

T cell receptor (TCR) clustering in the immunological synapse integrates TCR and costimulatory signaling in selected T cells

Bozidar Purtic*, Lisa A. Pitcher*, Nicolai S. C. van Oers*[†], and Christoph Wülfing*^{‡§}

*Center for Immunology and Departments of [†]Microbiology and [‡]Cell Biology, University of Texas Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX 75390

Edited by James P. Allison, Memorial Sloan-Kettering Cancer Center, New York, NY, and approved January 6, 2005 (received for review September 15, 2004)

During T cell activation, T cell receptors (TCR) cluster at the center of the T cell/antigen-presenting cell interface forming a key component of the immunological synapse. The function of this TCR clustering is still unresolved. A comprehensive search for such a function yielded a very limited and specific result. A micrometer-scale receptor clustering integrated the TCR and CD28 signals required for IL-2 secretion in primary 5C.C7 T cells, a low-affinity/avidity TCR system. 5C.C7 TCR signaling itself was not affected. In addition, central TCR accumulation was not required for any T cell effector function tested in three other TCR transgenic models. Central TCR accumulation thus had a specific role in signaling integration in low-affinity T cells.

T cells are activated when the T cell receptor (TCR) engages cognate agonist peptide/MHC complexes expressed on the surface of the antigen-presenting cell (APC) (1). Complete T cell activation also requires the engagement of costimulatory receptors, in particular CD28 and LFA-1, by their APC ligands B7 and intercellular adhesion molecule-1 (ICAM-1) (2). T cell activation provides a striking example of localized signaling, the accumulation of TCR/MHC complexes at the center of the T cell/APC interface (“central TCR accumulation”), an event readily visualized by fluorescence microscopy (3–5). In response to strong T cell stimuli, 2,000–3,000 TCR and MHC molecules accumulate at the center of the interface (4, 6). Lower concentrations of agonist peptide can still elicit clearly detectable clustering (6, 7) with an estimated few hundred TCRs. Central TCR accumulation is a critical feature of the “mature immunological synapse,” the segregation of multiple receptors, signaling, and adaptor proteins into micrometer-sized central and peripheral supramolecular activation clusters (8). Yet the function of central TCR accumulation has remained elusive and controversial (9). A major obstacle is the lack of an experimental tool to distinguish TCR signaling from its localization. To circumvent interference with TCR signaling, we have related central TCR accumulation to critical T cell signaling and effector functions over a wide range of physiological activation conditions. We used primary T cell/APC interactions from four different class II- and class I-restricted TCR transgenic mouse models. The comprehensive nature of our approach revealed a surprisingly limited and specific role for central TCR accumulation. The integration of costimulatory with TCR signaling required micrometer-scale receptor clustering only in the low-affinity/avidity 5C.C7 T cells. TCR signaling itself was not affected. In three additional TCR transgenic systems, central TCR accumulation was not required for any T cell signaling or effector functions.

Experimental Procedures

Cells and Reagents. *In vitro*-primed primary T cells from 5C.C7 (10), DO11.10 (11), HY (12), and P14 (13) TCR transgenic mice were generated as described in ref. 6. I-E^k-GFP-transfected A20 B cell lymphoma cells (6), A20 cells, or EL4 thymoma cells (for both HY and P14 T cells) were used as APCs. In the case of 5C.C7 T cells, agonist peptide concentrations were adjusted by

dilutions into null peptide (6). In all other studies, the peptide was diluted in water. Costimulation blockade with antibodies against ICAM-1 or B7-1/B7-2 was as described in ref. 14. Use of Jaspakinolide and a membrane-permeable version of the Wiscott-Aldrich syndrome protein C-terminal domain has been described in ref. 15. The antibodies used were as follows: anti-IL-2 (JES6-5H4; Becton Dickinson), anti-IFN- γ (XMG1.2; Becton Dickinson), anti-phospho LAT Y191 and anti-phospho Akt S473 (Cell Signaling Technology, Beverly, MA), anti-CTLA-4 (UC10-4F10-11) (Becton Dickinson), anti-V α 2, anti-V β 8 (P14 TCR) (Becton Dickinson), anti-V α 11 (Becton Dickinson), anti-V β 3 (5C.C7 TCR) (Becton Dickinson), anti-DO11.10 (Becton Dickinson), anti-TCR β (H27-597) (Becton Dickinson), and anti-HY (eBiosciences, San Diego).

Imaging. As discussed in detail in *Supporting Text*, which is published as supporting information on the PNAS web site, TCR/MHC accumulation was determined by using GFP fusion proteins with I-E^k (for 5C.C7 T cells) (6), H2-D^b as generated in strict analogy (for P14 T cells), the TCR ζ -chain (for DO11.10 and HY T cells) (7), and the double Src homology 2 (SH2) domain of the kinase ZAP-70 (for P14 and HY T cells). The latter was generated by linking amino acids 1–276 of human ZAP-70 C-terminally through a 7-aa linker to EGFP. The location of ligand-engaged CD28 was determined with a B7-2/GFP fusion protein, as discussed in *Supporting Text*. Use of actin-GFP and tubulin-GFP has been described in refs. 15 and 16. TCR ζ -GFP, ZAP-70 double SH2-GFP, actin-GFP, and tubulin-GFP were introduced into primary T cells by retroviral transduction with a Moloney murine leukemia virus-derived system as described in ref. 15. The microscopy system, image acquisition, and image analysis have been described in detail in ref. 15. Briefly, primary T cells and APCs loaded with peptide were allowed to interact at 37°C on the microscope stage. Every 20 seconds, a differential interference contrast bright field image and GFP images were acquired (spaced 1 μ m in *z* covering the entire cell). For the analysis of MHC/TCR accumulation, actin accumulation, and reorientation of the microtubule organizing center (MTOC), three-dimensional reconstructions of productive cell couples were generated and classified according to strict analysis criteria (refs. 6 and 15 and *Supporting Text*). For actin-GFP analysis, interface accumulation with fluorescence intensity of 40% more than the cellular background was considered as long it constituted the highest intensity within the cell (strong and partial phenotypes as defined in ref. 16).

This paper was submitted directly (Track II) to the PNAS office.

Abbreviations: APC, antigen-presenting cell; ICAM-1, intercellular adhesion molecule-1; LAT, linker of activated T cell; MCC, moth cytochrome c; MTOC, microtubule organizing center; SH2, Src homology 2; TCR, T cell receptor.

[§]To whom correspondence should be addressed. E-mail: christoph.wuefing@utsouthwestern.edu.

© 2005 by The National Academy of Sciences of the USA

Effector Functions. IL-2 and IFN- γ secretion were determined by intracellular cytokine staining of primary T cell/APC couples after 4 and 16 h of T cell/APC interactions according to standard procedures in ref. 17. Target cell killing was determined in 1-h chromium-release assays (16). TCR down-regulation was determined by staining for surface TCR expression levels after 1.5 h of T cell/APC contact according to standard procedures in ref. 18. Linker of activated T cell (LAT) and Akt phosphorylation was determined in cell extracts from T cell/APC couples that interacted for 5 min (LAT and Akt) or 30 min (Akt) by Western blotting with standard procedures. In control experiments, APCs were fixed with glutaraldehyde to assure that APC signaling did not contribute to observed changes in LAT and Akt phosphorylation (data not shown). TCR ζ -phosphorylation was assayed in ZAP-70 immunoprecipitates from T cell/APC couples that interacted for 5 min (19). Data were quantified as described in *Supporting Text* and in the legend to Table 1, which is published as supporting information on the PNAS web site.

Results

Central TCR Accumulation Is Specifically Linked to IL-2 Secretion in 5C.C7 T Cells. T cells from 5C.C7 TCR transgenic mice (10) have been used extensively to study the immunological synapse. The 5C.C7 TCR recognizes a peptide from moth cytochrome *c* (MCC) (amino acids 82–103) presented by I-E^k. To identify T cell signaling and effector functions that are consistently linked to central TCR accumulation, we performed agonist peptide dose–response experiments. The dose–responses of central TCR accumulation, induction of LAT phosphorylation as a readout of TCR signaling (20), TCR downmodulation as a readout of TCR engagement (18), and IL-2 production (Fig. 5, which is published as supporting information on the PNAS web site) were superimposable (Fig. 1A). These results suggested a direct role for TCR clustering in the regulation of 5C.C7 T cell activation. To further address this link, we used two approaches to block TCR clustering while maintaining TCR engagement. First, we slowed T cell actin dynamics by using either the inhibitor of actin depolymerization, Jasp, or a membrane-permeable version of the effector domain of the Wiskott–Aldrich Syndrome protein, the C-terminal domain (15). Second, we used antibodies to block CD28/LFA-1-mediated costimulation (6, 14). TCR down-regulation and LAT phosphorylation were unaffected with these inhibitors. In contrast, IL-2 secretion was reduced in parallel with the loss of central TCR accumulation (Fig. 1A). IL-2 secretion thus was consistently related ($R^2 = 0.75$) to central TCR accumulation, whereas LAT phosphorylation and TCR down-regulation were not ($R^2 < 0.3$) (Fig. 6, which is published as supporting information on the PNAS web site). These results imply that IL-2 production in 5C.C7 T cells selectively depended on central TCR accumulation. Interestingly, TCR signaling itself was not, as further addressed below.

Costimulation Enhances Receptor Clustering and IL-2 Secretion Preferentially in 5C.C7 T Cells. To investigate whether central TCR accumulation was associated with IL-2 secretion in other T cells, we analyzed primary T cells from DO11.10 TCR transgenic mice (11). The DO11.10 TCR recognizes an ovalbumin peptide 324–340 presented by I-A^d. In an agonist peptide dose–response, central TCR accumulation occurred only at 10 μ M agonist peptide (Fig. 2A). In contrast, IL-2 production, LAT phosphorylation, TCR down-regulation, and naïve T cell proliferation occurred at peptide doses well below 10 μ M (10 nM to 10 μ M), severalfold less than that necessary for central TCR accumulation (Fig. 1B). Thus, central TCR accumulation was not associated with IL-2 production in all T cells. In addition, not a single DO11.10 signaling or effector function tested depended on central TCR accumulation, as further addressed below.

The disparate results between the DO11.10 and the 5C.C7 T

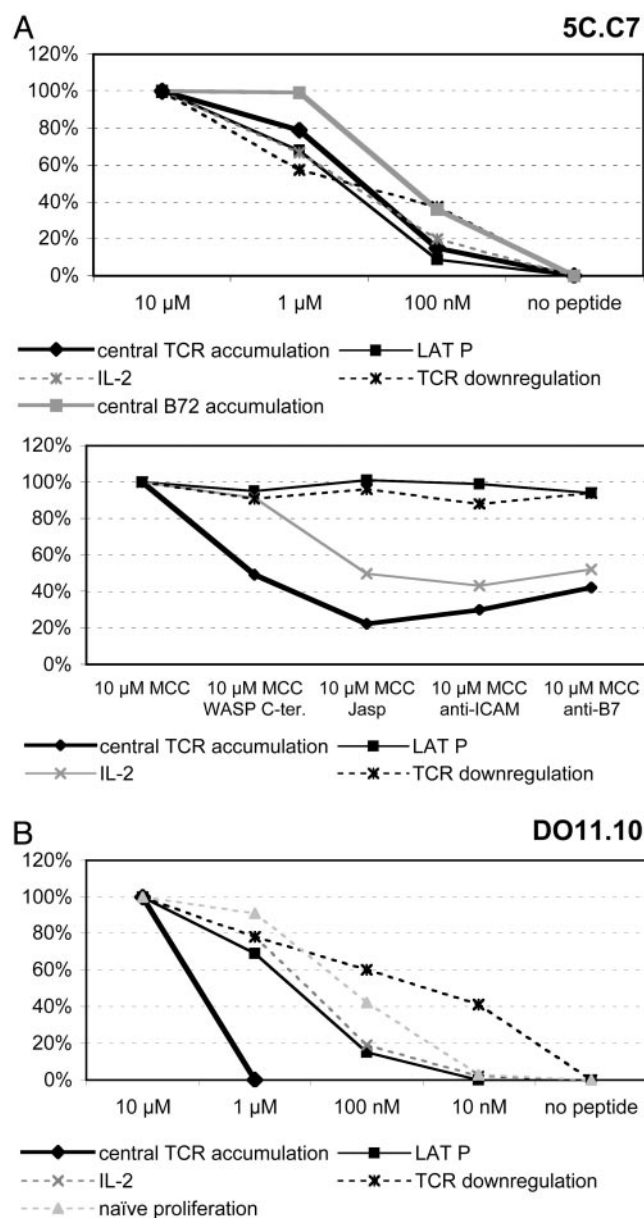


Fig. 1. Central TCR accumulation associates with IL-2 secretion in 5C.C7 T cells. (A) Central TCR and B7-2 accumulation and effector functions in 5C.C7/I-E^k-GFP transfected A20 B cell lymphoma APC interactions under the indicated conditions are shown as normalized data. Values for 10 μ M MCC are set to 100%, and values for no agonist peptide are set to 0%. All other values are scaled accordingly. Raw data are either published (TCR accumulation) (6) or given in Fig. 7 (B7 accumulation) or Table 1 (all other data). WASP C-ter, 200 nM of the rat Wiskott–Aldrich syndrome protein C-terminal domain; Jasp, 0.5 μ M Jaspakolinolide; anti-ICAM, and anti-B7¹, 10 μ g/ml blocking antibodies against ICAM-1 and B7-1/B7-2, respectively. (B) Normalized data for primary DO11.10/A20 APC interactions are shown similarly. Raw data are given in Table 1 and Fig. 2.

cells raised the question as to what distinguishes these two T cells. Most notably, I-E^k tetramer dissociation experiments showed that the avidity of the 5C.C7 TCR is at the very low end of the physiological range (21). The dissociation constant of the 5C.C7/MCC/I-E^k complex of 50 μ M is high (22). In contrast to this difference, TCR surface expression as assayed by anti-TCR- β staining was the same. Transgenic TCR expression was >95% of total TCR for both. The percentage of T cells secreting IL-2 and the amounts of IL-2 produced were the same at 10 μ M

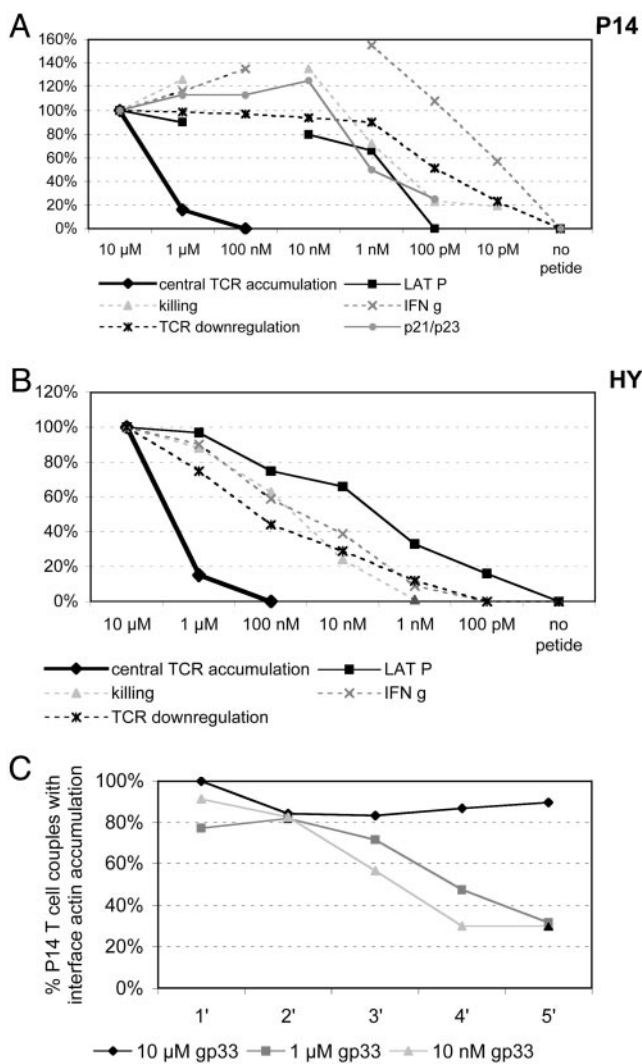


Fig. 4. Central TCR accumulation associates with sustained actin accumulation but not with critical effector functions in P14 and HY T cells. (A and B) Central TCR accumulation and effector functions in primary T cell/EL4 APC interactions (P14 T cells in A and HY T cells in B) under the indicated agonist peptide concentrations are shown as normalized data similar to Fig. 1. Raw data are given in Table 1 and Fig. 2. (C) The percent of actin-GFP-transduced P14/EL4 cell couples showing actin accumulation at the T cell/APC interface at >40% of the cellular background fluorescence intensity at the indicated time after cell couple formation in the presence of the given gp33 agonist peptide concentrations are displayed. Differences between values at 10 μ M versus 1 μ M and 100 nM gp33 peptide at 4' and 5' are significant ($P \leq 0.001$). Between 22 and 36 cell couples from at least two independent experiments were analyzed per condition.

the uropod to its final location behind the center of the interface. Efficient MTOC reorientation at low agonist peptide concentrations, where central TCR accumulation was dramatically reduced, was similarly observed in 5C.C7 T cells (15). In contrast to the efficient MTOC reorientation at low agonist peptide concentrations, the ability of P14 T cells to maintain actin at the T cell/APC interface, as determined with actin-GFP (16), was significantly impaired at 1 μ M gp33 and 10 nM gp33. Only the initial (i.e., within 2 min after cell couple formation) interface actin accumulation was comparable at all gp33 concentrations. However, although 90% of P14/EL4 cell couples showed interface actin accumulation 5 min after cell couple formation at 10 μ M gp33, only 32% and 30% did at 1 μ M gp33 and 10 nM gp33, respectively ($P < 0.001$) (Fig. 4C). This association of central

TCR accumulation with sustained actin accumulation establishes that T cell polarization was reduced when central TCR accumulation could not be observed. Interestingly, in the low-affinity 5C.C7 T cells, sustained actin accumulation was not only associated with central TCR accumulation (corroborating the P14 data) but also required for entry into the cell cycle (15). The role of sustained actin accumulation thus seems to depend on the TCR transgenic model similar to that of central TCR accumulation. T cells with a low-affinity TCR T cell required it for an effector function, and T cells with a high-affinity TCR did not. In contrast, the role of early actin accumulation is likely more general, possibly involving the formation of a wide, tight interface. In contrast to diminishing T cell polarization, the number of productively engaged TCRs, as read out by TCR phosphorylation and down-regulation, remained maximal down to 10 nM gp33 agonist peptide (Fig. 4A). High sensitivity of productive TCR engagement together with more easily diminished polarization (as illustrated in Fig. 10D) strongly argue that between 1 μ M gp33 and 10 nM gp33, the reduction of detectable TCR clustering was the consequence of incomplete T cell polarization, not of reduced TCR engagement. Central TCR accumulation thus constitutes a defined polarization phenotype.

Discussion

Large-scale clustering of the TCR at the center of the T cell/APC interface is one of the most prominent and intriguing features of the immunological synapse. We have addressed its function and have made three observations. First, central TCR accumulation constituted a defined T cell polarization phenotype. Second, central TCR accumulation was not required for critical T cell signaling or effector function in three TCR transgenic systems. Third, in the low-affinity/avidity 5C.C7 T cells, costimulatory signaling, receptor clustering, and IL-2 secretion were tightly associated. In combination, these data severely limit the possible functions of central TCR accumulation, leaving the mediation of combined TCR and CD28 signaling in the generation of IL-2 in a subset of T cells. The widespread and specific nature of the correlations in combination with selected functional interference provide reliable support for signal integration in IL-2 secretion as the function of micrometer-scale receptor clustering, including central TCR accumulation.

The formation of the immunological synapse has been assessed by central accumulation of TCR (3), PKC- θ (8), or phosphorylated ZAP-70 (37, 38) or by the central exclusion of LFA-1 (3, 39). It is unclear, however, whether such different aspects of T cell polarization reflect the same T cell organization or different, defined polarization states. We have shown that, in P14 and 5C.C7 T cells, central TCR accumulation and sustained actin accumulation require high agonist peptide concentrations, whereas early actin accumulation and MTOC reorientation are more sensitive. These data support the notion that T cell polarization consists of various defined states. They suggest that the two elements of cellular polarization at the center of the cytotoxic T lymphocyte/APC interface that are seen at high agonist peptide concentrations, accumulation of the TCR and secretory vesicles (40), have also differential sensitivity to agonist peptide. The existence of multiple T cell polarization states is further supported by the selective dissociation of TCR and PKC- θ clustering in DOCK2-deficient mice (41) and by differential agonist peptide dose-responses of CD2 accumulation and MTOC reorientation in human cytotoxic T lymphocyte clones (42). The immunological synapse, rather than being a single structure, seems to be a continuum of polarization states, one of which with very stringent activation requirements is central TCR accumulation.

We have shown that central TCR accumulation was not required for critical effector functions in three of four TCR

transgenic systems. Although these data have been generated by using primed primary T cells as a model of effector T cells, the similar dose-responses of naïve and primed DO11.10 (Fig. 1B) and P14 T cells (as discussed) argue that they also apply to naïve T cells. Previous work has linked central PKC- θ accumulation to cytolytic function and IFN- γ secretion (35), dissociated central LFA-1 exclusion from cytolytic function (43), and linked IFN- γ secretion but not cytolytic function to the enrichment of CD2 and phosphotyrosine (42), arguing for and against a requirement of the immunological synapse for T cell effector function. Together with our data, these studies suggest that some T cell polarization states are required for T cell effector function, whereas others are not. Central TCR accumulation as a polarization state with a very stringent activation requirement was not required for effector functions in the majority of T cells studied.

Initially, TCR clustering generated substantial enthusiasm as a potential mechanism of signal amplification through receptor proximity (3, 4). Later work, however, showed that substantial T cell signaling occurs in its absence (38) and even suggested that TCR clustering enhanced TCR down-regulation (44). The data presented here address this apparent contradiction. We have shown that TCR signaling itself, as assayed by TCR and LAT phosphorylation, and TCR down-regulation are independent of TCR clustering. However, the integration of TCR with costimulatory signaling required a micrometer-scale signaling complex

in low-affinity/avidity 5C.C7 T cells. These data suggest that signal amplification through receptor clustering is used for only one particular aspect of signaling, the integration of TCR with costimulatory signaling, and is used only when required to compensate for a weak TCR signal. Interestingly, the dependence of cytokine secretion on receptor clustering seemed to be an intrinsic property of low-affinity T cells, because stimulation of high-affinity P14 T cells with a low-affinity Y4A partial agonist/MHC complex (30) did not restore it (data not shown). We speculate that, during T cell selection, a marginal TCR/MHC affinity imprints dependence of IL-2 secretion on costimulation-mediated receptor clustering on the developing T cell. Marginal TCR/MHC affinity is most likely to give rise to autoreactive T cells by allowing more self-peptide/MHC complexes to remain under the threshold for negative selection. Therefore, the imprinting of enhanced dependence of peripheral T cell activation on receptor clustering for such T cells should safeguard against autoimmune disease by enforcing costimulation dependence.

We thank Dr. M. Davis (Howard Hughes Medical Institute and Stanford University, Stanford, CA) for the retroviral TCR- ζ /GFP expression construct and Dr. D. Farrar (University of Texas Southwestern Medical Center) for DO11.10 mice and naïve DO11.10 T cell proliferation data. This work was supported by grants from the National Institutes of Health (to C.W. and N.S.C.v.O.) and the Welch Foundation (to C.W.).

- Davis, M. M., Boniface, J. J., Reich, Z., Lyons, D., Hampl, J., Arden, B. & Chien, Y. (1998) *Annu. Rev. Immunol.* **16**, 523–544.
- Sprent, J. (1999) *J. Immunol.* **163**, 4629–4636.
- Grakoui, A., Bromley, S. K., Sumen, C., Davis, M. M., Shaw, A. S., Allen, P. M. & Dustin, M. L. (1999) *Science* **285**, 221–226.
- Monks, C. R., Freiberg, B. A., Kupfer, H., Sciaky, N. & Kupfer, A. (1998) *Nature* **395**, 82–86.
- Wülfing, C., Tskvitaría-Fuller, I., Burroughs, N. J., Sjaastad, M. D., Klem, J. & Schatzle, J. D. (2002) *Immunol. Rev.* **189**, 64–83.
- Wülfing, C., Sumen, C., Sjaastad, M. D., Wu, L. C., Dustin, M. L. & Davis, M. M. (2002) *Nat. Immunol.* **3**, 42–47.
- Krummel, M. F., Sjaastad, M. D., Wülfing, C. & Davis, M. M. (2000) *Science* **289**, 1349–1352.
- Monks, C. R., Kupfer, H., Tamir, I., Barlow, A. & Kupfer, A. (1997) *Nature* **385**, 83–86.
- Davis, D. M. & Dustin, M. L. (2004) *Trends Immunol.* **25**, 323–327.
- Seder, R. A., Paul, W. E., Davis, M. M. & Fazekas de St. Groth, B. (1992) *J. Exp. Med.* **176**, 1091–1098.
- Szabo, S. J., Dighe, A. S., Gubler, U. & Murphy, K. M. (1997) *J. Exp. Med.* **185**, 817–824.
- Markiewicz, M. A., Girao, C., Opferman, J. T., Sun, J., Hu, Q., Agulnik, A. A., Bishop, C. E., Thompson, C. B. & Ashton-Rickardt, P. G. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 3065–3070.
- Pircher, H., Burki, K., Lang, R., Hengartner, H. & Zinkernagel, R. M. (1989) *Nature* **342**, 559–561.
- Wülfing, C. & Davis, M. M. (1998) *Science* **282**, 2266–2270.
- Tskvitaría-Fuller, I., Rozelle, A. L., Yin, H. L. & Wülfing, C. (2003) *J. Immunol.* **171**, 2287–2295.
- Wülfing, C., Puritic, B., Klem, J. & Schatzle, J. D. (2003) *Proc. Natl. Acad. Sci. USA* **100**, 7767–7772.
- Prussin, C. & Metcalfe, D. D. (1995) *J. Immunol. Meth.* **188**, 117–128.
- Valitutti, S., Muller, S., Cella, M., Padovan, E. & Lanzavecchia, A. (1995) *Nature* **375**, 148–151.
- van Oers, N. S., Killeen, N. & Weiss, A. (1994) *Immunity* **1**, 675–685.
- Zhang, W., Sloan-Lancaster, J., Kitchen, J., Tribble, R. P. & Samelson, L. E. (1998) *Cell* **92**, 83–92.
- Savage, P. A. & Davis, M. M. (2001) *Immunity* **14**, 243–252.
- Matsui, K., Boniface, J. J., Reay, P. A., Schild, H., Fazekas de St Groth, B. & Davis, M. M. (1991) *Science* **254**, 1788–1791.
- Egen, J. G. & Allison, J. P. (2002) *Immunity* **16**, 23–35.
- Bromley, S. K., Iaboni, A., Davis, S. J., Whitty, A., Green, J. M., Shaw, A. S., Weiss, A. & Dustin, M. L. (2001) *Nat. Immunol.* **2**, 1159–1166.
- Kane, L. P. & Weiss, A. (2003) *Immunol. Rev.* **192**, 7–20.
- Jones, R. G., Parsons, M., Bonnard, M., Chan, V. S., Yeh, W. C., Woodgett, J. R. & Ohashi, P. S. (2000) *J. Exp. Med.* **191**, 1721–1734.
- Ward, S. G. & Cantrell, D. A. (2001) *Curr. Opin. Immunol.* **13**, 332–338.
- Ueda, Y., Levine, B. L., Huang, M. L., Freeman, G. J., Nadler, L. M., June, C. H. & Ward, S. G. (1995) *Int. Immunol.* **7**, 957–966.
- Kane, L. P., Mollenauer, M. & Weiss, A. (2004) *J. Immunol.* **172**, 5441–5449.
- Tissot, A. C., Ciatto, C., Mittl, P. R., Grutter, M. G. & Pluckthun, A. (2000) *J. Mol. Biol.* **302**, 873–885.
- Weiss, A. & Littman, D. R. (1994) *Cell* **76**, 263–274.
- Ardouin, L., Boyer, C., Gillet, A., Trucy, J., Bernard, A. M., Nunes, J., Delon, J., Trautmann, A., He, H. T., Malissen, B. & Malissen, M. (1999) *Immunity* **10**, 409–420.
- Kersh, E. N., Kaech, S. M., Onami, T. M., Moran, M., Wherry, E. J., Miceli, M. C. & Ahmed, R. (2003) *J. Immunol.* **170**, 5455–5463.
- Bachmann, M. F., McKall-Faienza, K., Schmits, R., Bouchard, D., Beach, J., Speiser, D. E., Mak, T. W. & Ohashi, P. S. (1997) *Immunity* **7**, 549–557.
- Potter, T. A., Grebe, K., Freiberg, B. & Kupfer, A. (2001) *Proc. Natl. Acad. Sci. USA* **98**, 12624–12629.
- van Oers, N. S., Tohlen, B., Malissen, B., Moomaw, C. R., Afendis, S. & Slaughter, C. A. (2000) *Nat. Immunol.* **1**, 322–328.
- Freiberg, B. A., Kupfer, H., Maslani, W., Delli, J., Kappler, J., Zaller, D. M. & Kupfer, A. (2002) *Nat. Immunol.* **3**, 911–917.
- Lee, K. H., Holdorf, A. D., Dustin, M. L., Chan, A. C., Allen, P. M. & Shaw, A. S. (2002) *Science* **295**, 1539–1542.
- Irvine, D. J., Purbhoo, M. A., Krosgaard, M. & Davis, M. M. (2002) *Nature* **419**, 845–849.
- Stinchcombe, J. C., Bossi, G., Booth, S. & Griffiths, G. M. (2001) *Immunity* **15**, 751–761.
- Sanui, T., Inayoshi, A., Noda, M., Iwata, E., Oike, M., Sasazuki, T. & Fukui, Y. (2003) *Immunity* **19**, 119–129.
- Faroudi, M., Utzny, C., Salio, M., Cerundolo, V., Guiraud, M., Muller, S. & Valitutti, S. (2003) *Proc. Natl. Acad. Sci. USA* **100**, 14145–14150.
- Purbhoo, M. A., Irvine, D. J., Huppa, J. B. & Davis, M. M. (2004) *Nature Immunol.* **5**, 524–530.
- Lee, K. H., Dinner, A. R., Tu, C., Campi, G., Raychaudhuri, S., Varma, R., Sims, T. N., Burack, W. R., Wu, H., Wang, J., et al. (2003) *Science* **302**, 1218–1222.