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On the cover: Superposition of x-ray crystal structures of available nonameric peptide-H-2D^b complexes (MHC, blue; β -2 microglobulin, gray; peptides, orange). Computer modeling of peptide binding to MHC showed that, after binding, strong binders are less flexible than nonbinders. Combining this knowledge with sequence-based methods enhances the specificity of peptide–MHC binding prediction. Aranha, M. P., Y. S. M. Jewel, R. A. Beckman, L. M. Weiner, J. C. Mitchell, J. M. Parks, and J. C. Smith. 2020. Combining three-dimensional modeling with artificial intelligence to increase specificity and precision in peptide–MHC binding predictions. *J. Immunol.* 205: 1962–1977.

The Journal of Immunology (ISSN 0022-1767) is published twice each month by The American Association of Immunologists, Inc., 1451 Rockville Pike, Suite 650, Rockville, MD 20852, Phone: 301-634-7197, Fax: 301-246-8401. Subscription terms: New subscriptions and renewals begin January 1 and expire one year later (see <http://www.jimmunol.org/subscription> for prices and details). A special rate is available to members of The American Association of Immunologists, Inc. (see <http://www.aai.org/membership>). The American Association of Immunologists, Inc., is not responsible for undeliverable issues. Replacement issues can be obtained, if available, at the regular price of single issues (see <http://www.jimmunol.org/Subscription/Claims>). Reprints of individual articles are available only from authors. Periodicals postage paid at Rockville, MD 20852, and at additional mailing offices. Country of origin U.S.A. Printed on acid-free recyclable paper. Postmaster: Send address changes 60 days in advance to *The Journal of Immunology*, Subscription Department, 1451 Rockville Pike, Suite 650, Rockville, MD 20852. Copyright © 2020 by The American Association of Immunologists, Inc.

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