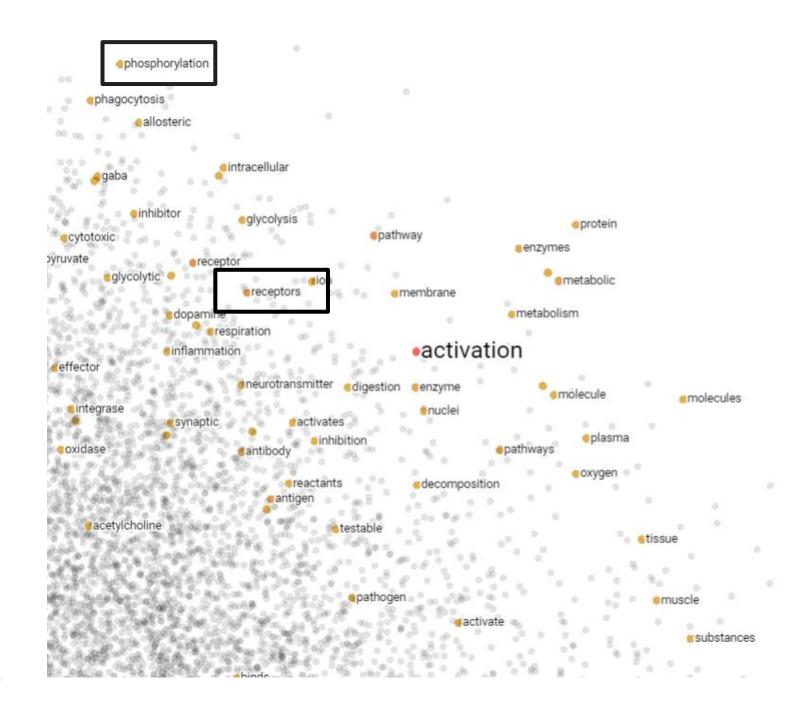
Feature extraction using BERT

Abstract label T cell receptor (TCR) activation and signaling precede immunological synapse formation and are sustained for hours after initiation. BERT BERT

Abstract sentences embeddings

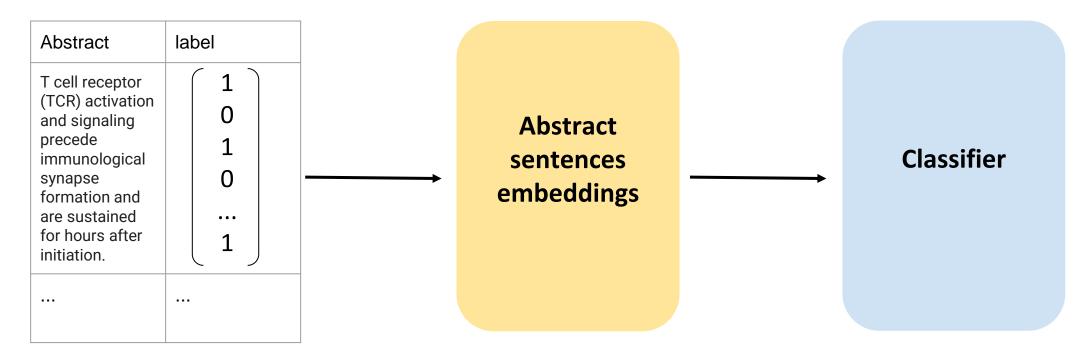
Abstract	label
-0.11	
0.123	0
-0.457	1 1
0.185	0
0.654	



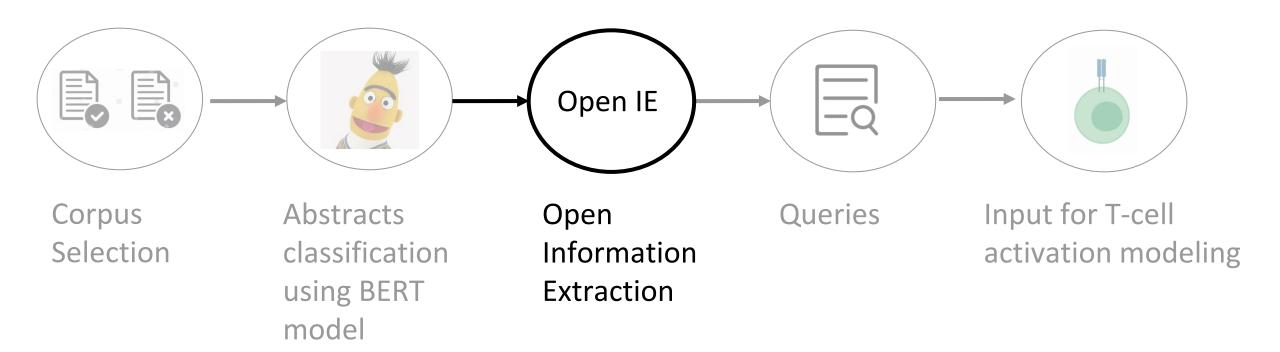


BERT Fine-tuning on classification

Input



Workflow



Open Information Extraction (Open IE)

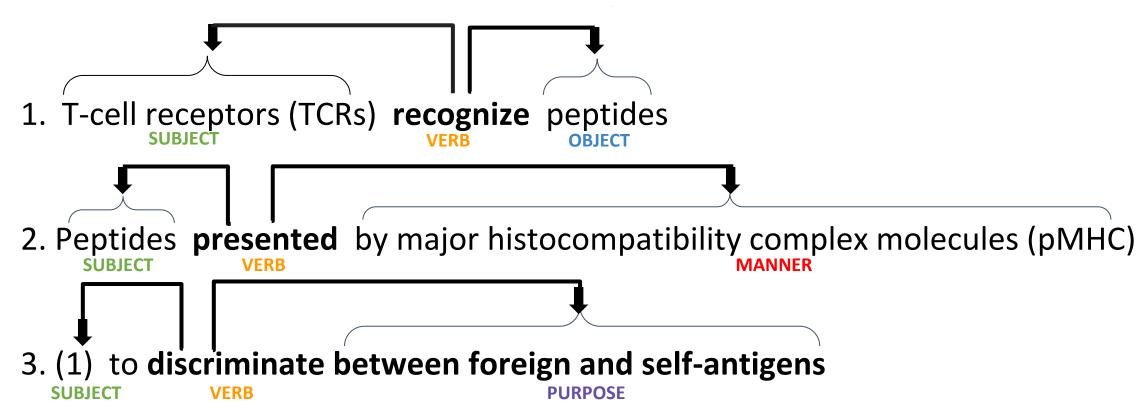
- ☐ Input: sentences of abstracts labeled as relevant
- ☐ Output: a set of statements mentioned in the abstract



Stanovky et. al., 2018

Open Information Extraction (Open IE)

"T-cell receptors (TCRs) recognize peptides presented by major histocompatibility complex molecules (pMHC) to discriminate between foreign and self-antigens."

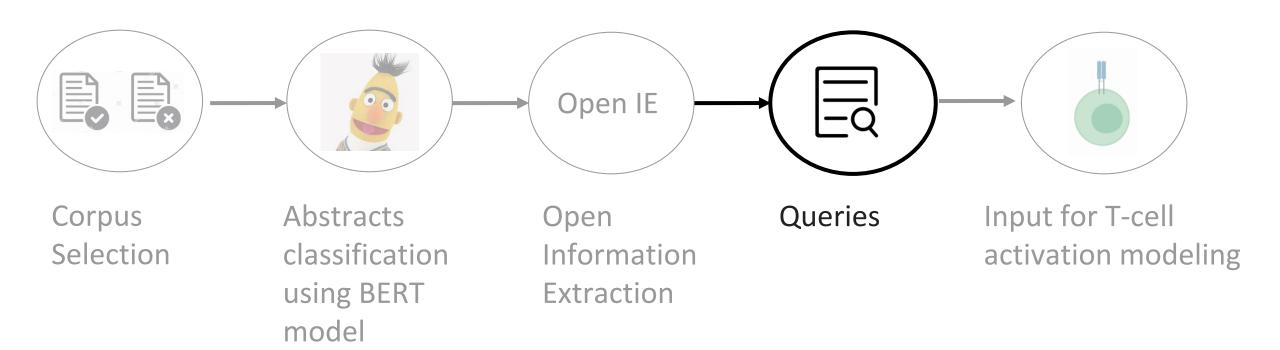


Yin et.al., 2012

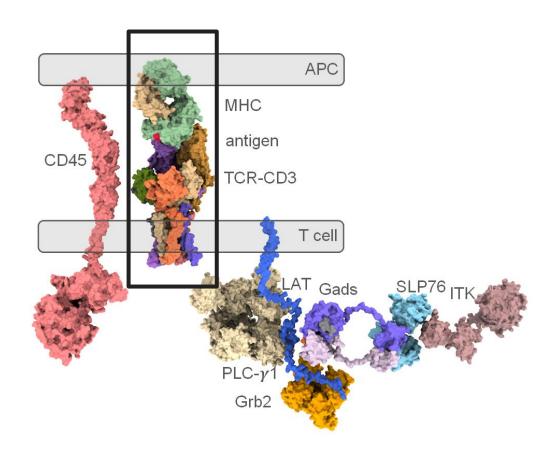
From statements to database



Workflow



- ☐ Triggers to T-cell Activation
- ☐ TCR-MHC interaction



- ☐ Triggers to T-cell Activation
- ☐ TCR-MHC interaction
- ☐ Binding affinity

TCR-MHC interaction

Cellular scale

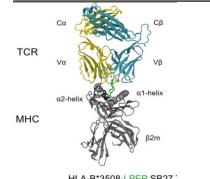


Molecule scale

Sherman lab



Atoms scale



- ☐ Triggers to T-cell Activation
- ☐ TCR-MHC interaction
- ☐ Binding affinity
- \square K_D value: low value \rightarrow high-affinity

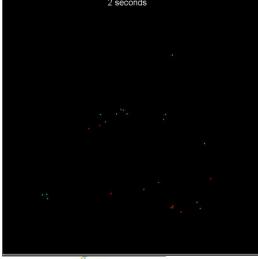
TCR-MHC interaction

Cellular scale

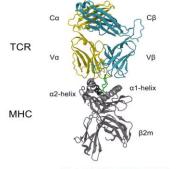


Molecule scale

Sherman lab



Atoms scale



- ☐ Triggers to T-cell Activation
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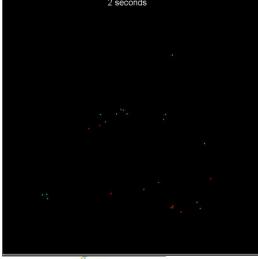
TCR-MHC interaction

Cellular scale

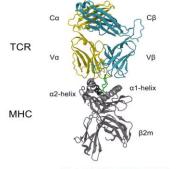


Molecule scale

Sherman lab



Atoms scale



Query & answers: example

 \square Query: dissociation constant (K_D) values

$$TCR + pepMHC \stackrel{k_{on}}{\underset{k_{off}}{\rightleftharpoons}} TCR:pepMHC$$



Query & answers: example

```
SELECT * FROM Database_Table
WHERE SUBJECT = 'T-cell receptor'
AND OBJECT = 'pepMHC';
```

☐ Answers examples:

"wild-type TCR affinities (K_D values) with pepMHC have been shown to be in the **range of 1–100 \muM**"

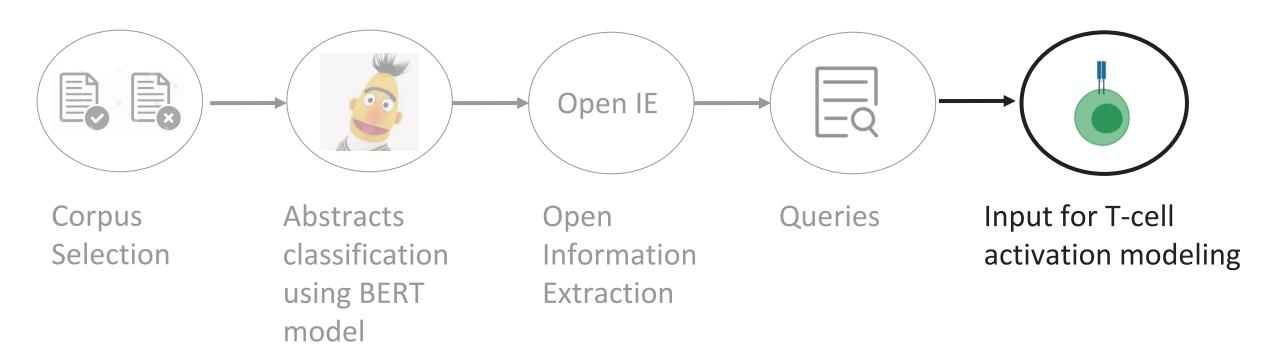
OBJECT

OBJECT

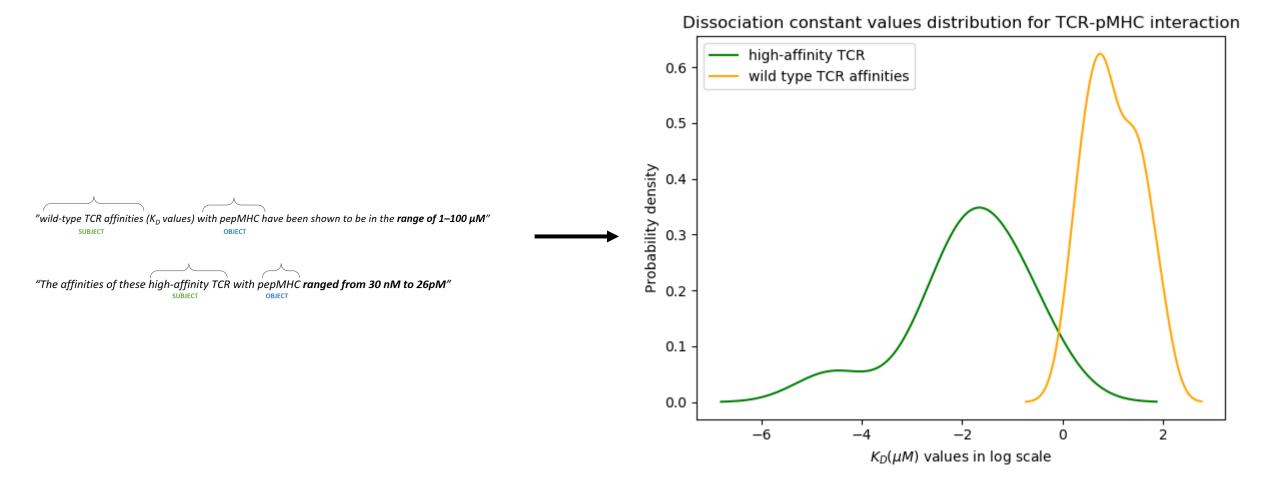
"The affinities of these high-affinity TCR with pepMHC ranged from 30 nM to 26pM"

SUBJECT OBJECT

Workflow



From queries output to T-cell activation modeling



IMMUNOLOGY REVIEW ARTICLE

T-cell receptor binding affinities and kinetics: impact on T-cell activity and specificity

Jennifer D. Stone*, Adam S. Chervin* and David M. Kranz Department of Biochemistry, University of Illinois at Urbana-Champaign, Urbana, IL, USA

doi:10.1111/j.1365-2567.2008.03015.x Received 1 November 2008; revised 6 November 2008; accepted 7 November 2008. *These authors contributed equally to this

Correspondence: D. M. Kranz, Department of Biochemistry, University of Illinois, 600 S. Mathews Avenue, Urbana, IL 61801, USA. Email: d-kranz@uiuc.edu Senior author: David M. Kranz

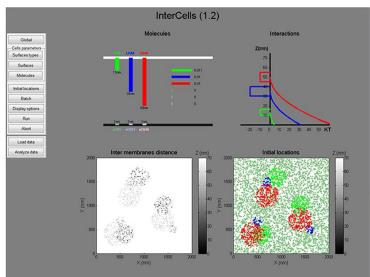
The interaction between the T-cell receptor (TCR) and its peptide-major histocompatibility complex (pepMHC) ligand plays a critical role in determining the activity and specificity of the T cell. The binding properties associated with these interactions have now been studied in many systems, providing a framework for a mechanistic understanding of the initial events that govern T-cell function. There have been various other reviews that have described the structural and biochemical features of TCR: pepMHC interactions. Here we provide an overview of four areas that directly impact our understanding of T-cell function, as viewed from the perspective of the TCR: pepMHC interaction: (1) relationships between T-cell activity and TCR: pepMHC binding parameters, (2) TCR affinity, avidity and clustering, (3) influence of coreceptors on pepMHC binding by TCRs and T-cell activity, and (4) impact of TCR binding affinity on antigenic peptide specificity.

Keywords: agonists; antagonists; binding affinity; coreceptors; dissociation rate; major histocompatibility complex; peptide specificity; peptide-major histocompatibility complex; serial triggering; T-cell receptor; T-cell receptor clustering



"wild-type TCR affinities (K_D values) with pepMHC have been shown to be in the range of 1–100 μ M" SUBJECT **OBJECT**

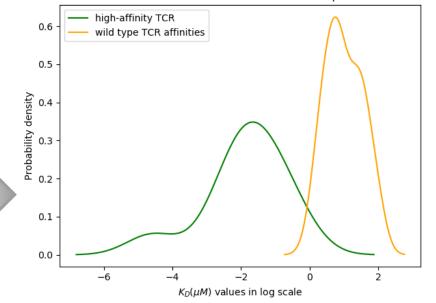
"The affinities of these high-affinity TCR with pepMHC ranged from 30 nM to 26pM" **SUBJECT OBJECT**





Neve-Oz et. al., 2018

Dissociation constant values distribution for TCR-pMHC interaction



Summary



Classification model for relevant papers



Database contains statements from relevant abstracts



Asking questions in large scale



Answers to part of the asked questions

Future work



Extracting information from the paper content



Context between abstract sentences to the content



Using the found parameters as input to the T-cell activation model

Thank you!

☐ Barak & Gabi

☐ Amir Bar

☐ For your listening









Questions?