

# Παθογένεια Ρευματοειδούς Αρθρίτιδας



ΠΑΝΕΠΙΣΤΗΜΙΑΚΟ  
ΝΟΣΟΚΟΜΕΙΟ ΗΡΑΚΛΕΙΟΥ

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ΠΑΝΕΠΙΣΤΗΜΙΟ ΚΡΗΤΗΣ  
ΙΑΤΡΙΚΗ ΣΧΟΛΗ



# References

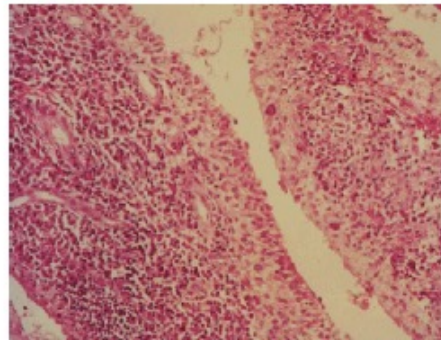
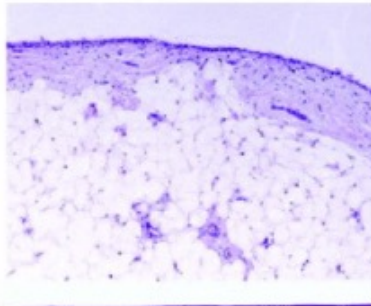
- Nat Immunol. 2021 Jan;22(1):10-18
- Sci Transl Med. 2016 Mar 23;8(331):331ra38
- Immunity. 2016, 45, 903–916
- Cell Metabolism. 2019, 30, 1–16
- Nat Immunol. 2019 Jul;20(7):928-942
- Nat Rev Immunol. 2017 Jan;17(1):60-75.

# Outline

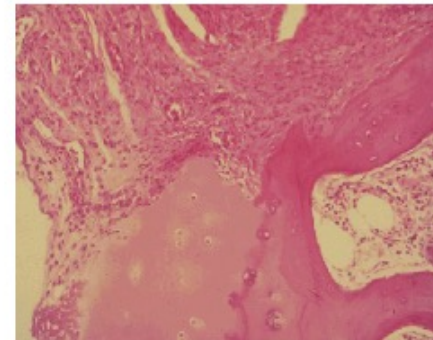
- Autoimmunity development in RA
  - Genes
  - Environment
  - Autoimmunity
  - Citrullination
- Synovial targeting
  - CD4
  - Fibroblasts
  - Macrophages/monocytes

# Rheumatoid arthritis target tissue of inflammation: Synovium

Normal



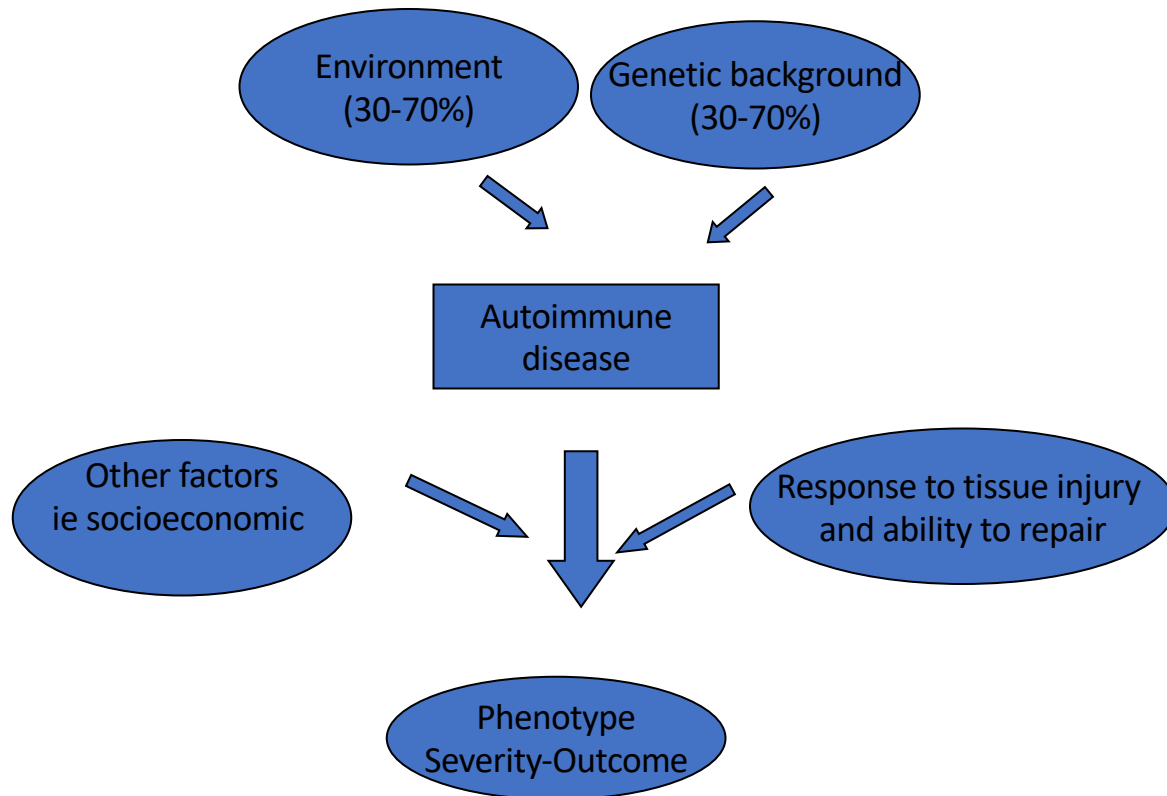
**Pathophysiological  
process:**



Tissue hyperplasia  
Inflammatory cell infiltration  
Angiogenesis  
Bone destruction

The cause of autoimmune disease is generally unknown.

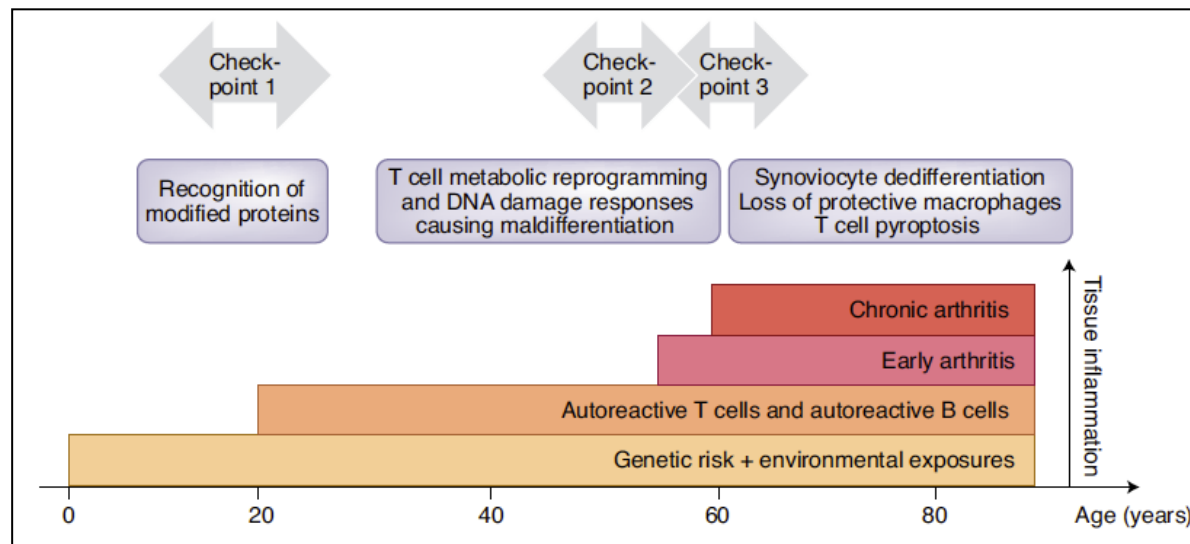
Tissue damage pathogenesis is complex but rather well characterized



# General concept for RA pathogenesis

“RA is an almost lifelong process in with distinct phases:

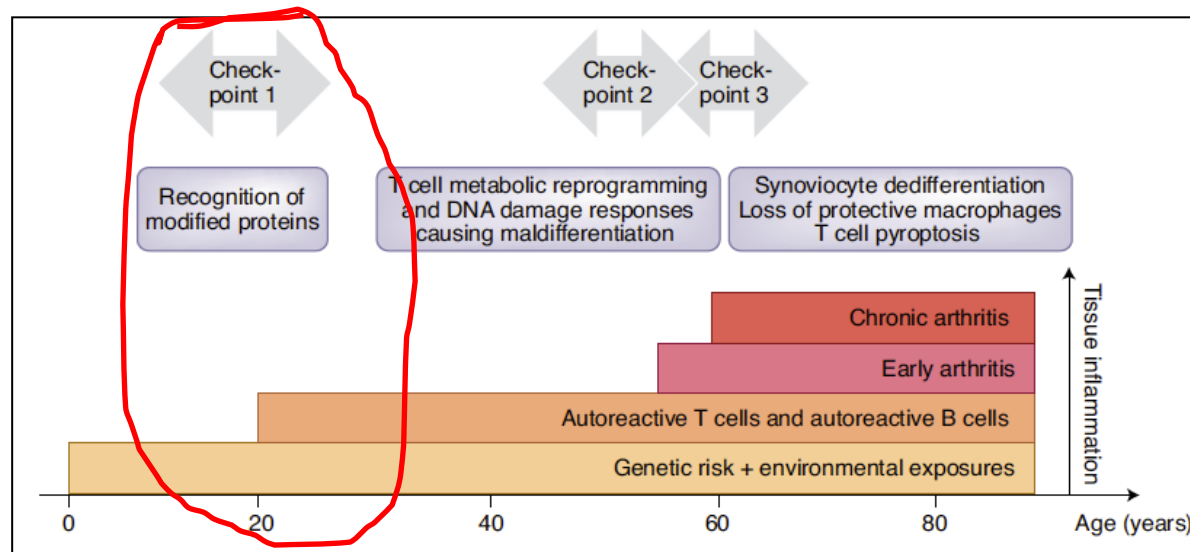
- ✓ **disease risk:** genetically predisposed individuals lose self-tolerance, produce autoantibodies.
- ✓ **asymptomatic autoimmunity:** characterized by prototypic autoantibodies reactive against post-translationally modified proteins, often citrullinated antigens.
- ✓ **symptomatic synovitis:** Acute joint inflammation transitions into chronic, destructive synovitis. Tissue responds with a maladaptive wound healing response (pannus), which by itself has destructive features and will lead to irreversible tissue injury”



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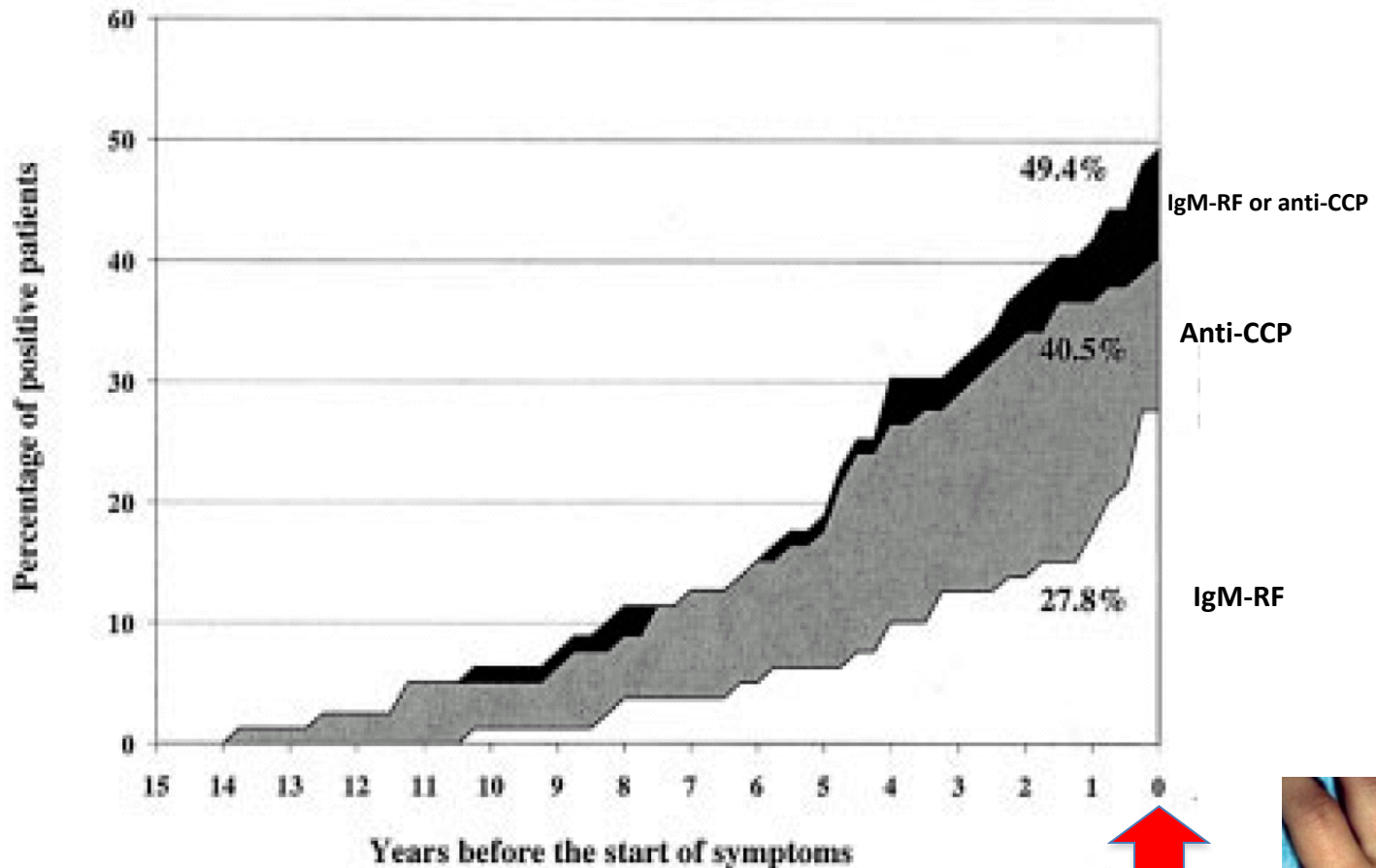
“RA is an almost lifelong process in with distinct phases:

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# Autoimmunity in RA starts long before symptoms:

ACPA (anti citrullinated peptide antibodies) and RFs (Rheumatoid factors) decades before symptoms



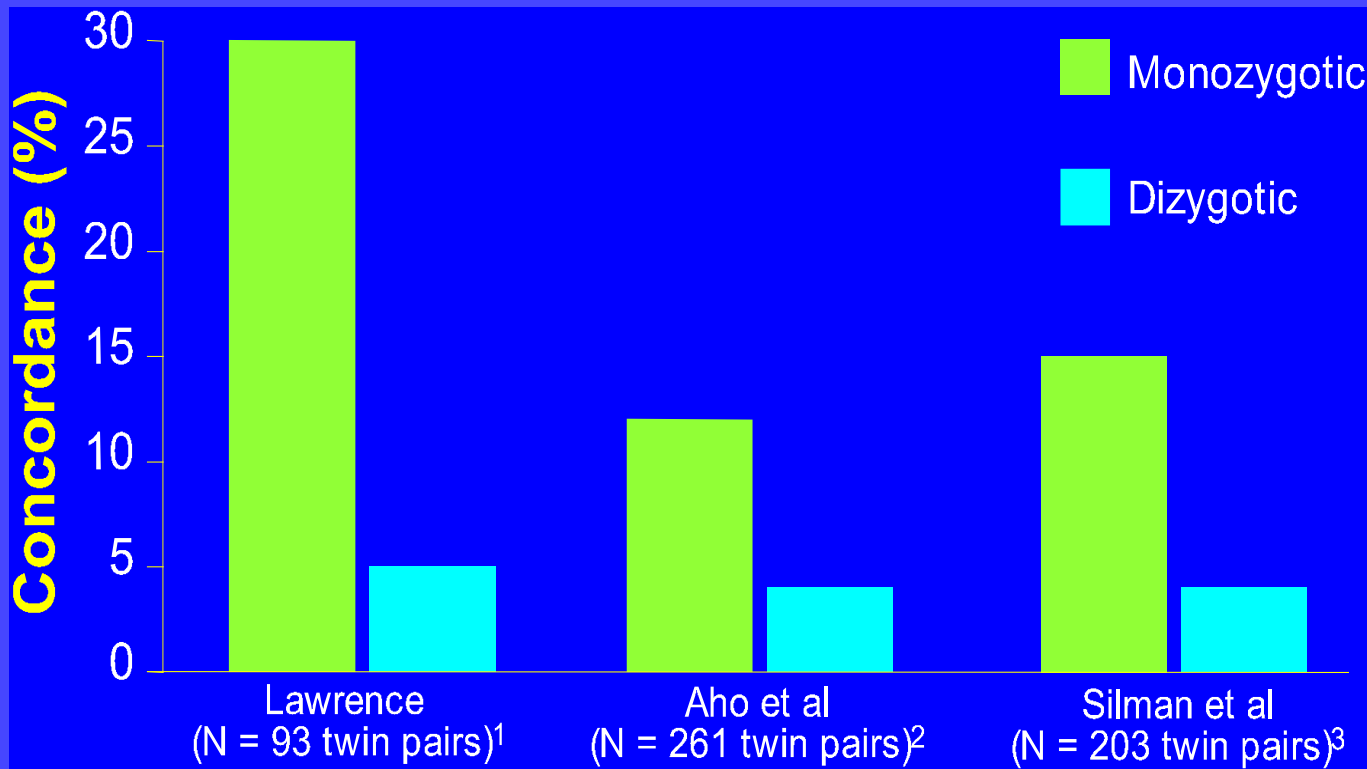
Arthritis!!!





# Twin Studies in Rheumatoid Arthritis:

Increased incidence in twins and in families with affected members



1. Lawrence JS. *Ann Rheum Dis*. 1970;28:357-379.

2. Aho K et al. *J Rheumatol*. 1986;13:899-902.

3. Silman AJ et al. *Br J Rheumatol*. 1993;32:903-907.

# Genetic risk for RA:

## Major contribution of HLA-DR

- Studies in twins → genetic contribution to RA accounts for **~60%** of the variation in liability to disease.
- The most important genetic risk : class **MHC class II** region (HLA-DR).
- MHC contribute **18–37%** of the total genetic susceptibility to RA, increasing disease liability **4–6-fold**.
- For **ACPA +ve RA**: **HLA-DRβ1** and two additional amino acid positions in **HLA-B** and **HLA-DP** in conferring risk to anti-CCP–positive rheumatoid arthritis.
  - These variants account for **12.7%** of the phenotypic variance of seropositive RA risk
  - common validated alleles outside the MHC explain **~4%** of this variance



# Shared Epitope Hypothesis

## Alleles Associated with Rheumatoid Arthritis

	67	68	69	70	71	72	73	74
DR4/Dw4 ( $\beta 1^*0401$ )	L	L	E	Q	K	R	A	A
DR4/Dw14 ( $\beta 1^*0404$ )	L	L	E	Q	R	R	A	A
DR4/Dw15 ( $\beta 1^*0405$ )	L	L	E	Q	R	R	A	A
DR1 ( $\beta 1^*0101$ )	L	L	E	Q	R	R	A	A
DR16 ( $\beta 1^*0401$ )	L	L	E	Q	R	R	A	A

# Shared epitope hypothesis

All *HLADRB1* alleles associated with RA risk encode a conserved sequence of 5 amino acids (positions 70–74) that surrounds the **peptide-binding pocket** of the antigen-presenting molecule.

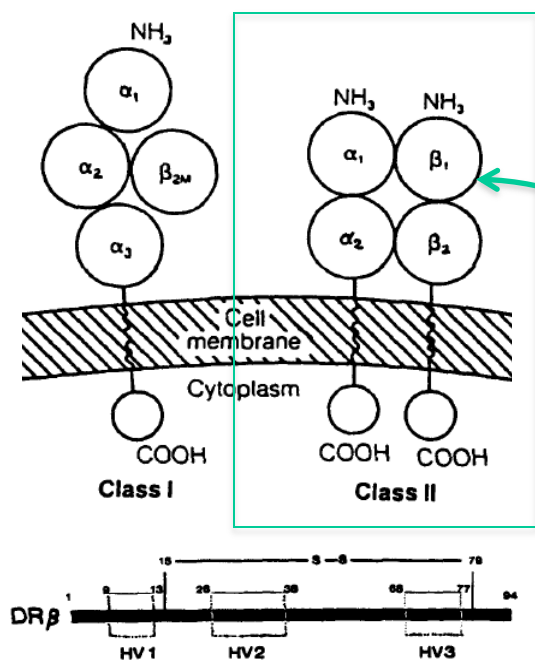


Figure 2. Top, Schematic diagram comparing the structural features of class II molecules at the cell surface with those of class I molecules. Bottom, The first domain, which contains regions of variability that alternate with invariant regions.

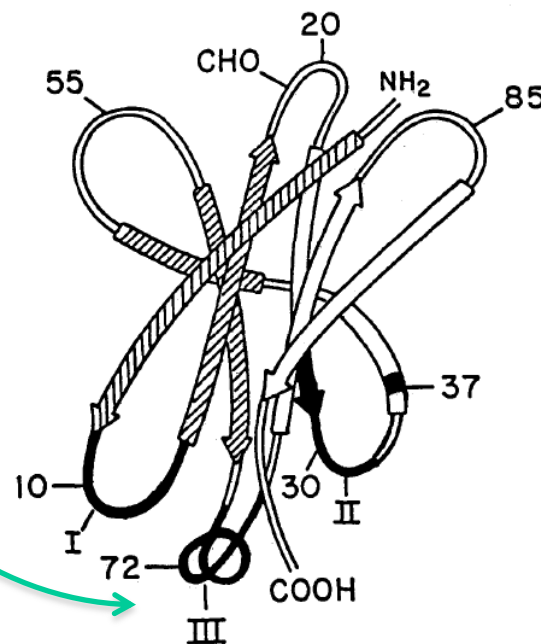
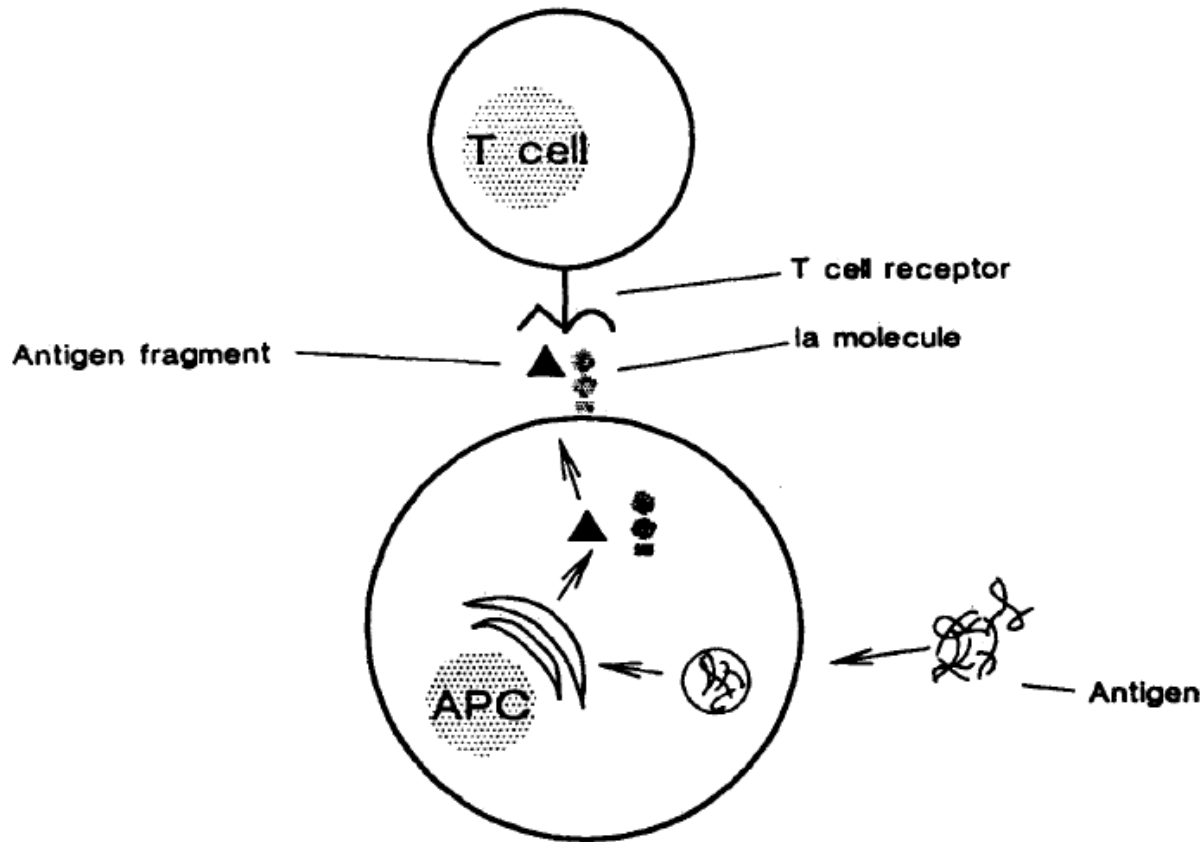


Figure 4. The predicted 3-dimensional structure of a class II β chain. Note that the third hypervariable region around position 70 is predicted to contain a region of α helical structure. It is this region which differs among the DR4 subtypes. Adapted from the *Scandinavian Journal of Immunology* (Norcross and Kanehisa [4]), copyright 1985, and used with the permission of Blackwell Scientific Publications.

# Shared epitope hypothesis

The presence of this shared epitope suggests that the molecules containing it might:

- ✓ bind the **same antigen**, induce altered T-cell–antigen presenting cell interactions,
- ✓ and/or shape the T-cell repertoire participating in broader adaptive immune responses.



RA related Genes → autoimmunity

Τα HLA-DRB1 αλληλόμορφα σχετίζονται ΜΟΝΟ με ACPA θετική νόσο!

# Genetic association to autoimmunity

Shared Epitope alleles (HLA-DRB1) are associated with development of anti-CCP (and RFs) antibodies and thus only to seropositive

**Table 1.** Distribution of SE and anti-CCP positivity\*

SE	Dutch controls (n = 423), no. (%)	Dutch EAC RA patients			
		Anti-CCP positive (n = 195)		Anti-CCP negative (n = 213)	
		No. (%)	OR (95% CI)	No. (%)	OR (95% CI)
+/+	26 (6)	49 (25)	11.79 (6.58–21.13)	16 (8)	1.38 (0.71–2.67)
+/-	153 (36)	107 (55)	4.37 (2.88–6.65)	88 (41)	1.29 (0.91–1.82)
-/-	244 (58)	39 (20)	1.0	109 (51)	1.0

\* The following alleles were classified as shared epitope (SE) positive: DRB1\*0101, \*0102, \*0104, \*0401, \*0404, \*0405, \*0408, \*0413, \*0416, \*1001, and \*1402 (4). EAC = Early Arthritis Clinic; RA = rheumatoid arthritis; CCP = cyclic citrullinated peptide; OR = odds ratio; 95% CI = 95% confidence interval.

# Mechanism of the shared epitope / ACPA-association:

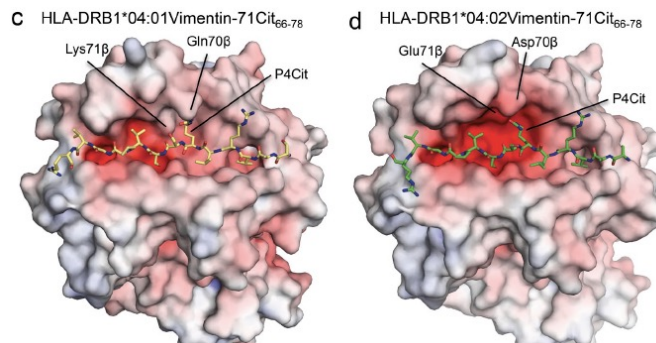
*DR-B1 alleles bind more avidly citrulline-containing peptides*

- It is partly attributable to the finding that **citrulline-containing peptides bind more avidly than unmodified molecules to the binding pocket of DRB1** molecules that contain the epitope, with subsequent activation of CD4+ T cells.

*J. Immunol.* 171, 538–541 (2003).

- The shared epitope also seems to function as an **immunostimulatory** ligand that polarizes T-cell differentiation towards type 17 T helper (TH17) cells, which are associated with autoimmunity.

*J. Immunol.* 185, 1927–1934 (2010).



*J. Exp. Med.* 2013 Vol. 210 No. 12 2569



# Genes → T cell function: HLA-DR4+ & T cell dysfunction

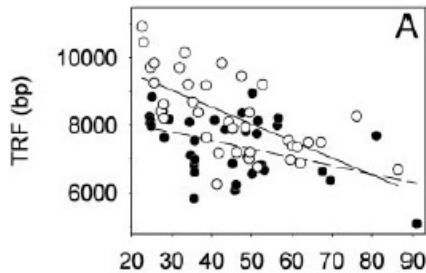
## HLA-DRB1 alleles are associated to T-cell senescence

Premature telomeric loss in rheumatoid arthritis is genetically determined and involves both myeloid and lymphoid cell lineages

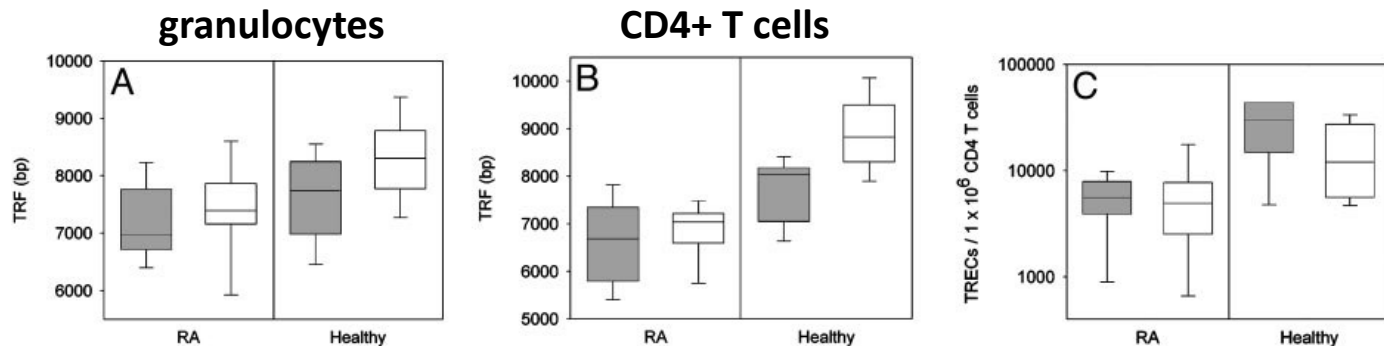
Stefan O. Schönland<sup>†</sup>, Consuelo Lopez<sup>†‡</sup>, Thomas Widmann<sup>†‡</sup>, Julia Zimmer<sup>†</sup>, Ewa Bryl<sup>†</sup>, Jörg J. Goronzy<sup>†§</sup>, and Cornelia M. Weyand<sup>†§¶</sup>

### HLA-DR4 Affects Telomeric Length in CD4 T Cells

HLA-DR4<sup>+</sup> (●) HLA-DR4<sup>-</sup> (○)



### Premature telomeric erosion in lymphocytes and granulocytes and decreased frequencies of TREC T cells in patients with RA.



HLA-DR4<sup>-</sup> (white) and HLA-DR4<sup>+</sup> (gray)

# RA - Genetic susceptibility of non-HLA genes

MHC: makes up 12.7% of total genetic variance

Non-MHC: makes up ~4% of total genetic variance

**Table 1. Candidate Genes with Single-Nucleotide Polymorphisms (SNPs) Linked to Rheumatoid Arthritis and Their Potential Function in Pathogenesis.\***

Candidate Gene and Pathway	SNP Locus	Function Relevant to Pathogenesis
<b>T-cell activation</b>		
<i>HLA-DRB1</i> †	6p21	HLA DRB1 allele (also known as the shared epitope) involved in MHC molecule-based antigen presentation and responsible for self-peptide selection and T-cell repertoire; first discovered and still by far the strongest genetic link to rheumatoid arthritis
<i>PTPN22</i>	1p13.2	Lymphocyte-specific nonreceptor tyrosine phosphatase involved in regulation of activation threshold of lymphocytes; second genetic link described in rheumatoid arthritis
<i>AFF3</i>	2q11.2	Transcription factor for lymphoid development
<i>CD28</i>	2q33.2	Costimulatory molecule for T-cell activation
<i>CD40</i>	20q13.12	Costimulatory molecule that enhances interactions between T and B cells and increases auto-antibody production
<i>CTLA4</i>	2q33.2	Costimulation suppressor that regulates interactions between T cells and antigen-presenting cells
<i>IL2RA</i>	10p15.1	High-affinity receptor for interleukin-2 on lymphocyte subsets
<i>IL2</i>	4q27	Cytokine that regulates activation of T cells, particularly regulatory T cells
<i>IL-21</i>	4q27	Cytokine that regulates differentiation of T cells, particularly Th17, and activation of B cells
<i>PRKQC</i>	10p15.1	Member of the protein kinase C family that regulates T-cell and macrophage activation
<i>STAT4</i>	2q32.3	Transducer of cytokine signals that regulate proliferation, survival, and differentiation of lymphocytes
<i>TAGAP</i>	6q25.3	Rho-GTPase enzyme involved in T-cell activation

# RA - Genetic susceptibility of non-HLA genes

**Table 1.** Candidate Genes with Single-Nucleotide Polymorphisms (SNPs) Linked to Rheumatoid Arthritis and Their Potential Function in Pathogenesis.\*

Candidate Gene and Pathway	SNP Locus	Function Relevant to Pathogenesis
<b>NF-<math>\kappa</math>B pathway</b>		
<i>REL</i>	2p16.1	Proto-oncogene member of the NF- $\kappa$ B family that regulates leukocyte activation and survival
<i>TNFAIP3</i>	6q23.3	Signaling protein and negative regulator of TNF- $\alpha$ -induced NF- $\kappa$ B activation
<i>TRAF1</i>	9q33.1	Regulator of TNF- $\alpha$ -receptor superfamily signaling (e.g., to NF- $\kappa$ B and JNK)
<b>Other pathways</b>		
<i>BLK</i>	8p23.1	B-lymphoid tyrosine kinase involved in B-cell receptor signaling and B-cell development
<i>CCL21</i>	9q13.3	Chemokine implicated in germinal-center formation
<i>FCGR2A</i>	1q23.2	Low-affinity IgG Fc receptor that regulates macrophage and neutrophil activation and immune-complex clearance
<i>PADI4</i>	1p36.2	Enzyme that converts arginine to citrulline, creating autoantigens in rheumatoid arthritis
<i>PRDM1</i>	6q21	Protein that acts as a repressor of $\beta$ -interferon gene expression
<i>TNFRSF14</i>	1p36.32	TNF- $\alpha$ -receptor superfamily member with proinflammatory activity

## Complex interactions:

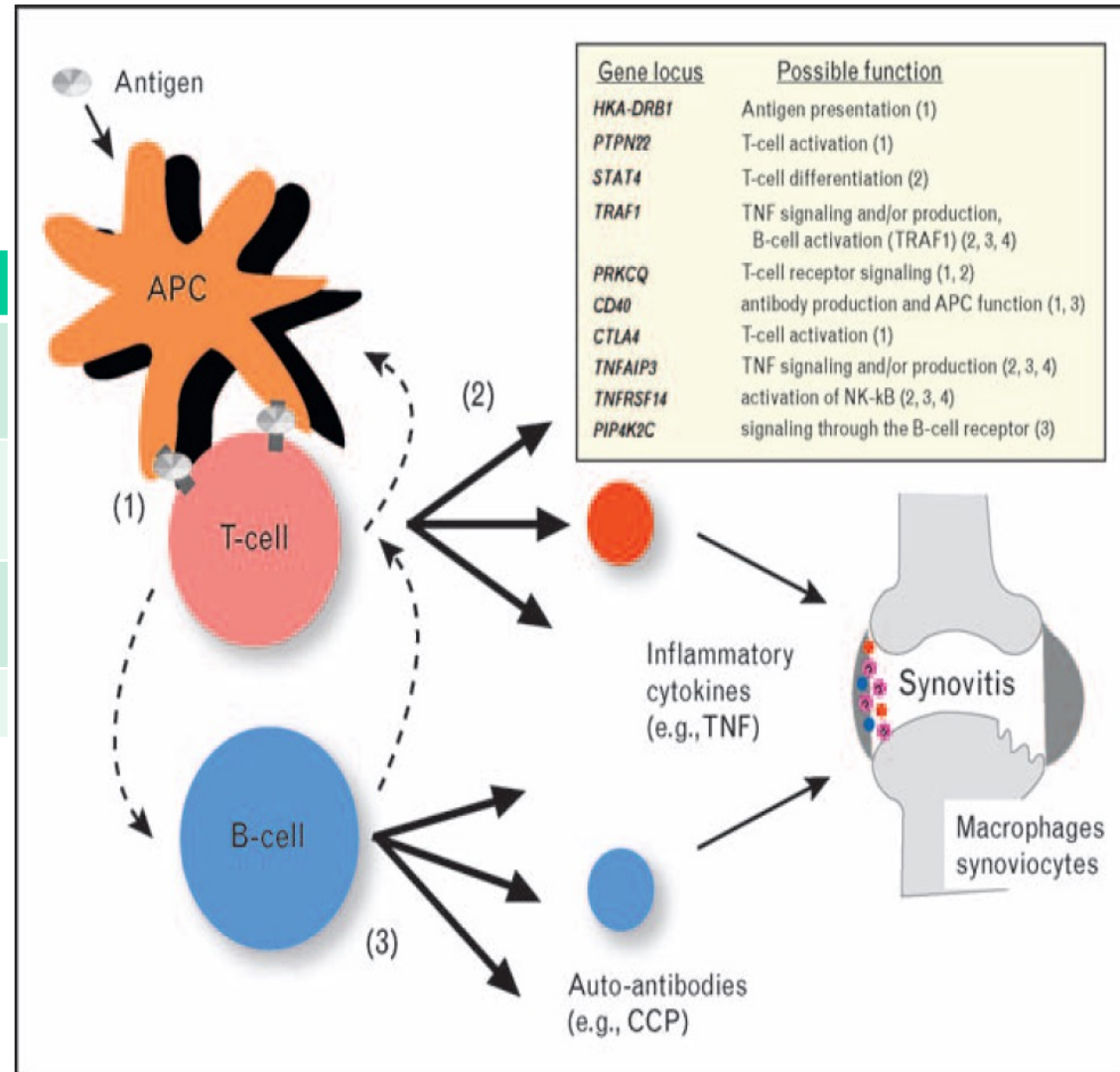
Gene–gene interactions that increase disease risk, as described between *HLA-DRB1* and *PTPN22*, exemplify the complexity of the net risk conferred by any given gene

## Genetics /Autoimmunity / Clinical correlations:

The above genetic background, mainly for ACPA + patients

# Genes & RA pathogenesis

Function	Genes
Antigen presentation	<i>DRB1, CD40</i>
T-cell activation/ differentiation	<i>PTPN22, STAT4, CTLA4, TNFAIP3</i>
Ab production	<i>TRAF1, CD40, TNFAIP3, PIP4K2C</i>
Inflammation	<i>TRAF1, TNFAIP3</i>

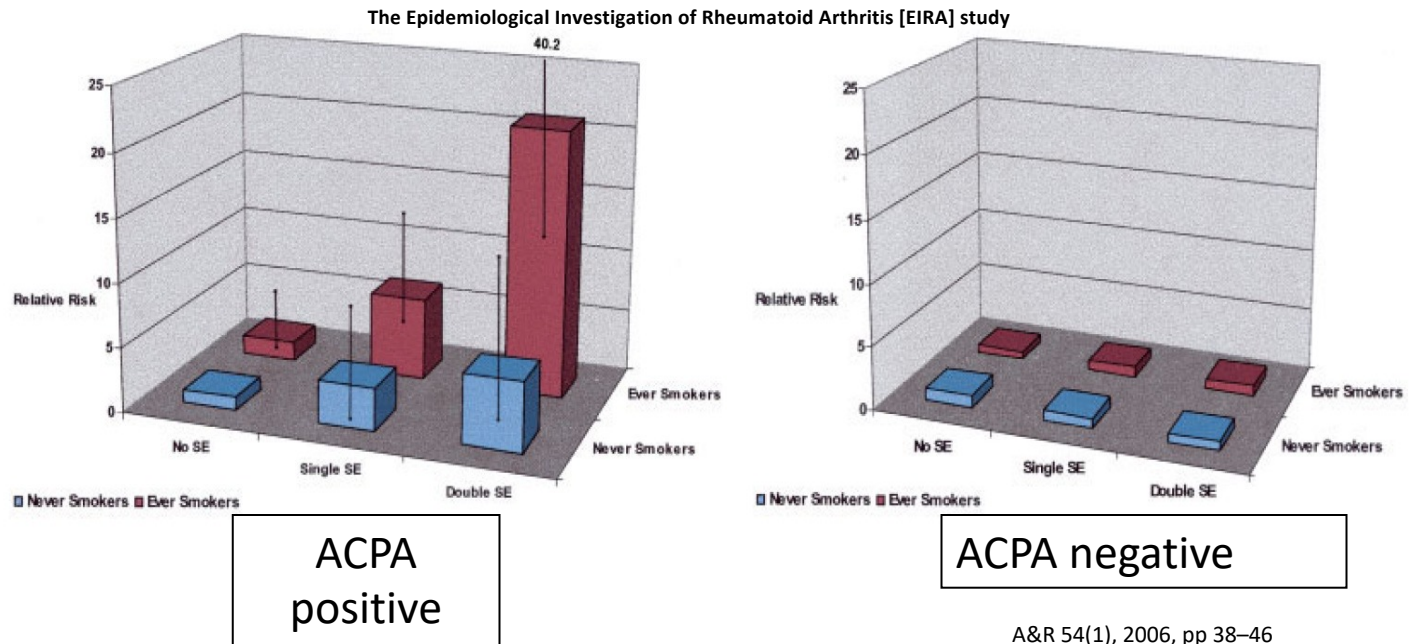


# Environment and gene interaction in autoimmunity/ disease development

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**Smoking** increased the risk of **developing ACPA** only in HLA-SE RA carriers

Relative risk of developing rheumatoid arthritis (RA) in subjects exposed to different combinations of smoking and HLA-DR shared epitope (SE) genes



If not in the joints where autoimmunity starts?

# If not in the joints where autoimmunity starts?

- **Mucosal tissue sites** and **neutrophil extracellular traps** may provide relevant contextual signals through which **citrullinated antigens** gain immunogenicity, supporting that early steps of tolerance loss may occur in the lung and the gut.
- Nevertheless, how tolerance to the modified peptides is broken remains unclear, and a common denominator is not clear



# Lung as the site of citrullination and initial ACPA development

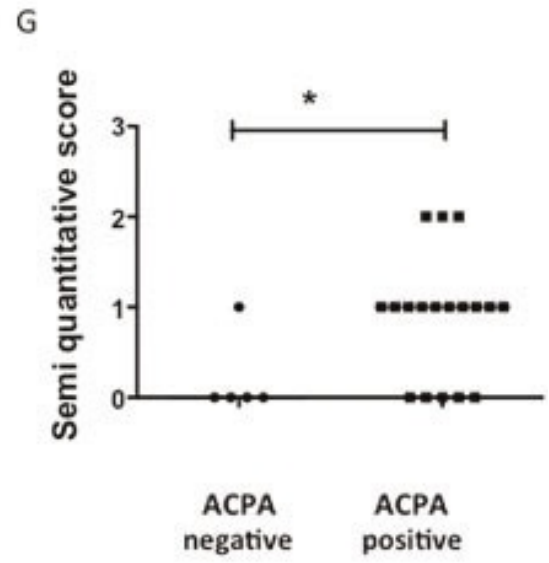
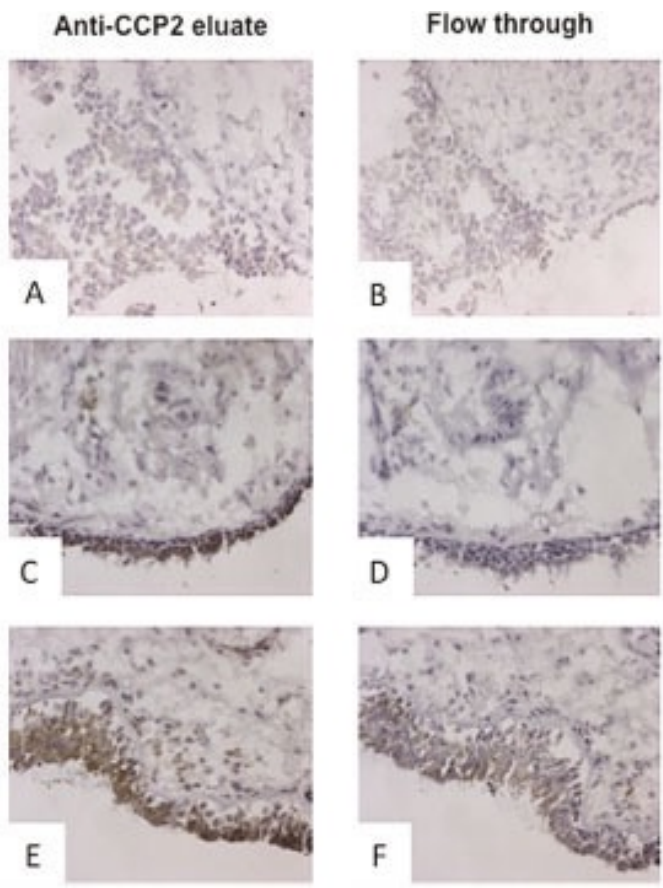
Early, untreated ACPA +ve RA exhibit higher levels of expression of the citrullinated protein in large bronchial biopsy tissue.

RA patients

ACPA negative non-smoker

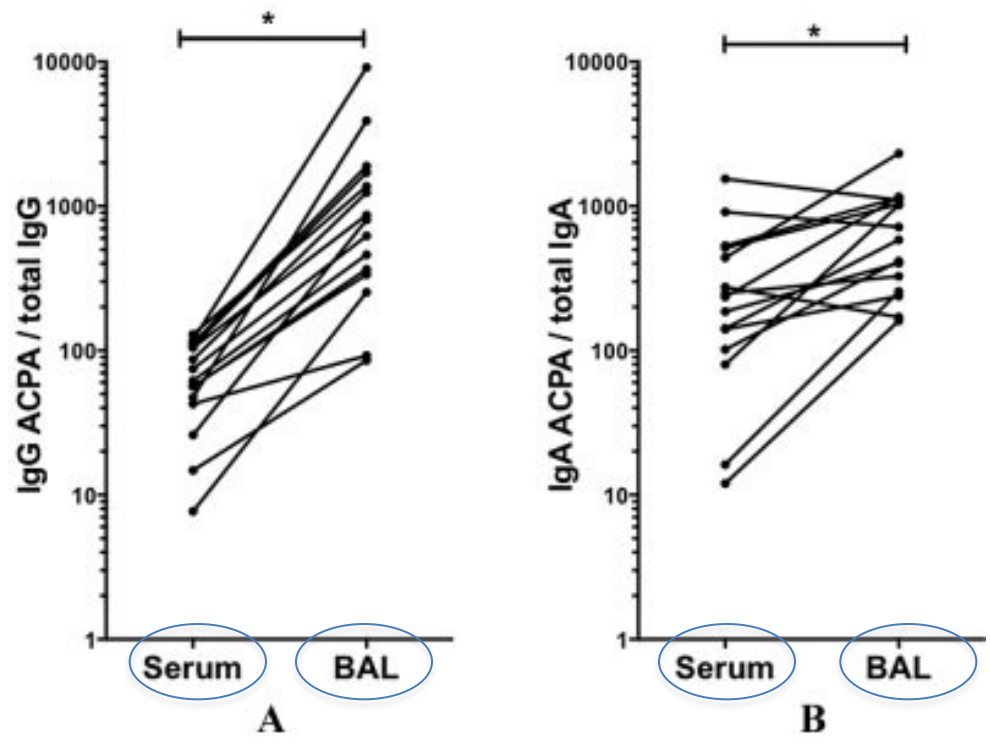
ACPA positive non-smoker

ACPA positive smoker



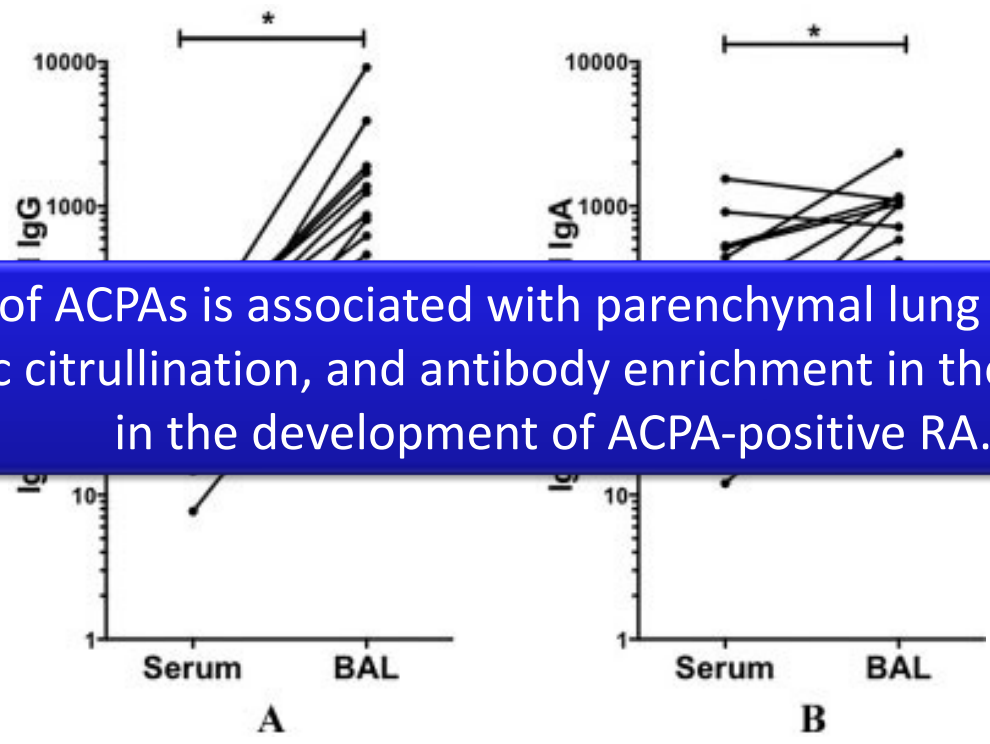
# Lung as the site of citrullination and initial ACPA development

Enrichment of ACPAs in the lungs vs serum of ACPA-positive patients with early, untreated RA



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Enrichment of ACPAs in the lungs vs serum of ACPA-positive patients with early, untreated RA



The presence of ACPAs is associated with parenchymal lung abnormalities, site-specific citrullination, and antibody enrichment in the lungs early in the development of ACPA-positive RA.

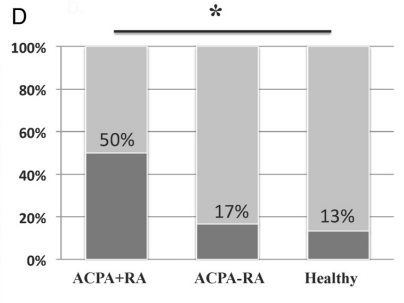
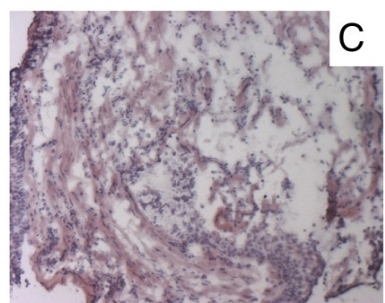
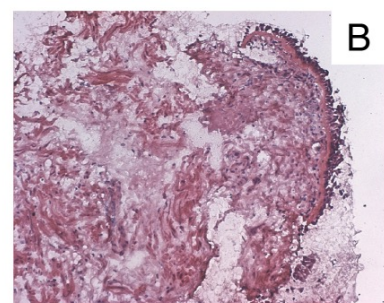
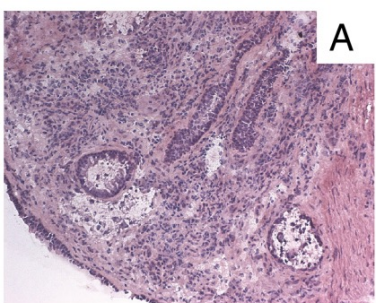
# Immune activation in BAL and bronchial biopsies of patients with early untreated ACPA-positive RA

## Lymphocytic infiltration in the bronchial biopsies of patients with ACPA-positive untreated early rheumatoid arthritis

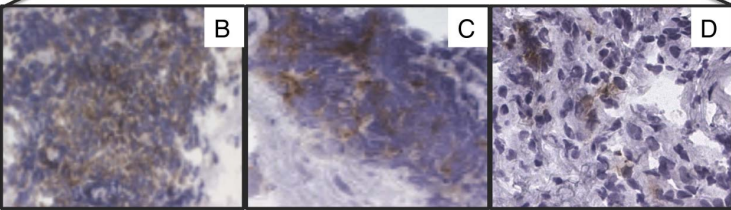
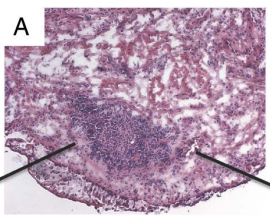
ACPA+RA

ACPA-RA

Healthy



■ No lymphocyte infiltrate  
■ Lymphocyte infiltrate



Germinal centre-like structures are present in bronchial biopsies

AID

CD19

CD138



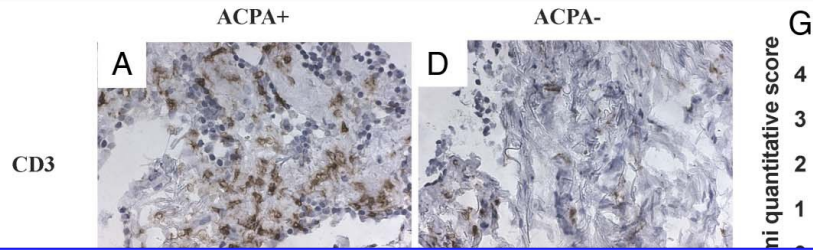
arg-enolase

cit-enolase

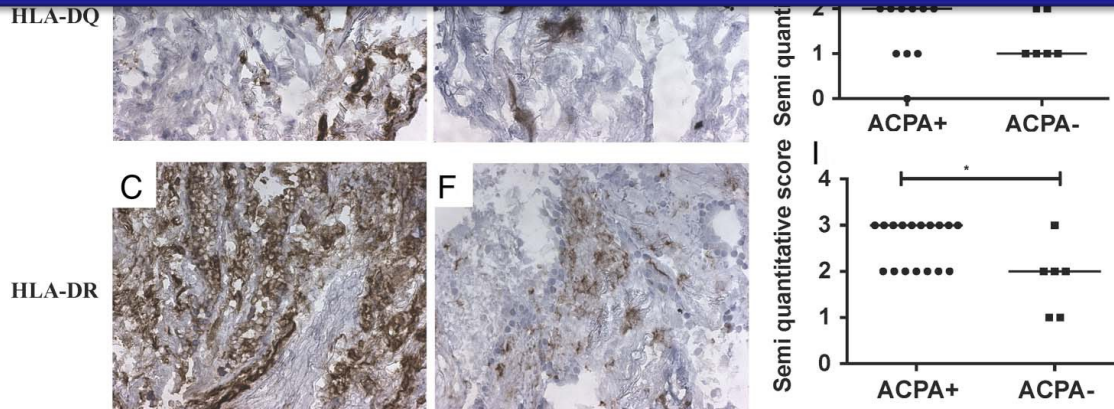


# Immune activation in BAL and bronchial biopsies of patients with early untreated ACPA-positive RA

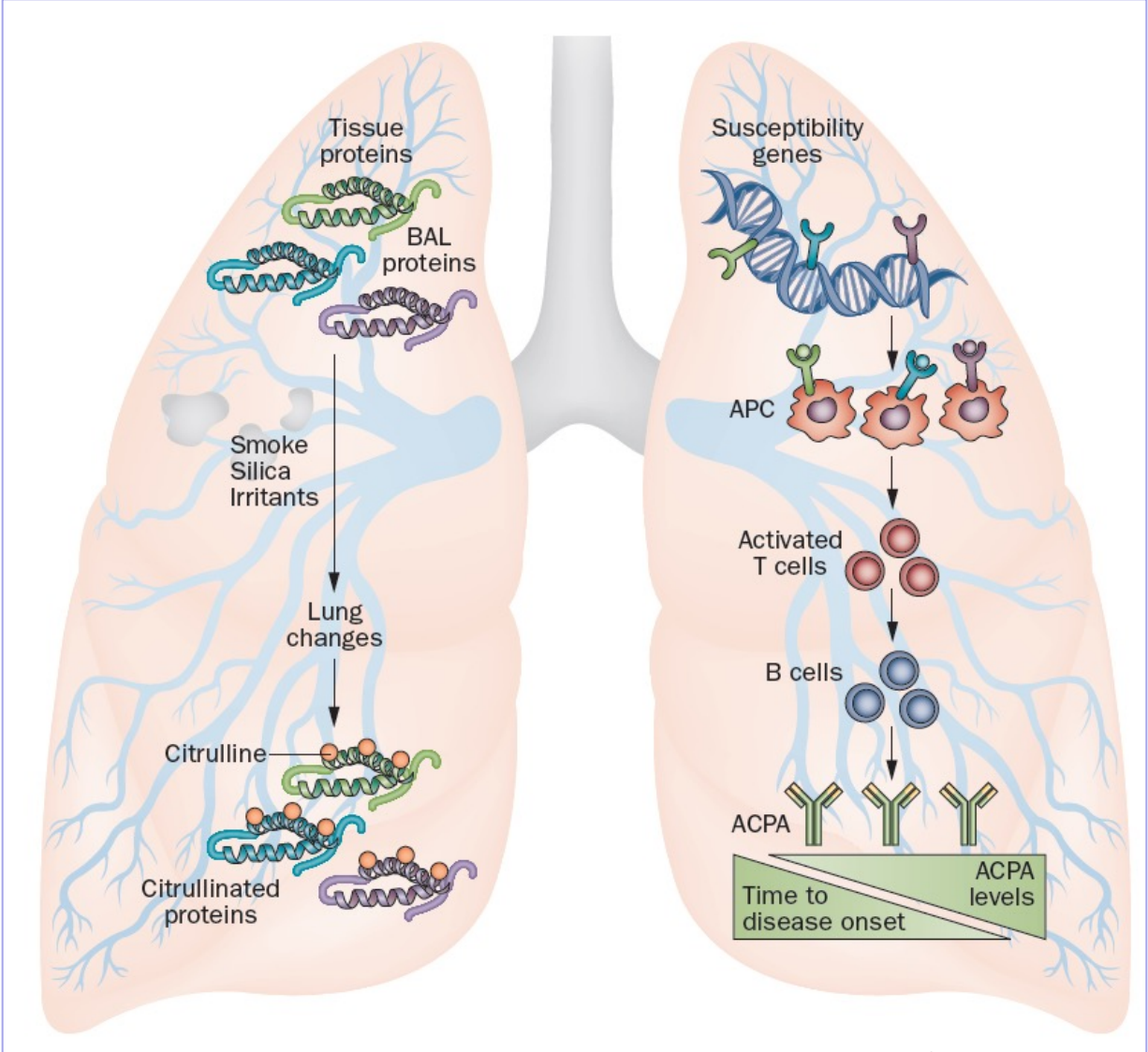
Immune activation are present in bronchial biopsies of patients with ACPA-positive untreated early RA



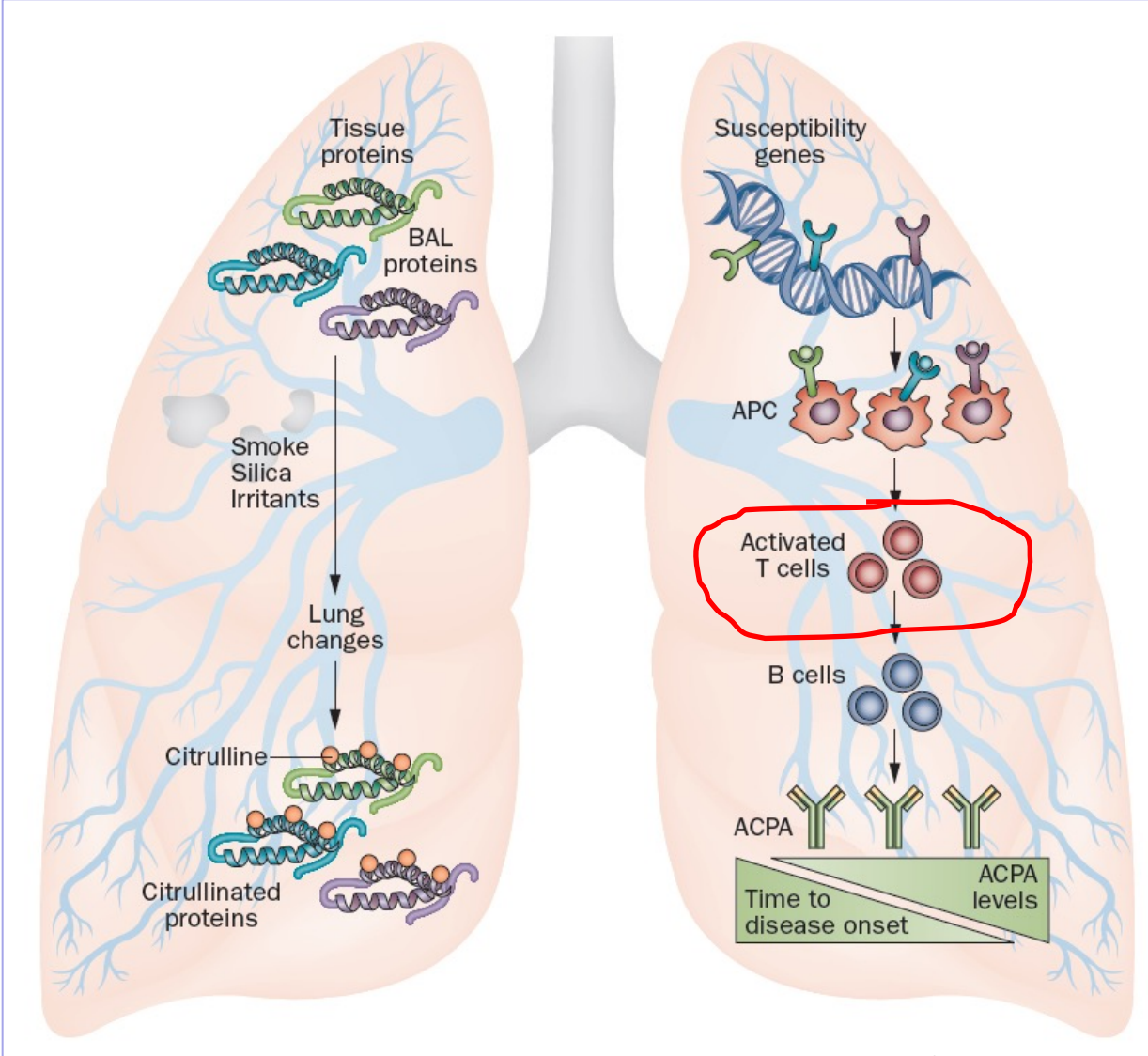
Lung plays an important role in the immunological reactions responsible for the development of ACPA-positive RA



# Initiation of RA-associated immunity against citrullinated proteins in the lungs.



# Initiation of RA-associated immunity against citrullinated proteins in the lungs.

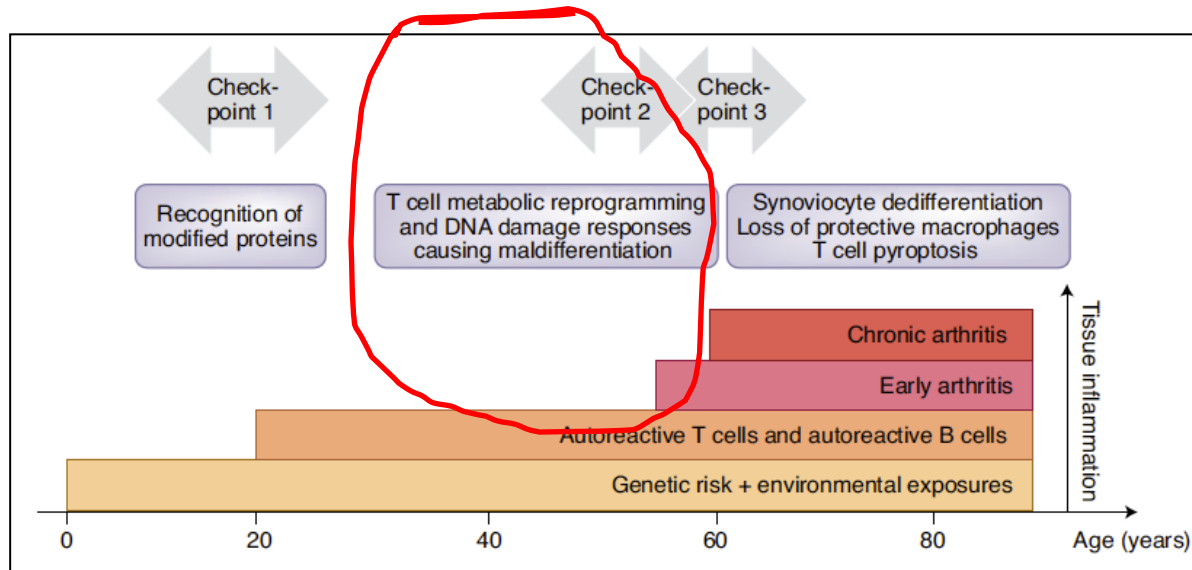




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# Immune factors contributing to synovial localization of inflammation

“The onset of synovial inflammation, is closely linked to cell-intrinsic defects in CD4+ T cells and is functionally caused by a mis-differentiation step during the conversion of naive resting CD4+ T cells into memory and effector T cells”

- ✓ **CD3+ T cells** are present in most **early synovitis** cases and the **histologic phenotype** of synovial biopsy samples **predicts** disease persistence and severity.

Ann. Rheum. Dis. 78, 761–772 (2019). Cell Rep. 28,2455–2470.e5 (2019)

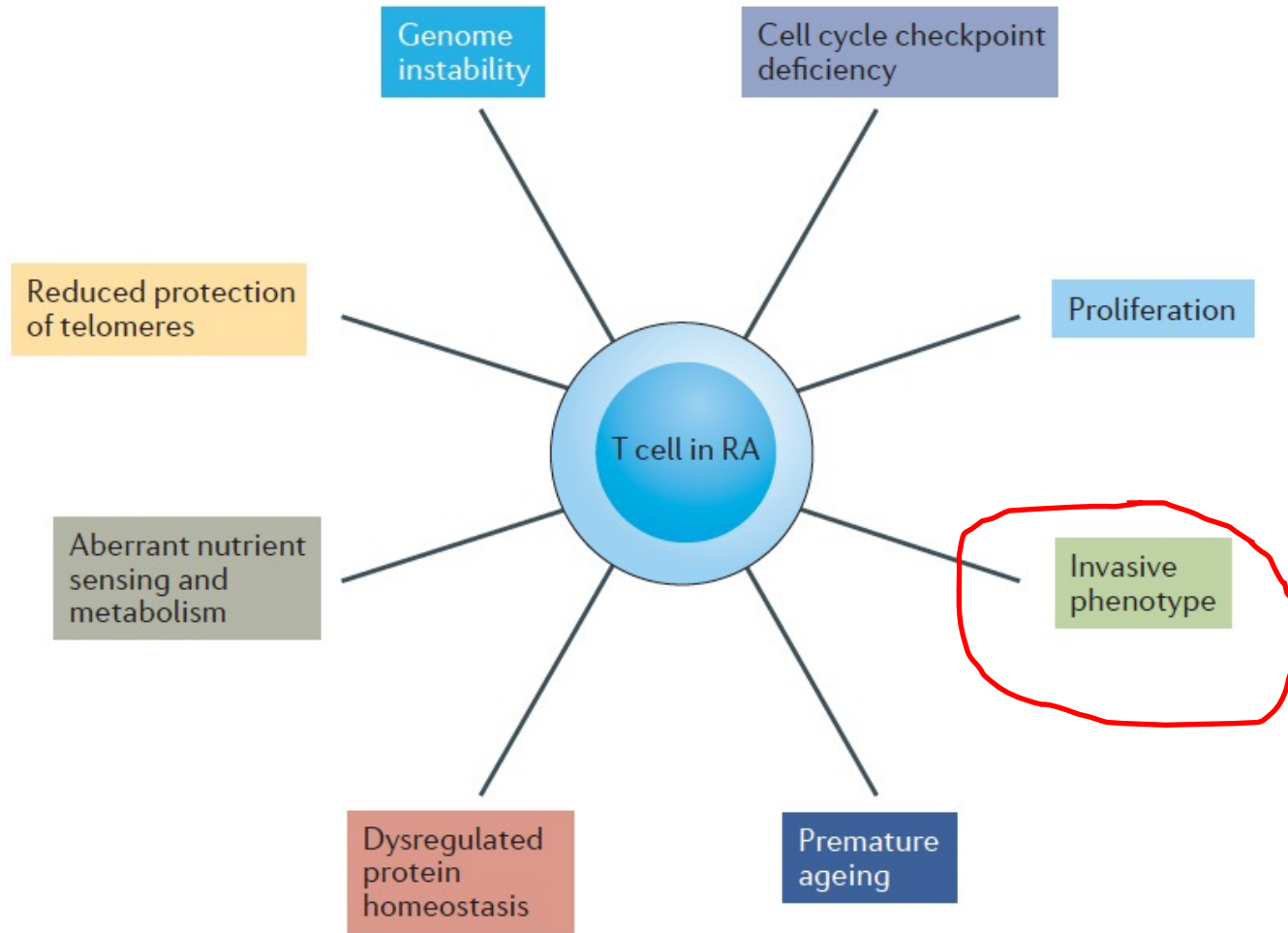
- ✓ **Decreased frequency of naïve CD4+ T cells** is the strongest predictor for the progression from **ACPA positivity to synovitis**.

Sci. Rep. 10, 3669 (2020)

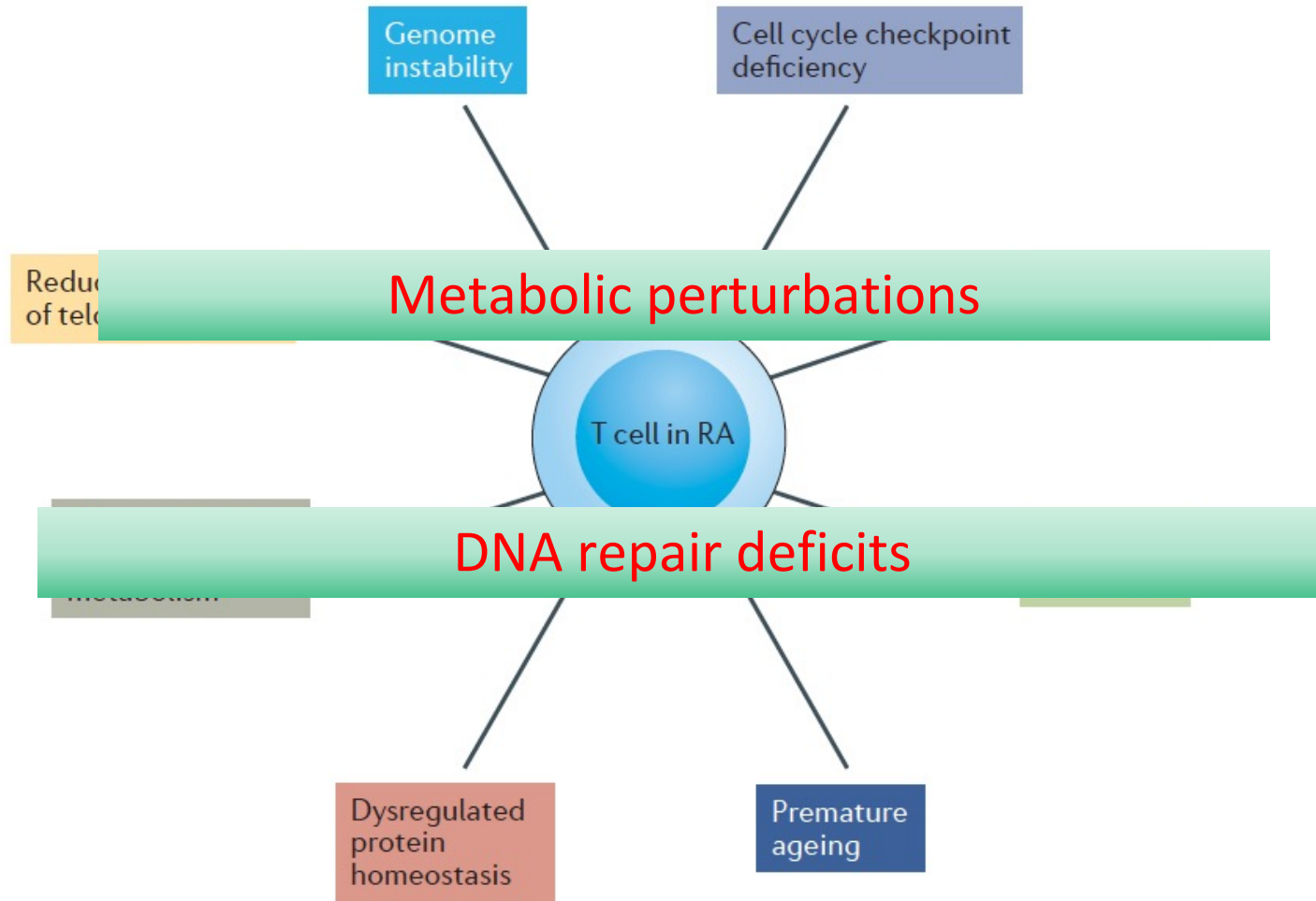
- ✓ **Differential methylation** patterns of naïve CD4+ T cells characterize the **earliest stages** of joint inflammation in patients who were drug naïve

Clin. Epigenetics 12,54 (2020)

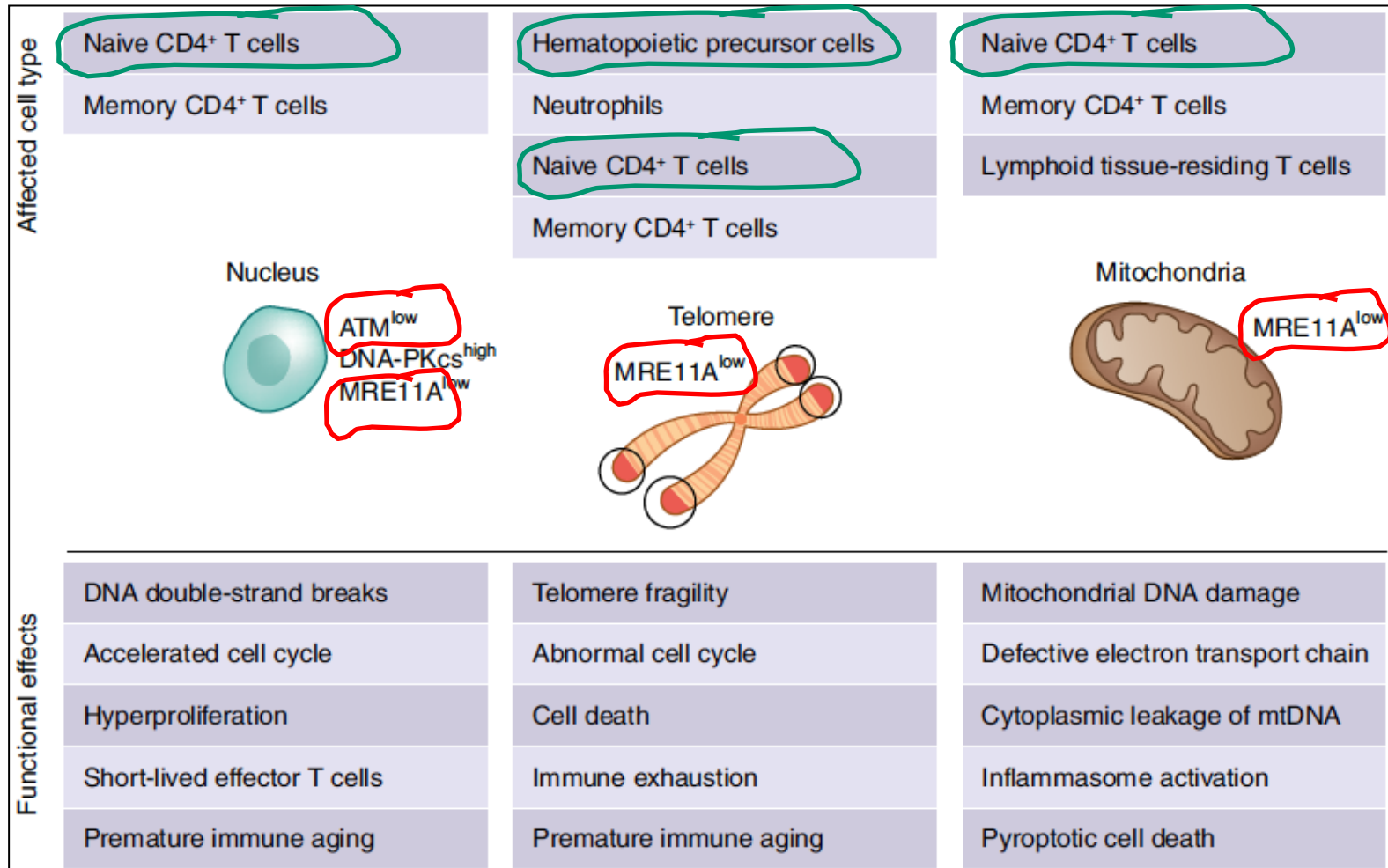
# Hallmarks of T cells in rheumatoid arthritis



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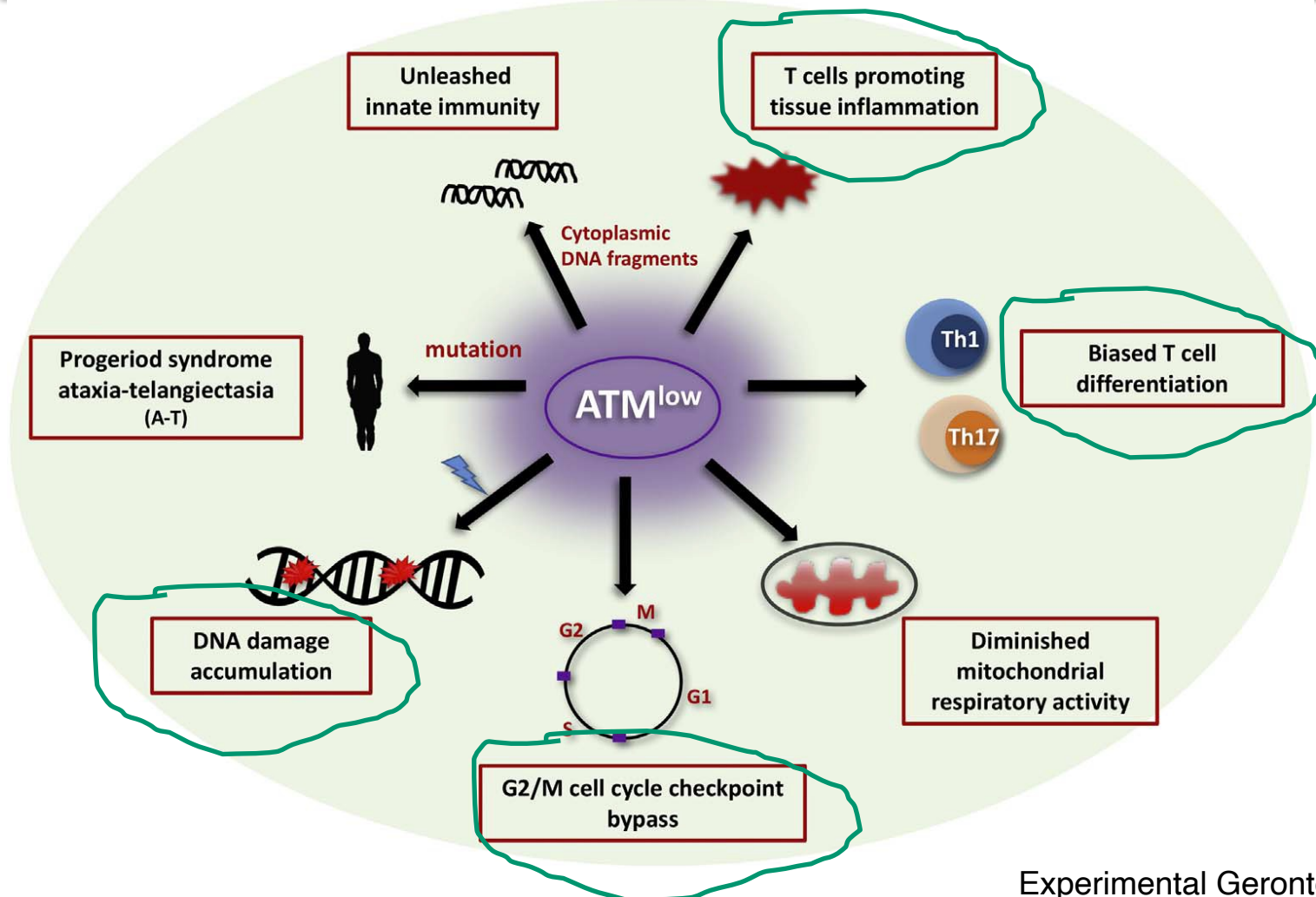


# DNA repair deficits in rheumatoid arthritis



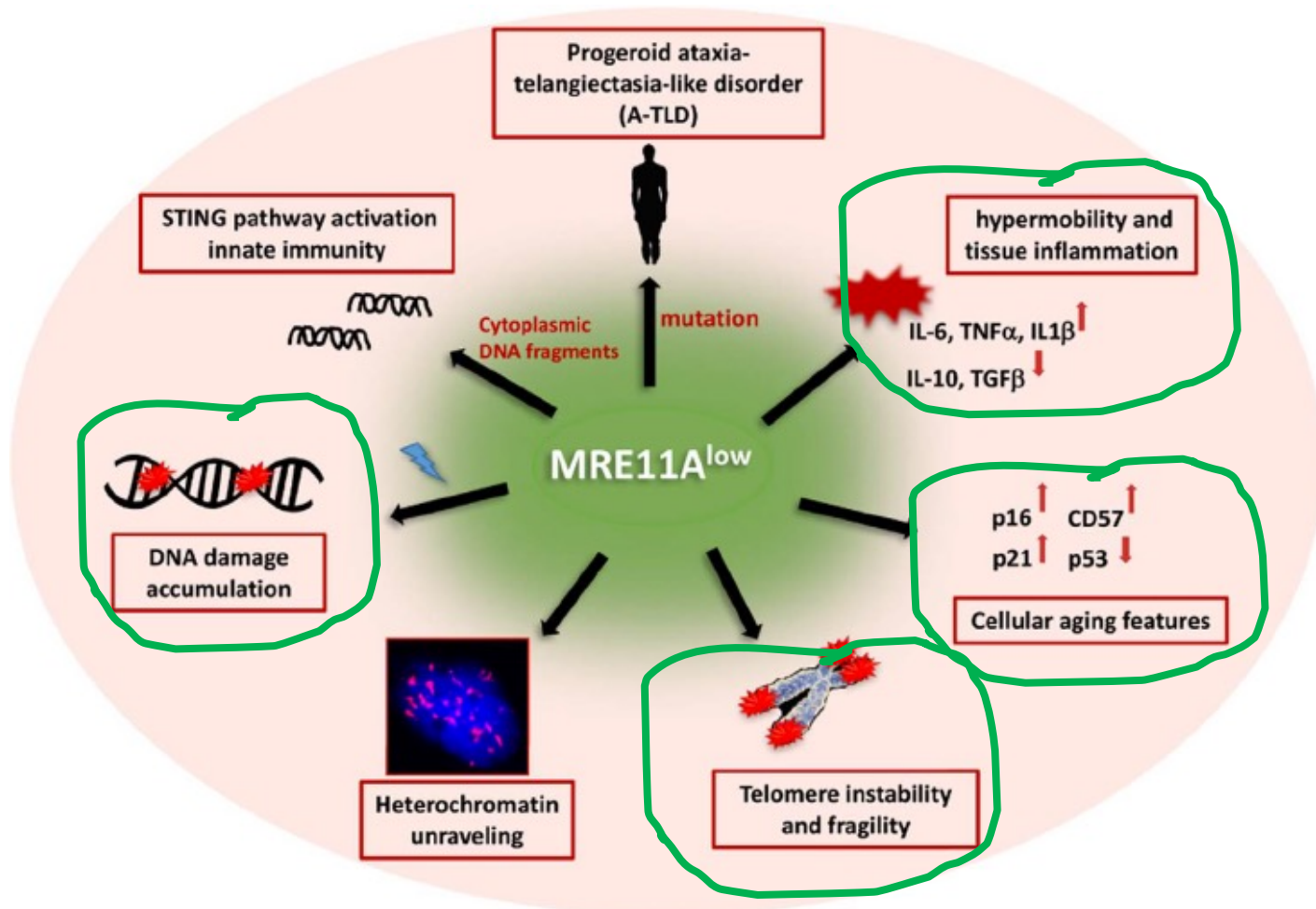
# ATM<sup>low</sup> T cells in RA patients promote tissue inflammation

- (ATM) : superfamily of phosphatidylinositol 3-kinase-related kinases.
  - activator of the DNA damage response and DNA repair.
- ATM function is redox sensitive, connecting metabolic activity with the DNA repair machinery.



# MRE11A Protects Synovial Tissue from Inflammation

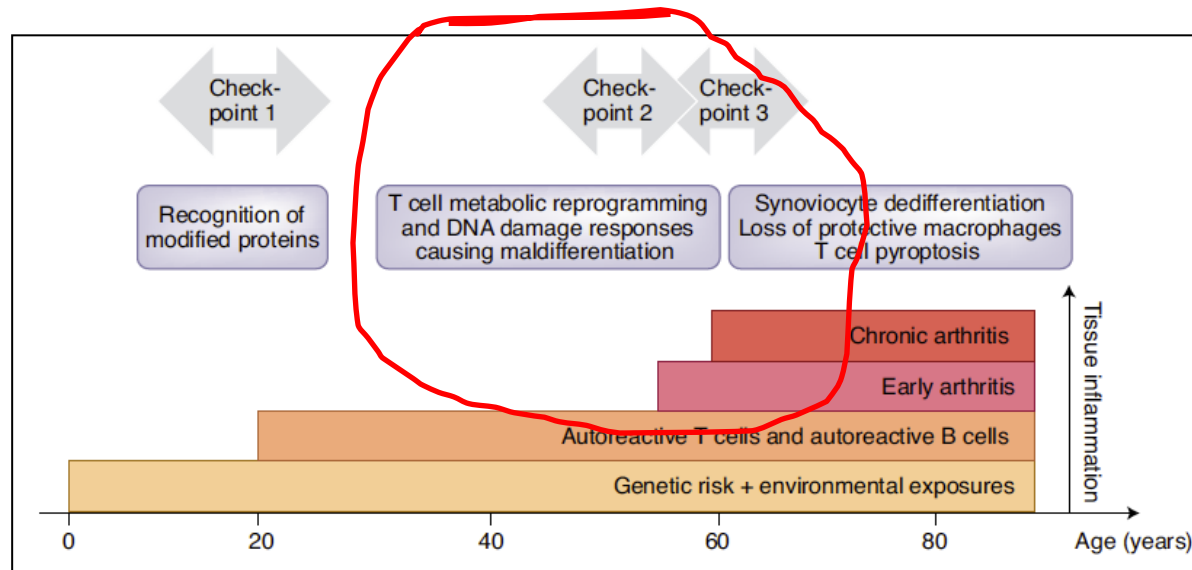
## Early RA patients have low MRE11A expression



# General concept for RA pathogenesis

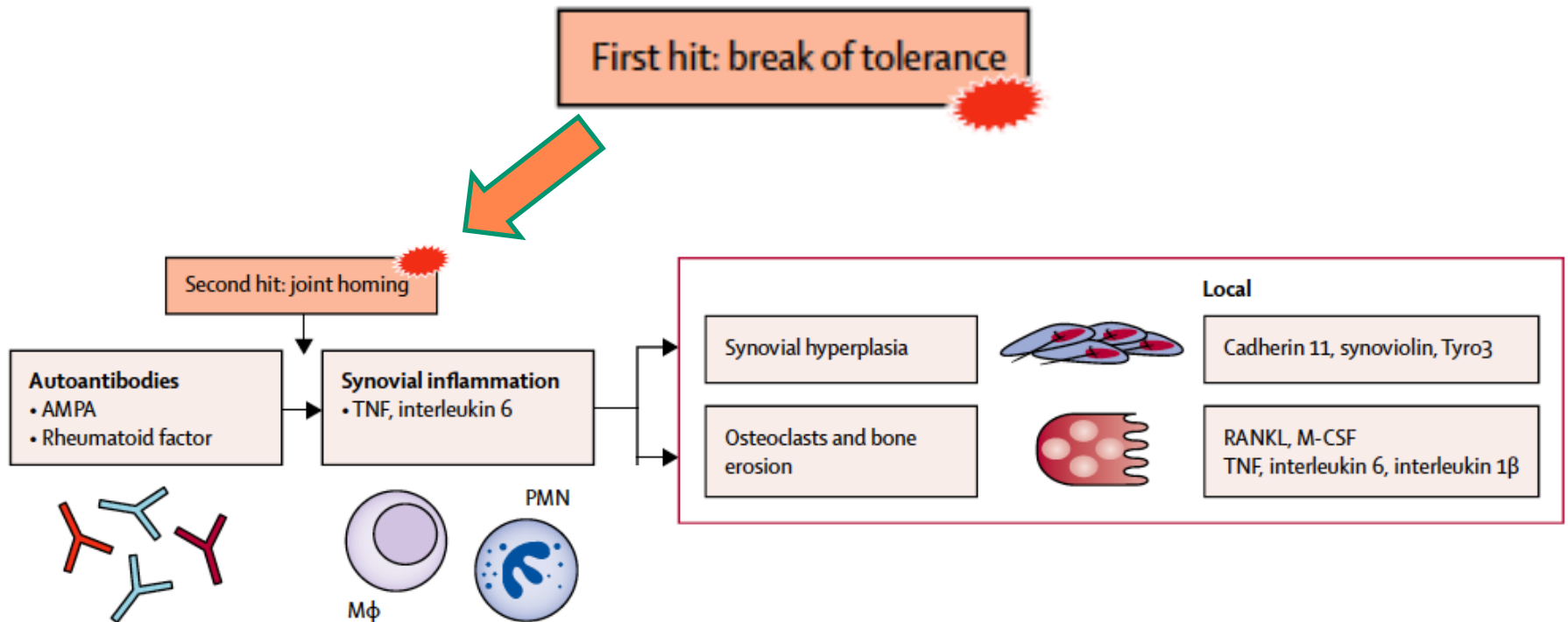
“RA is an almost lifelong process in with distinct phases:

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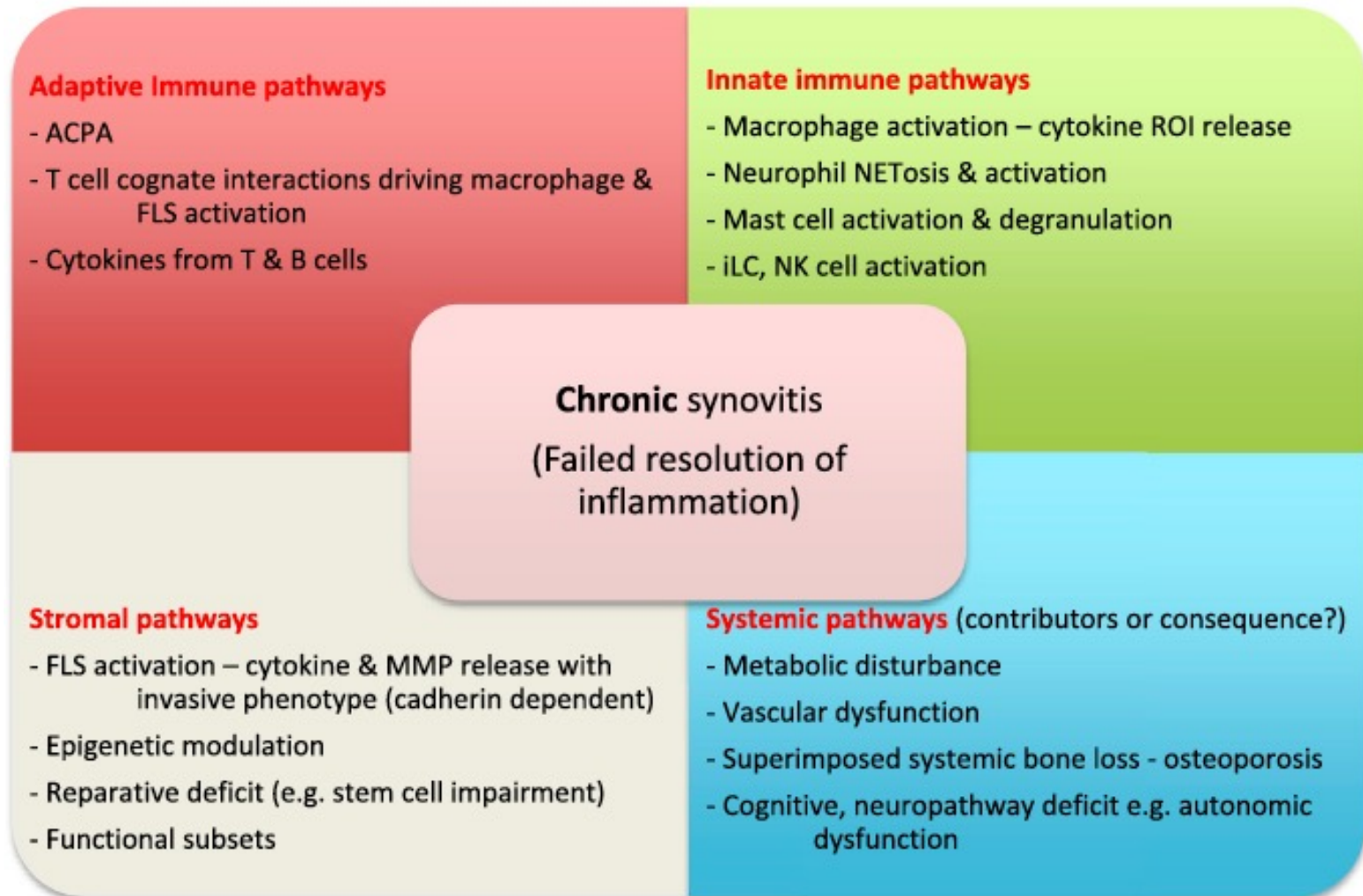


# Chronic, destructive synovitis: Hyperplasia (pannus) and osteoclastogenesis

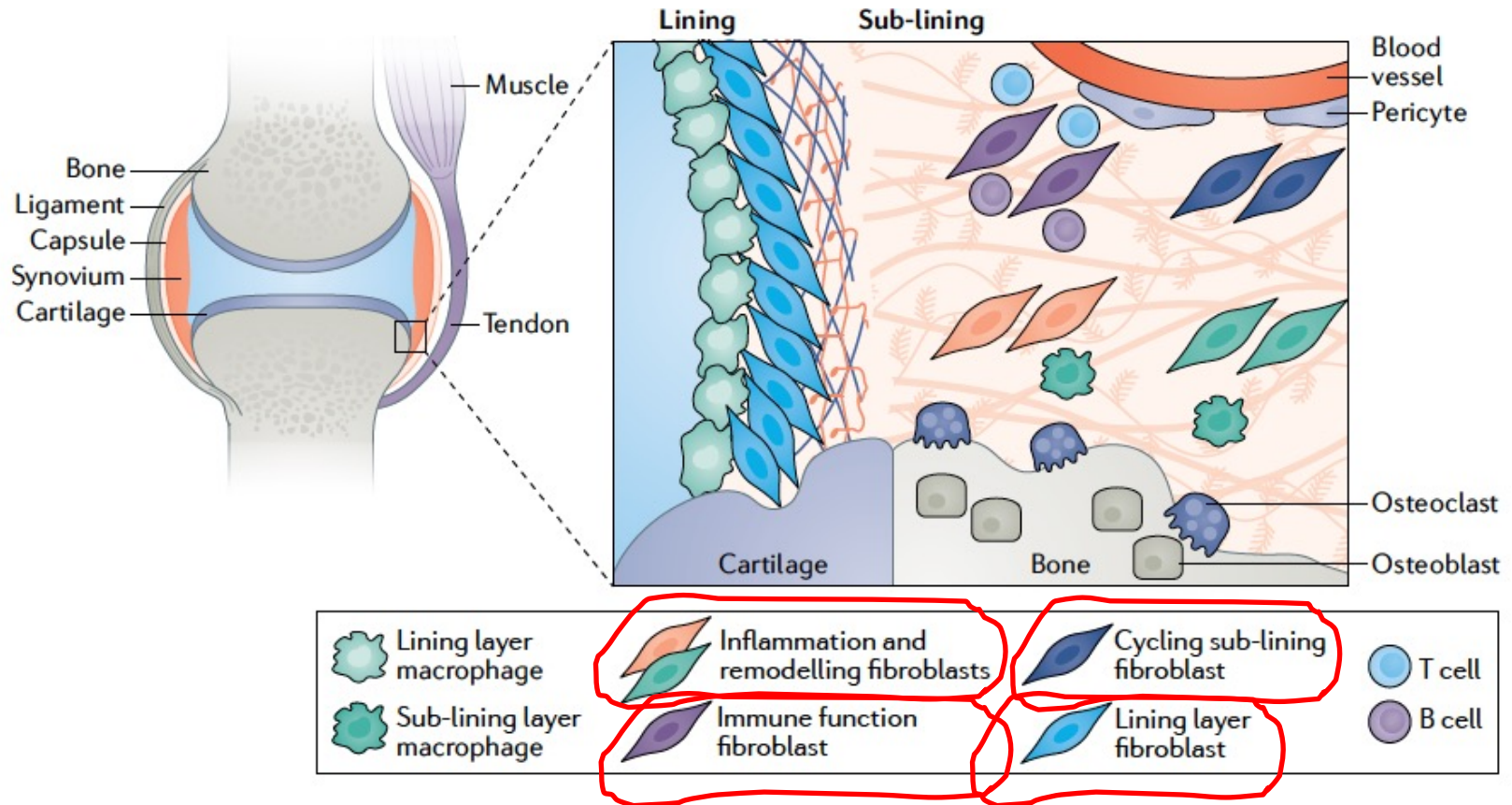


# Mechanisms that Drive the Chronicity of RA:

## Distinct pathways combine to mediate failed resolution of disease



# The multiple faces of fibroblasts in RA

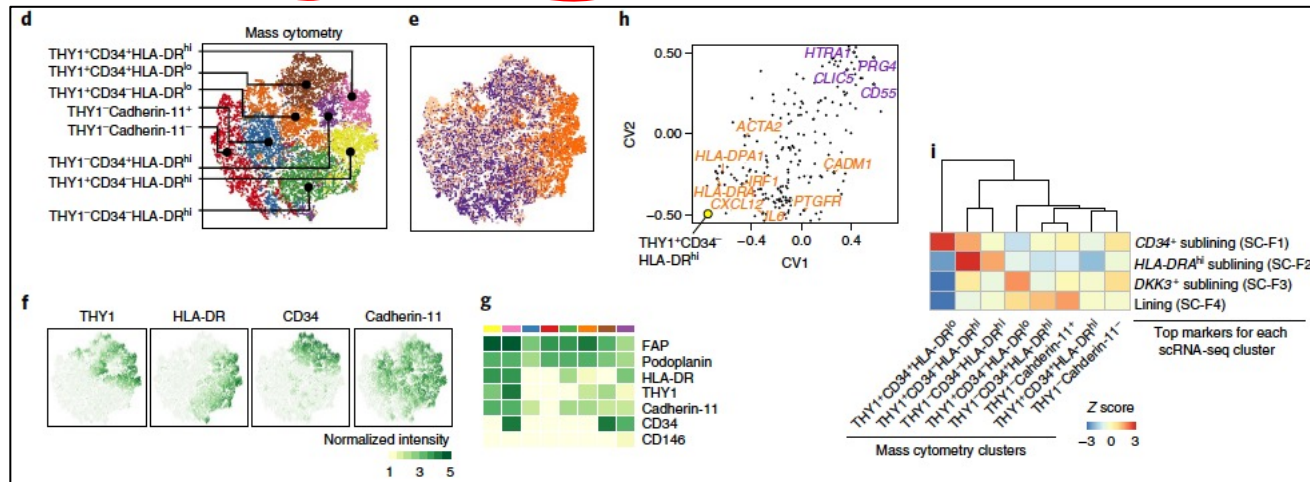


# Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry

Nat Immunol. 2019 Jul;20(7):928-942

Table 1 | Conserved cell populations in rheumatoid arthritis joints

Cell subsets	Marker genes (human)	Marker genes (mouse)	Activation marker or effector genes
<b>Fibroblasts</b>			
Lining layer	Negative ( <i>CD90</i> ); positive ( <i>CD55</i> and <i>PGR4</i> )	Negative ( <i>Cd90</i> ); positive ( <i>Pgr4</i> )	<i>RANKL:OPG</i> ratio, <i>CCL9</i> , <i>CLIC5</i> , <i>MMP1</i> , <i>MMP2</i> , <i>MMP3</i> , <i>MMP9</i> , <i>MMP13</i> , <i>HAS1</i> , <i>HTRA4</i> and <i>DNASE1L3</i>
Sub-lining layer (immunomodulatory)	Positive ( <i>CD90</i> and <i>CD34</i> ) Negative ( <i>CD34</i> ); positive ( <i>CD90</i> and <i>DKK</i> )	Positive ( <i>Cd90</i> and <i>Cd34</i> )	<i>IL6</i> , <i>IL33</i> , <i>IL34</i> , <i>IFI30</i> , <i>LIF</i> , <i>CXCL9</i> , <i>CXCL12</i> , <i>CXCL13</i> , <i>CCL2</i> , <i>CCL19</i> and <i>CCL21</i>
Sub-lining layer (perivascular)	Negative ( <i>CD34</i> ); positive ( <i>CD90</i> and <i>HLA-DRA</i> )	Negative ( <i>Cd34</i> ); positive ( <i>Cd90</i> )	



## 4-5 Functionally distinct fibroblast subgroups

Sublining fibroblasts as a potential therapeutic target in RA:

- Are a major source of pro-inflammatory cytokines such as IL6
- All SF subsets express TNF receptor 1, **but none is a TNF producer**
- Express MHC II (SC-F2, THY1<sup>+</sup>CD34<sup>-</sup>HLA-DR<sup>hi</sup>)

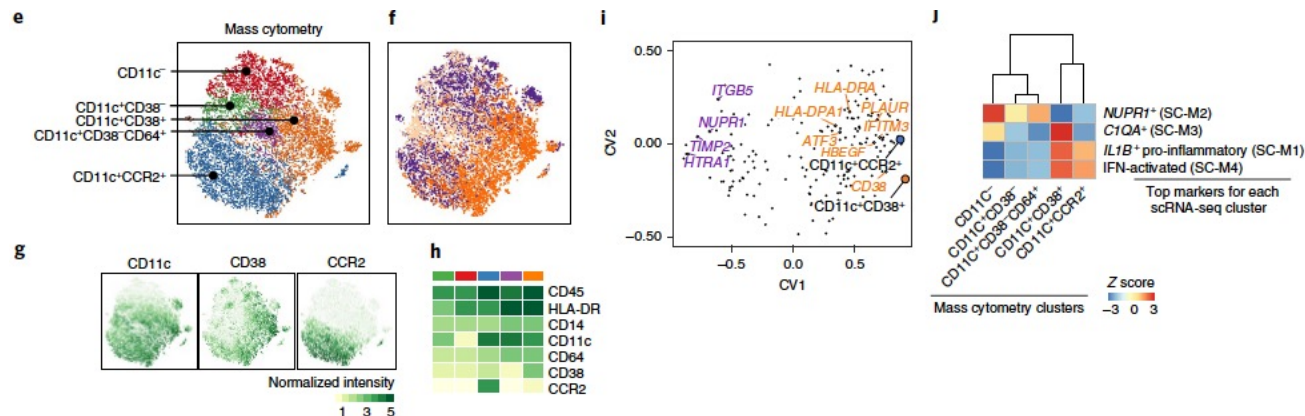
Further studies are needed to define molecular mechanisms that regulate sublining fibroblast expansion in RA.

# Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry

Nat Immunol. 2019 Jul;20(7):928-942

Table 1 | Conserved cell populations in rheumatoid arthritis joints

Cell subsets	Marker genes (human)	Marker genes (mouse)	Activation marker or effector genes
<i>Macrophages</i>			
Lining layer	Not reported	Negative ( <i>Cfsr1</i> ); positive ( <i>Cx3cr1</i> )	<i>TREM2</i> , <i>VSIG4</i> , <i>AXL</i> , <i>MFGE8</i> , <i>JAM1</i> , <i>ZO1</i> , <i>CLDN5</i> , <i>FAT4</i> and <i>VANGL2</i>
Interstitial	Negative ( <i>CD11C</i> and <i>CD38</i> ); positive ( <i>NURP1</i> )	Negative ( <i>Cx3cr1</i> ); positive ( <i>Cfsr1</i> , MHC class II genes and <i>Aqp1</i> )	<i>MERTK</i> , <i>CTSK</i> , <i>HTRA1</i> , <i>GPNMB</i> and <i>ITGB5</i>
	Positive ( <i>C1QA</i> , <i>CD11C</i> and <i>CD38</i> )	Negative ( <i>Cx3cr1</i> ); positive ( <i>Cfsr1</i> and <i>Relma</i> )	<i>MRC1</i> , <i>CD163</i> and <i>MARCO</i>
Monocyte-derived (infiltrating)	Positive ( <i>SPP1</i> , <i>CD11C</i> , <i>CCR2</i> and <i>CD38</i> ) when activated by interferon	Negative ( <i>Ly6c2</i> ); positive ( <i>Ccr2</i> and <i>Arg1</i> )	<i>ARG1</i> , <i>IFI6</i> , <i>IFI44L</i> , <i>LY6E</i> and <i>SPP1</i>
	Positive ( <i>IL1B</i> , <i>CD11C</i> , <i>CCR2</i> and <i>CD38</i> )	Negative ( <i>Ly6c2</i> ); positive ( <i>Ccr2</i> and <i>Il1b</i> )	<i>NR4A2</i> , <i>HBEGF</i> , <i>PLAUR</i> , <i>RGS2</i> , <i>IL1B</i> , <i>HTF3</i> , <i>CXCL2</i> and <i>EREG</i>

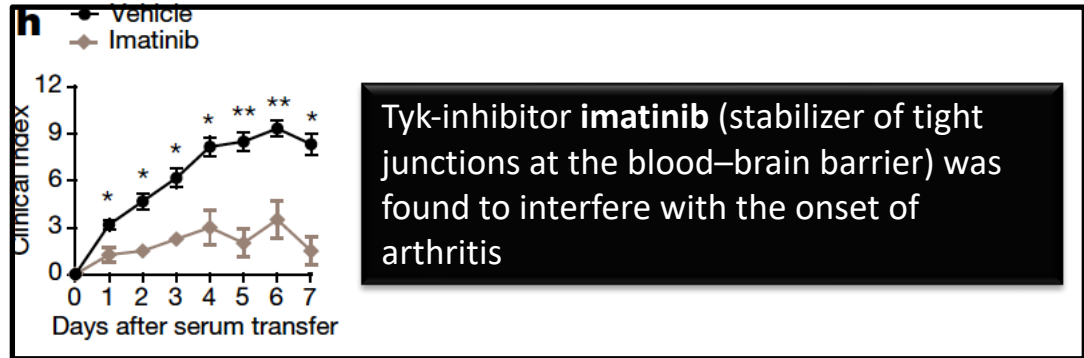
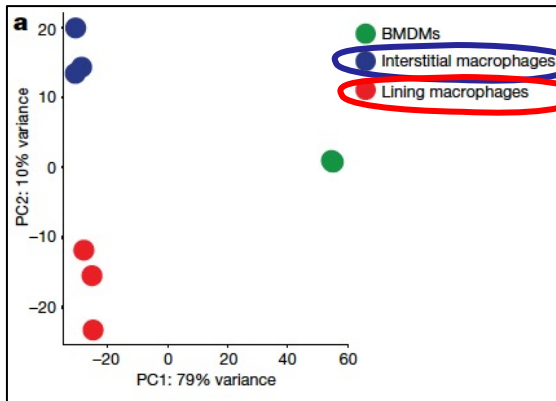


# Locally renewing resident synovial macrophages provide a protective barrier for the joint

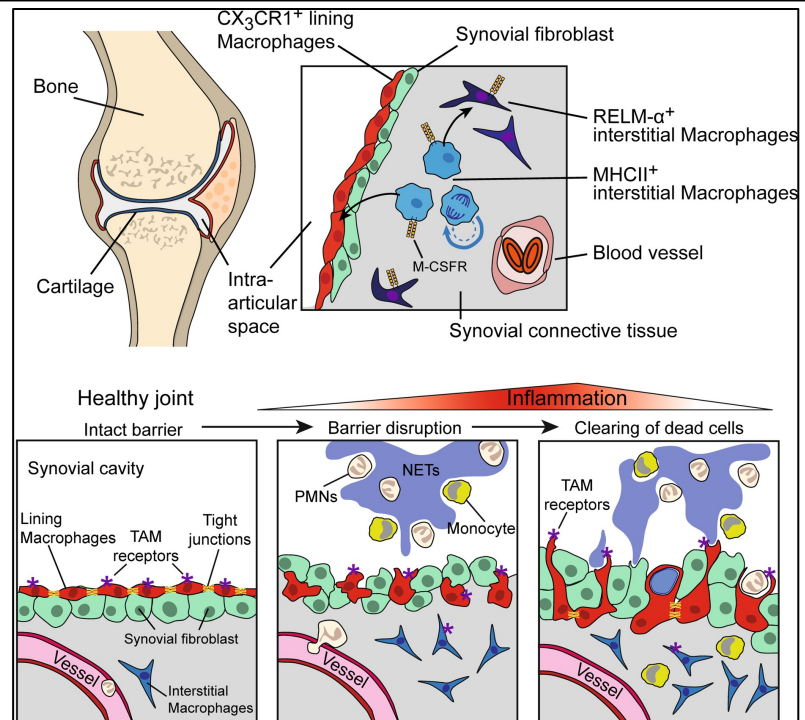
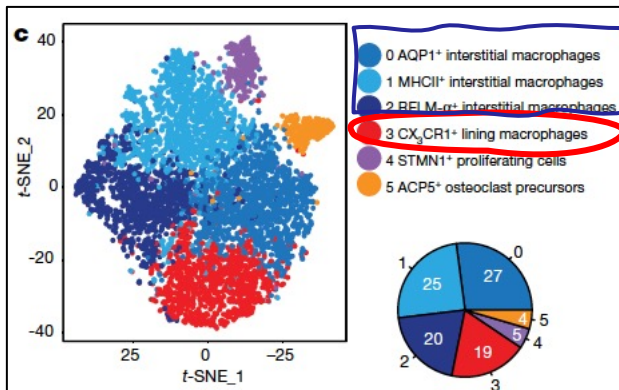
Stephan Culemann<sup>1,2,11</sup>, Anika Grüneboom<sup>1,2,11</sup>, José Ángel Nicolás-Ávila<sup>3</sup>, Daniela Weidner<sup>1,2</sup>, Katrin Franziska Lämmle<sup>1,2</sup>, Tobias Rothe<sup>1,2</sup>, Juan A. Quintana<sup>3</sup>, Philipp Kirchner<sup>4</sup>, Branislav Krljanac<sup>5</sup>, Martin Eberhardt<sup>6</sup>, Fulvia Ferrazzi<sup>4</sup>, Elke Kretzschmar<sup>7</sup>, Martin Schicht<sup>7</sup>, Kim Fischer<sup>1</sup>, Kolja Gelse<sup>8</sup>, Maria Faas<sup>1,2</sup>, René Pfeifle<sup>1,2</sup>, Jochen A. Ackermann<sup>1,2</sup>, Milena Pachowsky<sup>8</sup>, Nina Renner<sup>8</sup>, David Simon<sup>1</sup>, Reiner F. Haseloff<sup>9</sup>, Arif B. Ekici<sup>4</sup>, Tobias Bäuerle<sup>10</sup>, Ingolf E. Blasig<sup>9</sup>, Julio Vera<sup>6</sup>, David Voehringer<sup>5</sup>, Arnd Kleyer<sup>1</sup>, Friedrich Paulsen<sup>7</sup>, Georg Schett<sup>1</sup>, Andrés Hidalgo<sup>3</sup> & Gerhard Krönke<sup>1,2\*</sup>

Nature 2019;572(7771):670-675

Bulk RNA sequencing of sorted steady-state CX3CR1<sup>+</sup> lining Mφ



Single-cell RNA sequencing of total synovial CD45+CD11b+Ly6G-mononuclear phagocytes



# Key points

- **Genetic** (HLA DR) and **environmental factors** (smoking) contribute to autoimmunity to endogenous modified peptides (**citrullinated**)
- **T cell-endogenous abnormalities** present in naive T cells drive the differentiation program to favor the generation effector/inflammatory cells with tissue-invading properties
  - DNA-repair failure & a metabolic shift
- Subsets of **highly activated synovial fibroblasts** adopt proinflammatory and tissue-invasive functionalities
- **Anti-inflammatory macrophages** in the synovium fail to protect the synovium
- Potential of Novel therapies:
  - The recognition of stable stages and the molecular characterization of the relevant transition points has the potential to identify targets that could re-engineer the immune system to halt the disease process prior to irreversible tissue damage.