

# Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

## 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.

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

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

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

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.

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

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.