

Genetics of Primary Immunodeficiencies

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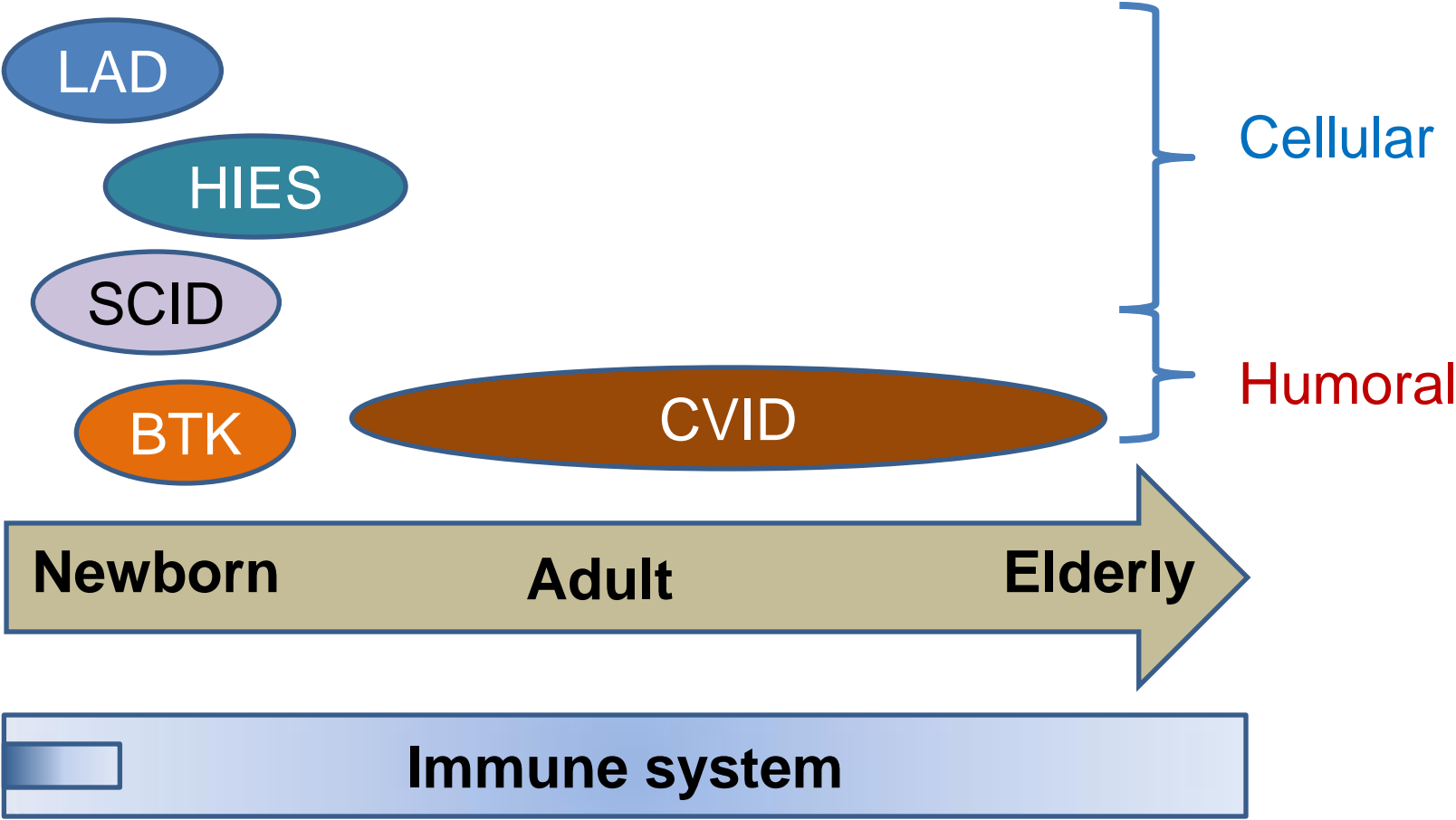
Learning Objectives

- Define and classify primary immunodeficiency diseases
 - changing definition
- Review the role of clinical laboratory in the diagnosis of primary immunodeficiency diseases
- Demonstrate the utility of molecular diagnosis in primary immunodeficiency diseases
 - changing methodology
- Review examples of genetic susceptibility to bacterial, fungal and viral infections:
 - Mendelian suscept. to chronic mucocutaneous candidiasis
 - Mendelian susceptibility to mycobacterial infections
 - Genetic susceptibility to herpes simplex encephalitis

Definitions

- Primary immunodeficiency (PID): genetic
- Secondary immunodeficiency: infection, malignancy, iatrogenic

Primary Immunodeficiencies

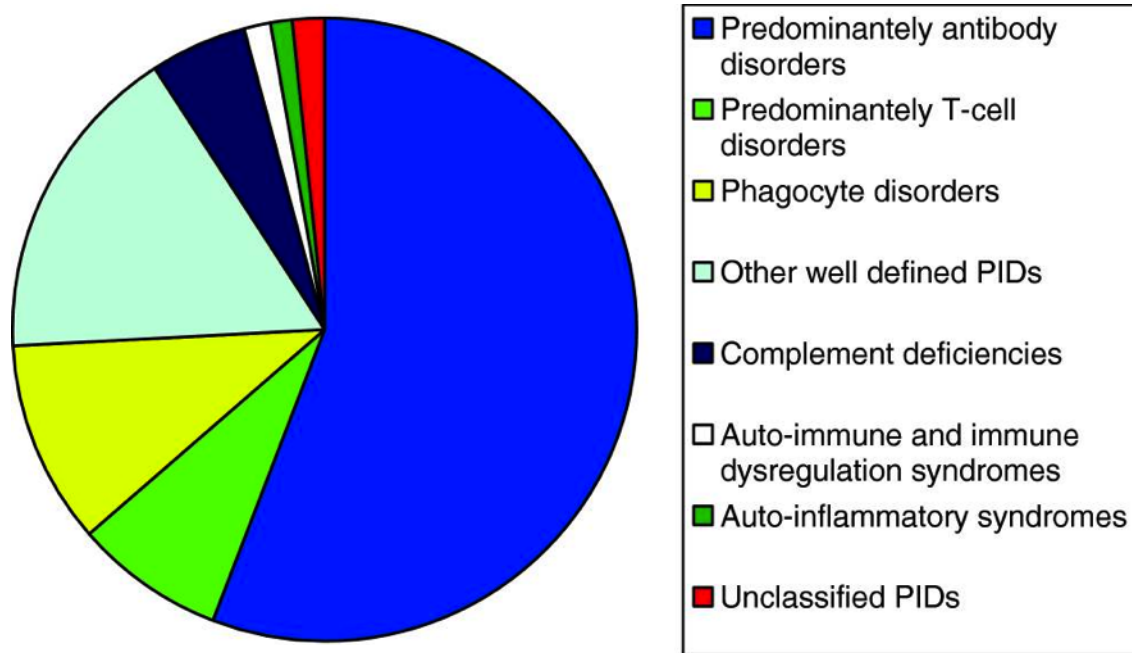


Maternal
Immunity

Immuno-
senescence

Primary antibody deficiencies are the most common PIDs

European ESID patient registry 2010



Antibody deficiencies:

Diagnosis ≥ 16 yo = 86%

Diagnosis ≤ 15 yo = 46%

PID

- Prevalence: 86.2/100,000
 - Incidence: 10.3/100,000
- (Joshi et al. 2009; Boyle and Buckley 2007)

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Leukemias

- Prevalence: 81.6/100,000
 - Incidence: 12.5/100,000
- (<http://seer.cancer.gov/statfacts/html/leuks.html>)

Identification of patients with PID

- Diagnosis of PIDs requires integration of data from clinical findings with laboratory immunological analyses and genetic testing

→ Infections

- recurrent
- life-threatening
- unusual

→ Autoimmune diseases

→ Malignancies

Diagnosis of PIDs

Clinical and family history-based diagnostic approach



Diagnostic immunology lab supports, refine phenotype



Molecular lab: diagnosis, genotype-phenotype, etc

Clinical and family history-based approach

Recur. respiratory
infections w/
diarrhea

Severe
viral/fungal
infections

Abscesses, delayed
separation of umbilical
cord



B cell and Ig.
evaluation



T cell
evaluation



Granulocyte
evaluation



- Immunoglobulins
- Flow cytometry

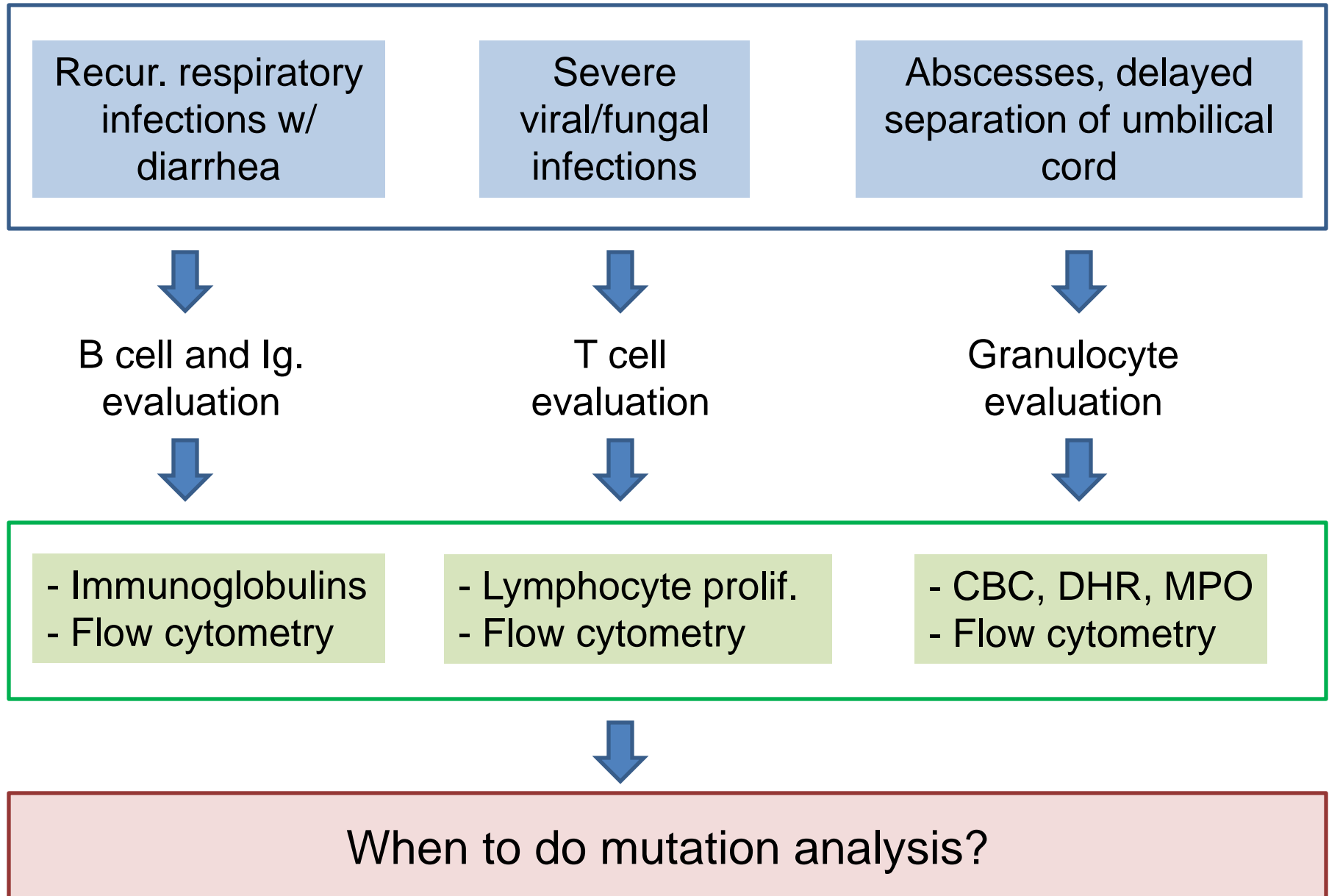


- Lymphocyte prolif.
- Flow cytometry



- CBC, DHR, MPO
- Flow cytometry

Clinical and family history-based approach



Mutation analysis in PIDs

- Definitive diagnosis (atypical presentations)
- Presymptomatic identification
- Carrier identification, genetic counseling, prenatal diagnosis
- Prognosis (strong genotype-phenotype correlation)
- Technical considerations (DNA stability vs. live cells)

Primary immunodeficiencies

PIDs are like other genetic diseases, but

- secondary causes of ID are more common than primary (esp. in adults)
- manifestations (infections) can be the same in both primary and secondary ID as well in “healthy” individuals

Primary immunodeficiencies

- PID: changing definition
 - from very severe Mendelian traits to varying degree of susceptibility to infections, including susceptibility to single infectious agents
 - not all-or-nothing (normal vs. immune deficient)
- ~150 recognized PIDS
- >200 genes (increasing fast)
 - candidate genes
 - mapping studies
 - novel technologies (genome/exome sequencing)
- Pathways not genes

Mendelian susceptibility to chronic mucocutaneous candidiasis

- *Candida albicans* is present in GI flora and and reproductive mucosa of **healthy** subjects
- **Immunocompromised** patients *C albicans* can cause systemic or mucosal disease
- Systemic candidiasis is an acute, disseminated, and invasive form mainly in patients with inherited or acquired neutrophil and T cell disorders
 - Candidemia is one of the most prevalent bloodstream infections in hospital settings and is associated with significant morbidity and mortality
- CMC is candidiasis localized to the skin, nails, and mucous membranes (no predisposition to invasive disease, such as sepsis or pneumonia)

Predisposition to systemic candidiasis

- invasive surgery
- total parenteral nutrition
- diabetes mellitus
- intensive care conditions
- central lines
- neoplasia
- long-term use of broad-spectrum antibiotics or immunosuppressive agents
- HIV
- any global T-cell deficiency or neutrophil disorders

Immunity to candida

- Impaired T cell immunity: HIV/AIDS, SCID, DiGeorge syn., DOCK8 deficiency, etc.
- Congenital neutropenias or secondary neutropenia (e.g. after chemotherapy)
- Recognition:
 - mannans (outer portion of the cell wall)
 - TLR4, Mannose Receptor, DC-SIGN, and Dectin2
 - β -glucans (inner portion of the fungal cell wall)
 - Dectin1, and MINCLE

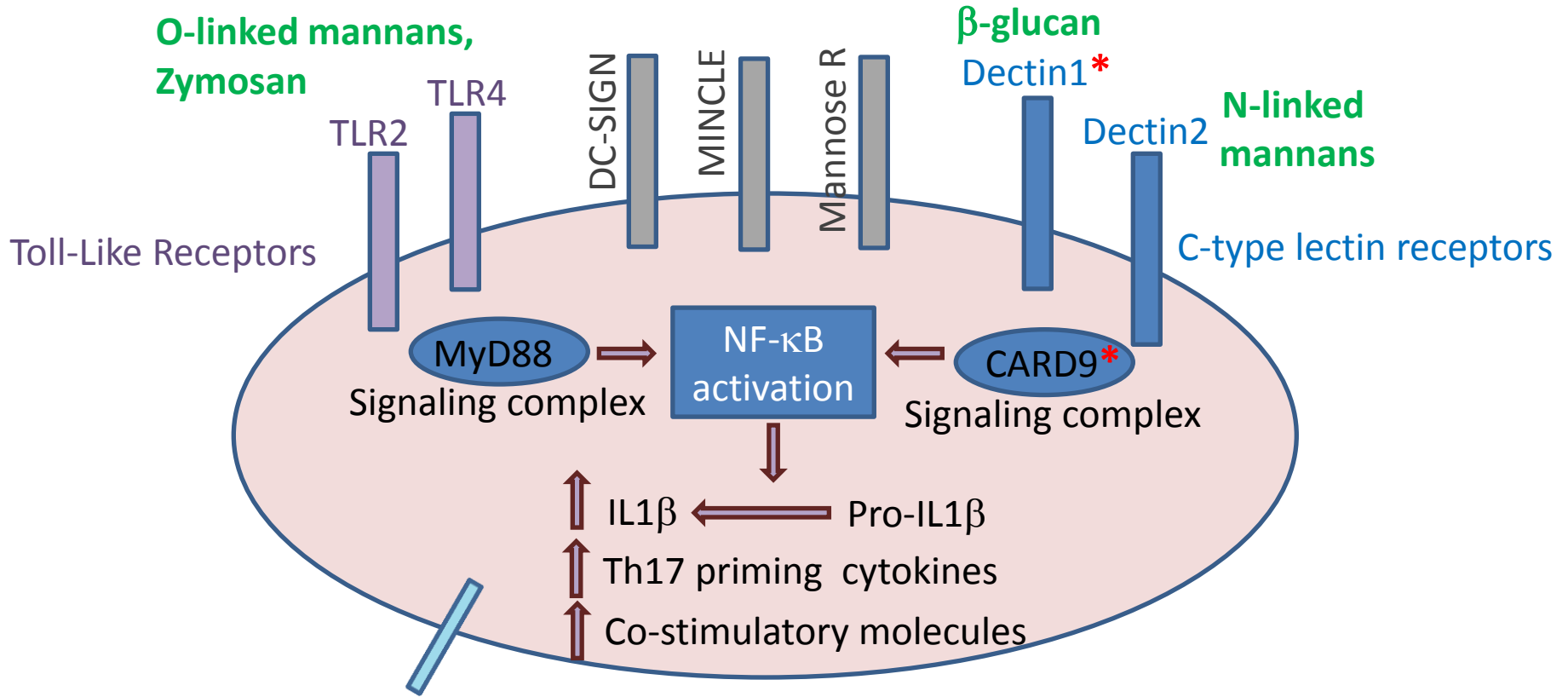
Genetics of CMC

- Dectin-1 deficiency (AR)
- CARD-9 deficiency (AR)
- AD Hyper IgE syndrome or Job syndrome: STAT3 deficiency
- AR Hyper IgE syndrome: DOCK8 deficiency
- STAT1 mutations (AD)
- IL-17F deficiency (AR)
- IL-17RA deficiency (AR)
- APECED (or APS type I): AIRE deficiency (AR)

Molecular testing → diagnosis, prognosis, inheritance

Immune response: receptors → signaling → effector functions

Fungal PAMPs

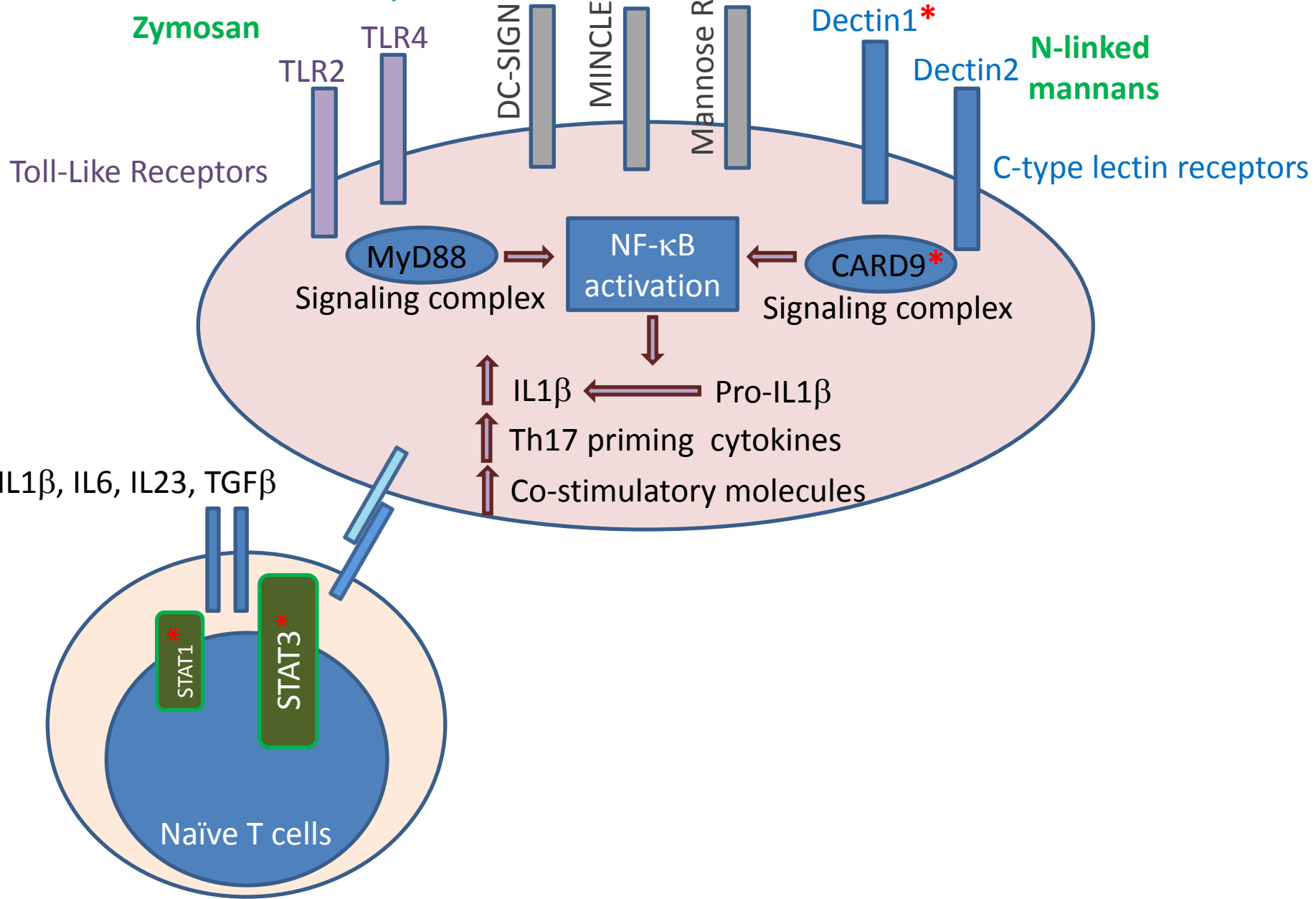


Fungal PAMPs

O-linked mannans,
Zymosan

β -glucan

N-linked
mannans

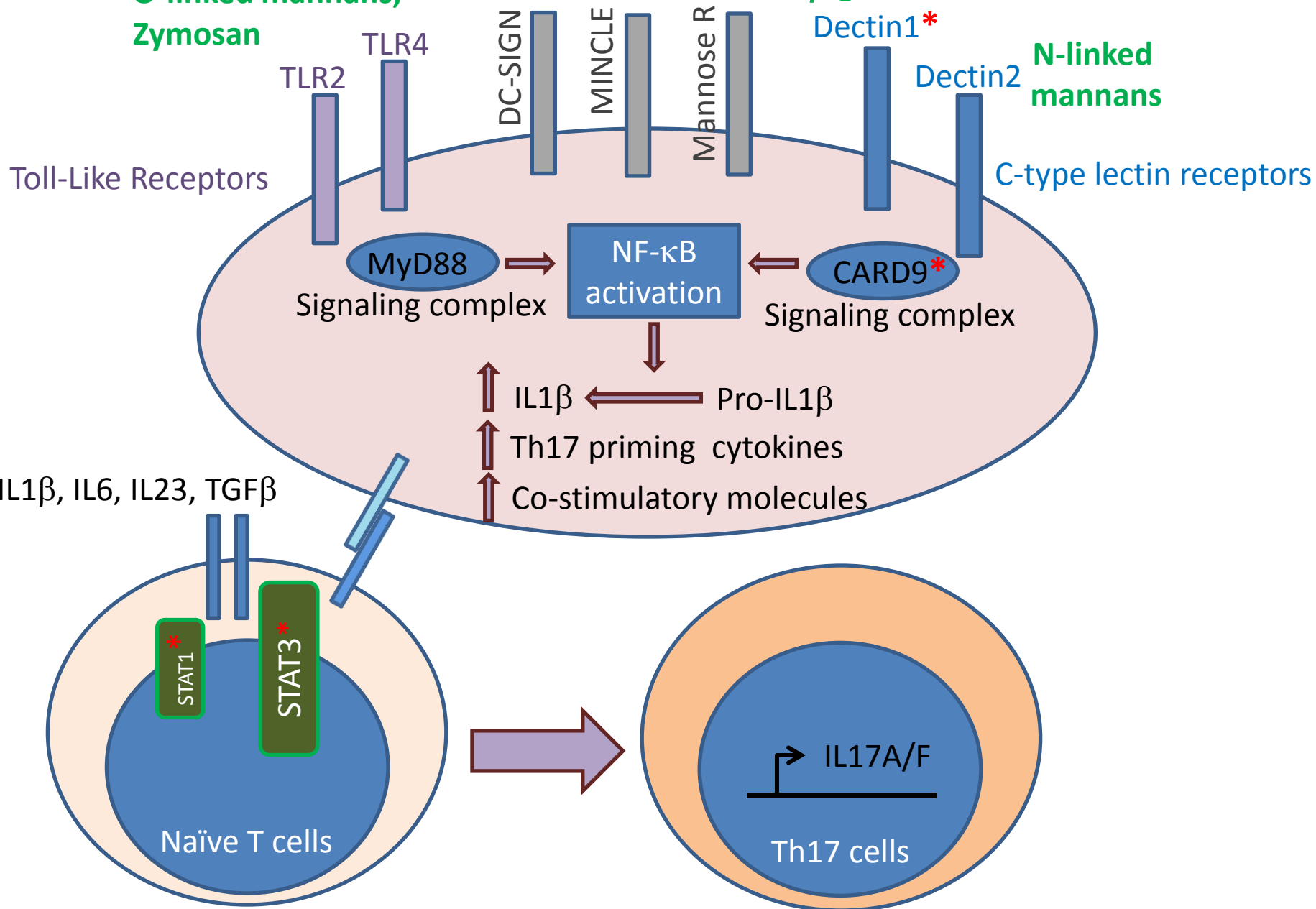


Fungal PAMPs

O-linked mannans,
Zyosan

β -glucan

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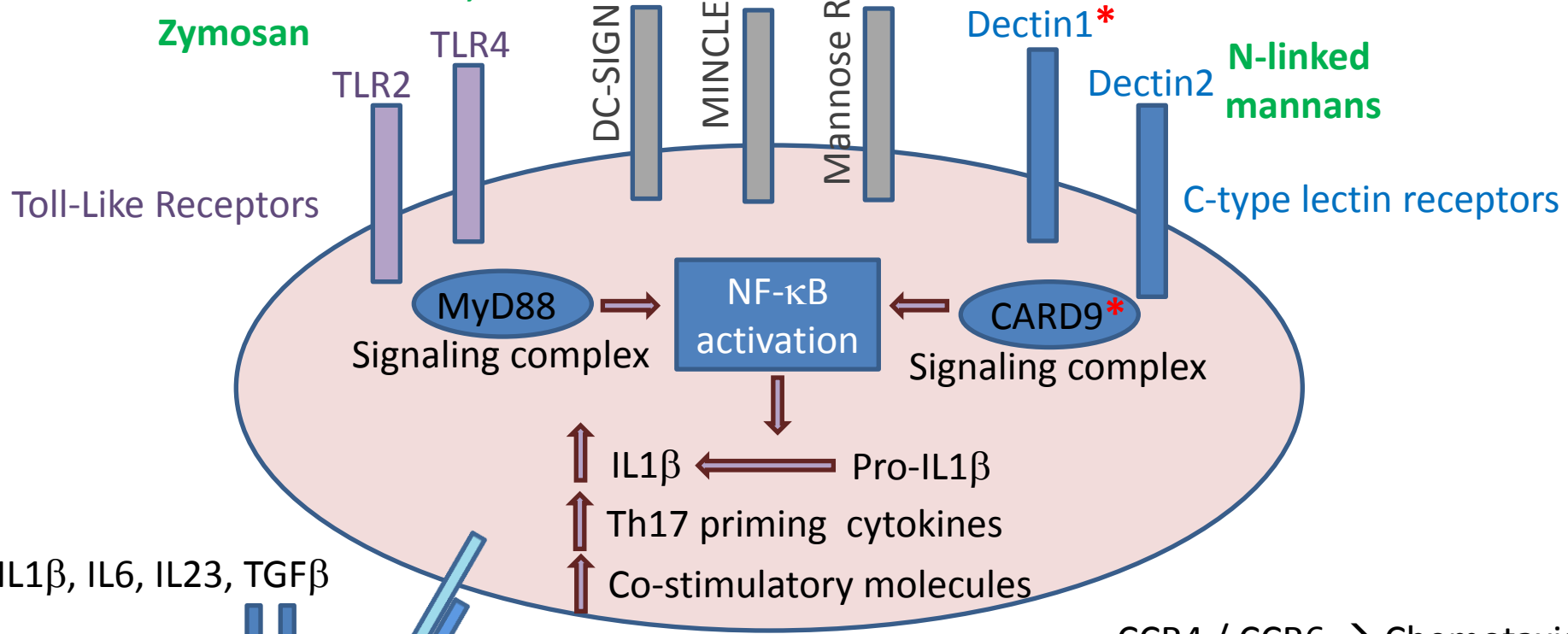


Fungal PAMPs

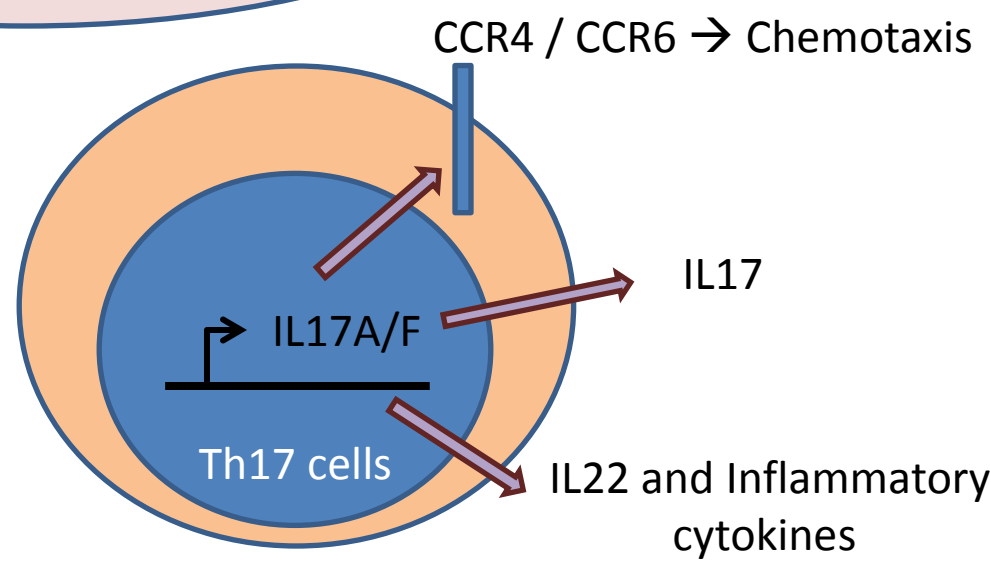
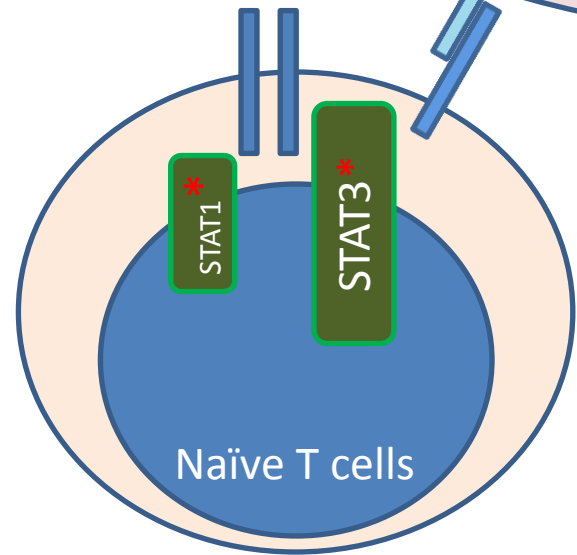
O-linked mannans,
Zyosan

β -glucan

N-linked
mannans



IL1 β , IL6, IL23, TGF β

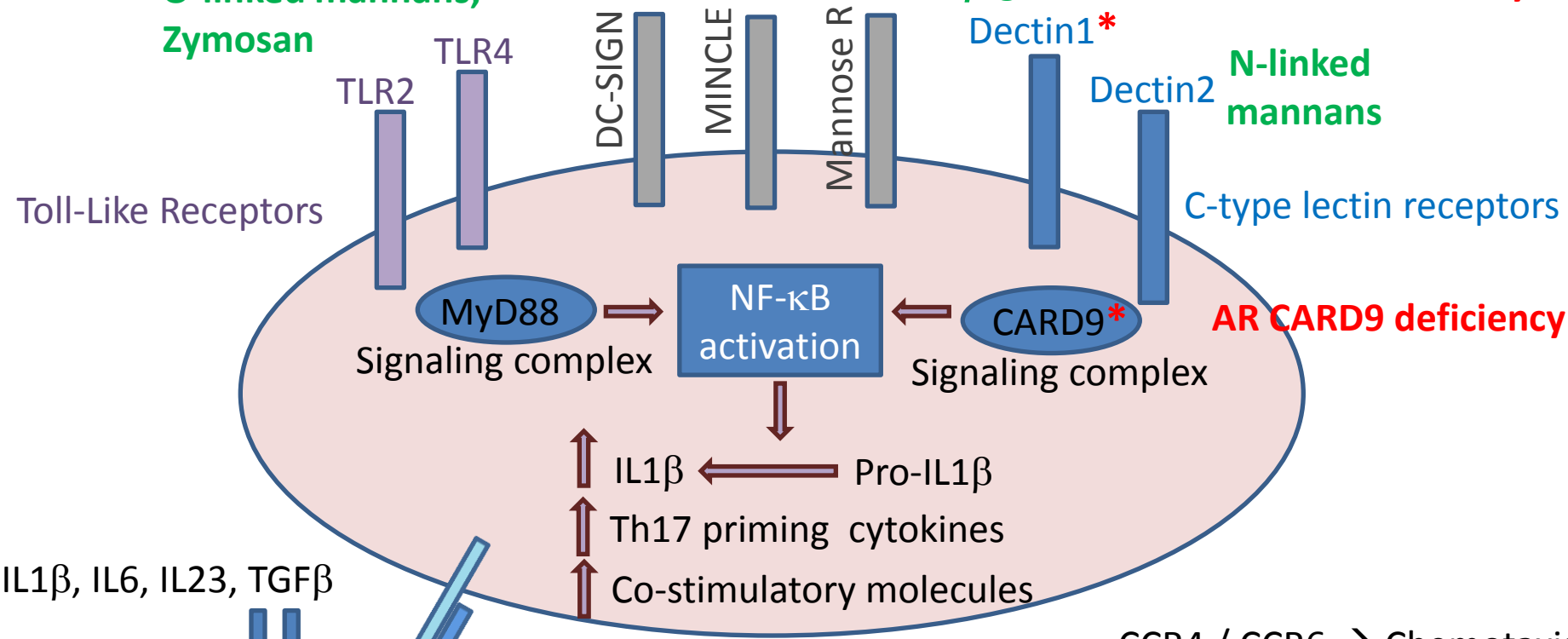


Fungal PAMPs

O-linked mannans,
Zymosan

β -glucan

AR Dectin1 deficiency



IL1 β , IL6, IL23, TGF β

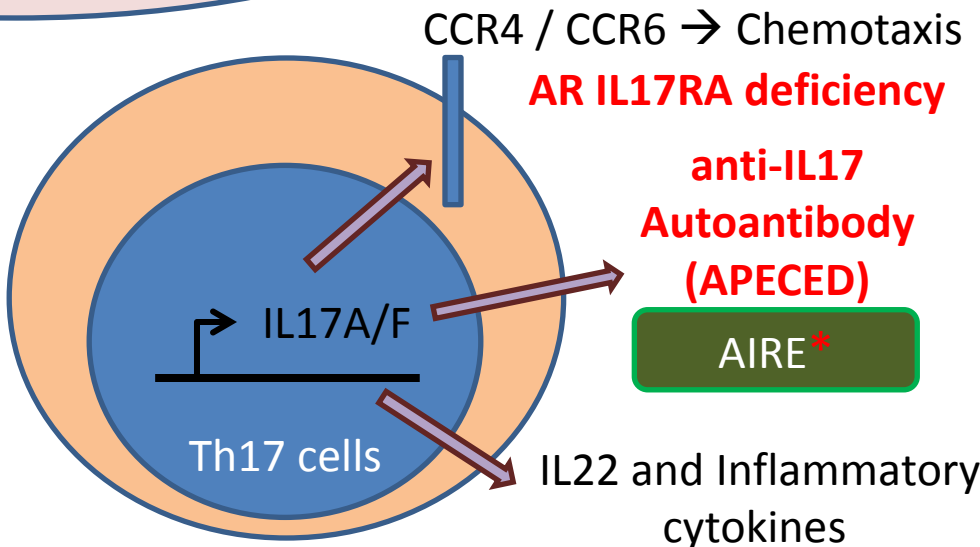
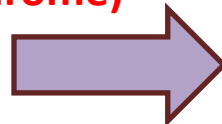
Gain-of-Function
STAT1

STAT1*

STAT3*

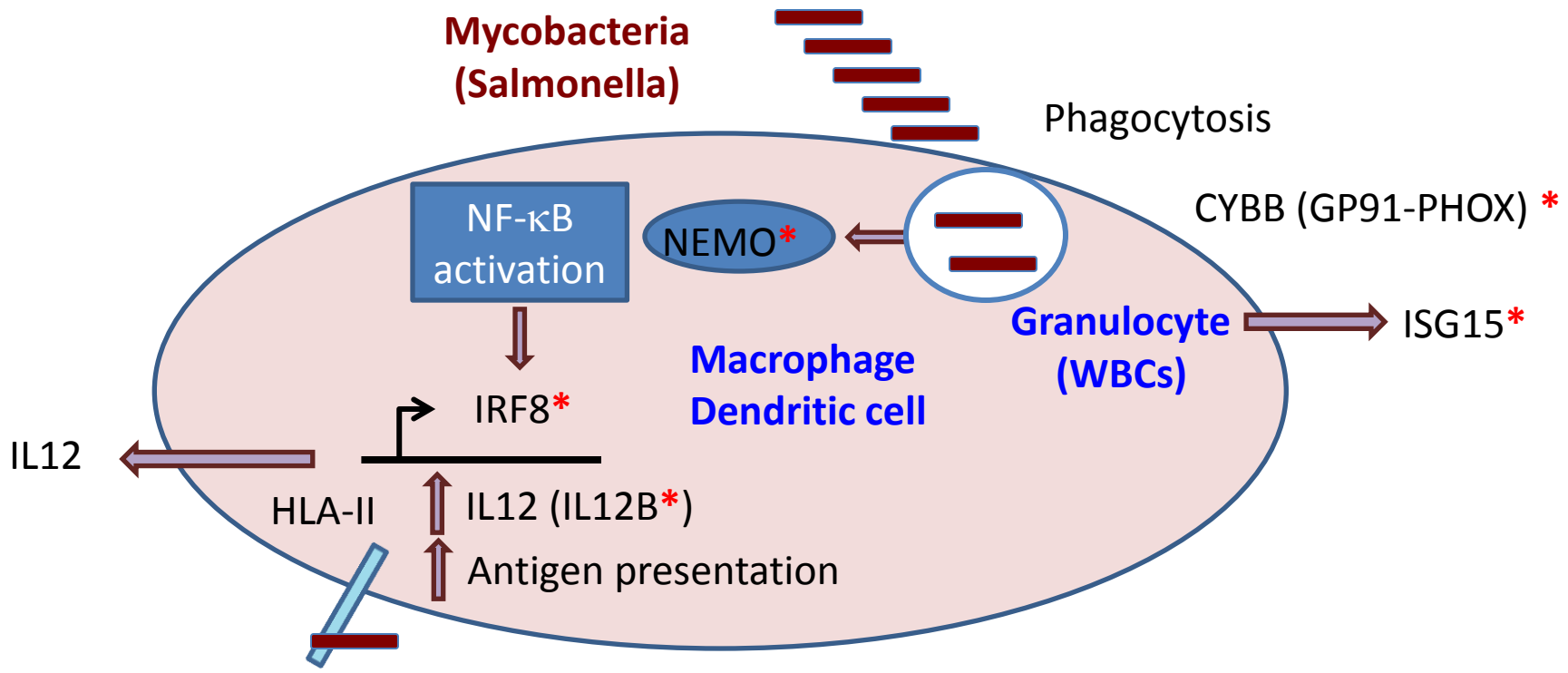
Dominant neg.
(Job syndrome)

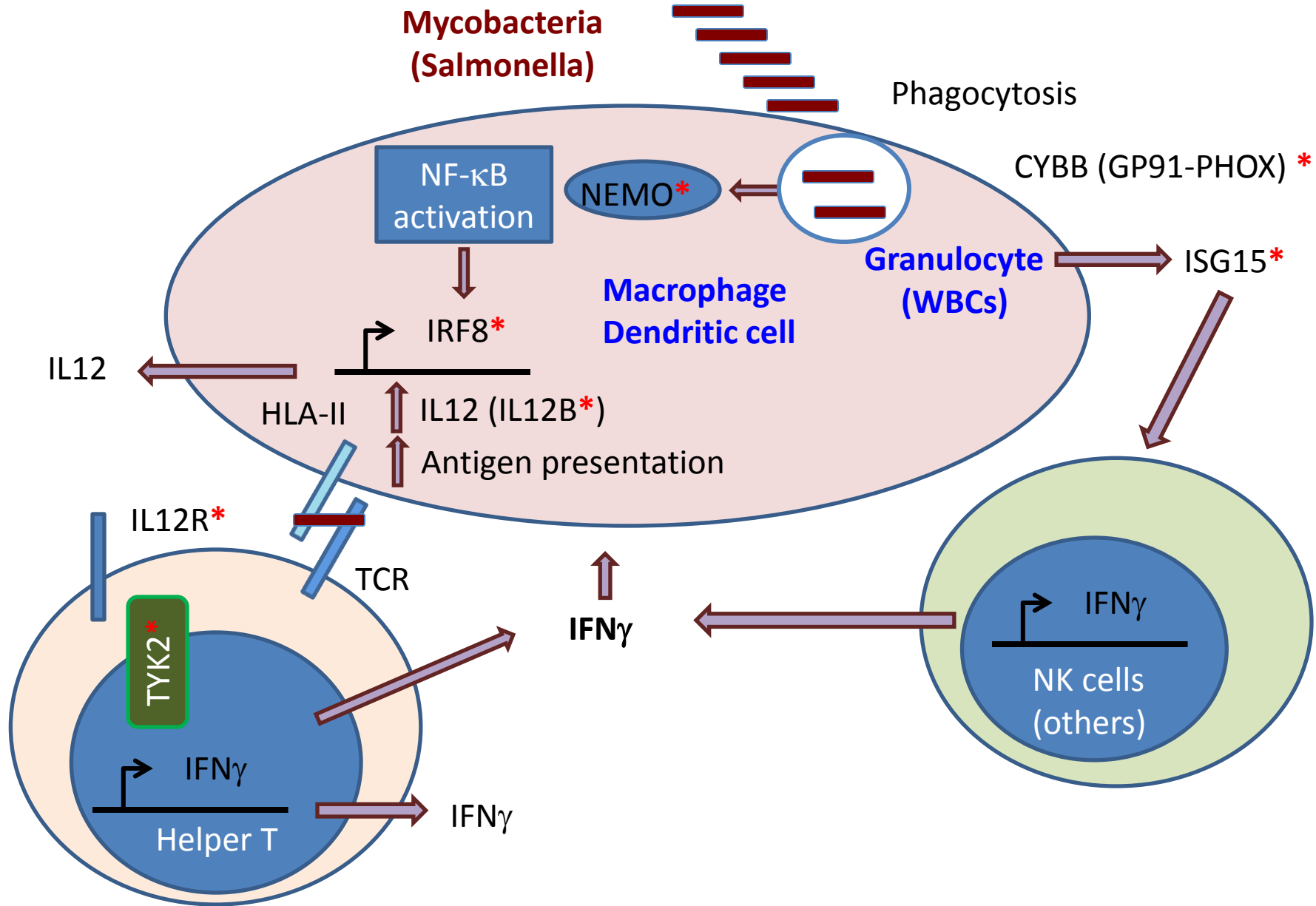
Naïve T cells

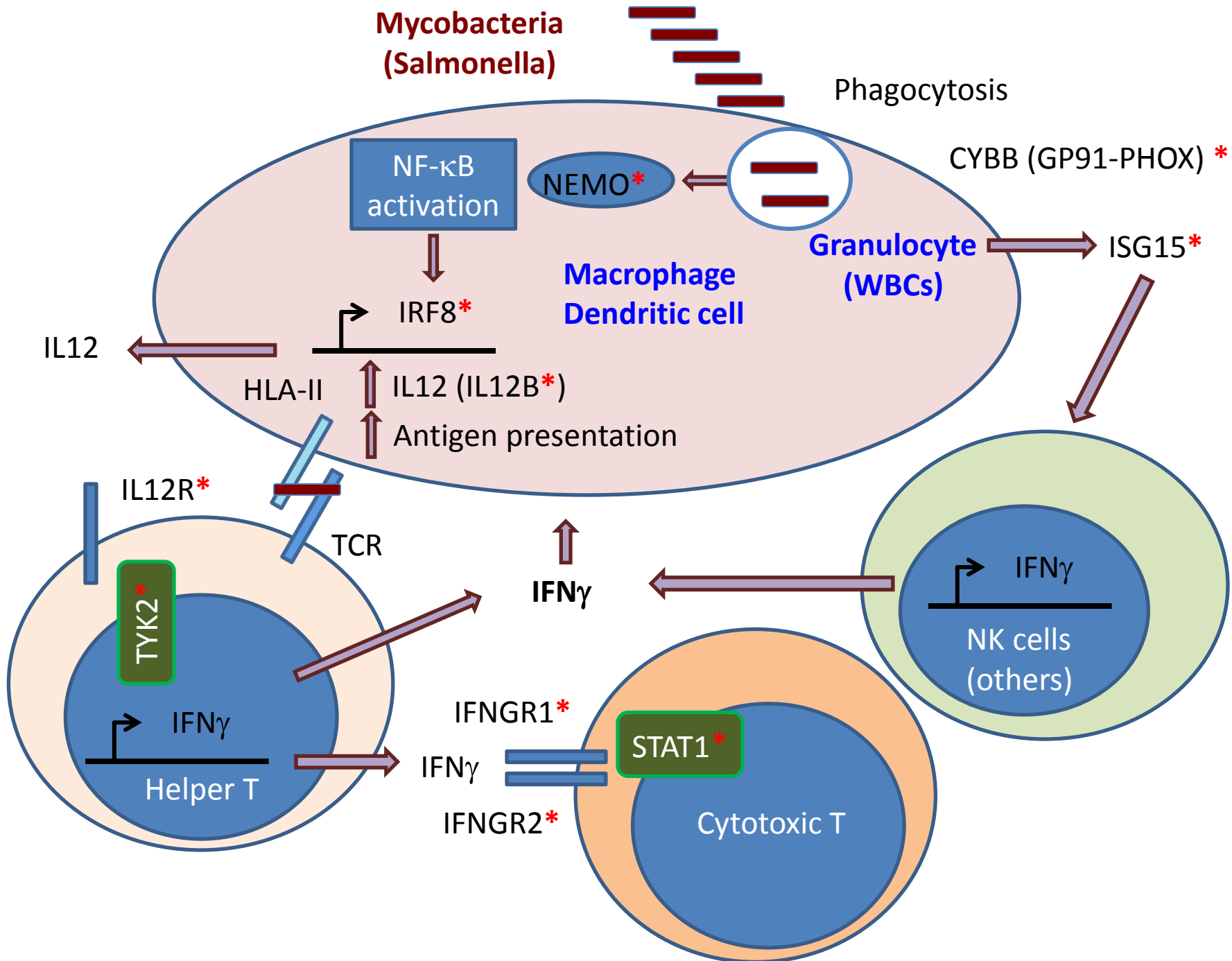


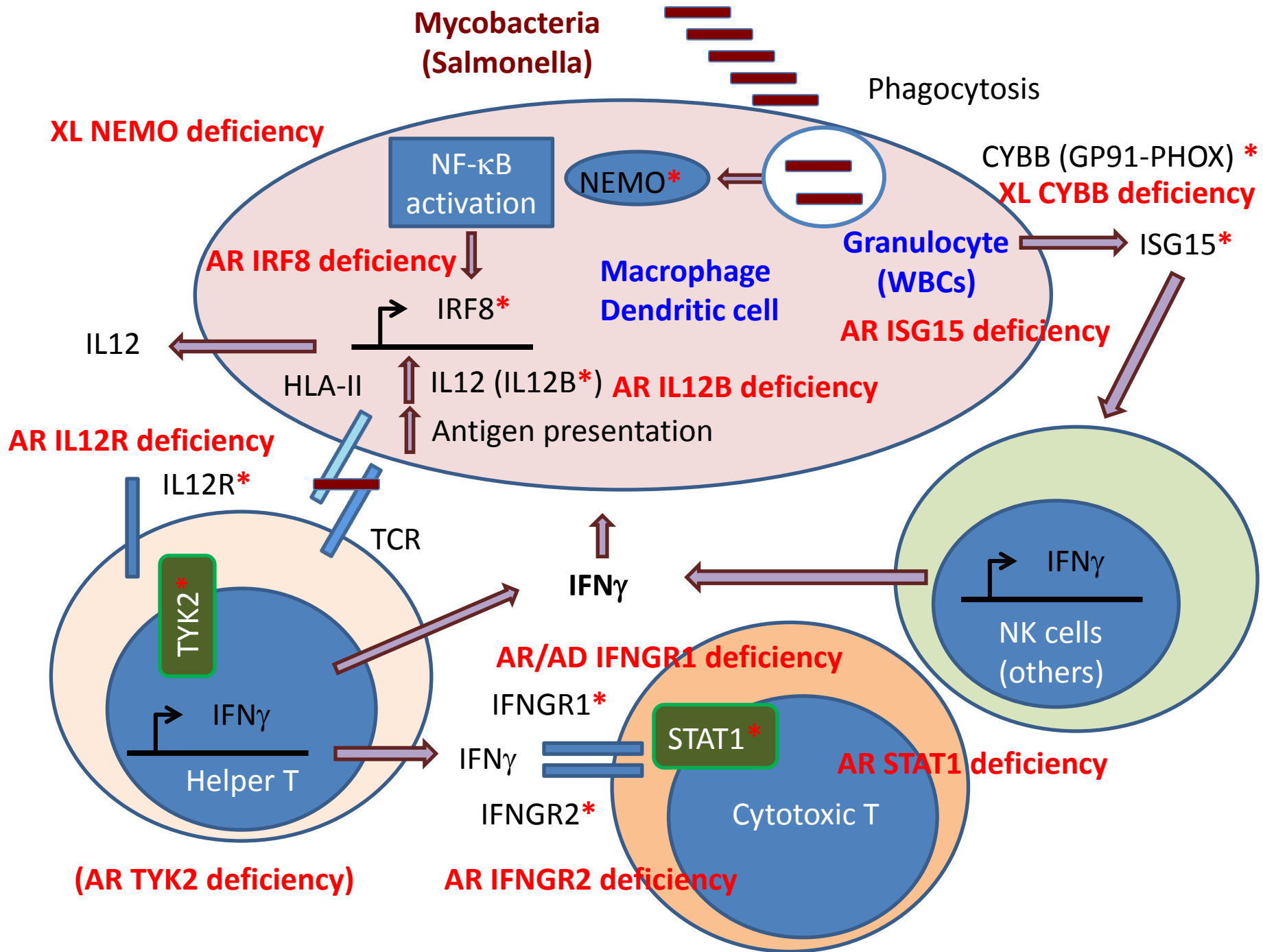
Mendelian susceptibility to mycobacterial disease

- Predisposition of otherwise apparently healthy individuals to infections caused by weakly virulent mycobacteria (BCG) and atypical (or nontuberculous) mycobacteria, *M. tuberculosis* and Salmonella
 - Genes:
 - IFNGR1 (AR/AD)
 - IFNGR2 (AR)
 - STAT1 (AD)
 - IL12B (AR)
 - IL12RB1 (AR)*
 - NEMO (IKBKG) (XL)
 - CYBB (XL)
 - IRF8 (AR/AD)
 - ISG15 (AR)
 - (TYK2 – AR)
- Impaired IFN- γ -mediated immunity (~50 % have unknown genetics)





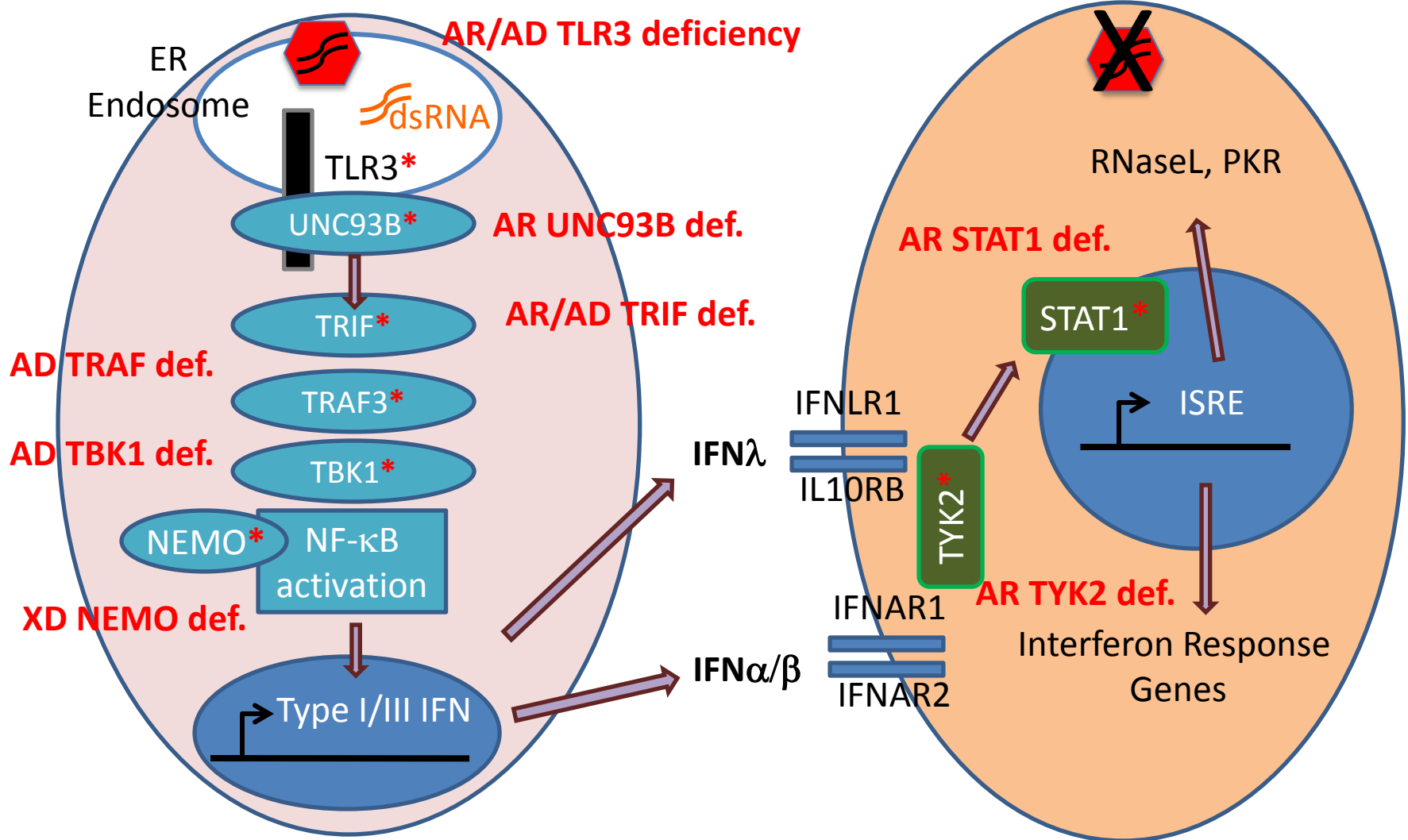




Herpes Simplex Encephalitis

- HSE is the most common cause of sporadic fatal encephalitis worldwide (70% mortality if untreated)
- Acyclovir
- Lifelong neurological sequelae of varying severity in survivors is common (>30%)
- Genes:
 - TLR3 (AR/AD)
 - UNC-93B (AR)
 - TRIF (AR/AD)
 - TRAF3 (AD)
 - TBK1 (AD)
 - NEMO (XR)
 - STAT1 (AR)
 - TYK2 (AR)

Herpes Simplex Encephalitis



Different genes – same/similar clinical phenotype

- **CMC:**

- IL-17RA, IL-17F, STAT1, DECTIN1, CARD9, STAT3, DOCK8, AIRE

- **MSMD:**

- IFNGR1, IFNGR2, STAT1, IL12B, IL12RB1, NEMO, CYBB, IRF8, ISG15, TYK2

- **HSE:**

- TLR3, UNC-93B, TRIF, TRAF3, TBK1, NEMO, STAT1

→ Molecular networks/pathways, not genes

→ Single gene testing vs. gene panels

One gene – multiple phenotypes

- AD **STAT1** deficiency: **dominant negative** mutations
→ susceptibility to mycobacterial and salmonella infections
- AD **STAT1** deficiency: **gain-of-function** mutations
→ chronic mucocutaneous candidiasis
- AR **STAT1** deficiency: **loss-of-function** mutations
→ susceptibility to severe viral and mycobacterial disease

Definition of PIDs

- defined based on clinical/immunological phenotype
 - defined based on the molecular defect
- none of these definitions are perfect

Genetics of PIDs

- Manifestations (infections) can be the same in both primary and secondary ID as well in “healthy” individuals
 - Genetics + Environment
- ~150 PIDs, >200 genes (both growing)
 - increasing role for mutation testing (PIDs defined by genes)
 - novel technologies (whole genome/exome)
- One disease multiple genes (overlapping phenotypes)
 - CMC, MSMD, HSE
- One gene, multiple diseases
 - STAT1, NEMO
- Inheritance: AR, AD, XL
 - AR/AD IFNGR1
- Molecular networks/pathways, not genes
 - recognition → signaling → effector function

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