logical response. Alternatively, α_s* may inhibit transformation by inhibiting other signaling pathways.

Alteration in cellular concentration of cAMP by itself does not affect regulation of mitogenesis in NIH 3T3 cells or in most other mammalian cell types (*18*). Mutations in *ras* occur commonly in human tumors (*19*). Thus activated Gα_s may suppress transformation of other cell types. Because expression of α_s* only modestly increases the cellular concentrations of cAMP, it is possible that the blockade of transformation by α_s* can be achieved without raising cellular cAMP concentrations to deleterious levels. NIH 3T3 cells are on the verge of transformation (*20*) and can be transformed without the introduction of foreign oncogenes (*21*). The use of such a system heightens the potential significance of our observations by indicating that α_s* can block the transformation of cells that have substantially progressed through the multiple steps involved in neoplastic transformation. Thus targeted implantation of α_s* may be a useful strategy for preventing the development of cancers in some predisposed cells or tissues.

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11. After transfection with the H-*ras* plasmid (pT24), which contains an activated c-H-*ras* oncogene isolated from human T24 bladder carcinoma cells [M. Goldfarb, *et al.*, *Nature* **296**, 404 (1982)], cells were induced for either 1 day (NIH 3T3 cells) or 3 days (RAT-1) with 1 mM dexamethasone before plating on soft agar plates. Procedures for the colony formation assay have been published (*7*). Transfection efficiencies for the various NIH 3T3 clonal lines were very similar (*12*). No differences were found in the transfection efficiencies for the different RAT-1 clonal lines (*12*).
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Fusion of a Kinase Gene, *ALK*, to a Nucleolar Protein Gene, *NPM*, in Non-Hodgkin's Lymphoma

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The 2;5 chromosomal translocation occurs in most anaplastic large-cell non-Hodgkin's lymphomas arising from activated T lymphocytes. This rearrangement was shown to fuse the *NPM* nucleolar phosphoprotein gene on chromosome 5q35 to a previously unidentified protein tyrosine kinase gene, *ALK*, on chromosome 2p23. In the predicted hybrid protein, the amino terminus of nucleophosmin (NPM) is linked to the catalytic domain of anaplastic lymphoma kinase (ALK). Expressed in the small intestine, testis, and brain but not in normal lymphoid cells, ALK shows greatest sequence similarity to the insulin receptor subfamily of kinases. Unscheduled expression of the truncated ALK may contribute to malignant transformation in these lymphomas.

Large-cell lymphomas comprise ~25% of all non-Hodgkin's lymphomas in children and young adults. Approximately one-third of these tumors have a t(2;5)(p23;q35) chromosomal translocation (*1*), which suggests that rearrangement of cellular proto-oncogenes on these chromosomes contributes to lymphomagenesis. Lymphomas with the t(2;5) typically involve lymph nodes, skin, lung, soft tissue, bone, and the gastrointestinal tract and arise predominantly from activated T lymphocytes (*2*). The malignant cells express interleukin-2 (IL-2) receptors and CD30 (Ki-1) antigen, a receptor for a ligand related to tumor necrosis factor (*3*). By the updated Kiel lymphoma classification, most tumors with the t(2;5) are classified as anaplastic large-cell non-Hodgkin's lymphomas (*4*).

To clone the genes altered by the t(2;5), we used a positional strategy that was based

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on fluorescence in situ hybridization (FISH) ordering of regionally derived cosmid clones (5). Bidirectional chromosome walks were performed from cosmids ~290 kilobases (kb) apart that flanked the breakpoint on chromosome 5; each walk spanned a genomic region of 150 kb. With genomic probes isolated 70 kb from the telomeric cosmid (6), we observed rearranged restriction fragments in the DNAs of two lymphoma cell lines containing the t(2;5) (Fig. 1A). One of the probes (p21-3/3E) was hybridized to a complementary DNA (cDNA) library prepared from the UOC-B1 pro-B leukemia cell line, which is t(2;5)-negative. Multiple cDNA clones were isolated that hybridized to a ubiquitously expressed 1.6-kb mRNA encoding nucleophosmin (NPM; also known as B23 or numatrin), a highly conserved nucleolar phosphoprotein that shuttles ribosomal components between the nucleolus and the cytoplasm in the later stages of ribosome assembly (7). Northern (RNA) blot analysis with a probe corresponding to 5′-specific *NPM* sequences revealed that t(2;5)-positive cell lines expressed both the normal 1.6-kb *NPM* transcript and a 2.4-kb transcript, whereas t(2;5)-negative cell lines expressed only the 1.6-kb transcript (Fig. 1B). In contrast, a probe containing 3′-untranslated *NPM* sequences detected only the normal 1.6-kb *NPM* transcript in all cell lines (8).

By screening a cDNA library prepared from the SU-DHL-1 t(2;5)-positive cell line, we isolated more than 20 clones that hybridized to 5′ but not 3′ *NPM* probes. Sequences from the 5′ ends of the three longest clones were identical to 5′ *NPM* cDNA sequences but diverged after the codon for Val^{117}. *NPM* sequences 3′ of this codon were replaced by 1223 nucleotides (nt), resulting in an open reading frame of 1575 nt (Fig. 2A). A probe (pS1.2) representing the 3′ end of the fusion cDNA identified the same 2.4-kb transcript that had been detected with the 5′-specific *NPM* probe in RNAs from t(2;5)-positive cells (Fig. 1B). This fragment was localized to chromosome 2p23 by hybridization to DNAs of human-rodent somatic cell hybrids and by metaphase FISH analysis (9), which indicates that the 2.4-kb mRNA was encoded by a fused gene created by the t(2;5).

The 3′ portion of the chimeric t(2;5) cDNA encodes conserved residues characteristic of the catalytic domain of protein tyrosine kinases (PTKs) (10) (Fig. 2, A and B). The newly identified anaplastic lymphoma kinase (ALK) showed the greatest sequence similarity to members of the insulin receptor kinase subfamily, including leukocyte tyrosine kinase (LTK; 64% amino acid identity), TRKA (38%), ROS (37%)

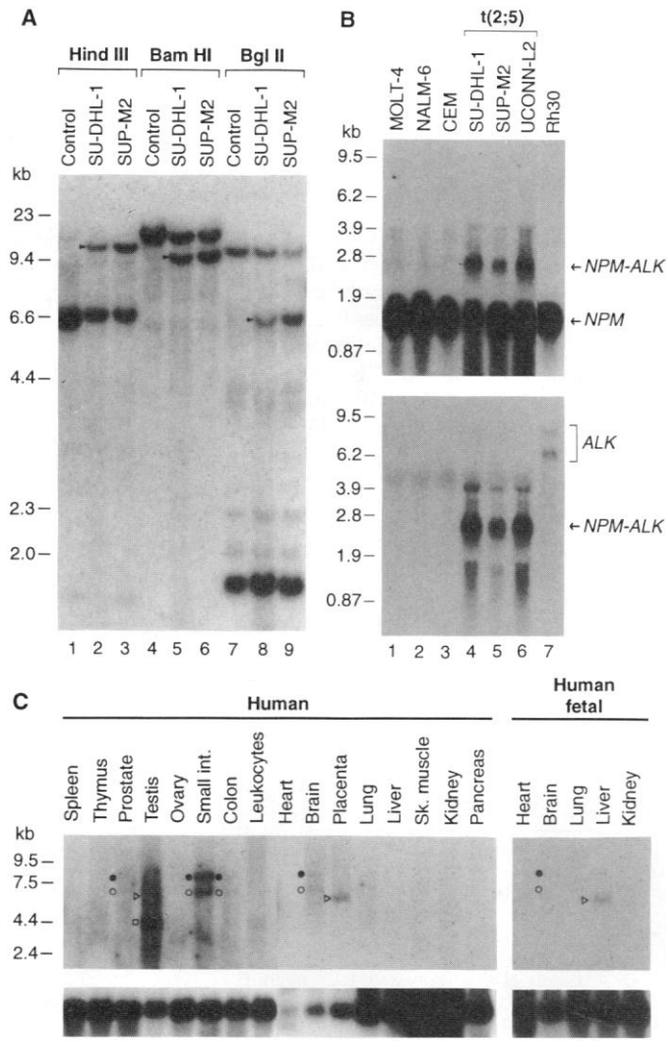

Fig. 1. (**A**) Southern blot analysis of DNAs from a human lymphocyte cell line that is karyotypically normal and Epstein-Barr virus–immortalized (control lanes) and from the t(2;5)-positive cell lines SU-DHL-1 and SUP-M2 with the p16-3/1.2S probe. Arrowheads indicate rearranged restriction fragments. (**B**) Northern blot analysis of RNAs from t(2;5)-negative B lymphoid (NALM-6), T lymphoid (MOLT-4 and CEM), and rhabdomyosarcoma (Rh30) cell lines and from the t(2;5)-positive lines SU-DHL-1, SUP-M2, and UCONN-L2. The probes were a 5′ fragment from the *NPM* cDNA (top) and a 3′ fragment from the *NPM-ALK* cDNA (pS1.2) (bottom) (19). Each lane contains 20 μg of total RNA, except for lane 7, which contains 8 μg of polyadenylated [poly(A)$^+$] RNA. (**C**) Analysis of RNAs [2 μg of poly(A)$^+$ RNA per lane; Clontech, San Diego, California] from various human tissues with a 3′ *NPM-ALK* cDNA probe (pS1.2). Open circles, 6.5-kb *ALK* transcripts; closed circles, 8.0-kb transcripts; open square, 4.4-kb transcript; arrowheads, 6.0-kb transcripts. Control hybridizations with a β-actin cDNA probe are shown below. The blots hybridized with pS1.2 are 6-day autoradiographic exposures; the blots hybridized with the β-actin probe are 4-hour exposures. Small int., small intestine; sk. muscle, skeletal muscle.

and its *Drosophila* homolog Sevenless (35%), the β chain of the insulin-like growth factor receptor (IGF-1 receptor; 37%), and the β chain of the insulin receptor (IR; 36%).

We determined the structure of normal ALK proteins by isolating cDNA clones from the Rh30 rhabdomyosarcoma cell line with the pS1.2 probe. Analysis of the inserts of the two largest clones, pRMS4 and pRMS17-2, revealed 3′ *ALK* sequences identical to those in the fusion gene cDNA, which indicates that mutations had not occurred in the chimeric protein. Sequences of *ALK* immediately upstream of the *NPM-ALK* junction encoded 23 hydrophobic amino acids typical of a transmembrane domain, whereas those from the extreme 5′ ends of the *ALK* clones were 50% identical to sequences encoding insulin-like growth factor binding protein (IBP-1) (8, 11). These comparisons indicate that the normal *ALK* product is a membrane-spanning tyrosine kinase receptor. Notably, the transmembrane and putative extracellular domains are not included in the NPM-ALK chimeric protein.

ALK mRNAs of 6.5 and 8.0 kb were abundantly expressed in rhabdomyosarcoma cell lines and in small intestine and were weakly expressed in brain (fetal and adult), colon, and prostate (Fig. 1, B and C). Large amounts of 4.4-kb and 6.0-kb mRNAs were detected in testis, whereas only a 6.0-kb mRNA was detected in placenta and fetal liver. All four mRNAs were also detected with a probe containing only 3′ untranslated *ALK* sequences, which suggests that they represent differentially spliced *ALK* mRNAs, not cross-hybridizing transcripts of other *PTK* genes. *ALK* transcripts were not detected in Northern analysis of RNA prepared from hematopoietic cells, including normal spleen, thymus, peripheral blood leukocytes, B lymphoblastoid cell lines, phytohemagglutinin-stimu-

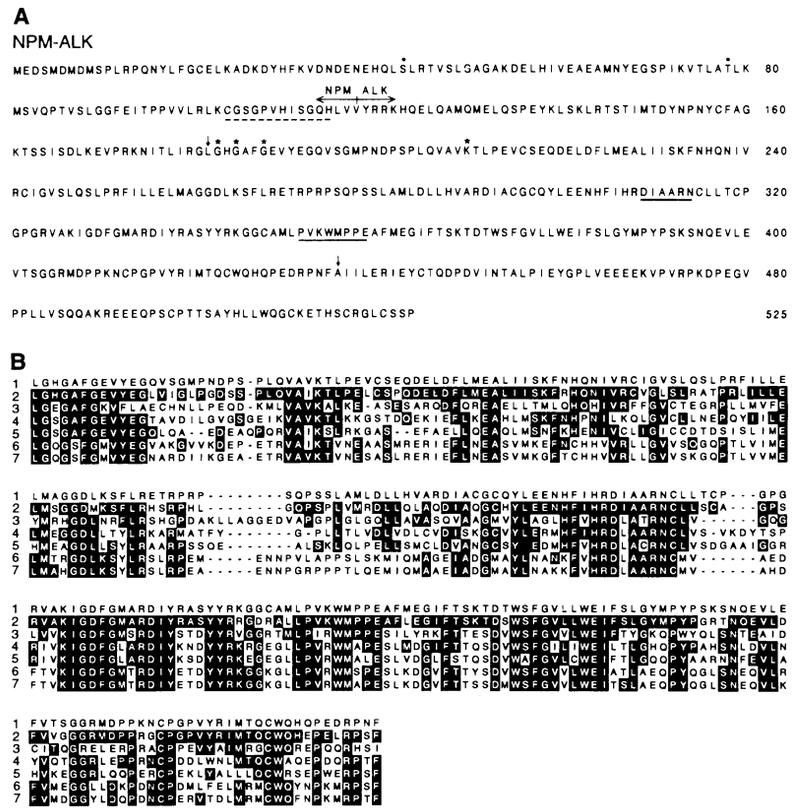

Fig. 2. (**A**) Deduced amino acid sequence of NPM-ALK (*20*). Solid circles, potential phosphorylation sites for protein kinase C; dashed underline, potential metal binding domain; arrows, boundaries of the ALK catalytic domain; asterisks, conserved residues of the consensus adenosine triphosphate (ATP) recognition sequence and the ATP-binding lysine residue; and solid underlines, consensus sequences specific for tyrosine kinases. (**B**) Alignment of the ALK catalytic domain with those in the insulin receptor subfamily of PTKs. Line 1, ALK; line 2, LTK; line 3, TRKA; line 4, ROS; line 5, Sevenless; line 6, IGF-1 receptor; and line 7, IR. Gaps are indicated by dashes, and amino acid identity is indicated by shaded boxes. All sequences are for human proteins, except for Sevenless, which is a *Drosophila* protein (*10*).

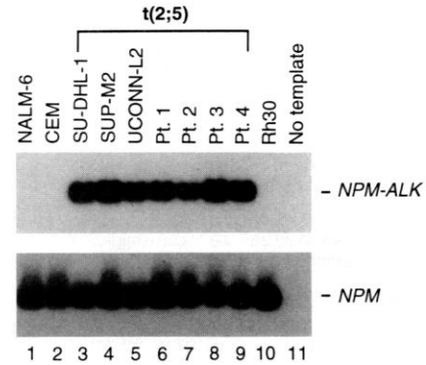

Fig. 3. Southern blot analysis of *NPM-ALK* and *NPM* RNA-PCR products. Total RNAs (1 μg) from t(2;5)-positive cell lines (SU-DHL-1, SUP-M2, and UCONN-L2) and patient (Pt.) samples (1 to 4) were analyzed. RNAs from the t(2;5)-negative B and T lymphoid leukemia cell lines (NALM-6 and CEM, respectively) and the Rh30 rhabdomyosarcoma cell line, which expresses normal *ALK*, were included as negative controls, as was a blank without an RNA template.

lated T lymphocytes, or t(2;5)-negative leukemia-lymphoma cell lines of myeloid or B or T lymphoid derivation.

FISH mapping indicated that *NPM* and *ALK* are transcribed in centromeric to telomeric orientations on chromosomes 5 and 2, respectively, with the 2.4-kb fusion transcript arising from the derivative 5 translocated chromosome. Northern blot analysis provided no evidence for expression of a reciprocal *ALK-NPM* chimeric transcript, which could have been generated from the derivative 2 chromosome.

An RNA-based polymerase chain reaction (RNA-PCR) method (*12*) confirmed the specificity of the fusion junctions in chimeric transcripts expressed in lymphomas having the t(2;5) (Fig. 3). Conversely, fusion transcripts were not detected in t(2;5)-negative cell lines, including several rhabdomyosarcoma lines that expressed *ALK* transcripts. Identical *NPM-ALK* junction sequences were found in the RNAs of all seven t(2;5)-positive samples, including the SU-DHL-1, SUP-M2, and UCONN-L2 cell lines and diagnostic samples from four patients with anaplastic large-cell lymphomas (*13*). The breakpoints of the 2;5 translocation therefore appear to consistently involve the same introns of the *NPM* and *ALK* genes, leading to identical junctions in the fusion mRNAs.

The normal NPM protein is a nonribosomal nucleolar phosphoprotein involved in the assembly of preribosomal particles into both small and large ribosomal subunits (*7*). It binds cooperatively with high affinity to single-stranded nucleic acids, exhibits activity that destabilizes the RNA helix, and is found in association with the most mature nucleolar preribosomal ribonucleoproteins (*14*). *NPM* transcription and translation are cell cycle–regulated, reaching peak levels just before the entry of the cells into the S phase, with a decline to the base line just before the onset of the G_2 phase (*15*). We postulate that the *NPM* gene contributes an active promoter to drive expression of the ALK catalytic domain in lymphoma cells containing the t(2;5). This role for *NPM* would appear to be crucial, because the *ALK* promoter is normally silent in lymphoid cells. An oncogenic role, if any, remains to be established for the NH_2-terminal *NPM* coding sequences incorporated into NPM-ALK, including those encoding potential protein kinase C phosphorylation sites (Ser^{43} and Thr^{78}) and a potential Cys-X_5-His-X_4-His metal binding motif (residues 104 to 115, where X is any amino acid) (*7*).

A consistent feature of tyrosine kinase oncogenes, including *TRKA, BCR-ABL, EGFR, ERBB2, CSF-1R,* and *LCK,* is that much of their potency can be attributed to mutations or gene fusions that lead to a constitutively active catalytic domain (*16*). Thus, in NPM-ALK fusion proteins, one would predict that the truncated ALK is deregulated and phosphorylates intracellular substrates to trigger malignant transformation. Anaplastic large-cell lymphomas arise from activated T lymphocytes, which depend on IL-2 for growth and viability (*17*). Conceivably, NPM-ALK phosphorylates substrates that are normally phosphorylated in response to IL-2 receptor– or T cell receptor–mediated signals (*18*), leading to constitutive activation of one of these signal transduction pathways.

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isolated microdissection clones from bands 5q34-q35 and used them to identify 39 cosmid clones [D. Saltman *et al.*, *Nucleic Acids Res.* **20**, 1401 (1992)], which then were oriented by FISH analysis of metaphase chromosomes from the SUP-M2 and SU-DHL-1 t(2;5)-positive cell lines [R. Morgan *et al.*, *Blood* **73**, 2155 (1989)]. Seventeen clones mapped centromeric and 22 clones telomeric to the breakpoint; clones from these groups were oriented relative to one another by two-color metaphase FISH analysis. The estimated genomic distance between the two cosmids that flanked the breakpoint most closely was 290 kb by interphase FISH analysis [J. B. Lawrence, R. H. Singer, J. A. McNeil, *Science* **249**, 928 (1990); B. Trask *et al.*, *Am. J. Hum. Genet.* **48**, 1 (1991)]. Probes prepared from these cosmids did not detect rearranged restriction fragments by Southern (DNA) blot analysis of pulsed-field gels containing DNA from t(2;5)-positive cell lines.

6. The genomic fragment p16-3/1.2S is located immediately centromeric to the chromosome 5 breakpoint, whereas fragment p21-3/3E lies just telomeric to the break. Both probes identified a 1.6-kb transcript in Northern analysis of RNAs prepared from t(2;5)-positive and t(2;5)-negative cell lines; in addition, p16-3/1.2S hybridized to a 2.4-kb transcript found only in t(2;5)-positive cells.
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19. The faint ~4-kb RNAs detected by pS1.2 in the t(2;5)-positive cells represent cross-hybridization of the probe with the 28*S* ribosomal RNA.
20. The nucleotide sequence of *NPM-ALK* (accession number UO4946) has been deposited in GenBank. Abbreviations for the amino acid residues are: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.
21. We thank A. Sinclair and J. Sublett for technical assistance; M. Lovett for support and advice; L. Deaven for the chromosome 5 cosmid library; J. Gilbert for editorial review; PC&T for their unwavering support; K. Williams, J. T. Sandlund, F. Behm, D. Head, and J. Whitlock for help with clinical lymphoma samples; and J. Cleveland, J. Downing, V. Kidd, J. Ihle, A. Nienhuis, and C. Sherr for critical review of the manuscript. Supported by National Cancer Institute grants KO8 CA 01702, PO1 CA 20180, and Core grant CA 21765, and by the American Lebanese Syrian Associated Charities of St. Jude Children's Research Hospital.

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Diversity of Endogenous Epitopes Bound to MHC Class II Molecules Limited by Invariant Chain

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The invariant chain (Ii) binds nascent major histocompatibility complex (MHC) class II molecules, blocking peptide binding until the complex dissociates in the endosomes. This may serve to differentiate the MHC class I and II antigen presentation pathways and enable class II molecules to efficiently bind peptides in the endosomes. This hypothesis was addressed by probing spleen cells from a combination of knock-out and transgenic mice with a large panel of T cell hybridomas. The Ii molecule blocked the presentation of a range of endogenously synthesized epitopes, but some epitopes actually required Ii. Thus, the influence of Ii on presentation does not follow simple rules. In addition, mice expressing Ii were not tolerant to epitopes unmasked in its absence, a finding with possible implications for autoimmunity.

The primary function of MHC class II molecules is to present peptides to $CD4^+$ T cells, often those derived from foreign, endocytosed proteins and encountered by class II molecules as they traffic through endocytic vesicles (*1*). In theory, peptides from exogenous antigen must compete for presentation with the vast quantities of endogenous proteins that transit through the endoplasmic reticulum (ER) and Golgi compartments and are known to engender MHC-binding peptides (*1–3*). It has been hypothesized that efficient loading of class II molecules in the ER and Golgi is prevented by Ii, a transmembrane protein that targets class II molecules to endosomes (*4–6*) and interferes with MHC class II–peptide interactions (*7*). However, this hypothesis has been challenged as unnecessary because many class II–peptide interactions are inefficient at the neutral pH of the ER and Golgi, requiring the more acidic conditions of the endosomes (*8*). In addition, recent studies on mice lacking Ii showed that, in the absence of Ii, class II molecules have a conformation which suggests that they are empty of peptide (*5, 6*). We have evaluated the effect of Ii on the presentation of endogenous proteins, using bona fide antigen-presenting cells (APCs) from mice derived by crossing a line devoid of Ii with transgenic lines expressing a segment of myelin basic protein (MBP) under the control of an MHC class II gene promoter. Processing and presentation of the various epitopes within the transgenic MBP segment was read out with a panel of MBP-reactive T cell hybridomas.

Mutant mice lacking the invariant chain (Ii^o) have been described previously (*5*). When crossed onto the $H\text{-}2^s$ genetic background, the Ii^o mutation leads to somewhat reduced A^s surface levels but full ability to present exogenous peptide, as when carried on the $H\text{-}2^b$ background (*5, 6*). Transgenic mice expressing a fragment of MBP (Tg) were produced as part of another study and will be described in detail elsewhere (*9*). As illustrated in Fig. 1A, they produce a chimeric protein consisting of residues 84 to 105 of MBP [MBP(84–105)] inserted between position 43 and 44 of hen egg lysozyme (HEL), selected as a relatively innocuous carrier. This MBP fragment contains several overlapping epitopes recognizable in the context of A^s and characterized extensively in past studies (*10*) and that can be distinguished with the peptides shown in Fig. 1B. The chimeric proteins are expressed in secreted form with the HEL signal sequence (sLM43) or are membrane-anchored as a result of fusion with the transmembrane and cytoplasmic domains of influenza A virus hemagglutanin (mLM43). Expression is driven by the MHC class II Eα promoter, which directs transcription in the thymus and in

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