

# Resource Summary Report

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## AntiJen

RRID:SCR\_001750

Type: Tool

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### Proper Citation

AntiJen (RRID:SCR\_001750)

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### Resource Information

**URL:** <http://www.ddg-pharmfac.net/antijen/AntiJen/antijenhomepage.htm>

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**Description:** Database with quantitative binding data for peptides binding to various cells including MHC Ligand, TCR-MHC complexes, T-cell epitopes, TAP, B-cell, and immunological protein-protein interactions. Information in each entry includes peptide libraries, copy numbers, and diffusion coefficient data.

**Synonyms:** AntiJen Database, AntiJen - A Kinetic, Thermodynamic and Cellular Database, AntiJen Database v2.0, AntiJen v2.0

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:11934742](#), [PMID:12870921](#)

**Keywords:** peptide, binding, antigen, antibodies, cellular, kinetic, diffusion coefficient

**Funding:** GlaxoSmithkline ;  
BBSRC ;  
MRC ;  
UK Department of Health

**Availability:** Free, Freely available

**Resource Name:** AntiJen

**Resource ID:** SCR\_001750

**Alternate IDs:** nif-0000-02551

**Old URLs:** <http://www.darrenflower.info/AntiJen/>

**Record Creation Time:** 20220129T080209+0000

## Ratings and Alerts

No rating or validation information has been found for AntiJen.

No alerts have been found for AntiJen.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 18 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

Grewal S, et al. (2024) Integrating machine learning to advance epitope mapping. *Frontiers in immunology*, 15, 1463931.

Wei Y, et al. (2024) Advances of computational methods enhance the development of multi-epitope vaccines. *Briefings in bioinformatics*, 26(1).

Deng N, et al. (2024) MONET: a database for prediction of neoantigens derived from microsatellite loci. *Frontiers in immunology*, 15, 1394593.

Khetan R, et al. (2022) Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. *mAbs*, 14(1), 2020082.

Mugunthan SP, et al. (2021) Multi-epitope-Based Vaccine Designed by Targeting Cytoadherence Proteins of *Mycoplasma gallisepticum*. *ACS omega*, 6(21), 13742.

Graves J, et al. (2020) A Review of Deep Learning Methods for Antibodies. *Antibodies (Basel, Switzerland)*, 9(2).

Oli AN, et al. (2020) Immunoinformatics and Vaccine Development: An Overview. *ImmunoTargets and therapy*, 9, 13.

Zhou WJ, et al. (2019) NeoPeptide: an immunoinformatic database of T-cell-defined neoantigens. *Database : the journal of biological databases and curation*, 2019.

Potocnakova L, et al. (2016) An Introduction to B-Cell Epitope Mapping and In Silico Epitope Prediction. *Journal of immunology research*, 2016, 6760830.

Luo H, et al. (2016) sNebula, a network-based algorithm to predict binding between human leukocyte antigens and peptides. *Scientific reports*, 6, 32115.

Backert L, et al. (2015) Immunoinformatics and epitope prediction in the age of genomic medicine. *Genome medicine*, 7, 119.

Molero-Abraham M, et al. (2015) EPIPOX: Immunoinformatic Characterization of the Shared T-Cell Epitome between Variola Virus and Related Pathogenic Orthopoxviruses. *Journal of immunology research*, 2015, 738020.

Kozlova E, et al. (2015) Classification epitopes in groups based on their protein family. *BMC bioinformatics*, 16 Suppl 19(Suppl 19), S7.

Luo H, et al. (2015) Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. *BMC bioinformatics*, 16 Suppl 13(Suppl 13), S9.

Kim Y, et al. (2014) Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC bioinformatics*, 15(1), 241.

Miller KR, et al. (2012) T cell receptor-like recognition of tumor in vivo by synthetic antibody fragment. *PloS one*, 7(8), e43746.

Woelke AL, et al. (2010) Theoretical modeling techniques and their impact on tumor immunology. *Clinical & developmental immunology*, 2010, 271794.

Vider-Shalit T, et al. (2007) Virus-epitope vaccine design: informatic matching the HLA-I polymorphism to the virus genome. *Molecular immunology*, 44(6), 1253.