

NeoScreen[®]

- In Vitro Analysis of Potential Cancer Neo-Epitopes

The majority of T cell epitopes used in vaccine development are identified using *in silico* prediction algorithms. The most widely used prediction algorithms are the Immune Epitope Database and Analysis Resource (IEBD) and netMHC (refs. 1-4).

Both algorithms identify epitopes using models that incorporate multiple aspects of MHC class-specific affinity, which are based on binding motifs as well as experimental affinity measurements. Although widely used, there are major limitations to affinity-based *in silico* strategies:

- For any epitope to be immunogenic, it must be able to bind a compatible MHC molecule and remain bound for long enough to be presented to and recognised by T cells to elicit an immune response. In other words, stable MHC/epitope interactions are required for immunogenicity.
- With the exception of very few alleles, the prediction tools are generally not precise.

Immunitrack is currently the only company in the world that proposes high throughput MHC/epitope stability measurements. Based on our experience, which is heavily supported by multiple peer-reviewed articles, stability is a better predictor of immunogenicity than affinity (refs. 5-6). In the example shown below, by screening E6 and E7 proteins from human papilloma virus (HPV) for stably-binding epitopes to A*0201, we were able to identify all 9 confirmed T cell epitopes among our top 13 most stably-binding epitopes.



В.

	A*0201	A*0201			
	Stab 1	Stab 2	Av stab	Pred aff nM	IEDB
1	82	84	83	50	Yes
2	75	77	76	NB	Yes
3	79	73	76	NB	Yes
4	72	72	72	NB	Yes
5	69	69	69	NB	
6	68	59	64	200	Yes
7	59	59	59	50	Yes
8	50	46	48	500	
9	50	44	47	50	Yes
10	46	47	46	200	Yes
11	47	42	44	NB	
12	44	44	44	NB	
13	41	47	44	NB	Yes

Figures A and B show the results of a stability analysis of 266 overlapping 9-mers from HPV E6 and E7. The red bar in **A** indicates a reference peptide that is a known T cell epitope, which is documented to bind stably to the MHC of interest. Stability of other peptides are calculated relative to this peptide (100% stability). Peptides marked in black are known A*0201-restricted HPV T cell epitopes from the Immune Epitope Database (IEDB). **B** displays stability measurements performed in duplicate (referred to as Stab 1 and Stab 2) for the 13 most stably-binding 9-mers. Remarkably, 9 of the top 13 binders are confirmed T cell epitopes (based on IEDB data). Prediction tools trained on affinity can only predict 5 confirmed T cell epitopes (see column Pred aff in nM – NB stands for non-binding).



Typical NeoScreen® Service Workflow

Immunitrack's NeoScreen® platform can help your company to identify MHC-restricted CD4 or CD8 epitopes from any cancer, biotherapeutic, viral or bacterial pathogen, fast and with unmatched precision.



Figure 1. Typical NeoScreen[®] Service Workflow. Note that customers may also approach Immunitrack with the sequence of a biotherapeutic or a viral or bacterial antigen of interest.



NeoScreen®

The ultimate selection of immunogenic cancer neo-epitopes

Do you work in the fields of immuno-oncology or vaccine design, or with the development of biologics?

Call us to learn more about how we can help you to assess the ability of any epitope to elicit a CD8 and/or CD4 T cell response.

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Read more about the NeoScreen® Technology on our webpage:

www.immunitrack.com/neoscreen-technology



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About Immunitrack

Immunitrack is founded upon world-leading research on MHC-epitope binding. Our proprietary epitope screening platform NeoScreen® measures the affinity and stability of MHC/epitope interactions, with capacity to rapidly screen libraries with thousands of (neo-)epitopes for applications within immuno-oncology, vaccine production, T cell therapies and immune monitoring.

Immunitrack's mission is to provide the pharmaceutical industry and research community with technology and reagents to select or redesign drug candidates during early R&D and to monitor the effects of lead drug candidates on patient immune responses.

References

¹ Nucleic Acids Res 2012, 40 (Web Server issue), W525-30.
² Protein Sci 2003, 12 (5), 1007-17.
³ Immunology 2010, 130 (3), 309-18.

⁴ Immunome Res 2008, 4, 2.

⁵ Cancer Immunol Res 2019, 7 (1), 50-61.

⁶ Eur J Immunol 2012, 42 (6), 1405-16