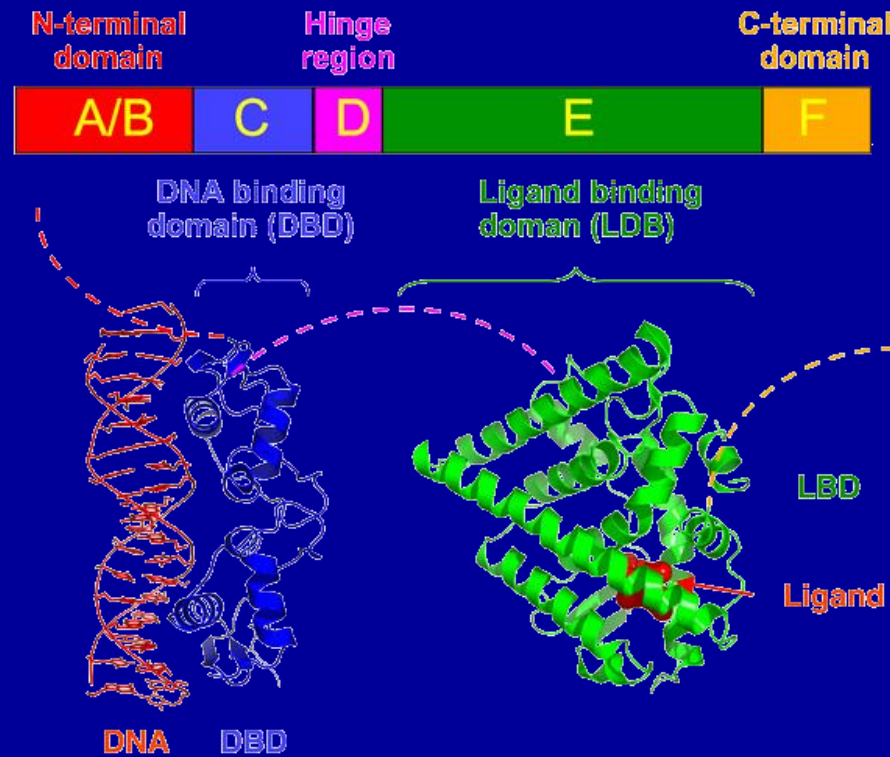


# Receptor & Signalling II



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# Learning Outcomes

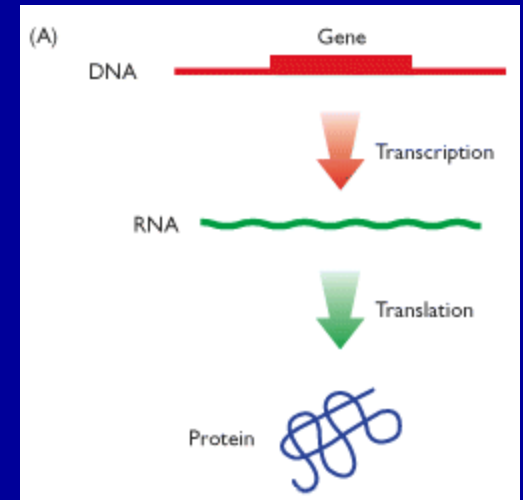
1. To list three key features of regulatory elements.
2. To list two functional domains of transcription factors.
3. To list the basic structural requirements for Nuclear Receptor (NR) action.
4. To classify the NRs as a 'superfamily' of proteins.
5. To classify the different types of ligands that modulate the activity of NRs.
6. To explain how NRs regulate the expression of a target gene.

# Gene Regulation in Eukaryotes

## Constitutive expression

Some of these genes expressed in all cells all the time.

House keeping genes are responsible for the routine metabolic functions common to all cells e.g respiration, basic metabolism, proteins of the cytoskeleton and chromosomes.



## Regulated expression

Some genes are only expressed in specialised cells. Other differences in gene expression between cell types may be more subtle.

# Transcription Factors Regulate Gene Expression

Why does gene expression need to be controlled anyway?

Primary purpose in multicellular organisms is to execute precise developmental decisions so that:

correct genes are expressed at:

- appropriate time
- correct place
- at the required levels

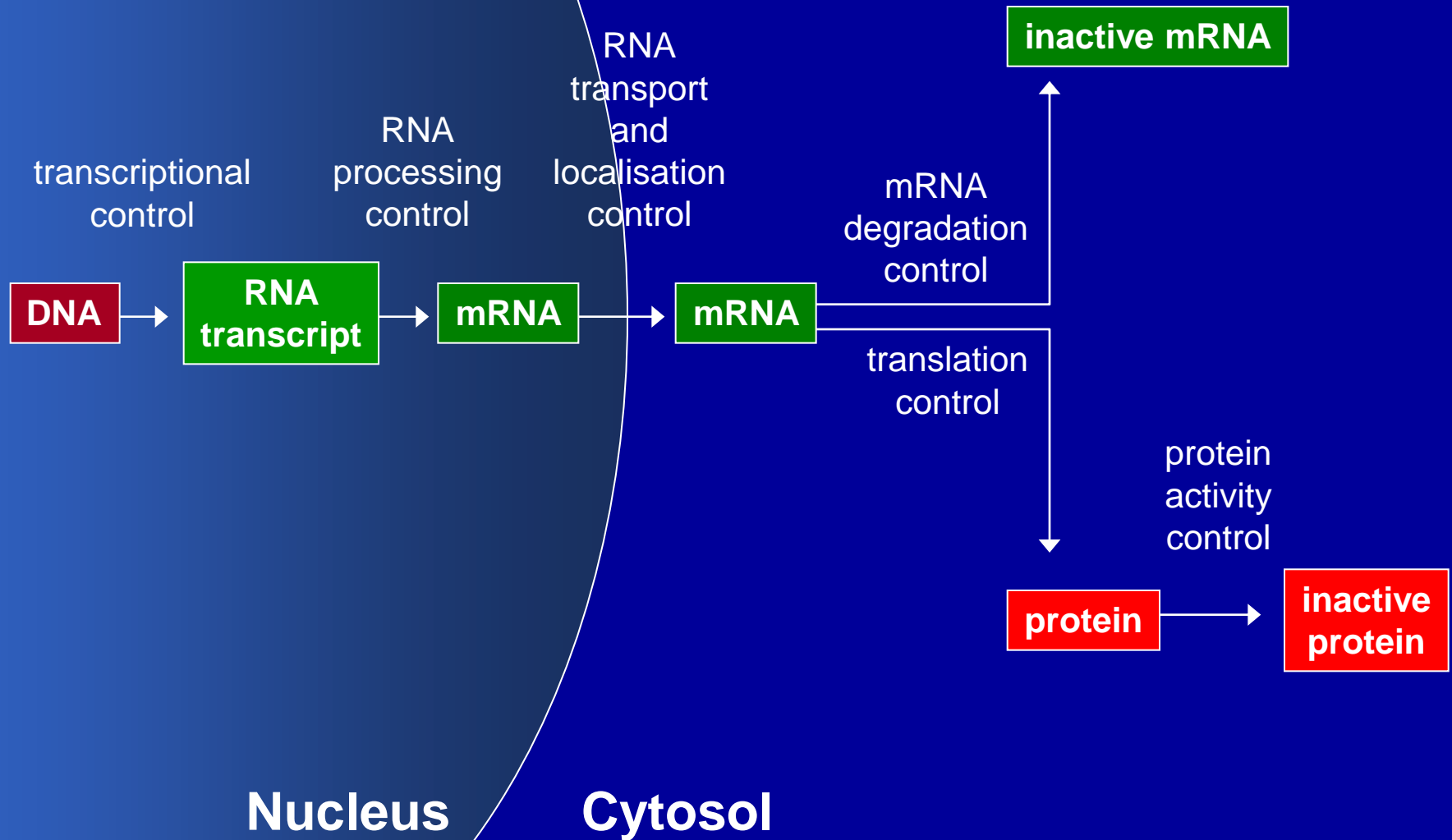
so that development, growth and differentiation proceed correctly.

Stimuli cause alterations in gene expression.

Some genes are expressed in response to nutritional/chemical stimuli (sugar, amino acid, hormone signal).

Environmental signal (light, temperature).

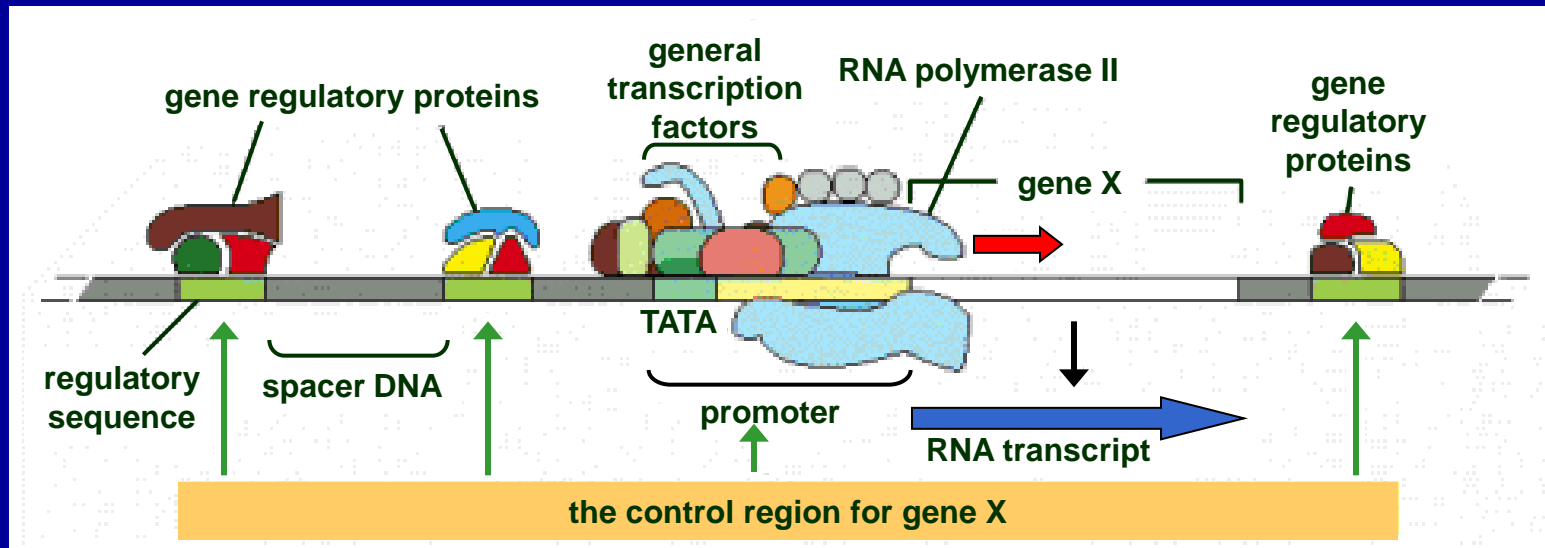
# Gene Expression Can be Regulated at Many Steps in the Pathway from DNA to RNA to Protein



# Protein-coding genes

- **Exons** whose sequence encodes the polypeptide
- **Introns**
- **Transcription start site**
- **RNA polymerase II** synthesizes precursors of mRNAs.
  
- **Proximal Promoter.**
  - i) **Basal** or **core** promoter located within 40bp of the start site.
  - ii) “Upstream” promoter which may extend over as many as 200bp upstream.
- **Enhancers**
- **Silencers**

# The Gene Control Region of a Typical Eukaryotic Gene

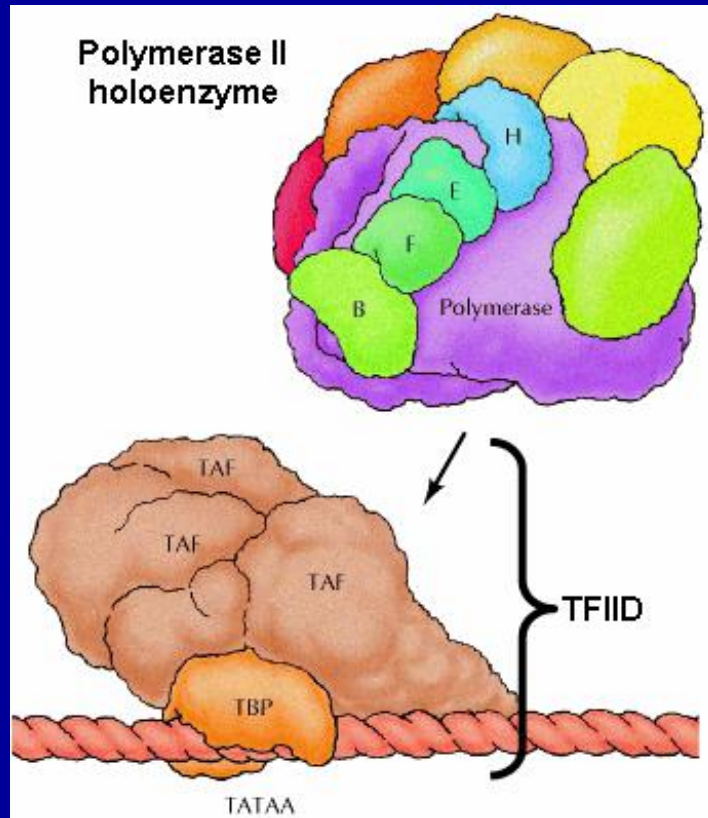


The **promoter** is the DNA sequence where the general transcription factors and the polymerase assemble.

The **regulatory sequences** serve as binding sites for gene regulatory proteins:  
affects the rate of transcription initiation  
can be located adjacent to the promoter, far upstream, within introns or downstream of the gene.

Whereas the **general transcription factors** that assemble at the promoter are similar for all polymerase II transcribed genes, the gene **regulatory proteins** and the locations of their **binding sites** relative to the promoter are different for each gene.

# RNA polymerase II holoenzyme

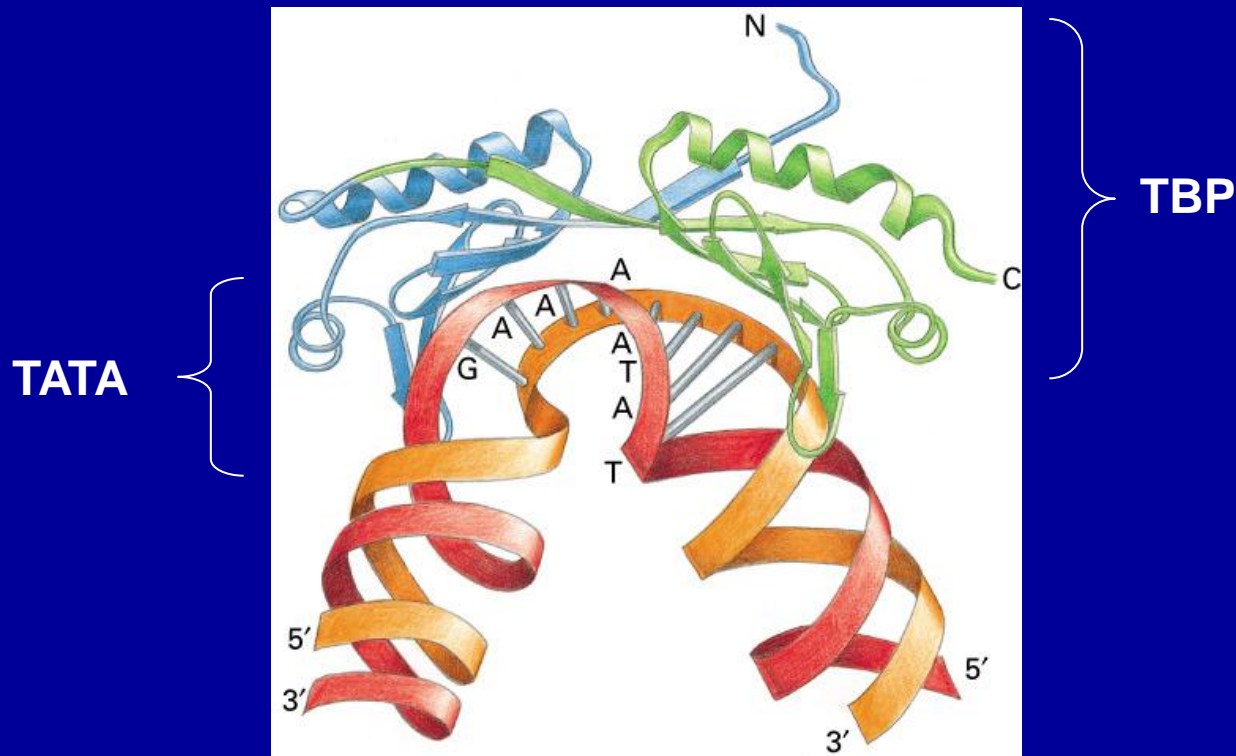


- RNA Polymerase II Requires General Transcription Factors
- The holoenzyme consists of a complex of RNA polymerase II, the general transcription factors **TFIIB**, **TFIIE**, **TFIIF**, and **TFIIH**, and several other proteins that activate transcription. (TFII = transcription factor for polymerase II)
- This complex can be recruited directly to a promoter via interaction with **TFIID**.
- **TFIID** is composed of **TBP** (TATA Binding Protein), and **TAFs** (TBP-associated Factors).



# TBP Induces Bending of DNA

The unique DNA bending at the TATA box caused by TBP generates two kinks in the double helix separated by partly unwound DNA may serve as a landmark for an active promoter that helps to attract the other general transcription factors (TFIIB).



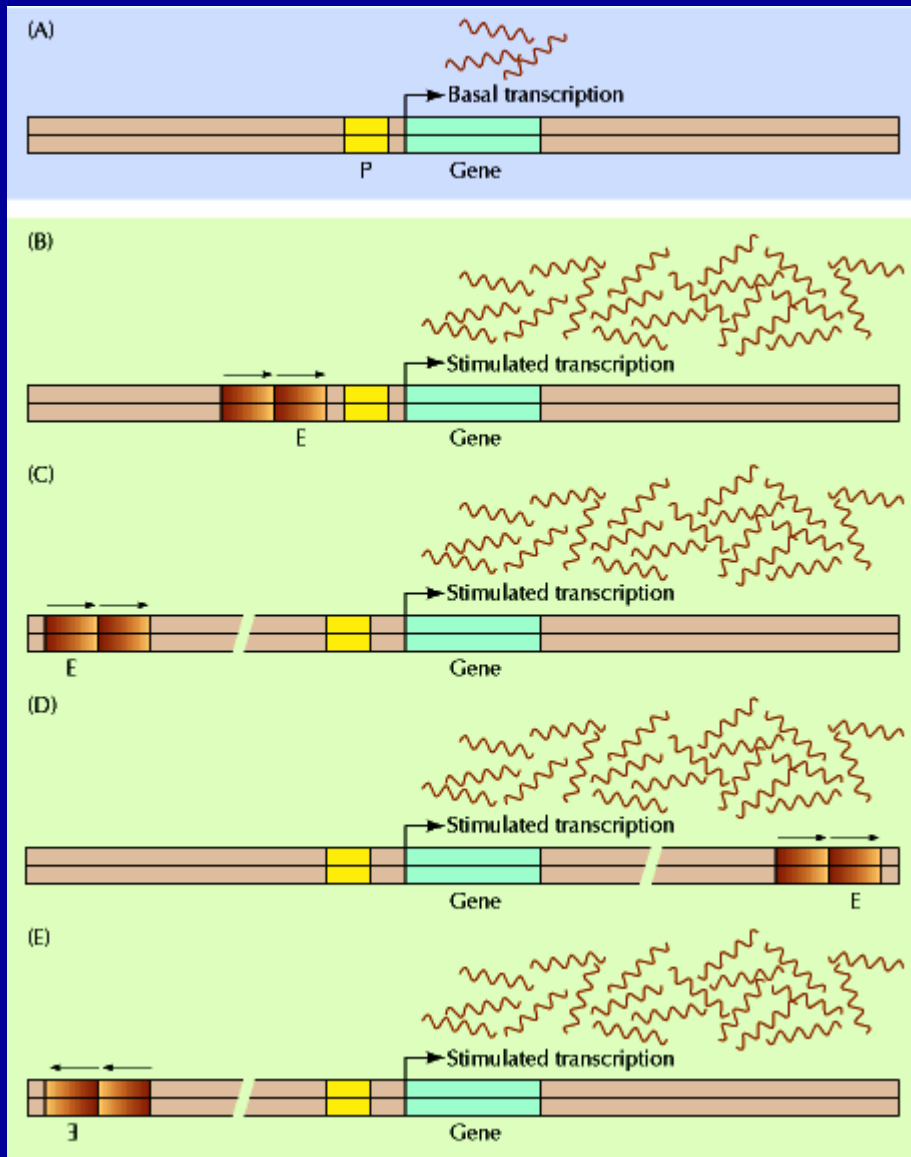
## TFIIH Enzymatic Activity

TFIIH - has **helicase** activity (ATP-dependent) and **protein kinase** activity - phosphorylation of the C-terminus of Pol II is required for its activity.

# Features of Response Elements

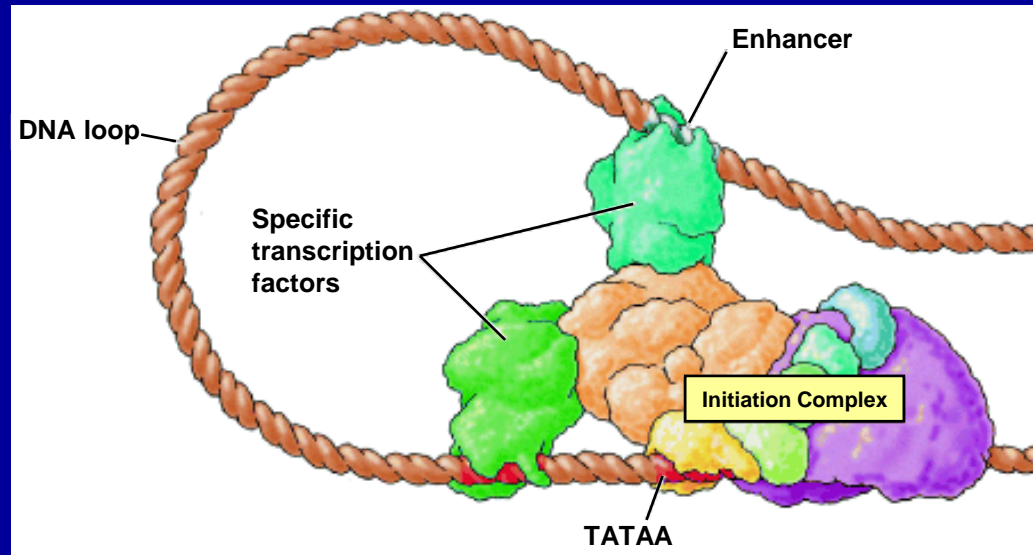
- contain short consensus sequences
- not fixed in location but usually within 200 bp upstream of the transcription start site
- a single element is usually sufficient to confer a regulatory response
- can be located in a promoter or an enhancer
- a specific protein (transcription factor) binds to the element and the presence of that protein is developmentally regulated

# Action of Enhancers



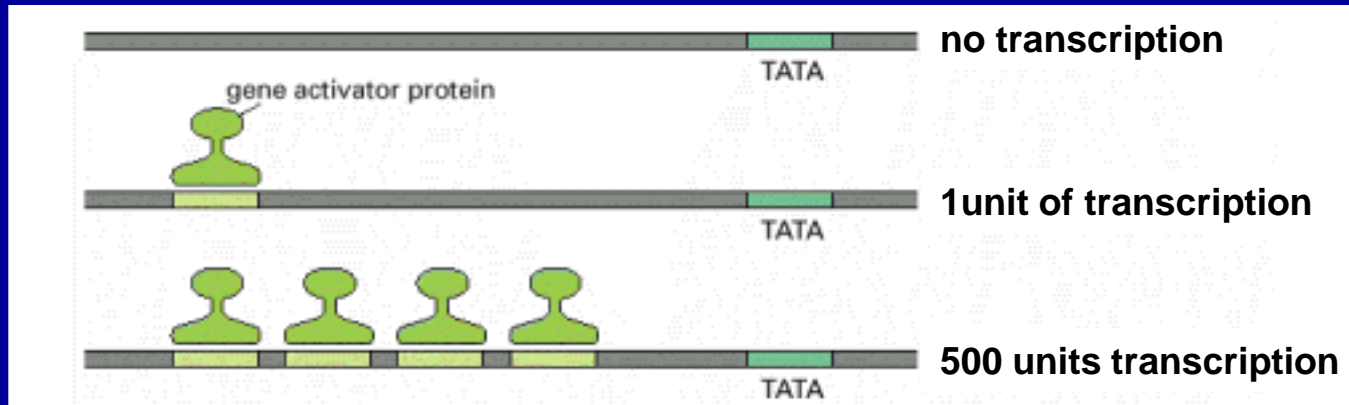
- Without an **enhancer**, the gene is transcribed at a low basal level.
- Addition of an **enhancer**, E for example, stimulates transcription.
- The enhancer is active not only when placed just **upstream** of the promoter, but also when inserted up to several kilobases either **upstream** or **downstream** from the transcription start site.
- In addition, enhancers are active in either the **forward** or **reverse orientation**.

## Gene Activation at a Distance: DNA Looping



- Transcription factors bound at distant enhancers are able to interact with general transcription factors at the promoter.
- The intervening DNA can form loops.
- There is therefore no fundamental difference between the action of transcription factors bound to DNA just upstream of the promoter and to distant enhancers.

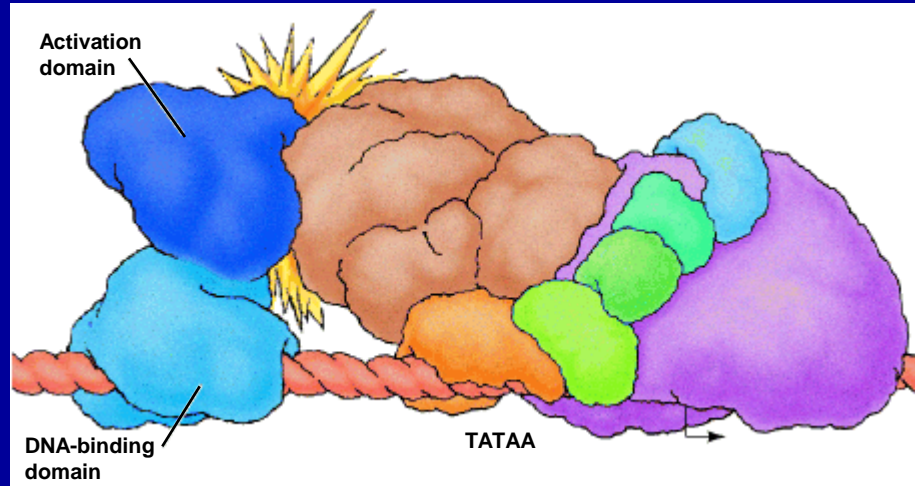
# Synergistic Action of Transcriptional Activators



## Transcriptional synergy:

- Greater than additive effect of the activators.
- Typically observed between different gene activator proteins (**transcription factors**) from the same organism.
- Also between activator proteins from widely different eukaryotic species when they are experimentally introduced into the same cell (The transcriptional machinery is highly conserved).

# Structure of Transcriptional Activators

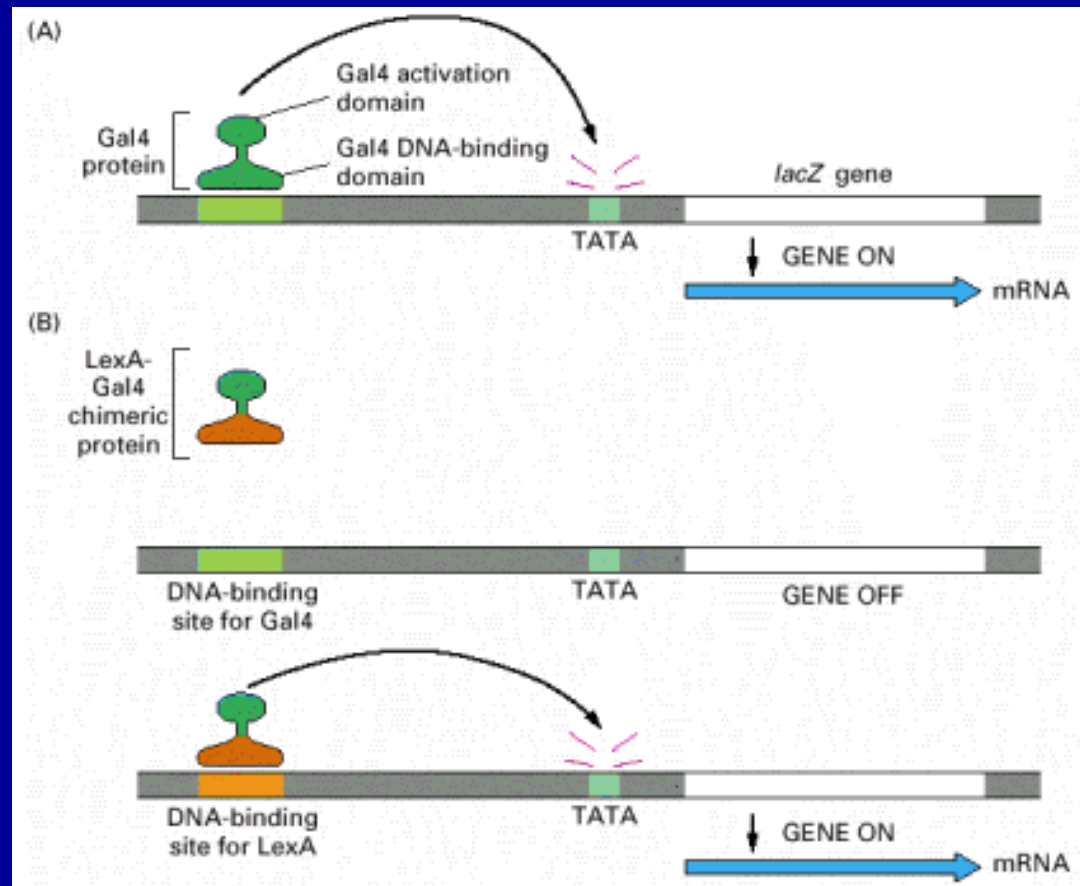


Transcriptional activators consist of two independent domains.

The DNA-binding domain recognises a specific DNA sequence.

The activation domain interacts with other components of the transcriptional machinery.

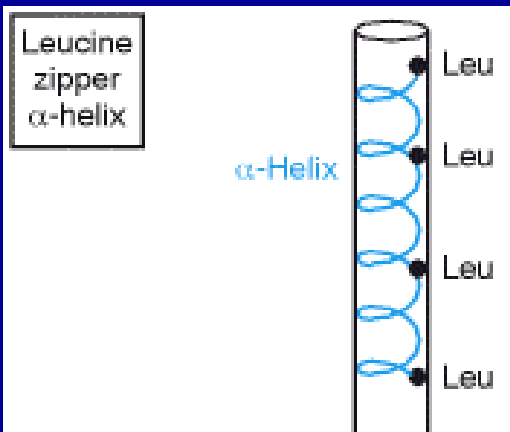
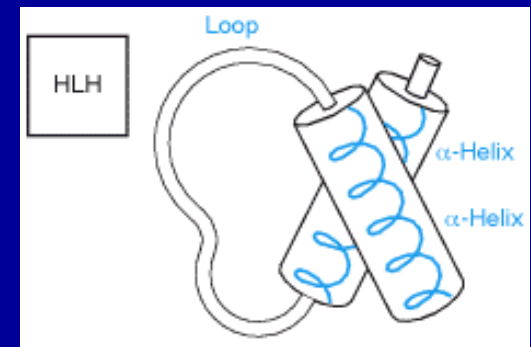
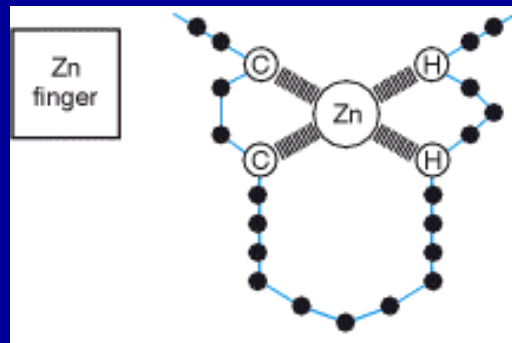
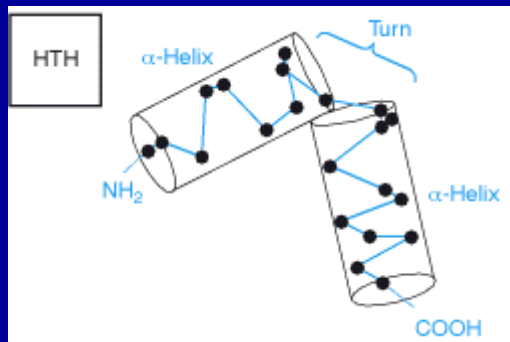
# The modular structure of a gene activator protein



A functional activator can be reconstituted from the C-terminal portion of the yeast Gal4 protein if it is attached to the DNA-binding domain of a bacterial gene regulatory protein (the LexA protein).

The resulting hybrid protein activates transcription from genes provided that the specific DNA-binding site is present.

# Structural motifs commonly found in transcription factors and DNA-binding proteins.



(HTH) **Helix-turn-helix** domains consist of 2  $\alpha$  helices connected by short chain of amino acids. C-terminal helix fits into major groove of DNA. N-terminal helix – structural component helps position the recognition helix.

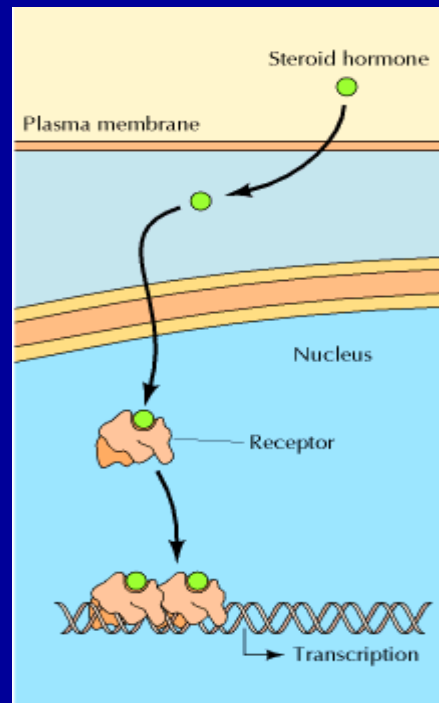
The **leucine zipper** monomer is *amphipathic* [i.e. has hydrophobic residues (leucines) consistently on one face of the helix]. Interactions between the hydrophobic side chains of leucine residues exposed on one side of a helical region are responsible for dimerization. Two  $\alpha$  helices form an inverted Y-shape structure that grips the DNA helix.

**Zinc finger** domains consist of loops in which an  $\alpha$  helix and a  $\beta$  sheet coordinately bind a zinc ion (via Cysteine-Cysteine-Histidine-Histidine). Clusters of Zn fingers mediate strong and sequence specific DNA binding.

(HLH) **Helix-loop-helix** domains are similar to leucine zippers, except that the dimerization domains of these proteins each consist of two helical regions separated by a loop.



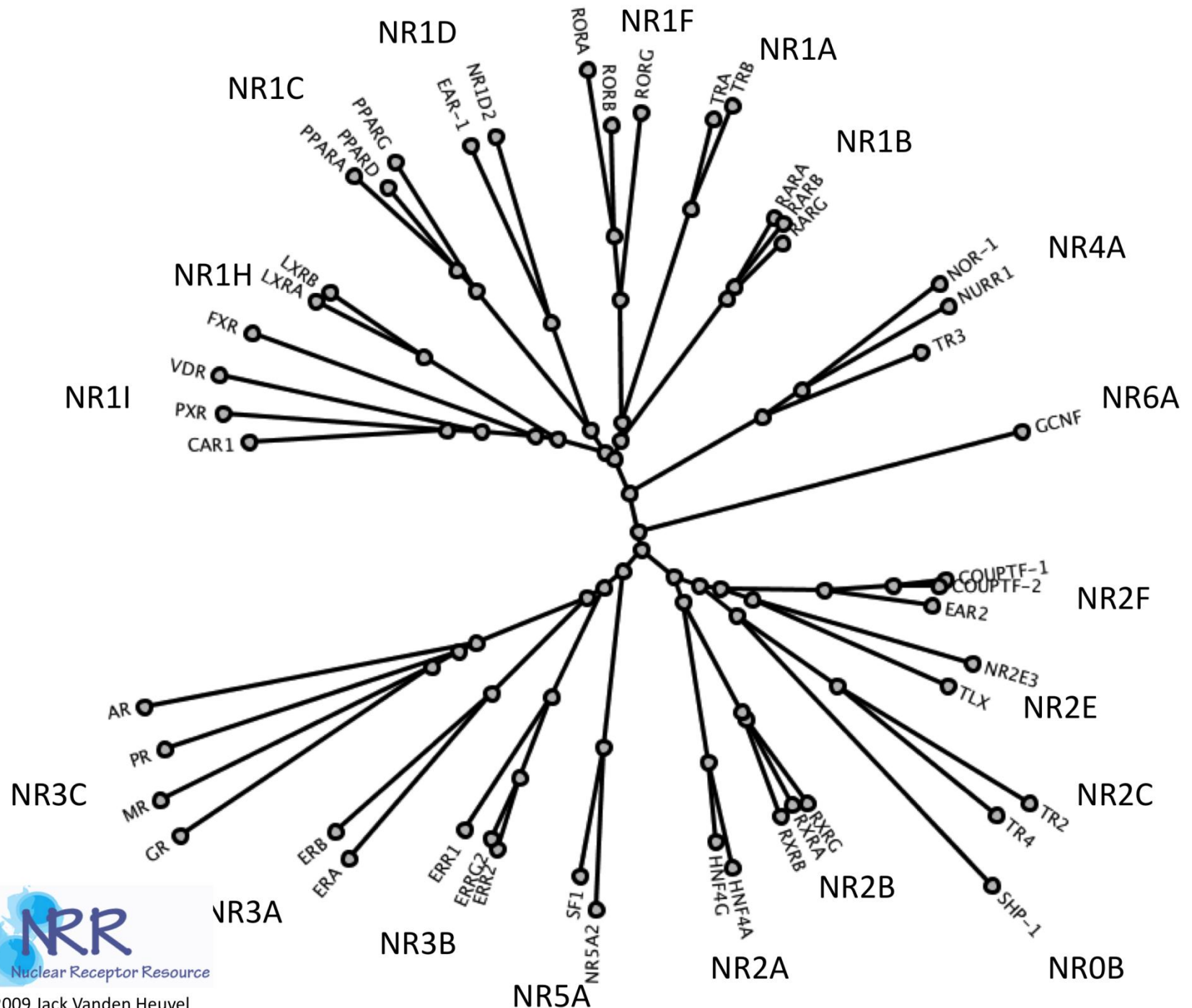
# Nuclear Receptors - Transcription Factor Family



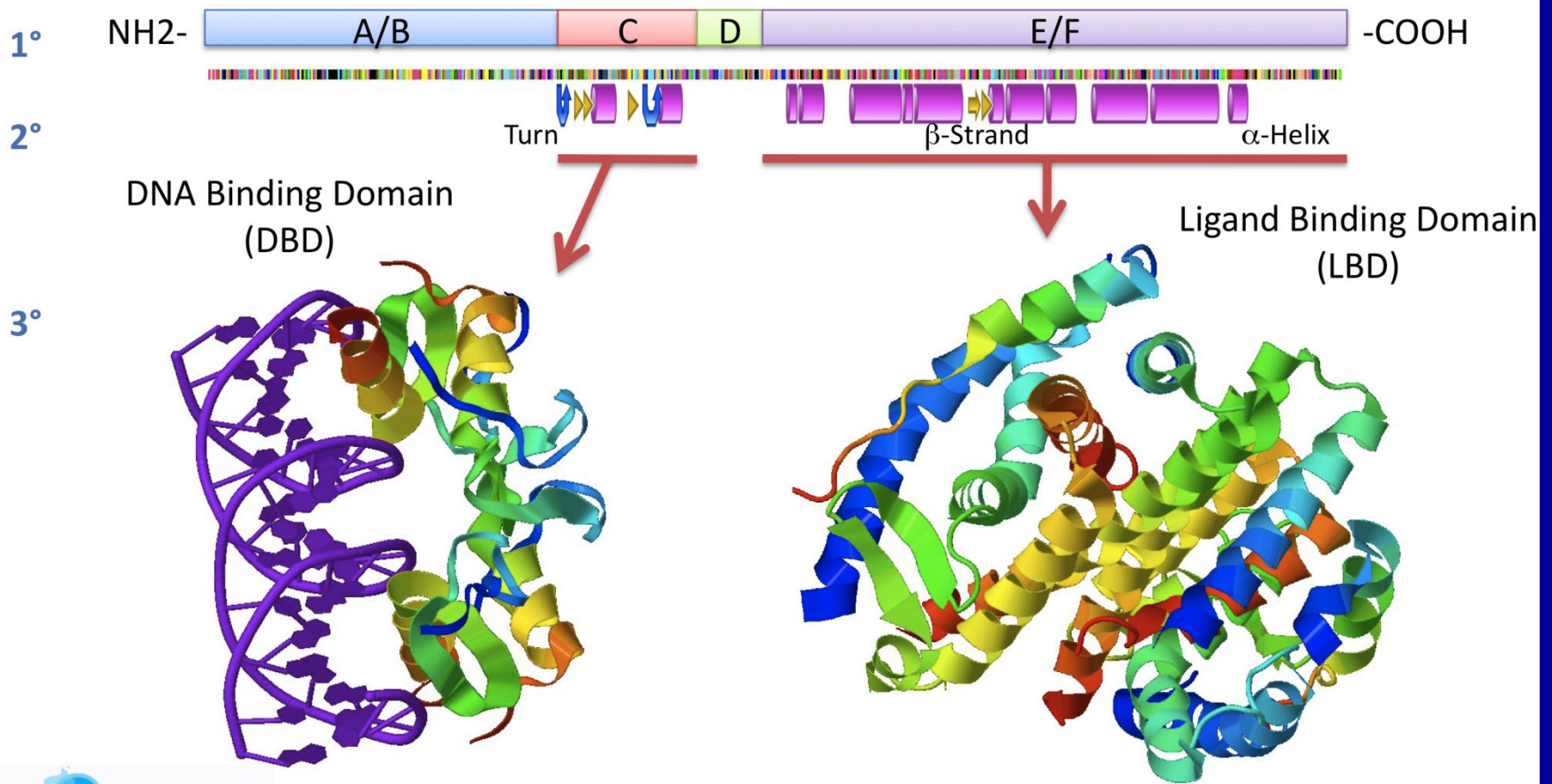
The **Nuclear Receptors** are intracellular proteins that:

- function as **transcription factors**
- bind to specific DNA sequences in the **promoters** or **enhancers** of target genes
- regulate **gene expression**
- 48 genes** coding for nuclear receptors in the human genome.
- Some are **widely expressed** while others are restricted to very **specific tissues** and cell types.

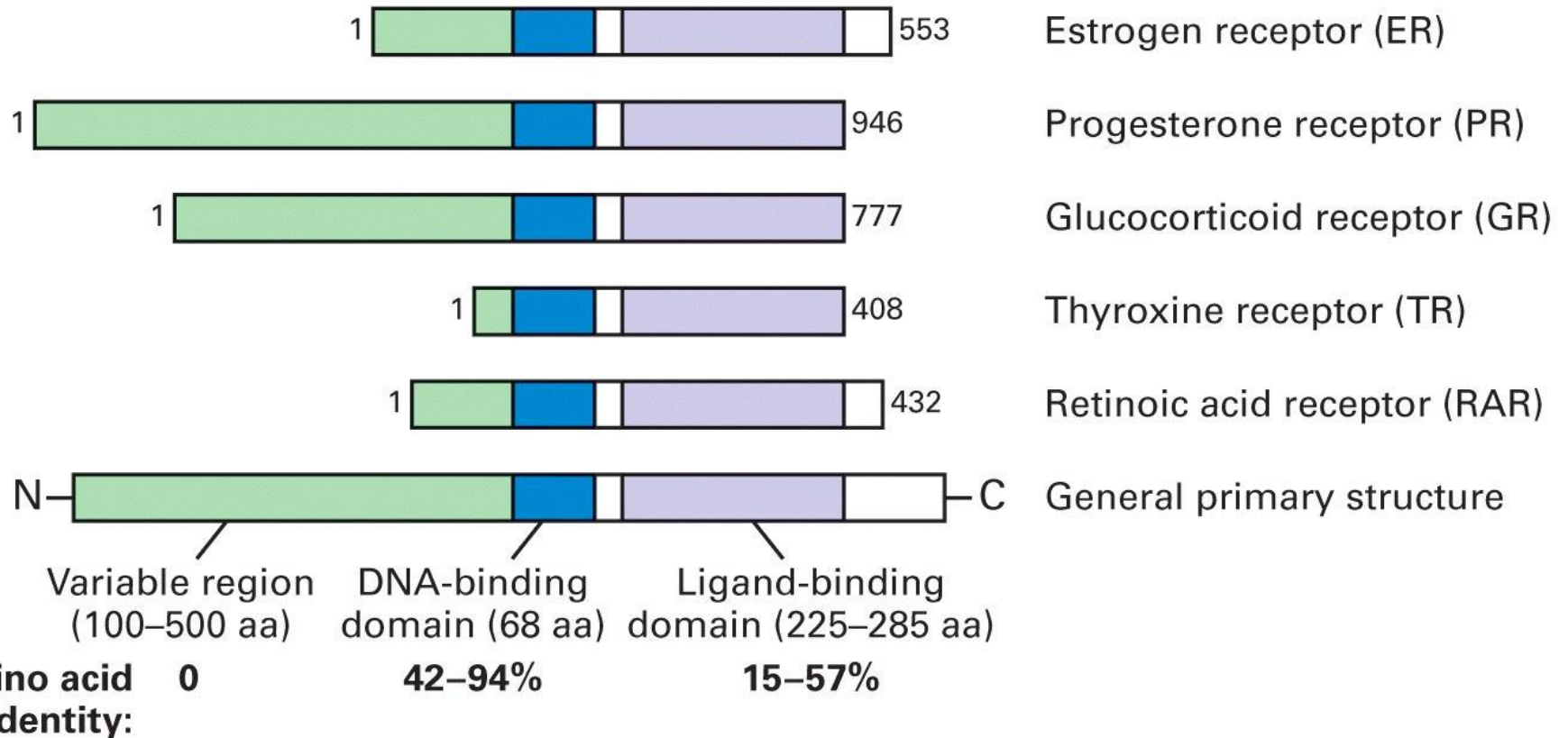
# Phylogeny and Nomenclature



# Structure of NRs



# Domain structure of Nuclear Receptors



# How can Nuclear Receptors be classified?

**LIGAND BINDING**

**DNA BINDING & DIMERISATION**

**EXPRESSION PATTERN**

# Ligands for Nuclear Receptors

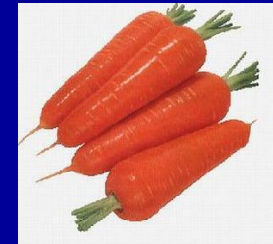
Task:

List 4 different substances that can act as ligands for NRs.

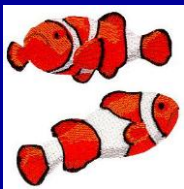
# *The biochemical origins of Nuclear Receptor ligands are varied:*



Cholesterol is the biosynthetic source of the steroid hormones

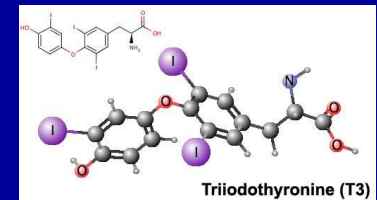


Retinoic acids are produced from  $\beta$ -carotene.



The eicosanoid, prostaglandin  $J_2$ , is a product of fatty acid metabolism.

Thyroid hormone is a tri-iodinated thyronine made as a degradation product of crosslinked iodinated tyrosines in the protein thyroglobulin.



***Although diverse in origin, NR ligands are all similar in mass and molecular size.***

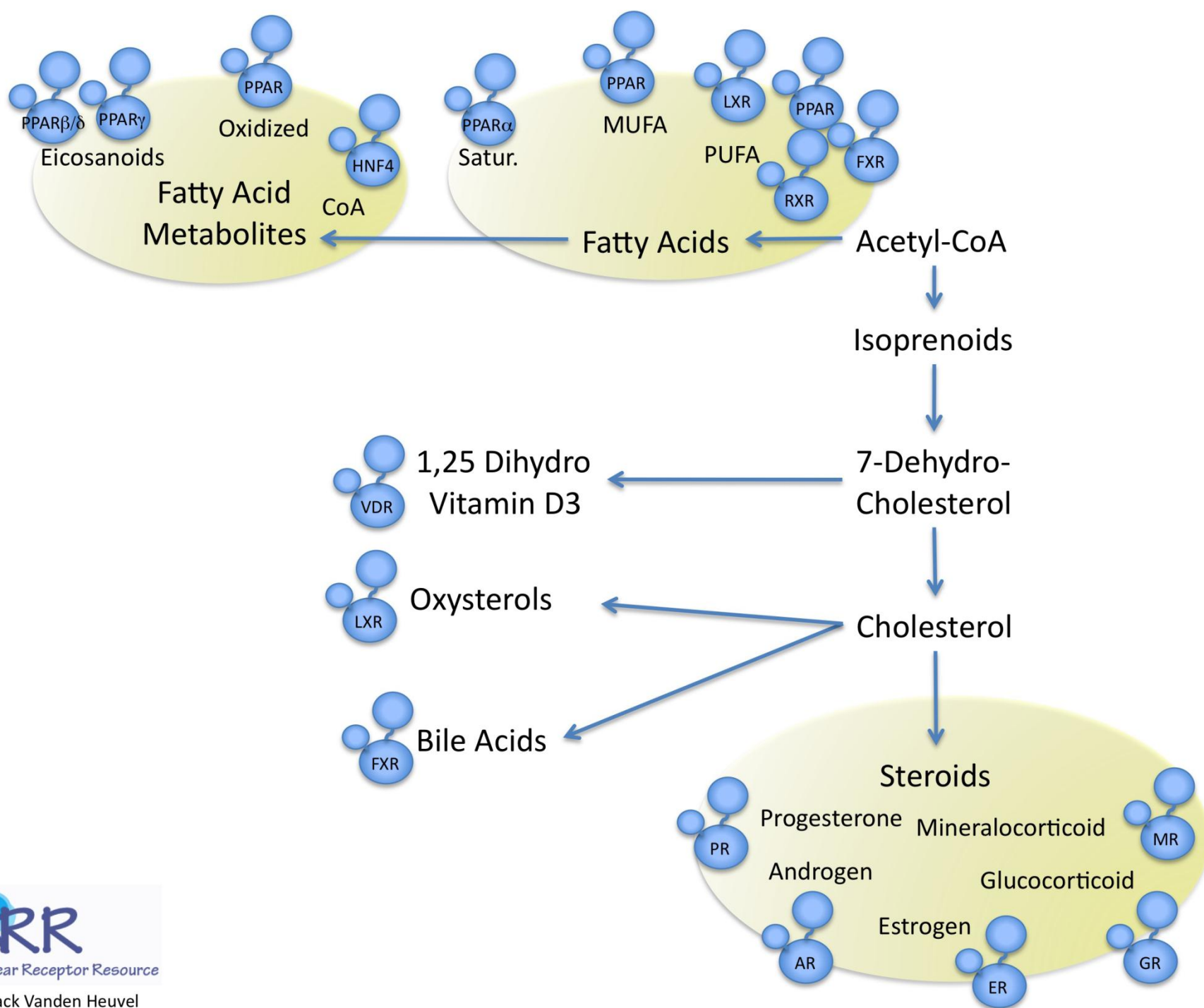


# Nuclear Receptor Family

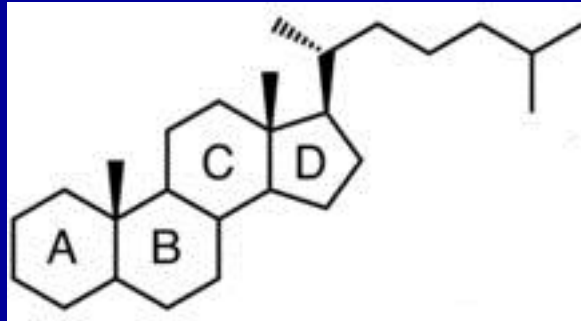


	<u>Receptors</u>	<u>Receptors</u>	<u>Receptors</u>
<b>Ligands:</b>	High-affinity, hormonal lipids	Low-affinity, dietary lipids	Unknown
	ER $\alpha, \beta$ PR AR GR MR  RAR $\alpha, \beta, \gamma$ TR $\alpha, \beta$ VDR	RXR $\alpha, \beta, \gamma$ PPAR $\alpha, \beta, \gamma$ LXR $\alpha, \beta$ FXR PXR/SXR CAR  <b>Ligands?</b> SF1 LRH-1	HNF-4 COUP-TF $\alpha, \beta, \gamma$ DAX-1 SHP TLX PNR NGFI-B $\alpha, \beta, \gamma$ ROR $\alpha, \beta, \gamma$ ERR $\alpha, \beta, \gamma$ RVR $\alpha, \beta, \gamma$ GCNF TR 2,4

Adapted and modified from (Chawla *et al* Science 294 p1866 2001)



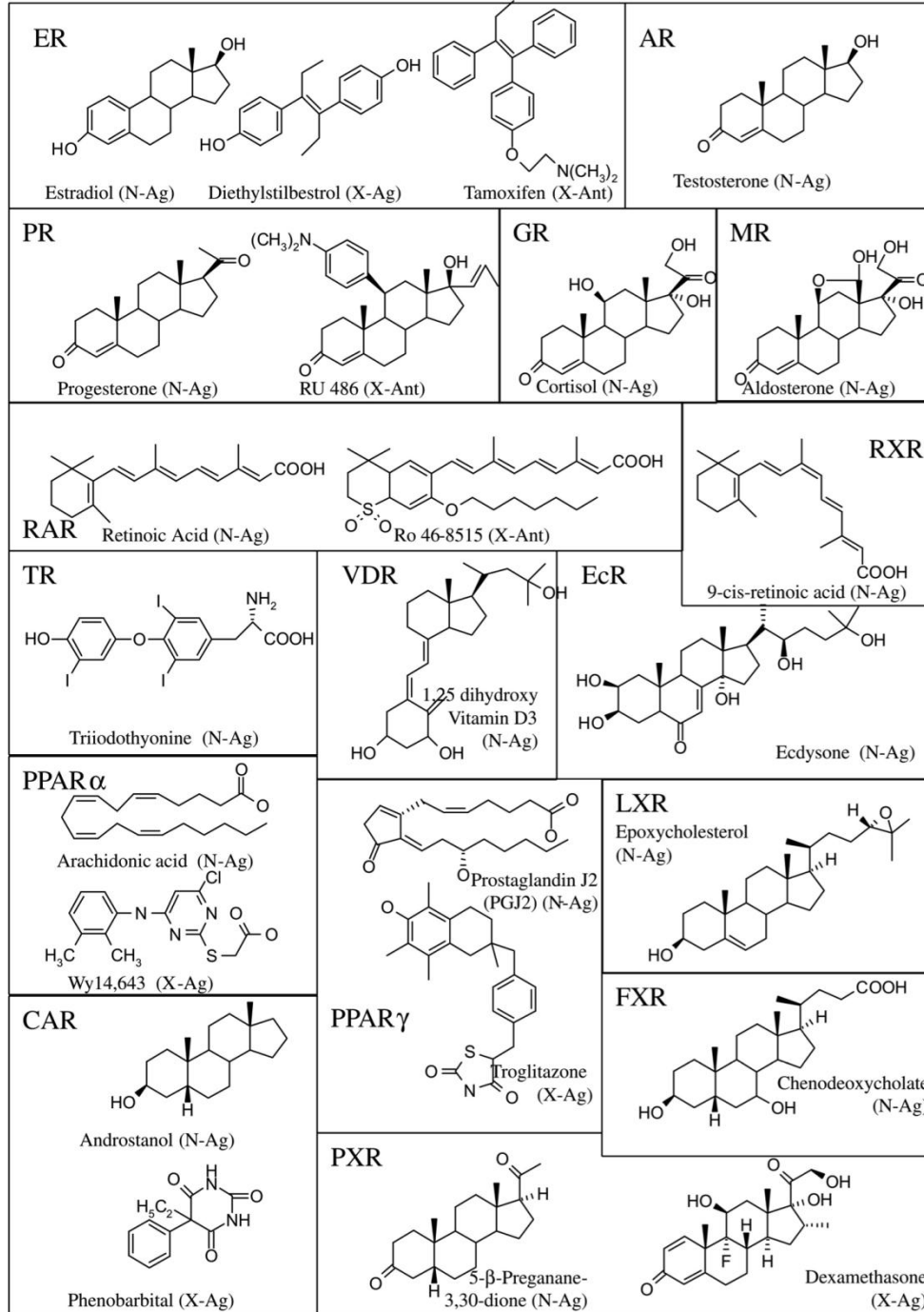
# Steroids



A **steroid** is composed of four fused carbon rings: three cyclohexane rings (A, B, C) and one cyclopentane ring (D) that determine the characteristic **sterane** core.

Steroids vary due to additional functional groups attached to the carbon rings and oxidation states of the rings.

# Representative NR Ligands

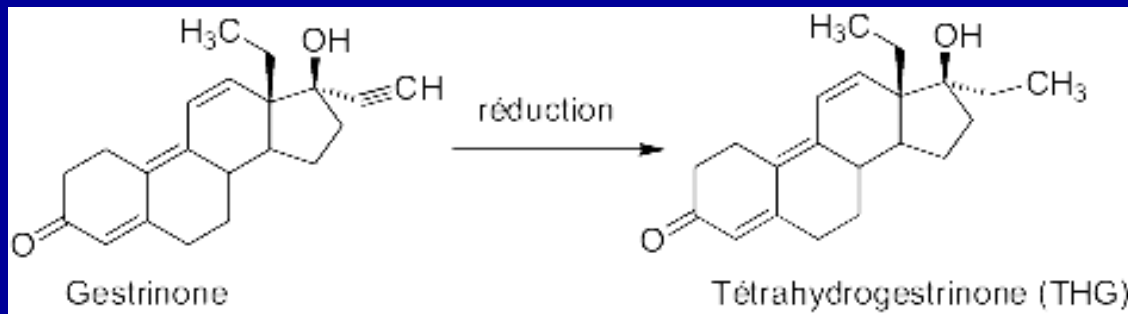


# Designer Androgens in Sport

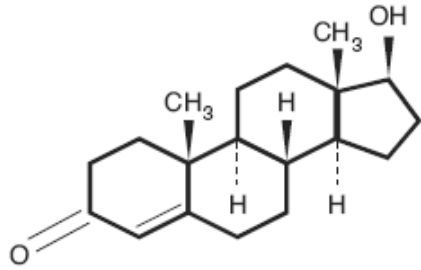
Dwain Chambers



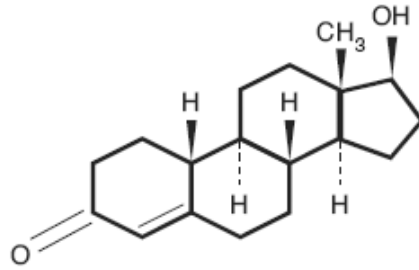
Marion Jones



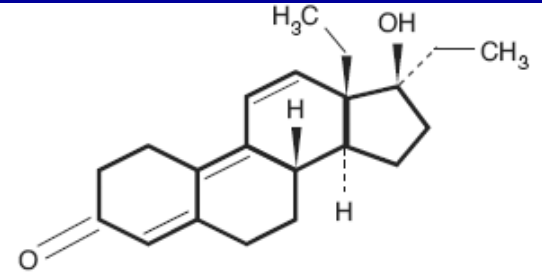
# Designer Androgens in Sport



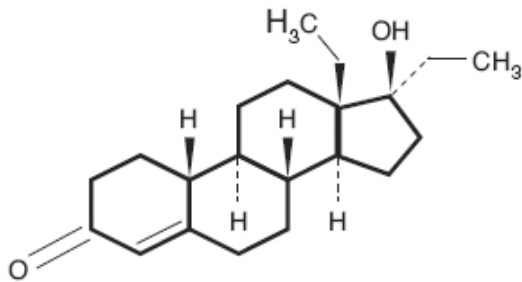
Testosterone



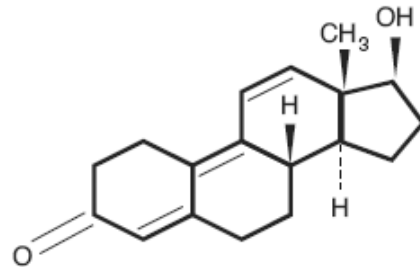
Nandrolone



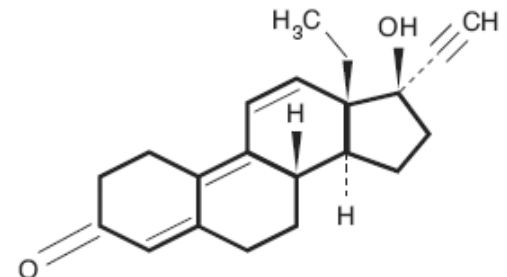
THG



Norbolethone



Trenbolone



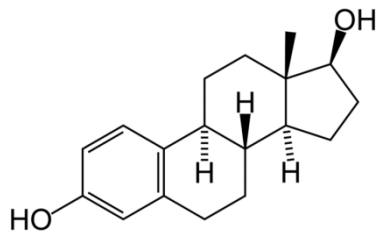
Gestrinone

THG and related natural and synthetic androgen structures. Note the structural similarities between the two designer androgens norbolethone and THG with THG's parent gestrinone (differing by only a side chain reduction) and the known potent androgens nandrolone and trenbolone.

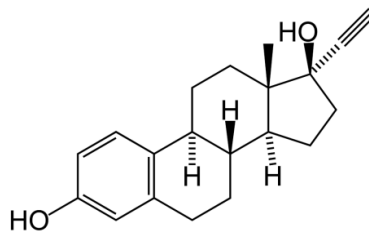
# Endocrine Disrupting Chemicals

**Endocrine disruptors** are exogenous substances that act like hormones in the endocrine system.

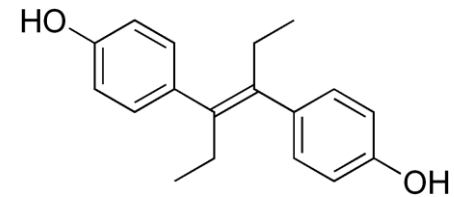
They disrupt the physiologic function of endogenous hormones.



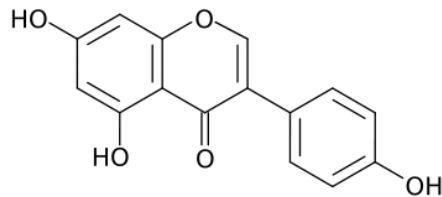
17β-Estradiol



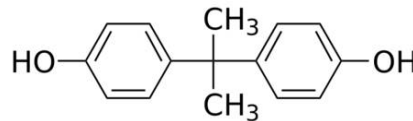
Ethinylestradiol



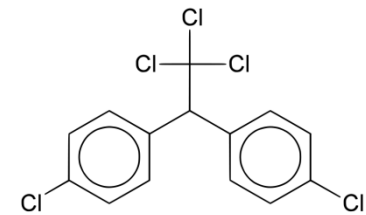
Diethylstilbestrol (DES)



Genistein



Bisphenol A



DDT

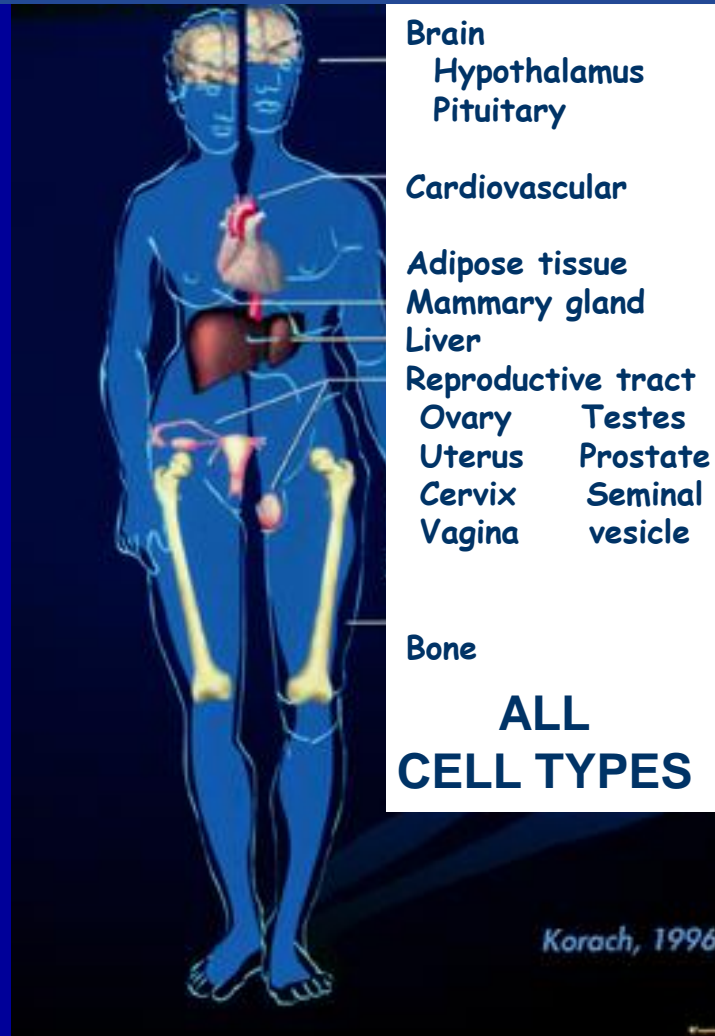


# What are the functions of Nuclear Receptors ?

## LIGANDS/HORMONES

- **Steroids** (androgens, estrogens, progestins, mineralocorticoids, glucocorticoids).
- **Retinoids**
- **Thyroid hormone**
- **Vitamin D**
- **Fatty acids**
- **Bile acids**
- **Phospholipids**
- *Environmental compounds*  
(eg plasticisers)

## TARGET TISSUES



## PROCESS

**Reproduction**

**Cell growth**

**Cell differentiation**

**Homeostasis**

**Inflammation**

**Apoptosis**

**Aberrant signalling**



**Clinical disorders**



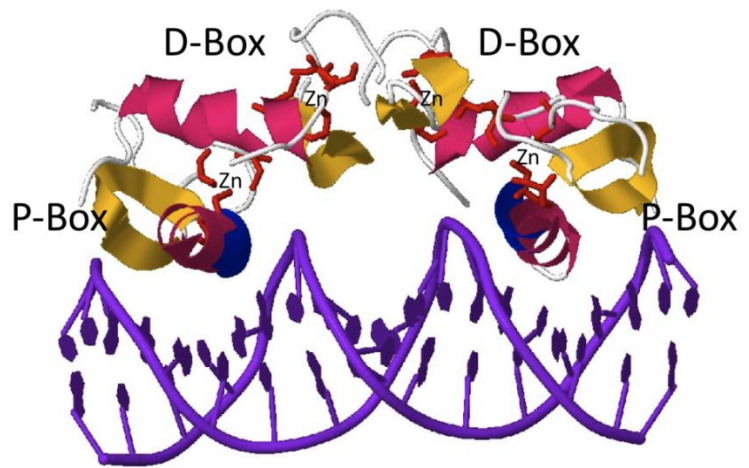
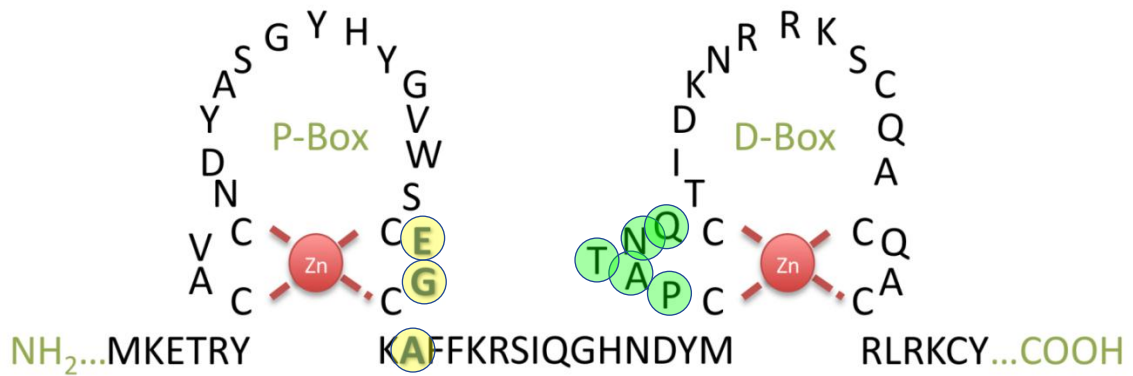
# Current and Potential Therapeutic Indications

- **TR $\beta$**  Obesity, dyslipidemia, **hypothyroidism**
- PPAR $\alpha$  Dyslipidemia, atherosclerosis, inflammation
- PPAR $\gamma$  Diabetes, obesity, cancer, inflammation, osteoporosis
- LXR $\alpha/\beta$  Dyslipidemia, atherosclerosis, diabetes
- VDR Osteoporosis, psoriasis, cancer, inflammation
- **GR** **Arthritis, asthma, immunosuppression,** obesity, diabetes
- MR Hypertension, CHF
- **PR** **Contraception,** cancer, osteoporosis
- AR Frailty, prostate cancer, sexual dysfunction, osteoporosis
- **ER $\alpha$**  **Breast cancer,** osteoporosis, cardiovascular disease, gynecological disorders, Alzheimer's
- ER $\beta$  Prostate cancer, osteoporosis, obesity, cardiovascular disease, Alzheimer's
- HNF4 $\alpha$  Diabetes, dyslipidemia
- RAR( $\alpha,\beta,\gamma$ ) Cancer, psoriasis
- RXR( $\alpha,\beta,\gamma$ ) Diabetes, cancer

# Possible Therapeutic Indications

- Rev-Erb ( $\alpha, \beta$ )      Circadian rhythm
- ROR $\alpha$               Atherosclerosis, dyslipidemia, inflammation, rheumatoid arthritis, osteoporosis, neurodegeneration
- ROR $\gamma$               Osteoporosis, immunosuppression
- FXR                  Dyslipidemia, liver disease
- PXR, CAR          Xenobiotic metabolism
- TR2, TR4          Cancer, male fertility
- TLX                  Neurodegeneration
- PNR                  Retinal degeneration
- COUP-TFI          Breast cancer, neural development
- COUP-TFII          Cancer, angiogenesis
- EAR2                Uterine/gynecological disorders
- NGFI-B             Drug abuse, cancer, schizophrenia, manic-depression, psychoses, neurodegeneration, immunomodulation
- NURR1             Parkinson's, schizophrenia, manic-depression, cancer
- NOR1              Drug abuse, cancer, immunomodulation
- SF-1                Adrenal disease, disorders of steroid metabolism
- LRH                Breast cancer, fertility, dyslipidemia
- GCNF              Fertility/contraception
- DAX-1             Adrenal disease, fertility, gynecologic disorders
- SHP                Obesity, dyslipidemia, diabetes, liver disease, cancer
- ERR $\alpha$             Osteoporosis, dyslipidemia
- ERR $\beta$              Fertility

# Nuclear Receptor Structure and DNA Binding



● Amino Acid residues that confer Response Element Binding Specificity  
 ● Amino Acid residues that are important for receptor dimerisation

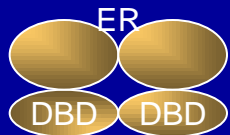
RECEPTORS	P-BOX	HALF-SITE	RESPONSE ELEMENT
ER	cEGckA	AGGTCA	AGGTCAnnnTGACCT
GR, MR, PR, AR	cGSckV	TGTTCT	AGGACAnnnTGTCTT
PPAR, RAR, VDR, PPAR	cEGckG	AGGTCA	AGGTCAnAGGTCA

# Consensus binding sites for Nuclear Receptors (AGGTCA)

## Inverse palindromes



- ER Estrogen
- GR Glucocorticoid
- MR Mineralocorticoid
- PR Progesterone
- AR Androgen



AGGTCA<sub>n</sub>nnTGACCT

AR, GR, MR, PR



AGAACA<sub>n</sub>nnTGTTCT

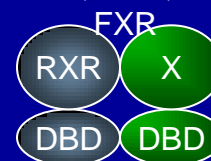
## Direct repeats



- TR Thyroid Hormone
- VDR Vitamin D3
- RAR Retinoic Acid
- PPAR Peroxisome proliferator

- |      |                                |   |
|------|--------------------------------|---|
| DR-1 | AGGTCA <sub>n</sub> AGGTCA     | RXR/RXR, PPAR/RXR,<br>RAR/RXR, COUP/RXR |
| DR-2 | AGGTCA <sub>nn</sub> AGGTCA    | RAR/RXR                                 |
| DR-3 | AGGTCA <sub>nnn</sub> AGGTCA   | VDR/RXR                                 |
| DR-4 | AGGTCA <sub>nnnn</sub> AGGTCA  | TR/RXR                                  |
| DR-5 | AGGTCA <sub>nnnnn</sub> AGGTCA | RAR/RXR                                 |

RAR, TR, VDR,  
PPAR, PXR, LXR,



AGGTCA<sub>n</sub><sub>1-5</sub>AGGTCA

RXR, COUP,  
HNF-4



AGGTCA<sub>n</sub>AGGTCA

NGFI-B, SF-1

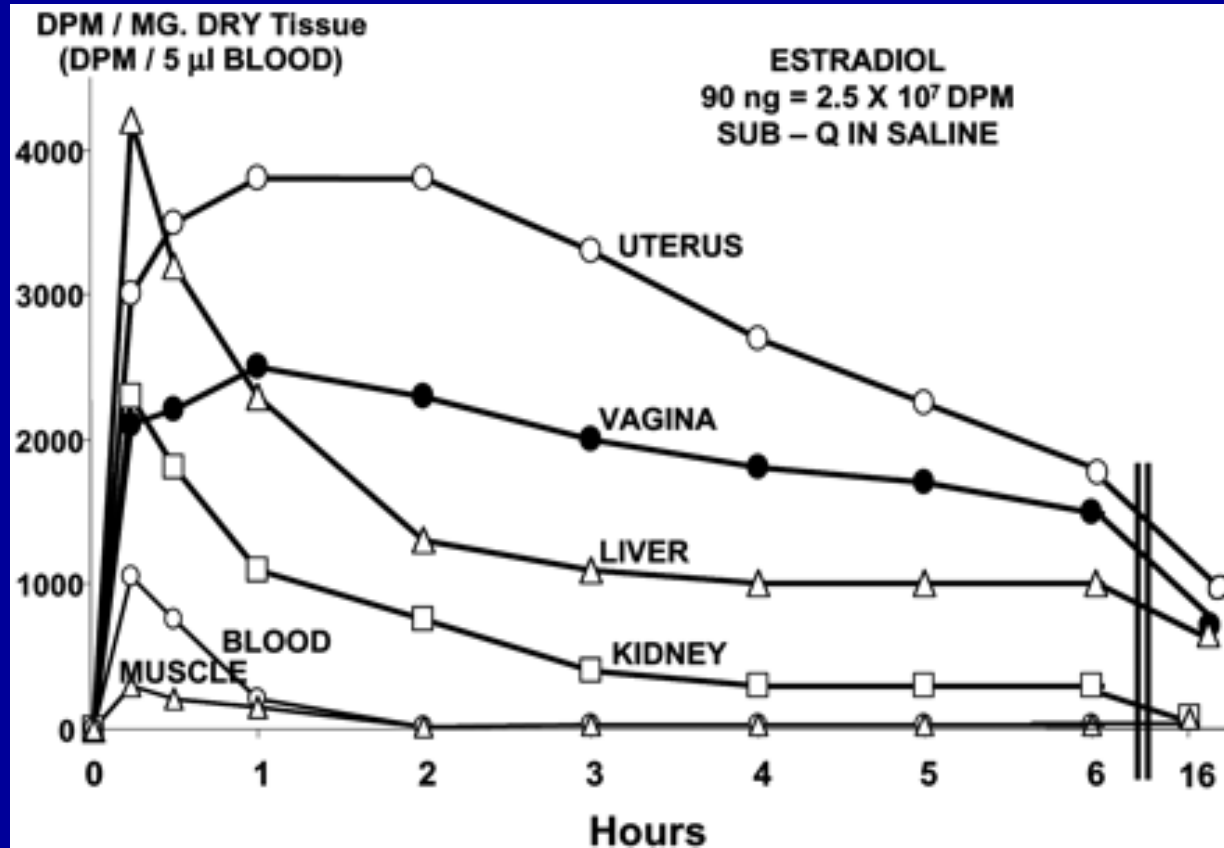


AGGTCA

**Which Nuclear Receptors are important for the normal function of reproductive tissues?**

# Tissue-specific concentration of $^3\text{H}$ Estradiol

Elwood Jensen 1962



The concentration of radioactivity in immature rat tissues after a single s.c. injection of  $^3\text{H}$  estradiol.



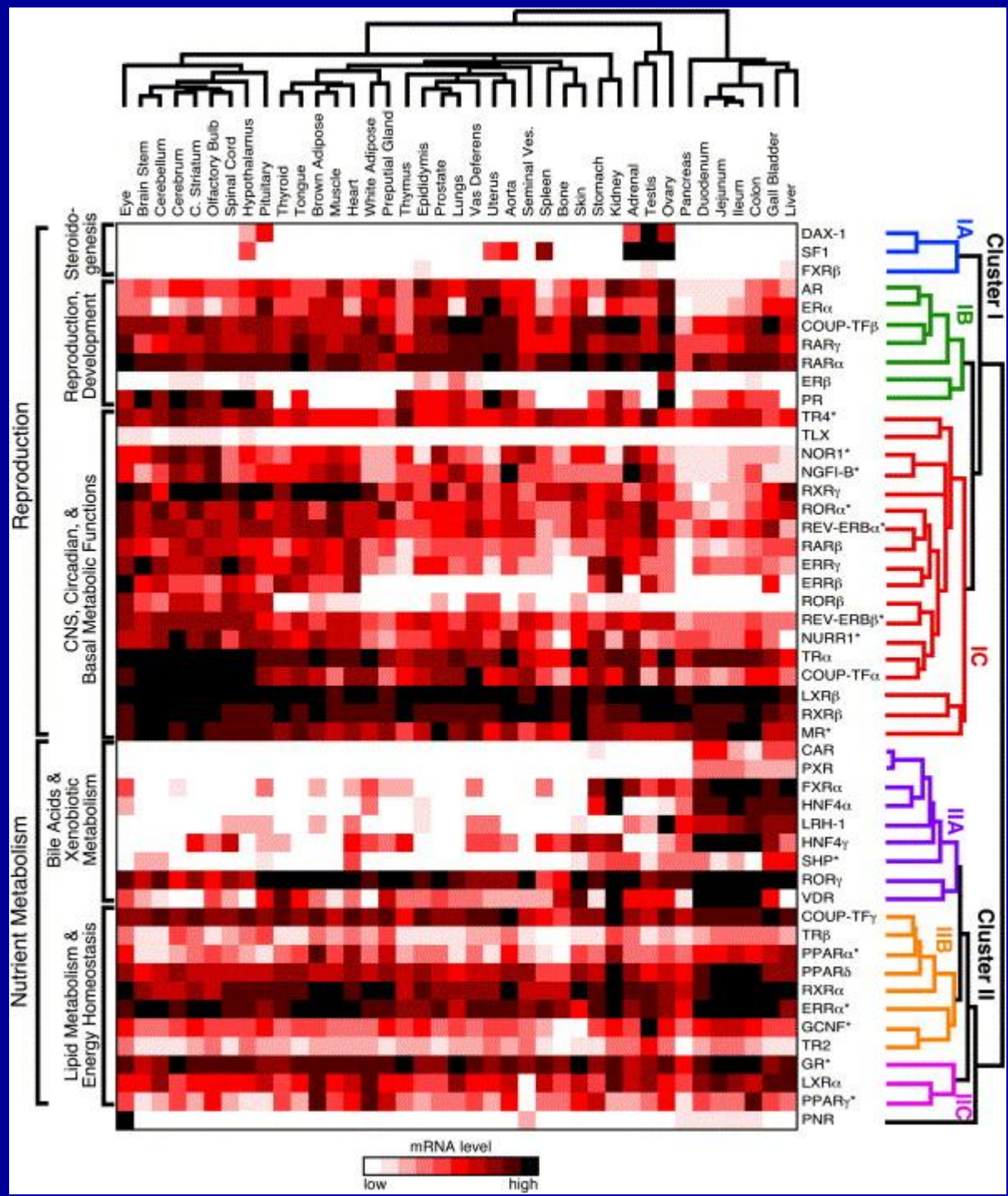
**STEROIDOGENESIS**

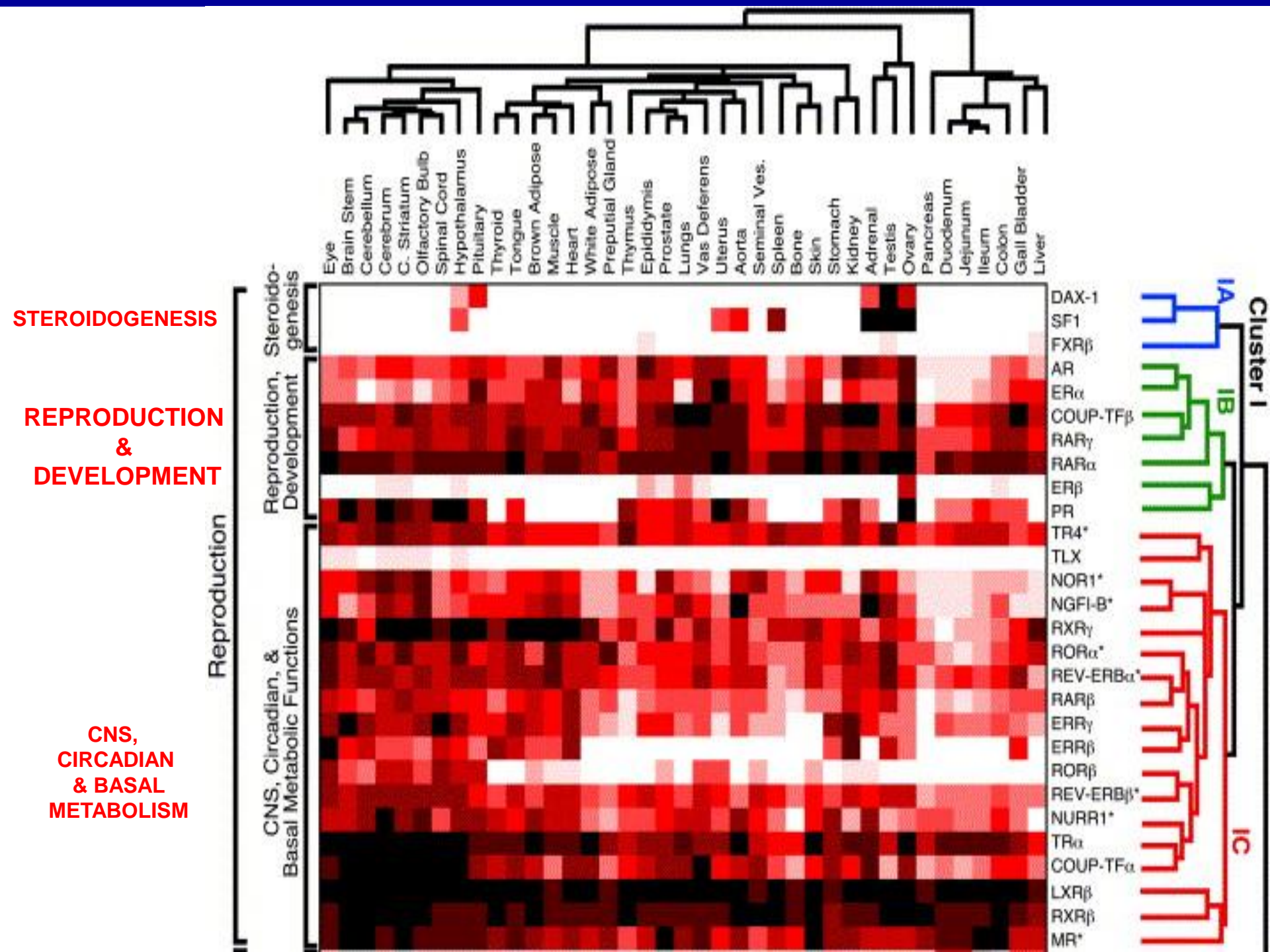
**REPRODUCTION & DEVELOPMENT**

**CNS, CIRCADIAN & BASAL METABOLISM**

**BILE ACID & XENOBIOTIC METABOLISM**

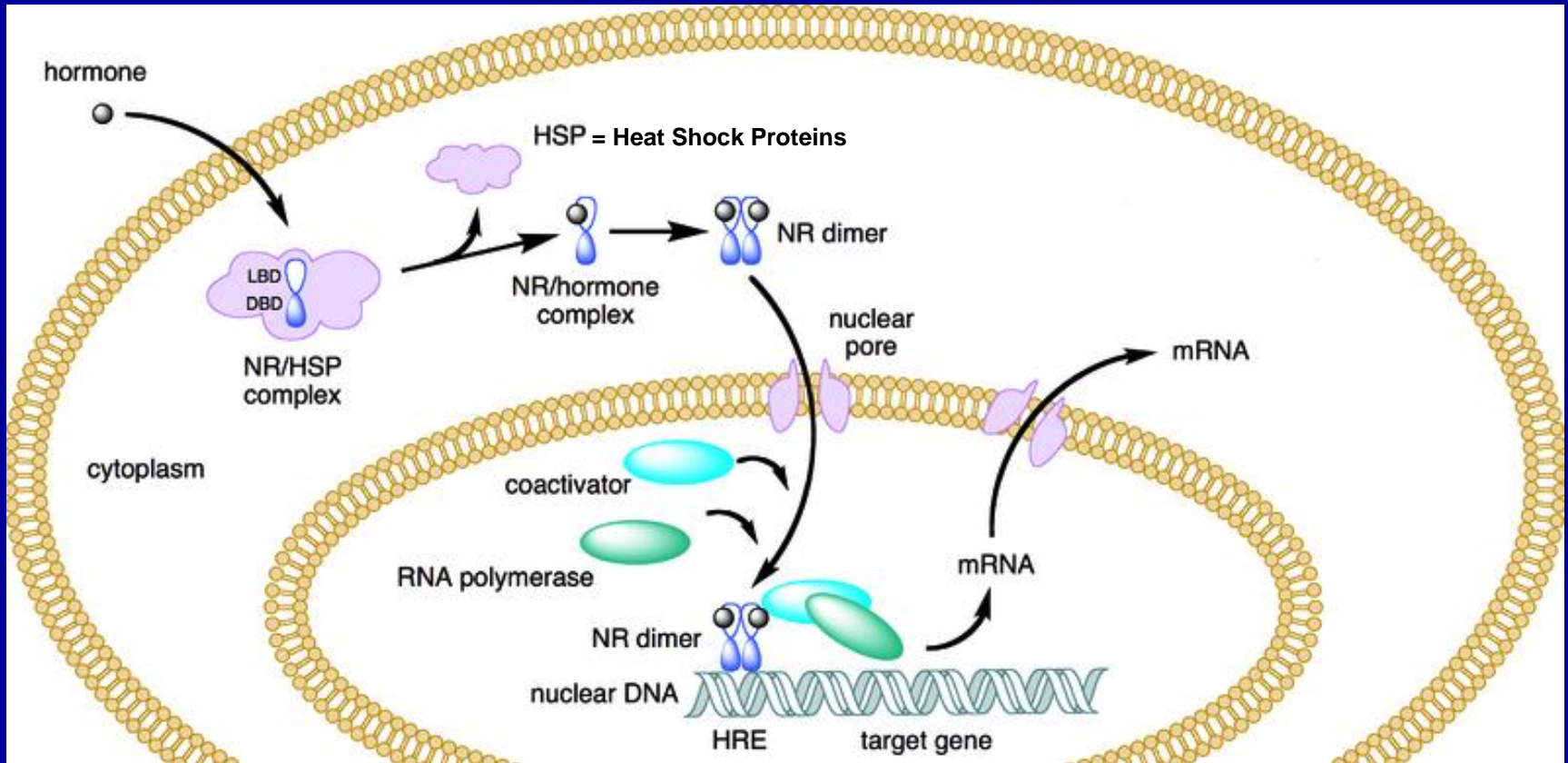
**LIPID METABOLISM & ENERGY HOMEOSTASIS**







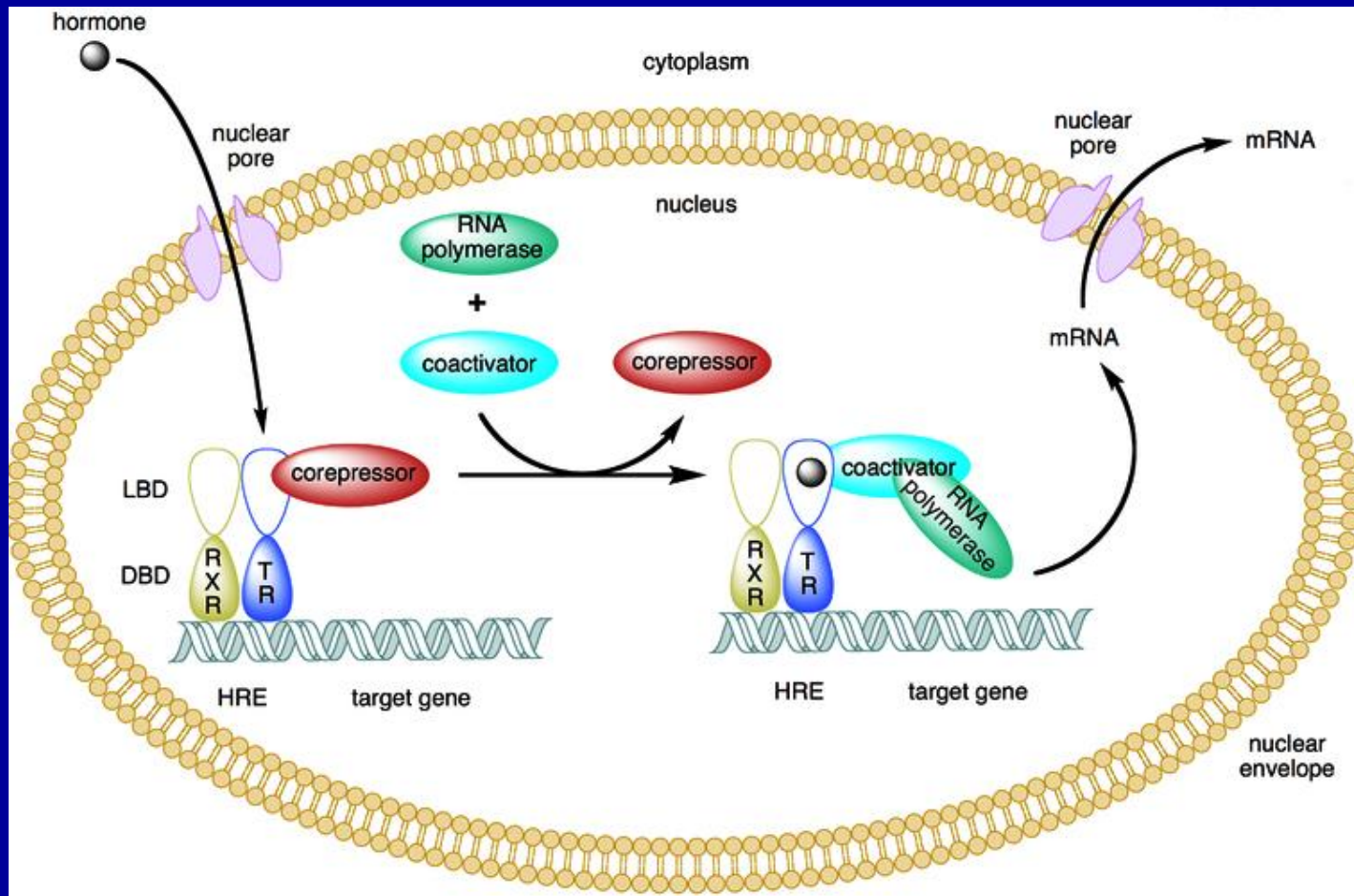
# The Mechanism of Nuclear Receptors Action



Following ligand binding NR dissociated from HSP complex, dimerizes and translocates to the nucleus.

Occurs for steroid receptors such as Androgen, Estrogen, Progesterone and Glucocorticoid Receptors (some receptor may be nuclear in absence of ligand).

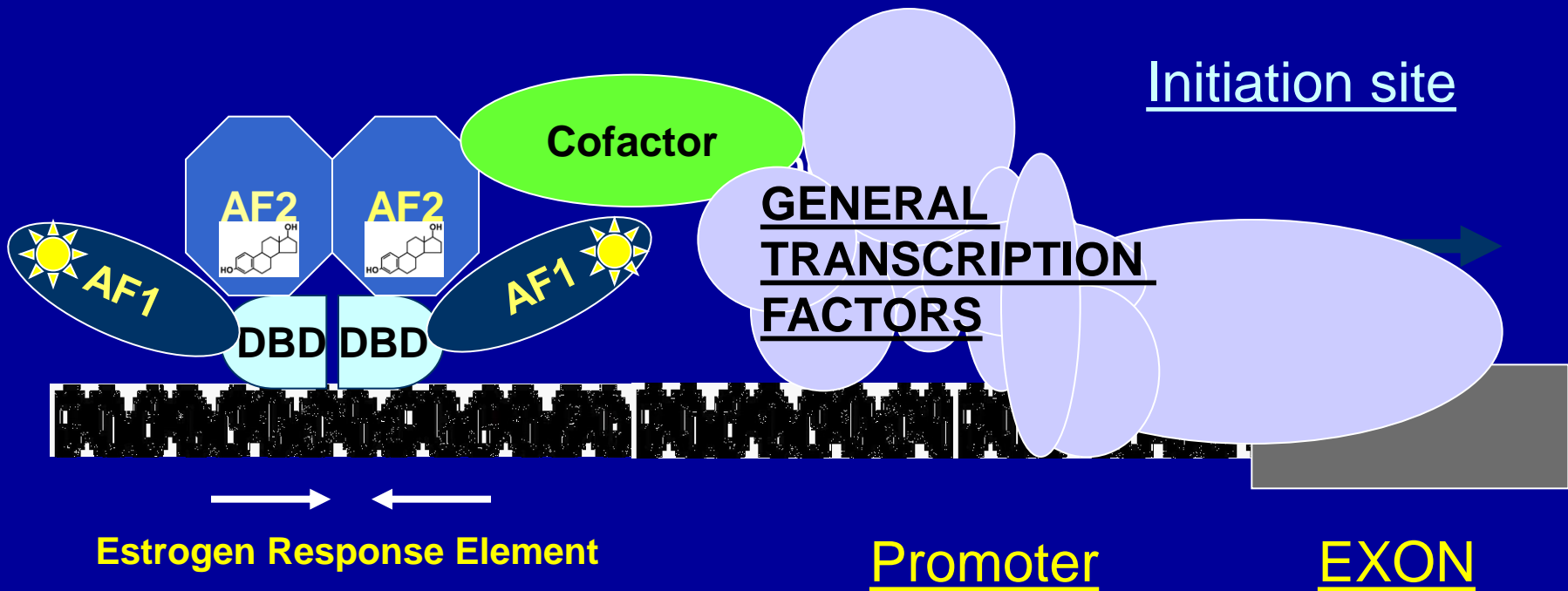
# The Mechanism of Nuclear Receptors Action



Nuclear receptors such as retinoic acid receptor, retinoid X receptor and thyroid hormone receptor are retained in the nucleus regardless of ligand availability.

Following ligand binding corepressors dissociate and coactivators bind to the NR.

# Activation of target gene expression



# Structure of the LBD

**Molecular structures have been determined for the LBD's of many NR**

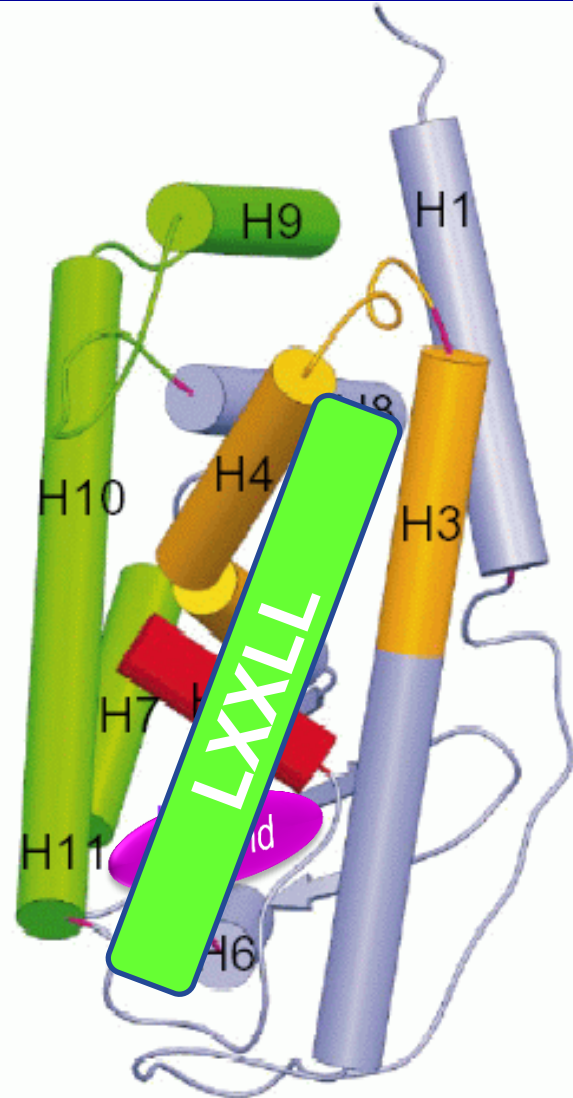
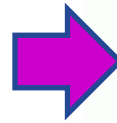
**12  $\alpha$ -helices (H1-H12) folded to form an " $\alpha$ -helical sandwich"**

**Helix 11 required in receptor dimerisation**

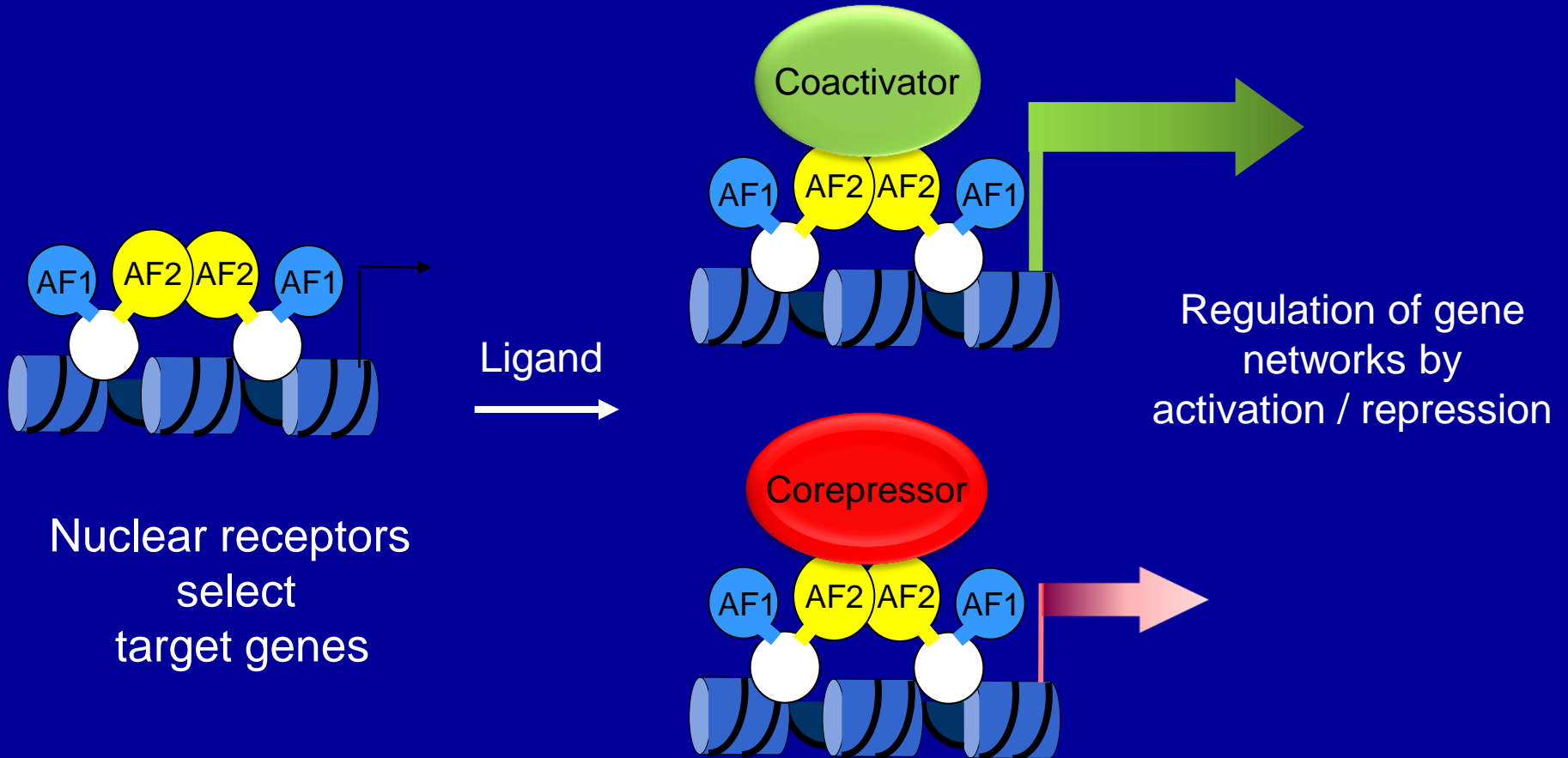
**Helices 3, 5, 6 and 11 form the ligand binding pocket**



# Ligand binding recruits LXXLL- motif containing coregulators to Nuclear Receptors



# Transcription by Nuclear Receptors is determined by cofactor recruitment





ATP-Dependent  
Chromatin remodeling



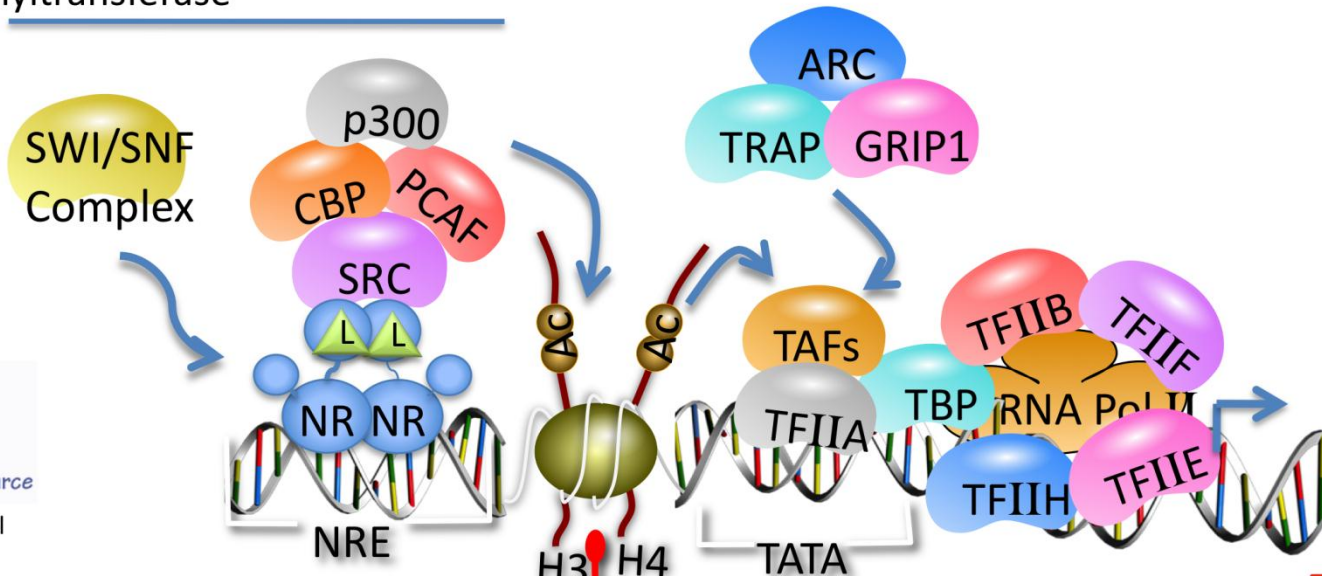
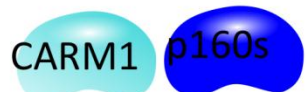
Histone Acetyltransferase



RNA and RNA  
Processing



ATP-Arginine  
Methyltransferase



Activation

Repression

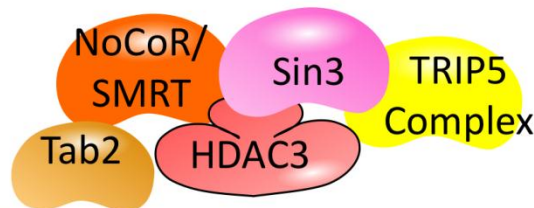
Ligand-Dependent  
Corepressors



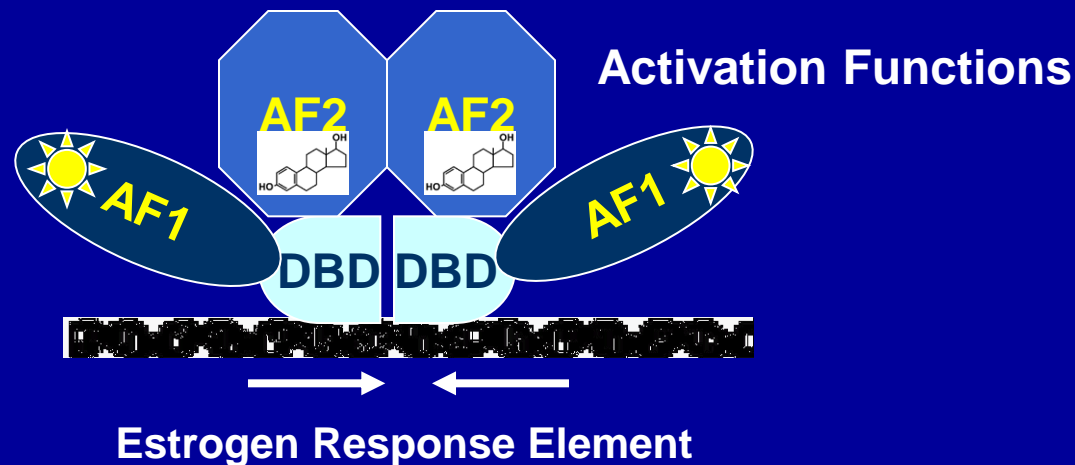
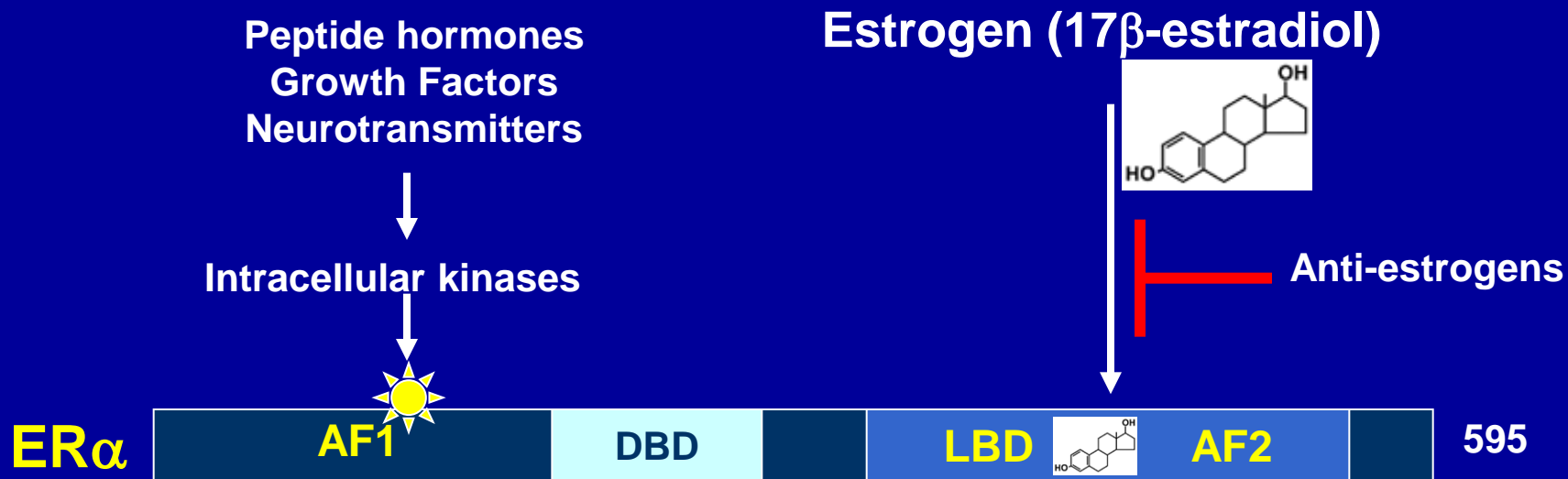
ATP-Dependent  
Chromatin Remodeling



Histone Deacetylase



# Regulation of Nuclear Receptor activity





# Summary

The basic modular structure of a Nuclear Receptor includes DBD, LBD/AF2 and AF1.

The Nuclear Receptor Superfamily can be classified according to:

- 1) Ligand binding
- 2) DNA binding and dimerization
- 3) Expression Pattern

Ligands for NRs include steroids, fatty acids, pharmaceuticals, environmental chemicals.

The Nuclear Receptor DBD contains two Zinc Fingers and is the most highly conserved domain.

Activated Nuclear Receptors recruit coregulators to facilitate the regulation of target gene expression.

## Further Reading

<http://www.nursa.org/flash/gene/nuclearreceptor/start.html>

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