

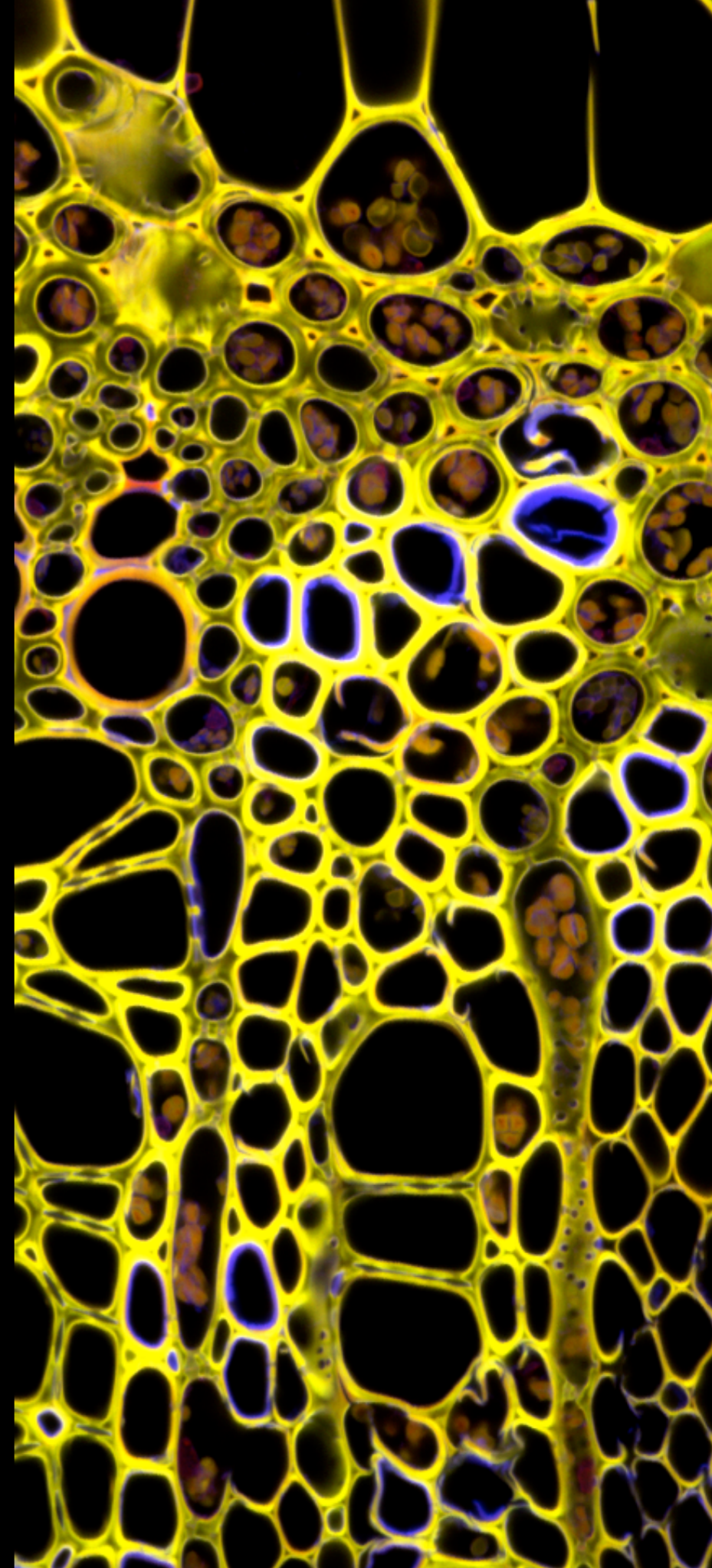
CDB Part IB

Plant Development

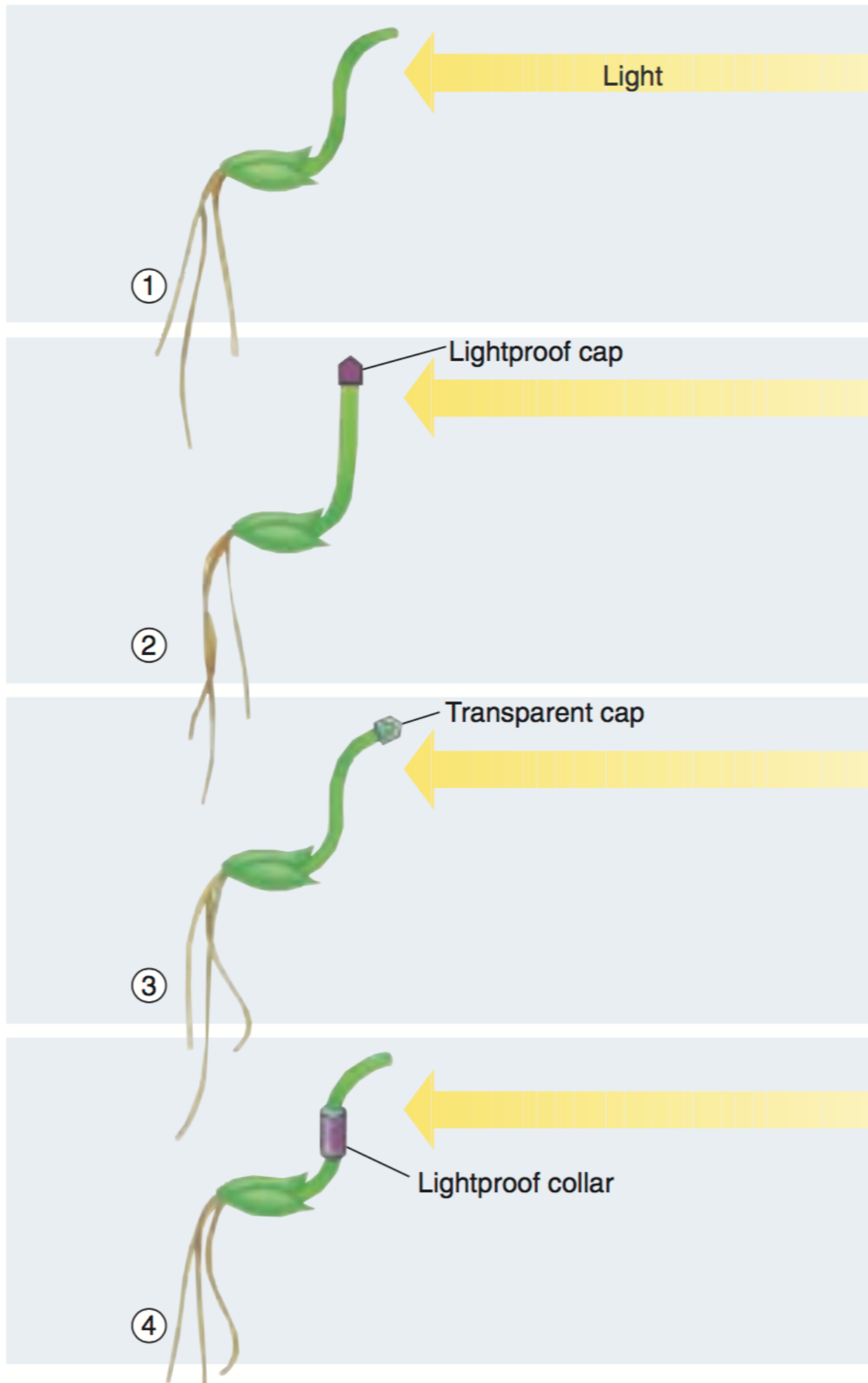
Lecture 2.

Polarity, auxin traffic and auxin response

Jim Haseloff
Department of Plant Sciences
(haseloff.plantsci.cam.ac.uk/education)



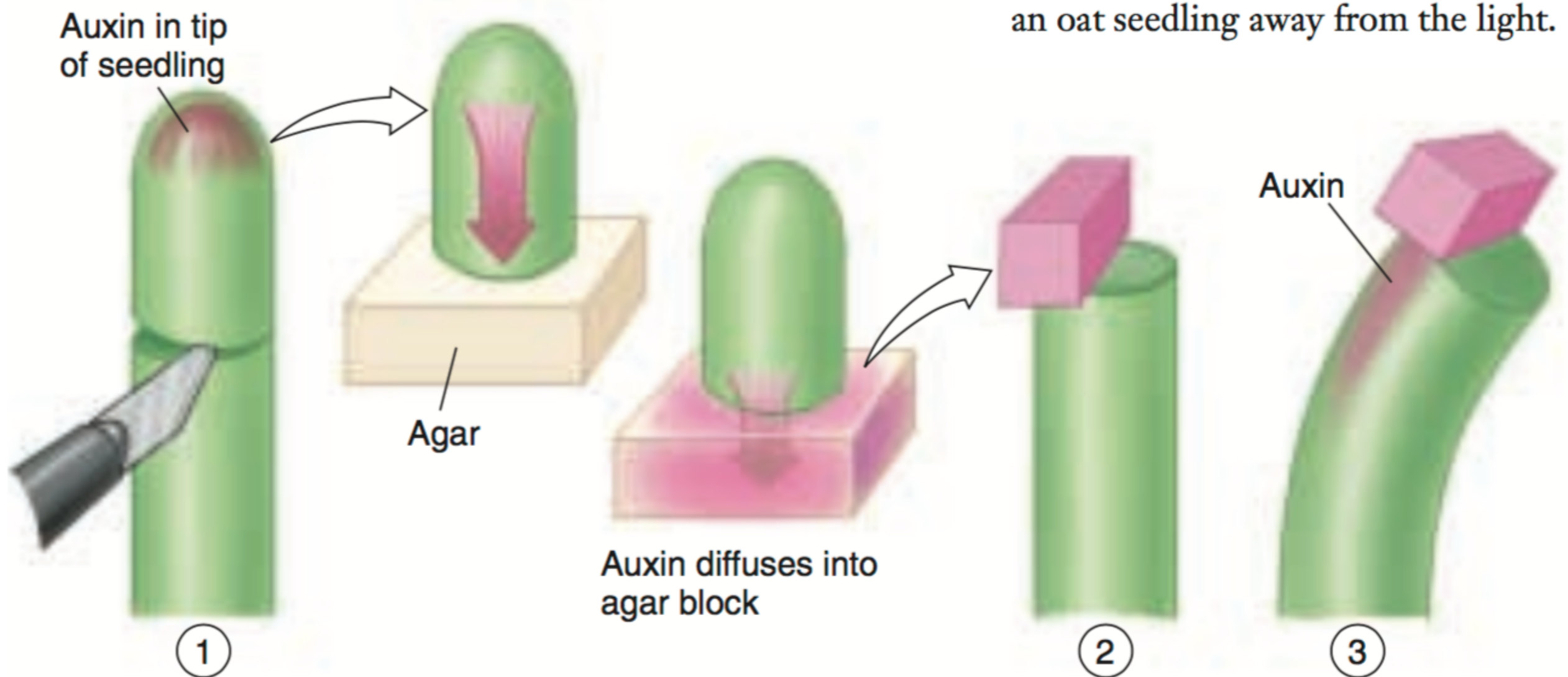
Charles and Francis Darwin's experiments on signalling during plant phototropism

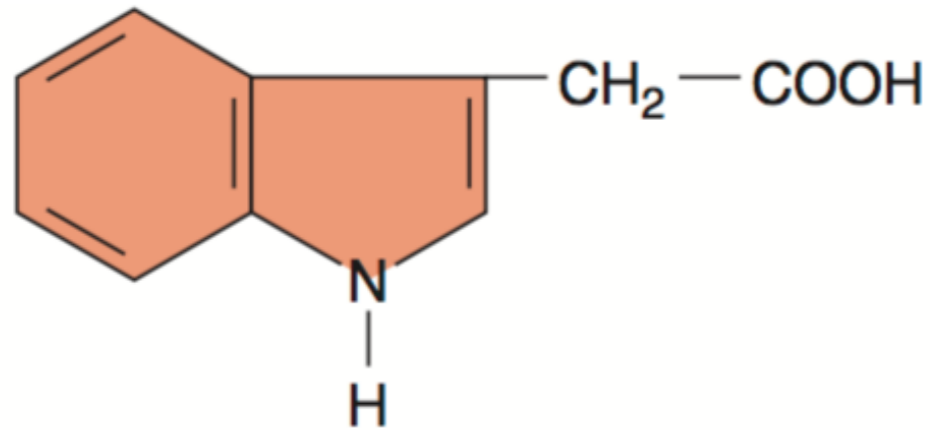


The Darwins' experiment. (a) Young grass seedlings normally bend toward the light. (b) The bending (1) did not occur when the tip of a seedling was covered with a lightproof cap (2), but did occur when it was covered with a transparent one (3). When a collar was placed below the tip (4), the characteristic light response took place. From these experiments, the Darwins concluded that, in response to light, an "influence" that caused bending was transmitted from the tip of the seedling to the area below, where bending normally occurs.

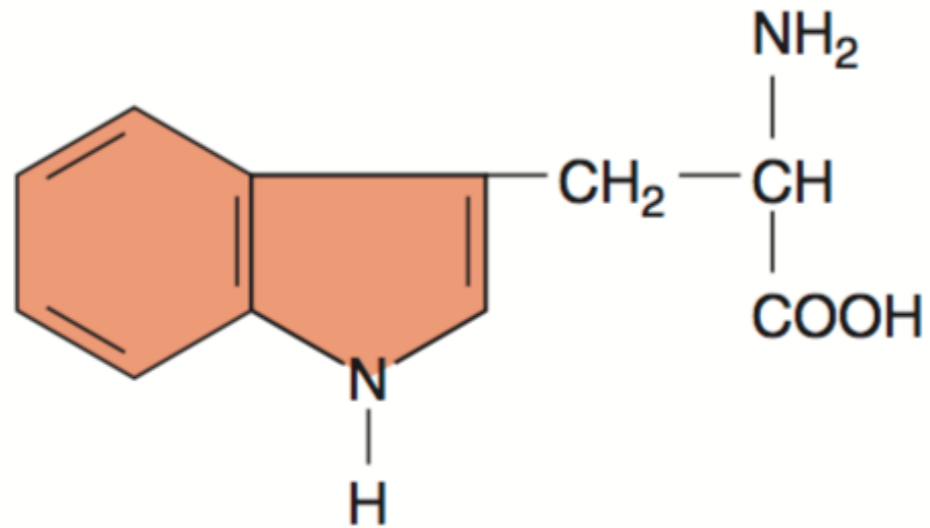
Demonstration of auxin signaling in plant tissues

Frits Went's experiment. (1) Went removed the tips of oat seedlings and put them in agar, an inert, gelatinous substance. (2) Blocks of agar were then placed off-center on the ends of other oat seedlings from which the tips had been removed. (3) The seedlings bent away from the side on which the agar block was placed. Went concluded that the substance that he named *auxin* promoted the elongation of the cells and that it accumulated on the side of an oat seedling away from the light.

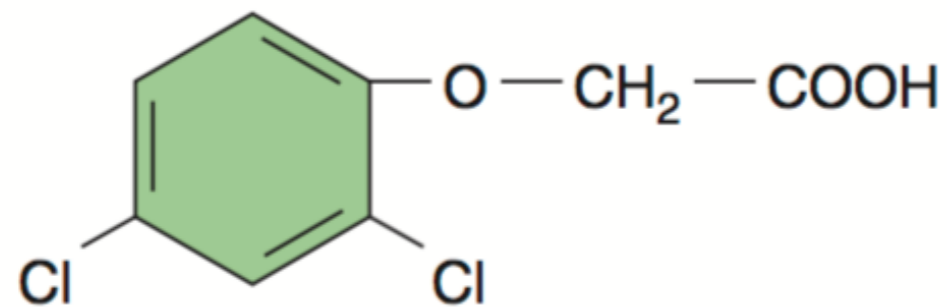




(a) **IAA (Indoleacetic acid)**



(b) **Tryptophan**



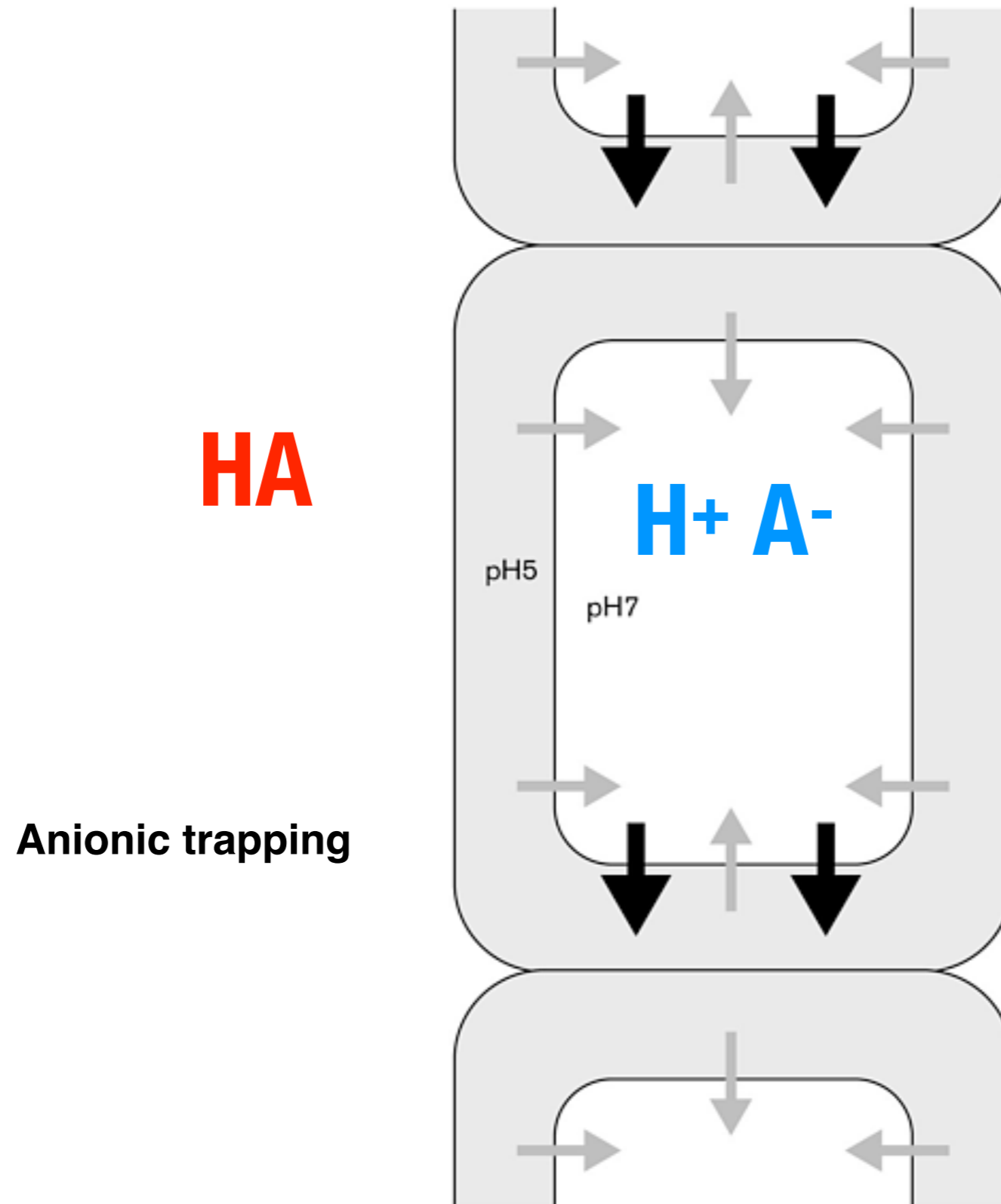
(c) **Dichlorophenoxyacetic acid
(2,4-D)**

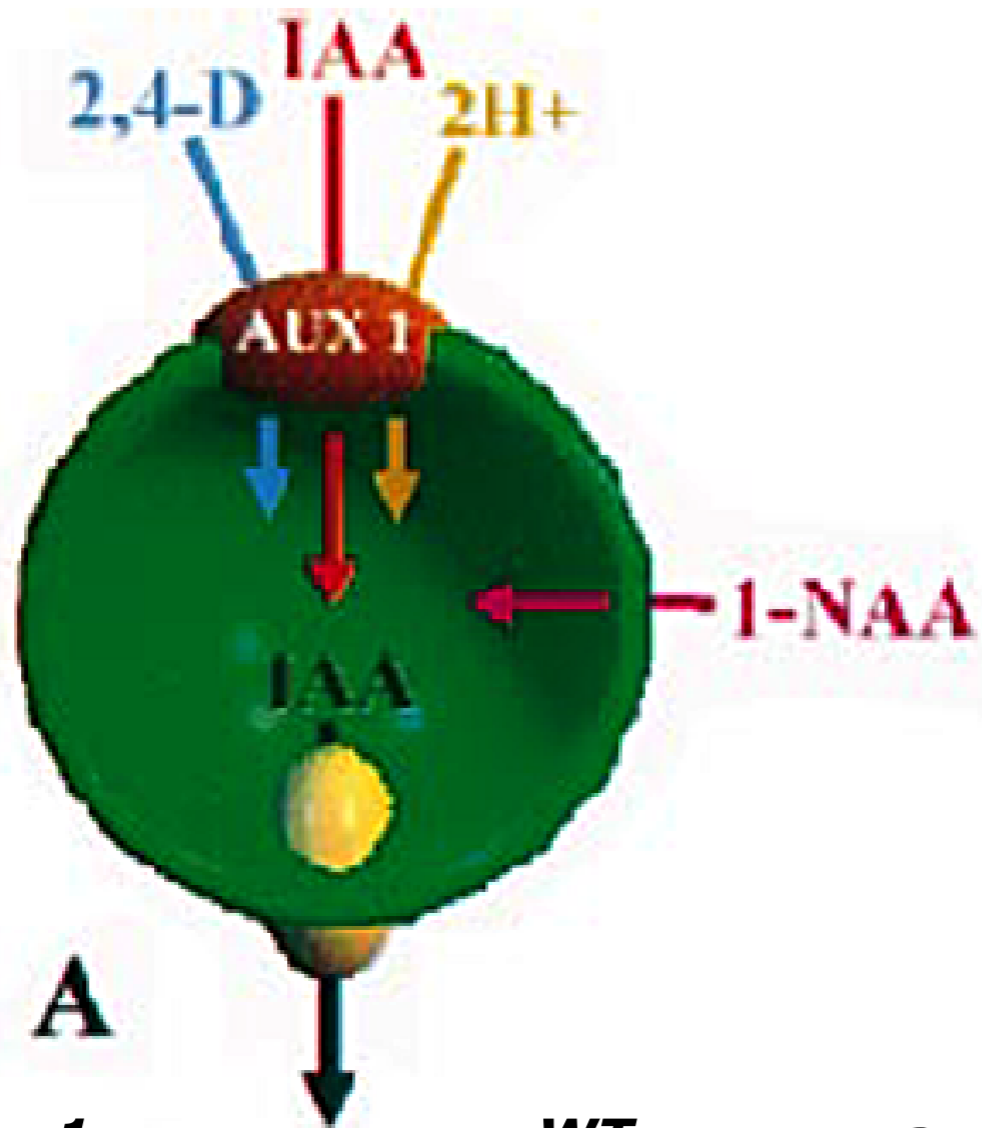
Auxin and apical-basal polarity:

Apical-basal polarity and the coordination of indeterminate growth and branching in plants is maintained by traffic of growth regulators.

These are not passive gradients, but are the product of active cellular transport.

The pathway of auxin traffic through the plant is determined by the activities of influx and efflux carriers.

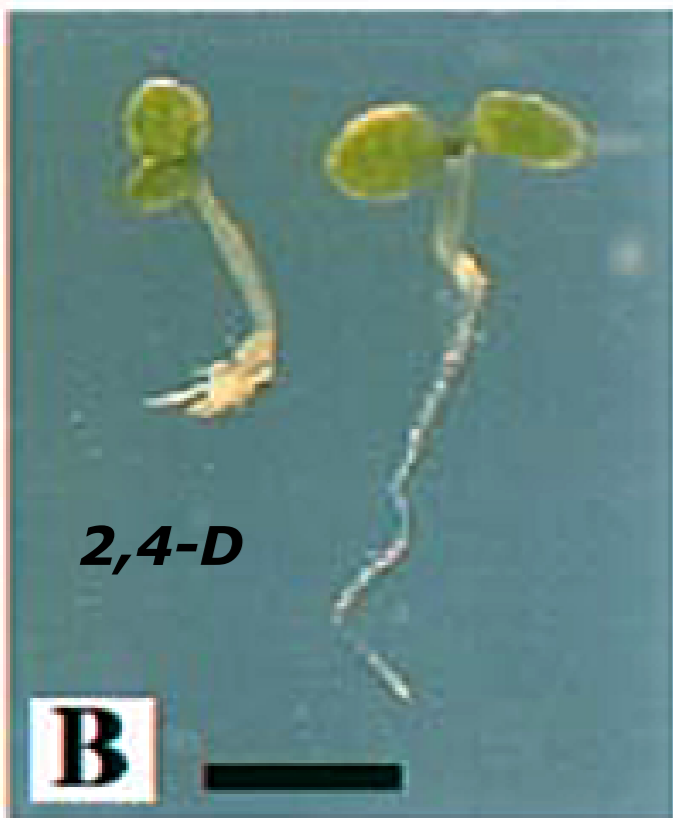




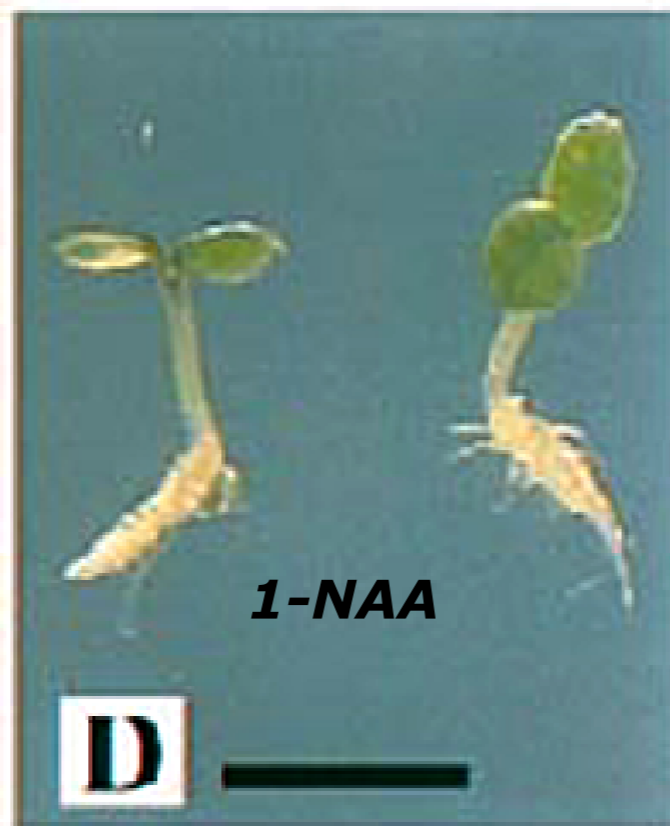
Auxin influx carrier: AUX1

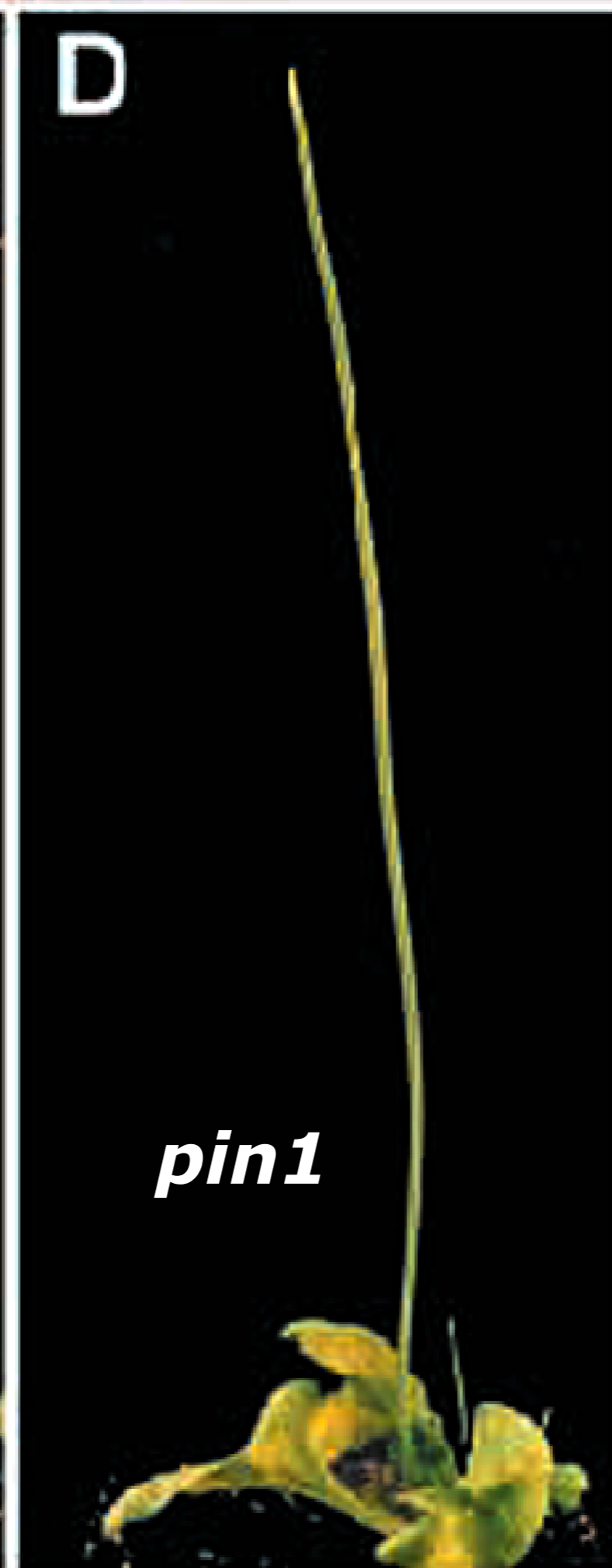
The *aux1* mutant confers resistance to the herbicide 2,4-D, an auxin mimic

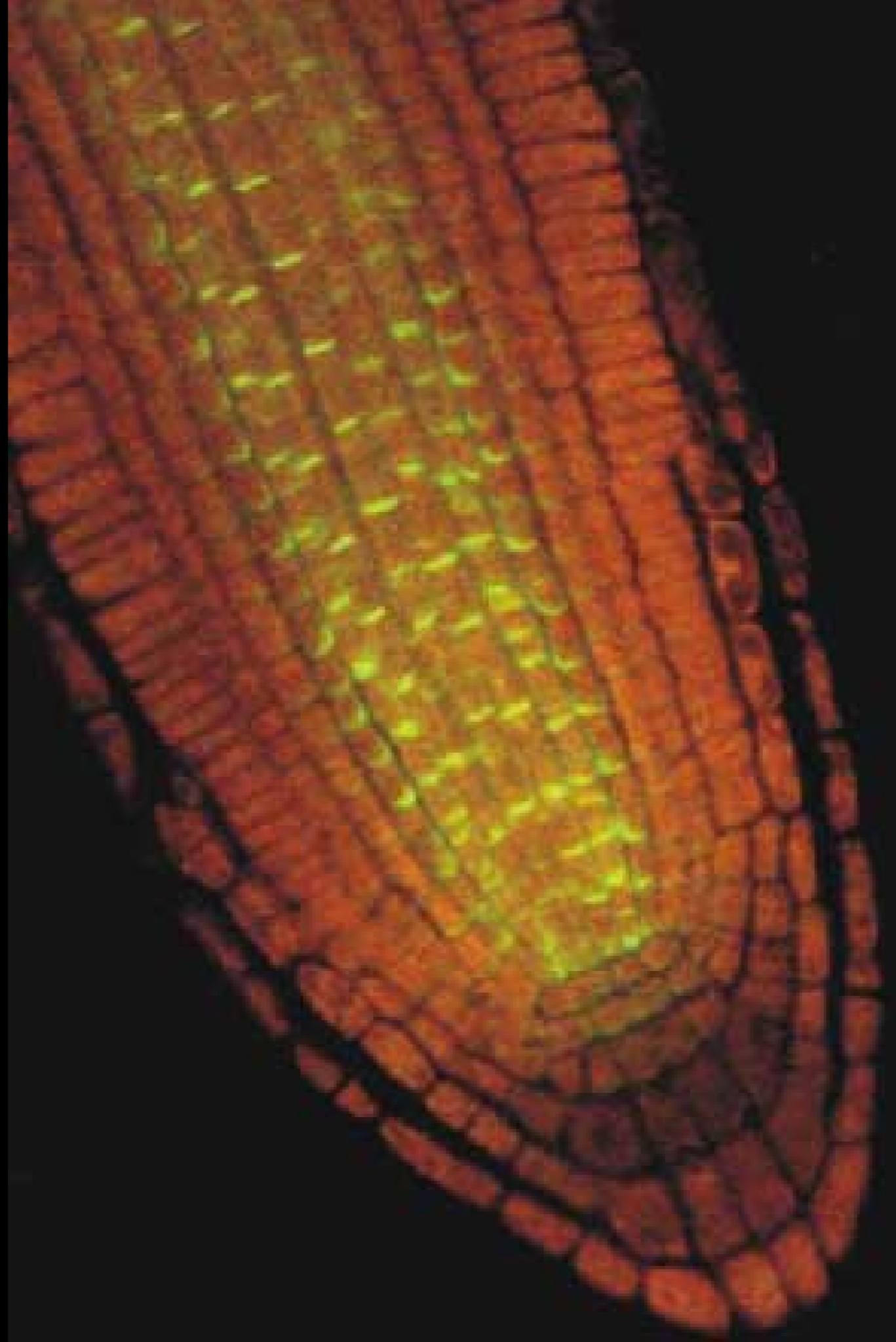
WT ***aux1***

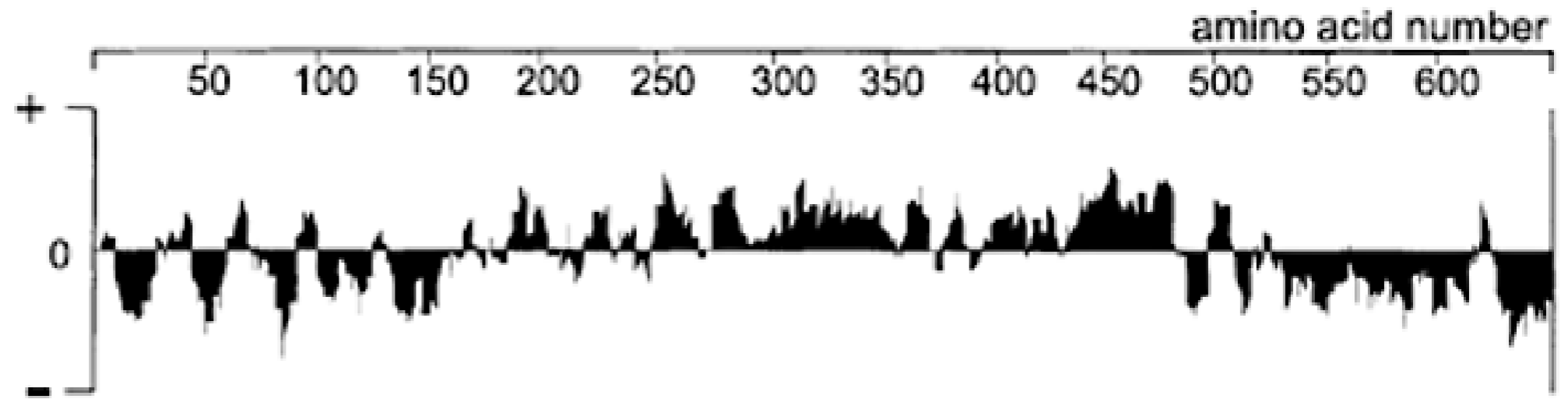


WT ***aux1***

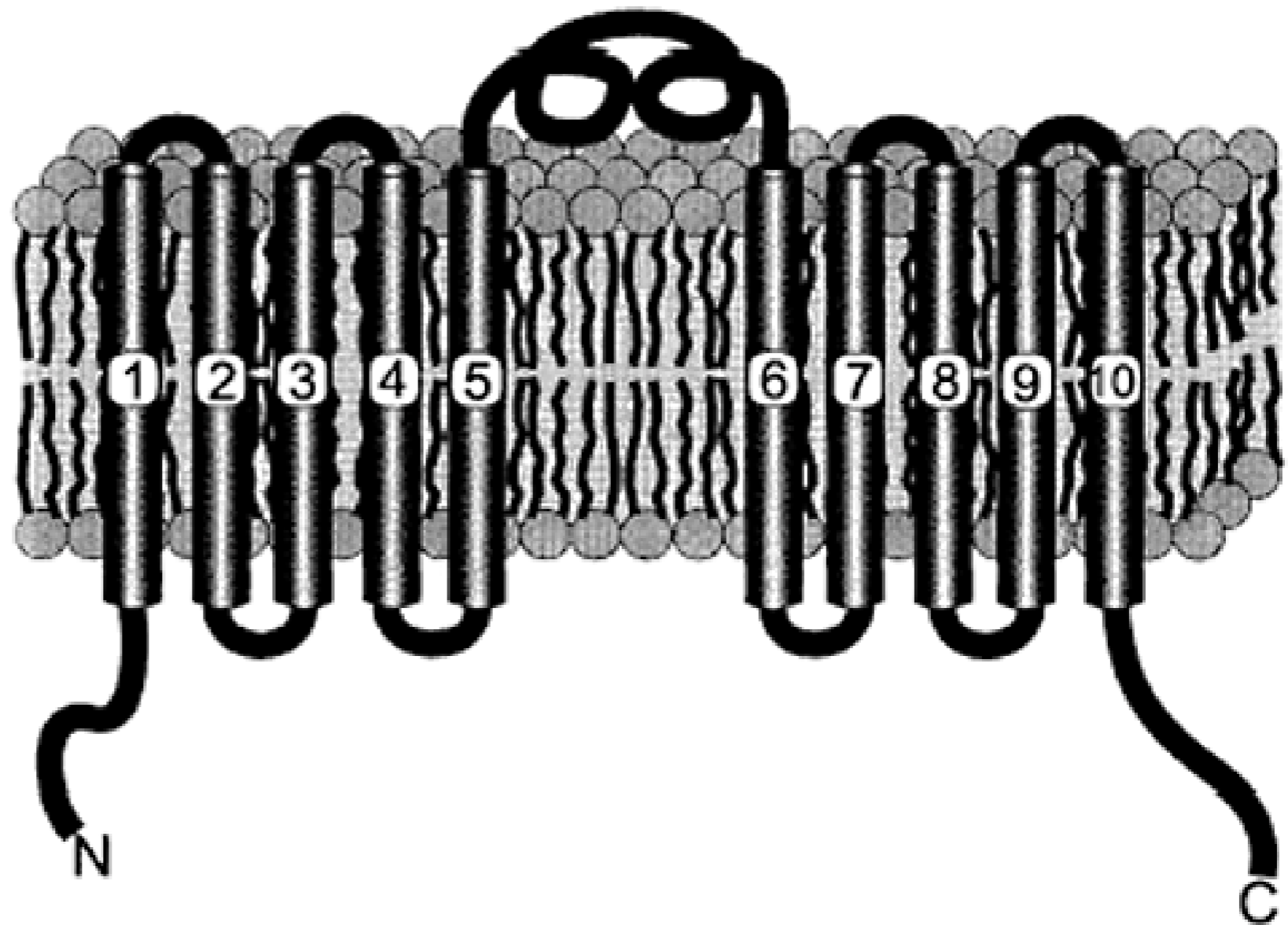




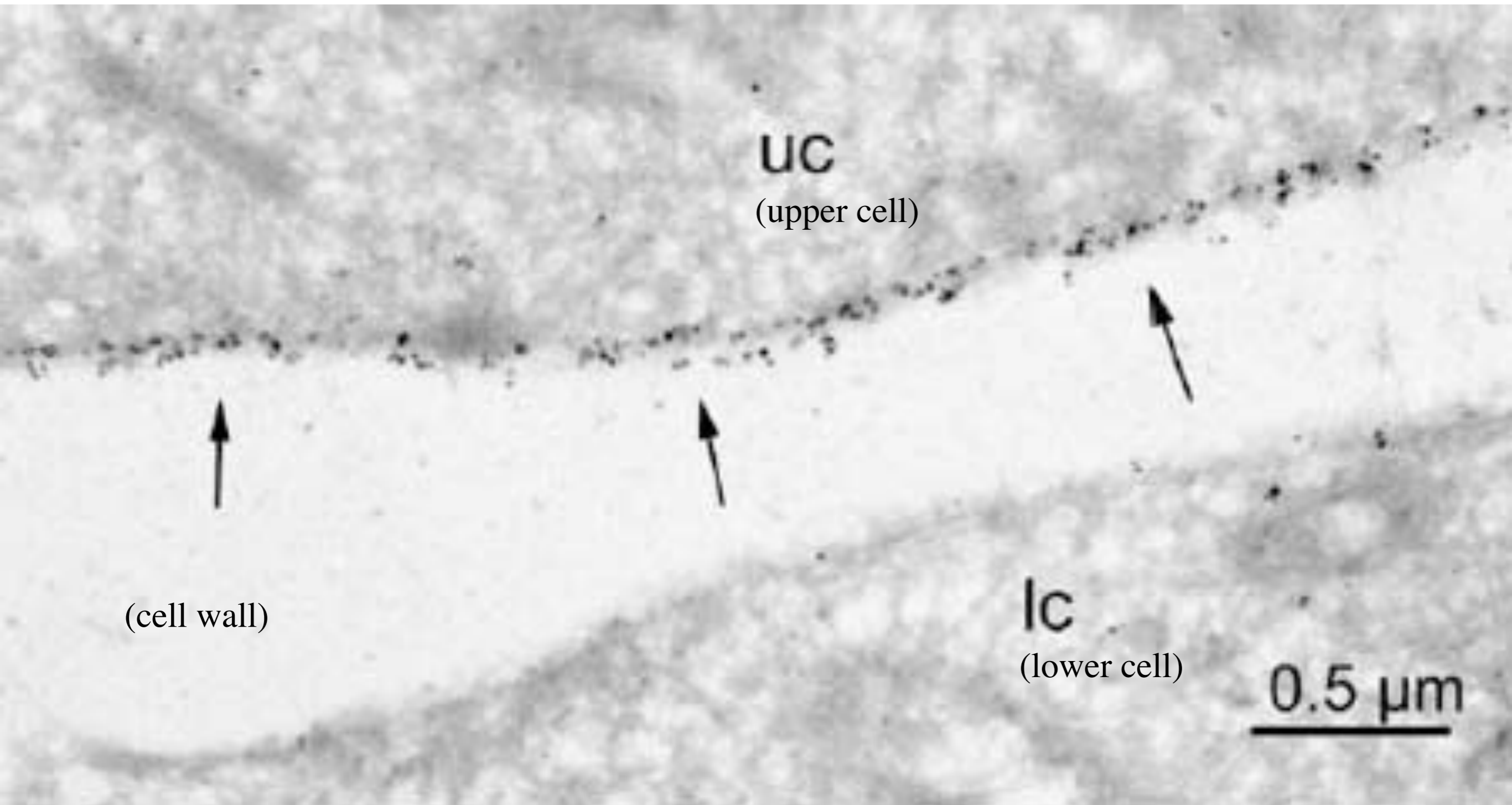




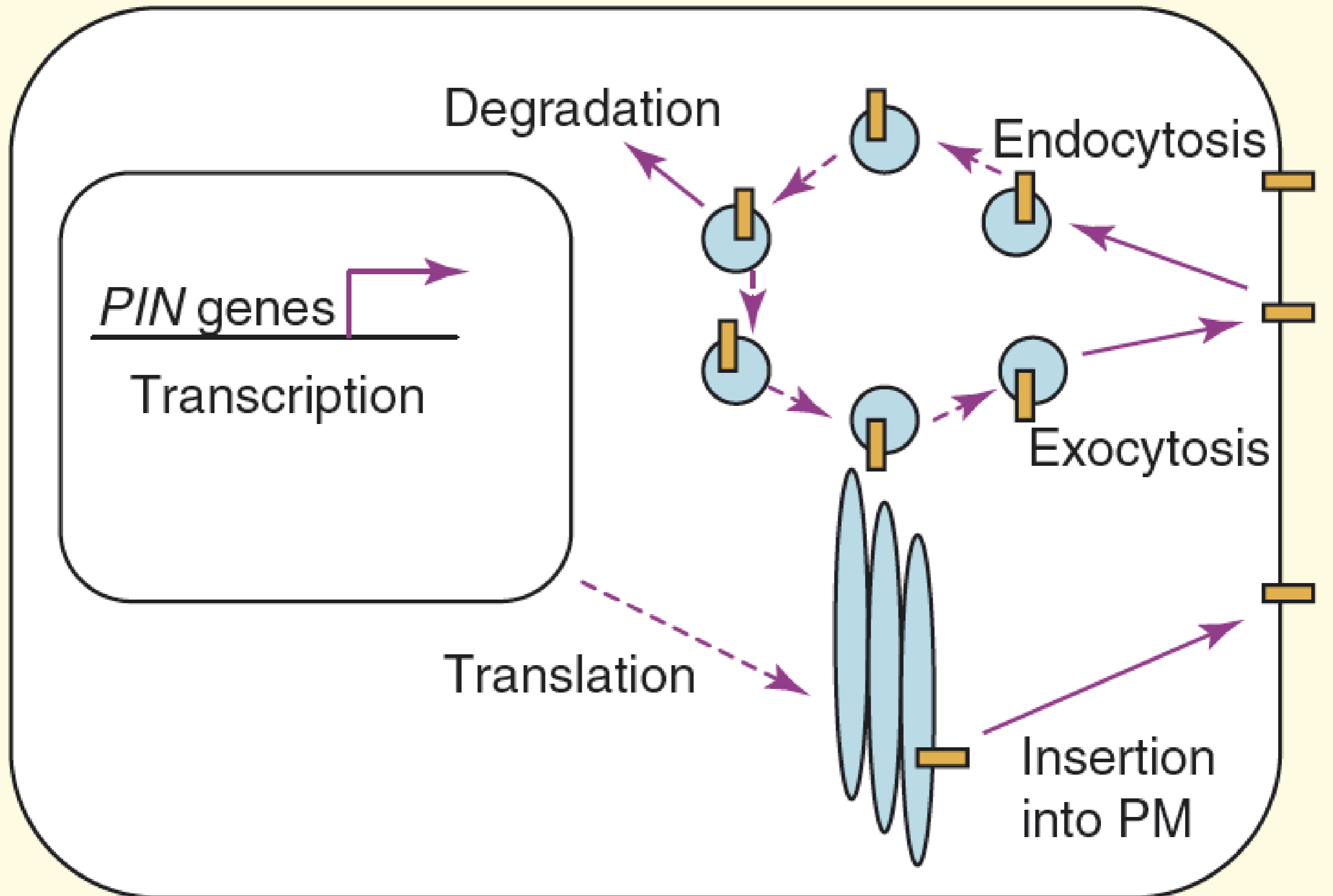
PIN1 auxin efflux carrier



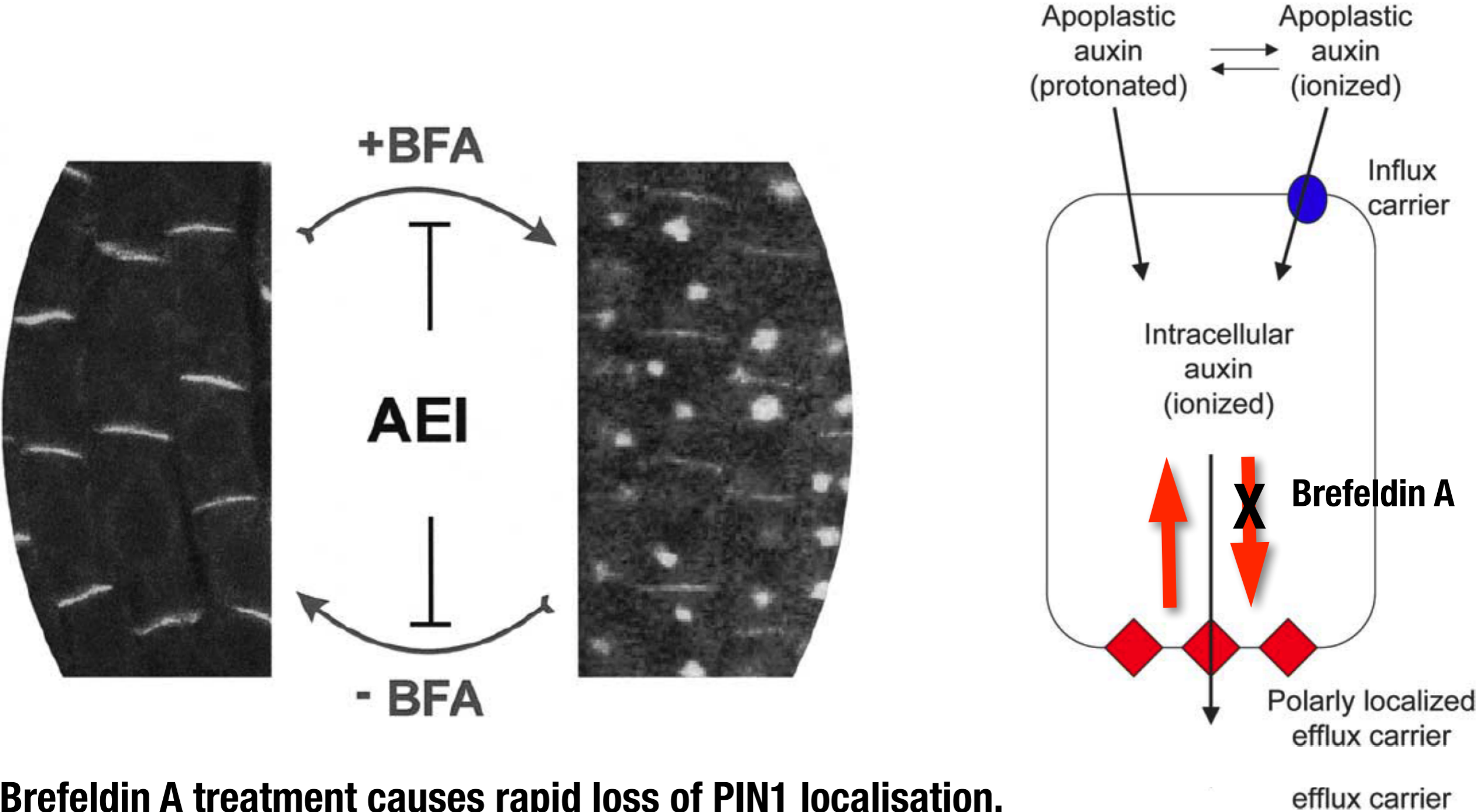
PIN1 is plasma membrane localised with a polar distribution within the cell



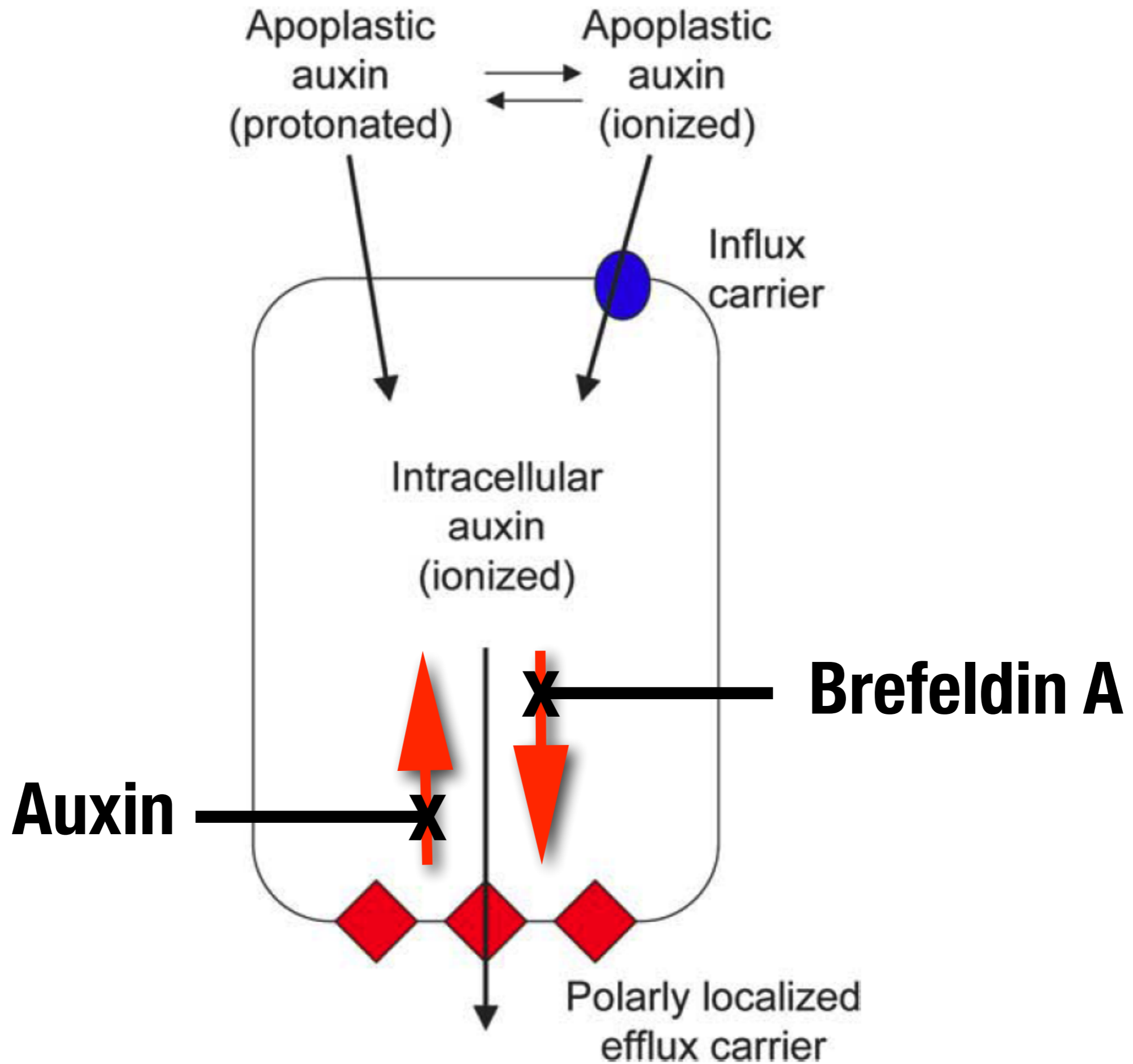
Feedback through regulated expression and localisation of PIN genes

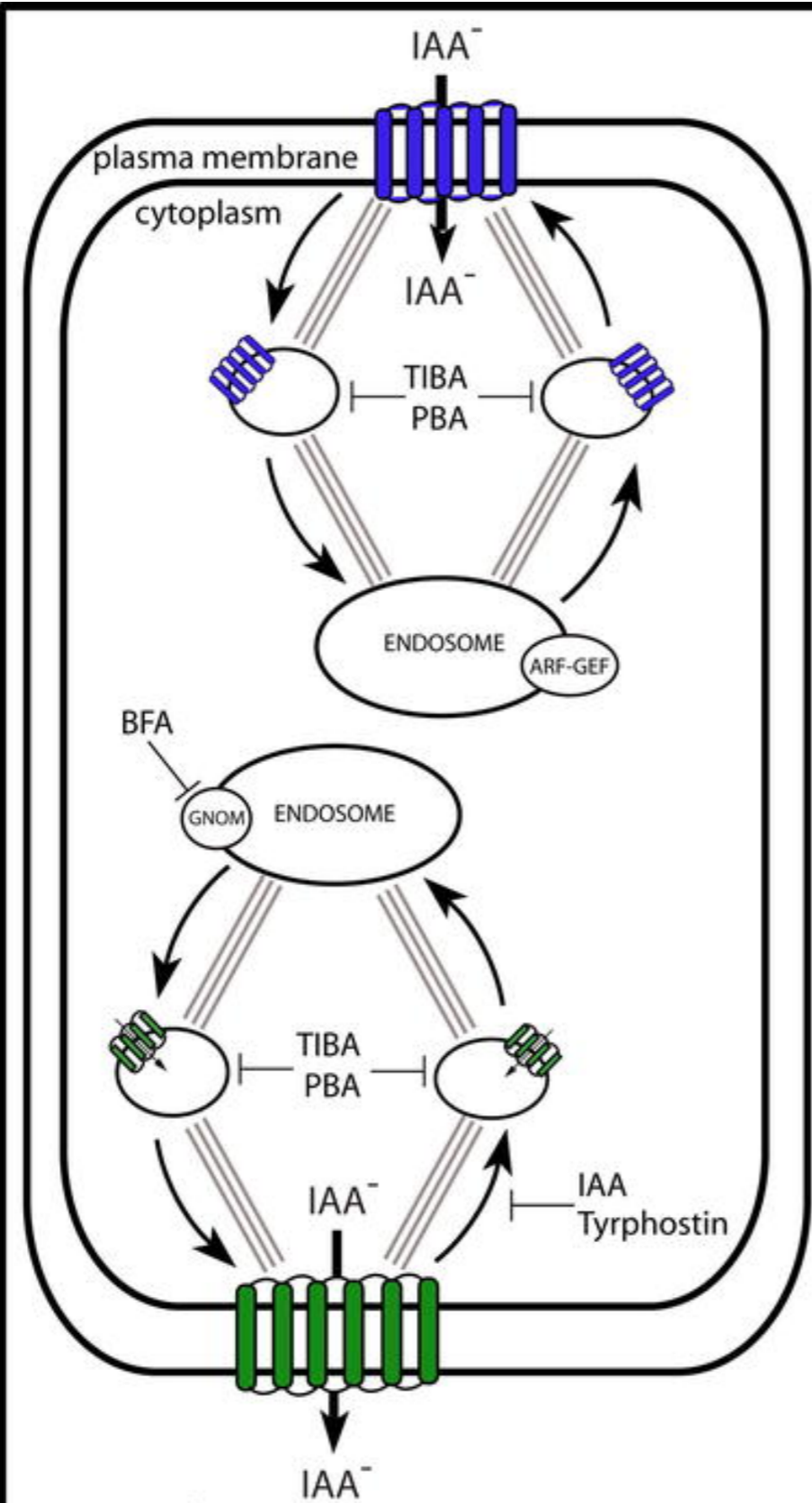


Asymmetric localisation of the PIN1 auxin efflux transporter is a dynamic process and requires the maintenance of polar secretion.



Brefeldin A treatment causes rapid loss of PIN1 localisation.

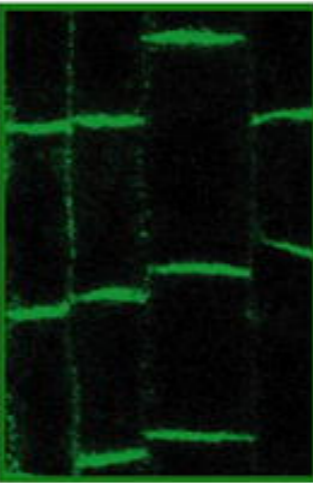




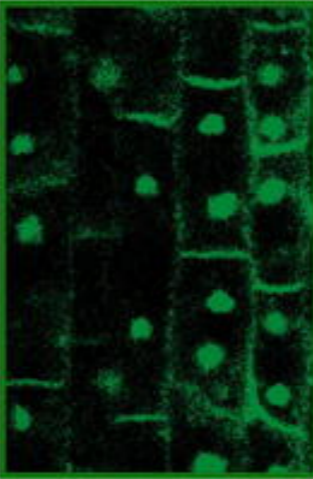
Legend:

- PIN efflux carriers
- AUX1 influx carrier
- actin filaments
- vesicle

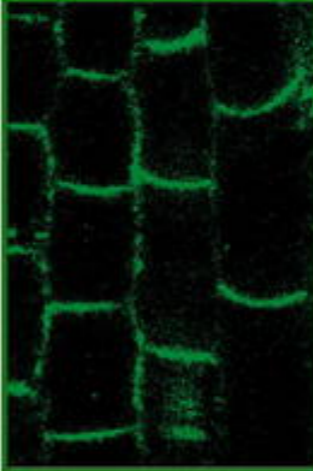
PIN1 plasma membrane localization in untreated roots

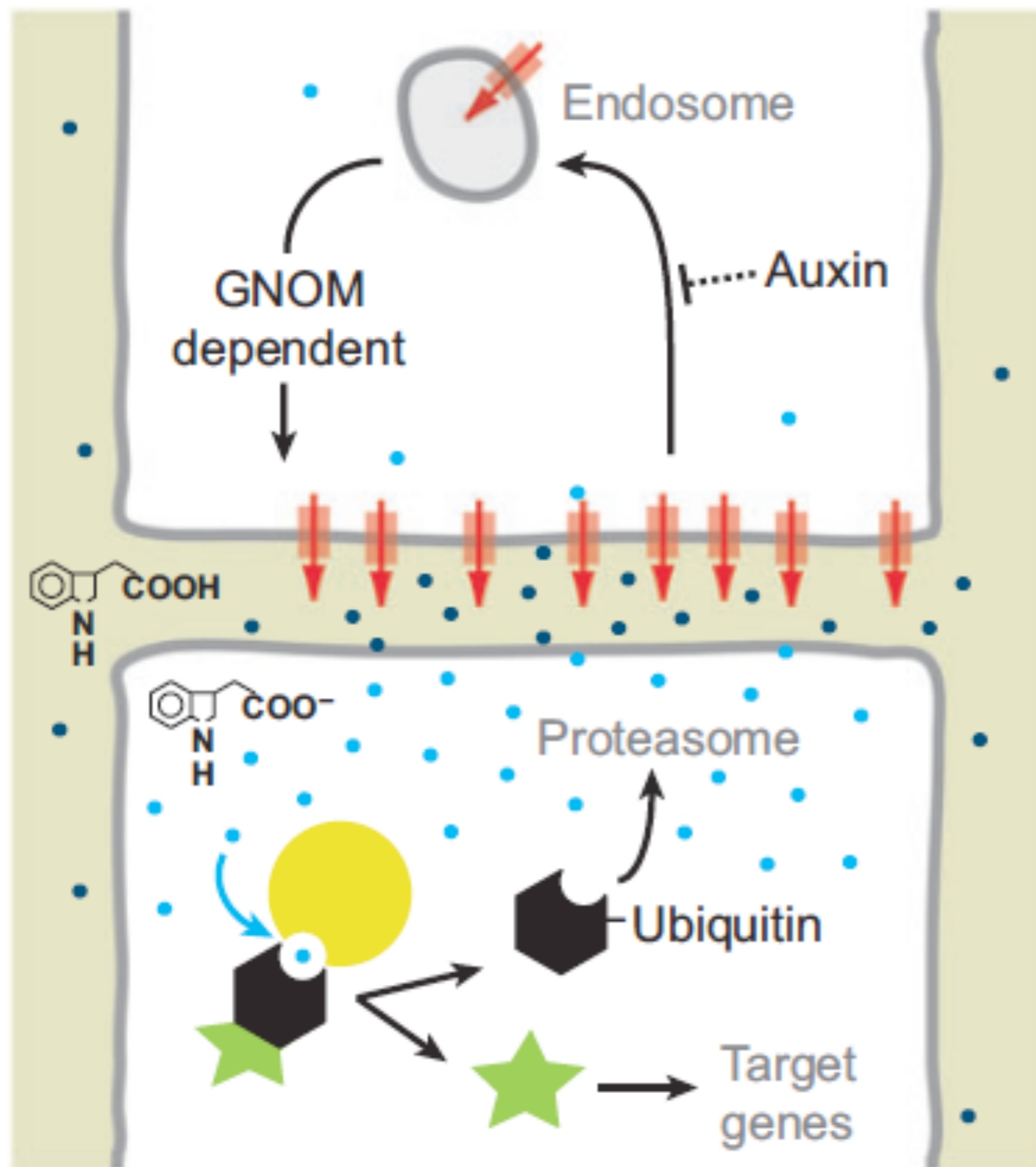


PIN1 internalization after BFA treatment



Recovery of PIN1 plasma membrane localization after washout of BFA





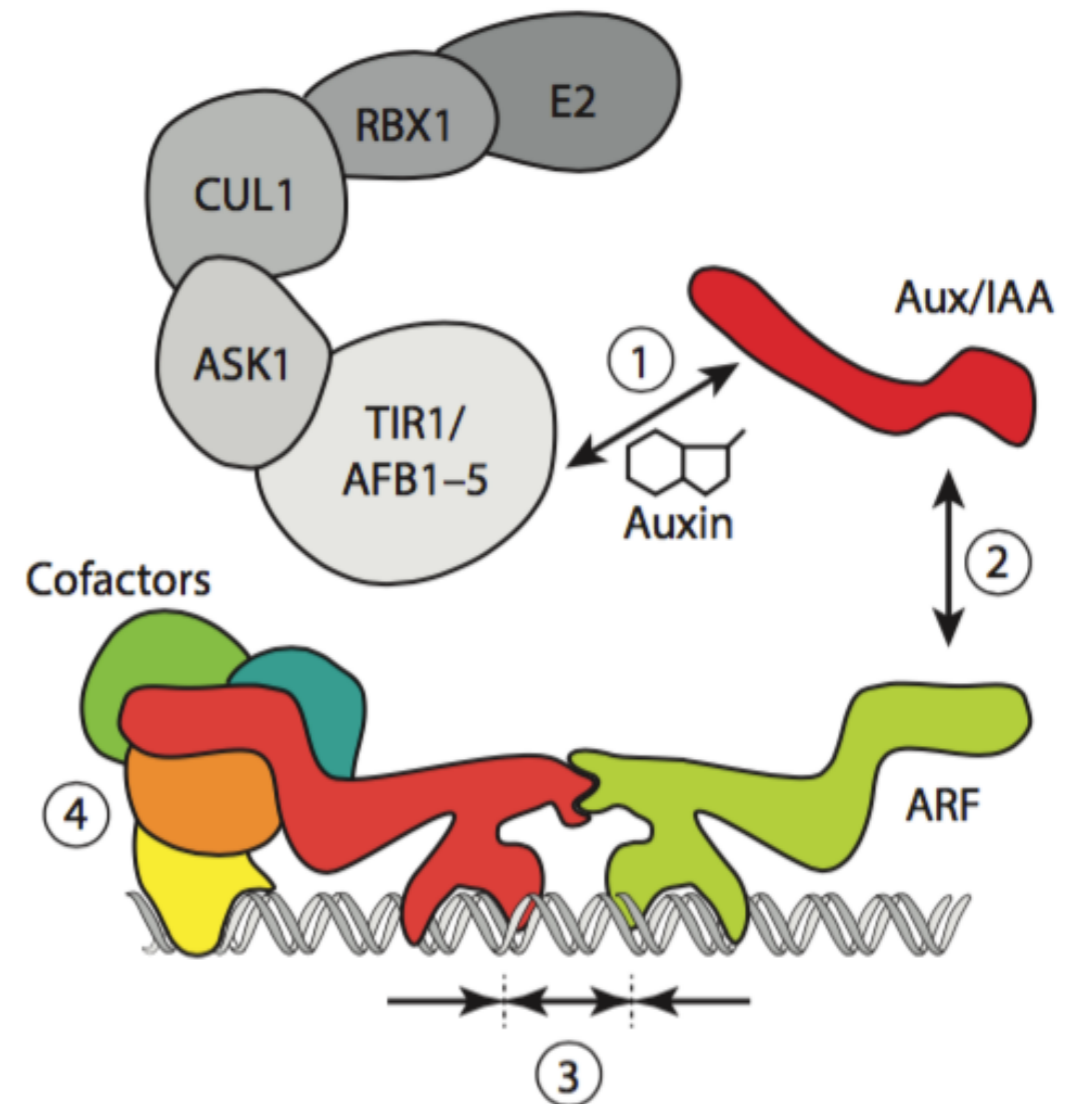
- Protonated IAA
- Dissociated IAA
- ↓ PIN efflux carrier
- SCF-TIR ubiquitin ligase
- Aux/IAA protein
- ★ Auxin response factor

How is auxin flux or accumulation converted to states of gene expression?

OVERVIEW:

Regulation of gene expression by auxin

1. Intracellular binding of auxin
2. Targeted degradation of Aux/IAA repressors
3. Selective activation of genes by ARF binding to auxin responsive promoter elements
4. Recruitment of protein co-factors for maintenance of gene expression and chromatin remodelling



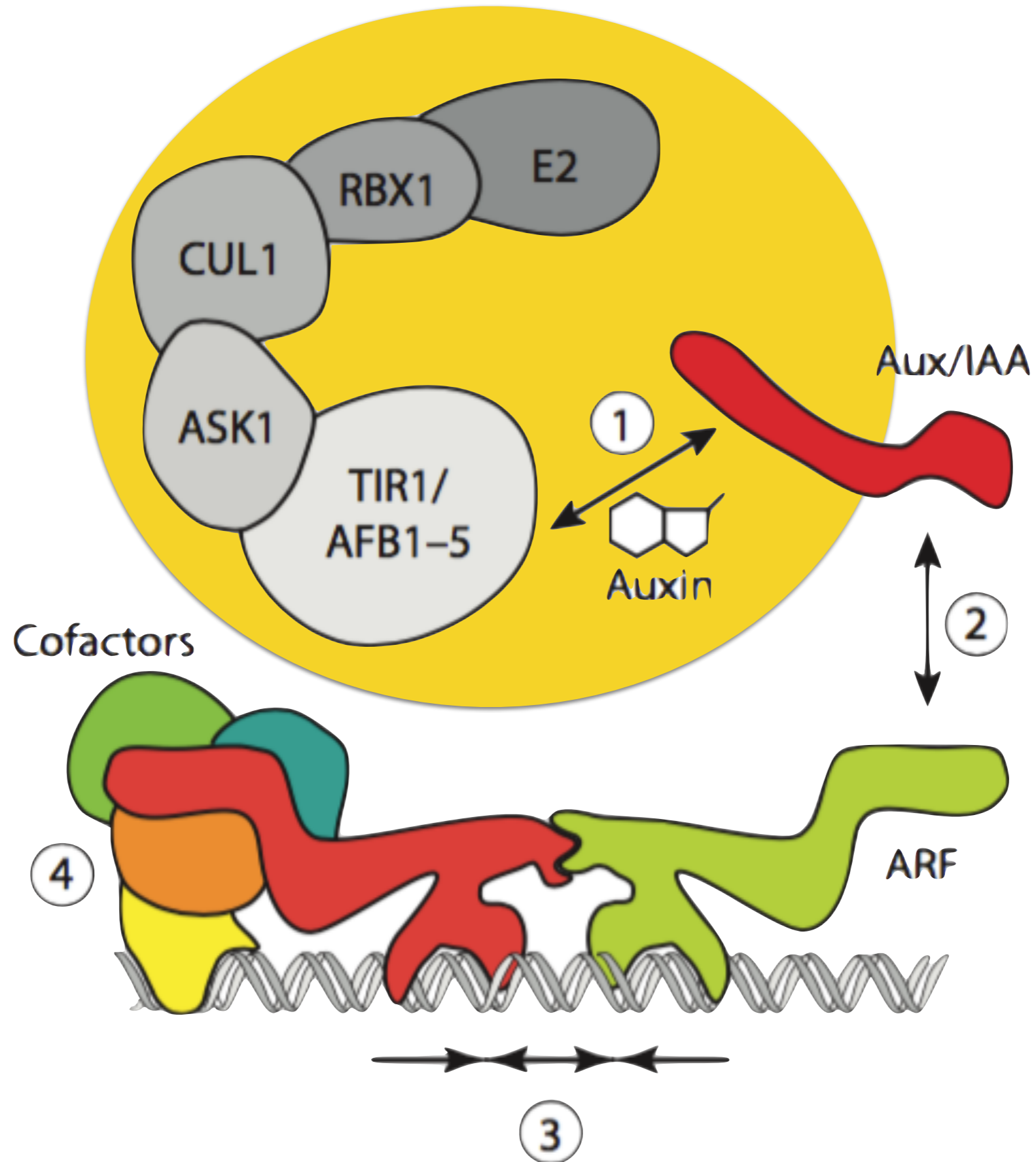
1. Intracellular binding of auxin

SCF complex

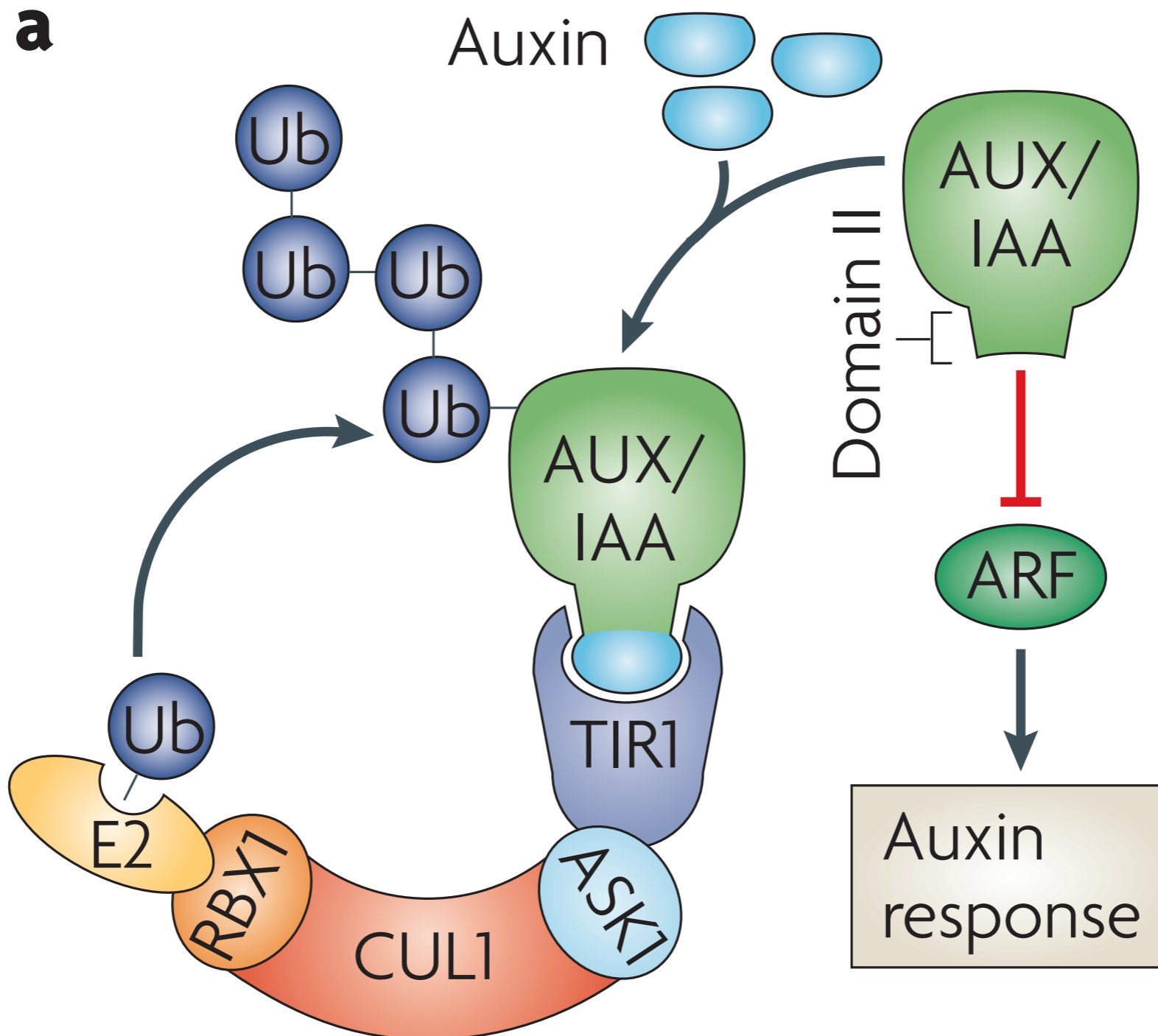
SKP/ASK1

Cullin/CUL1

F-Box/TIR1



TIR1-mediated mediated binding of auxin



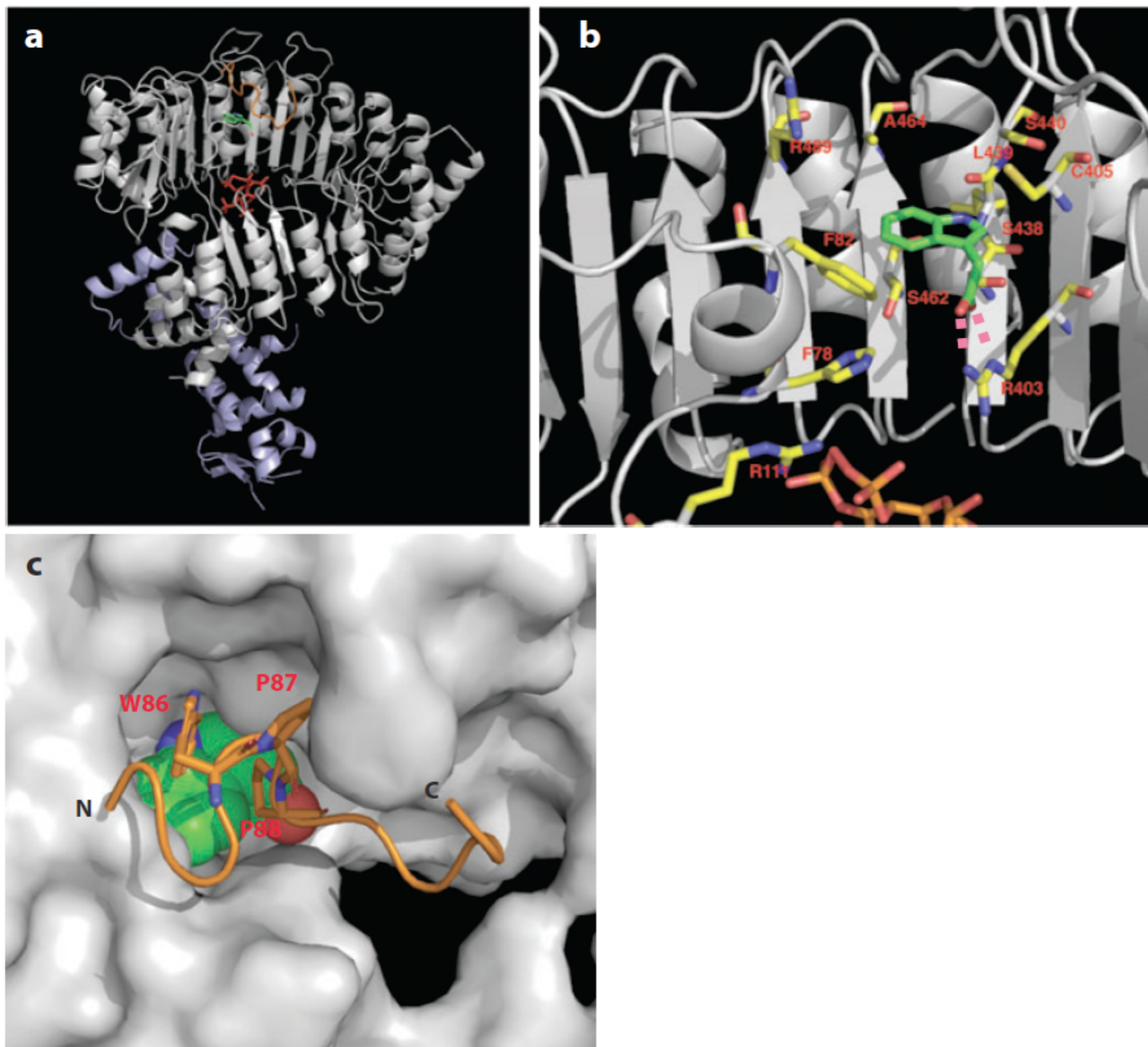
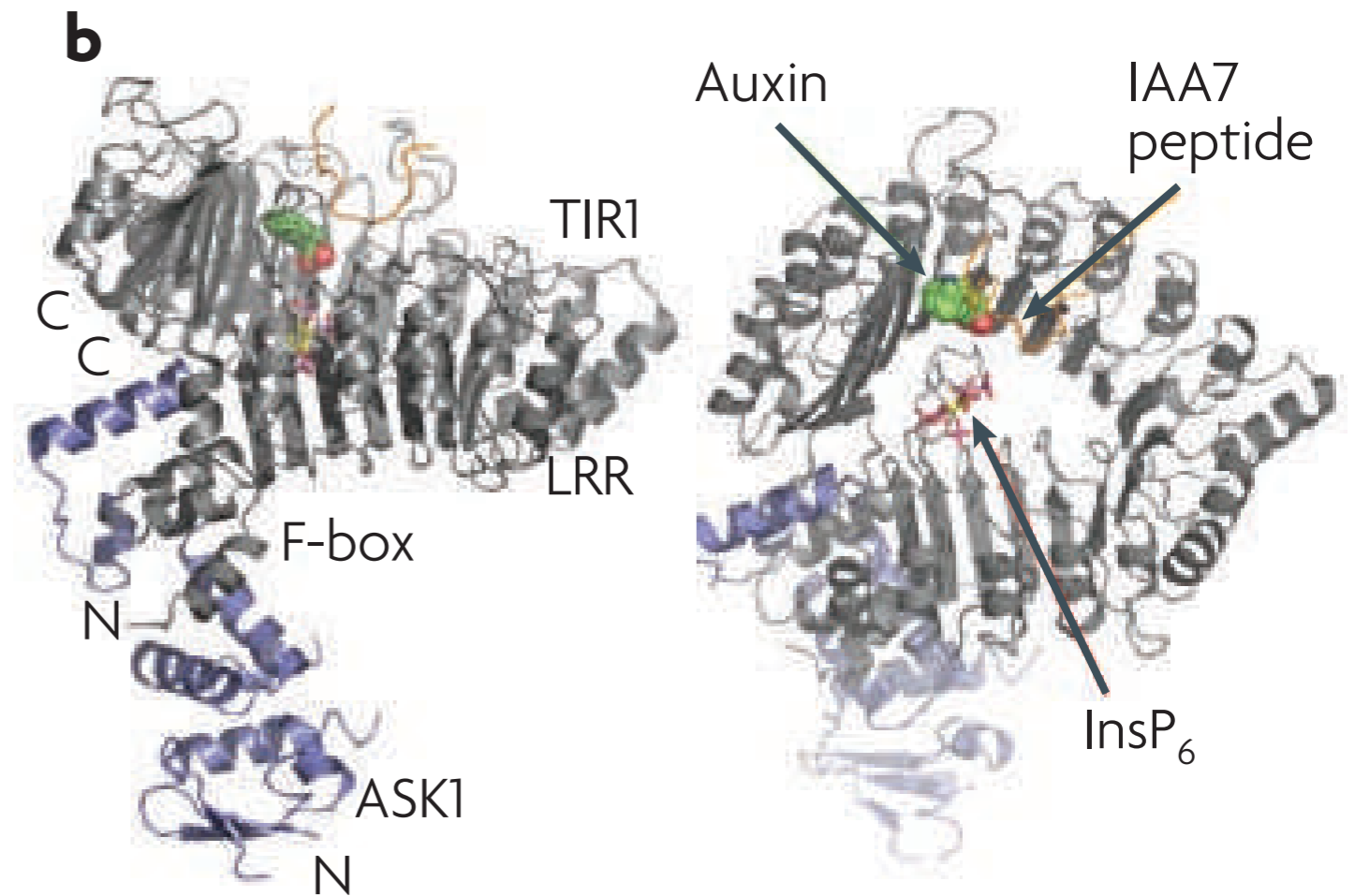
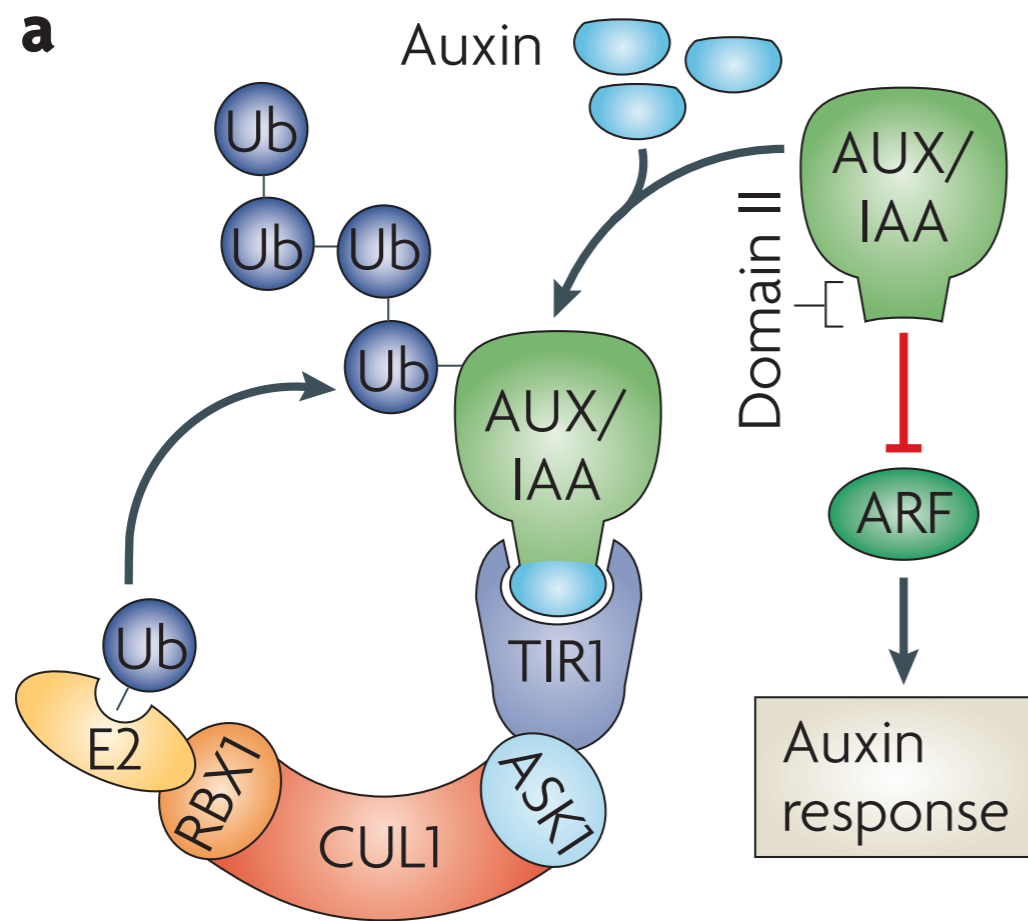


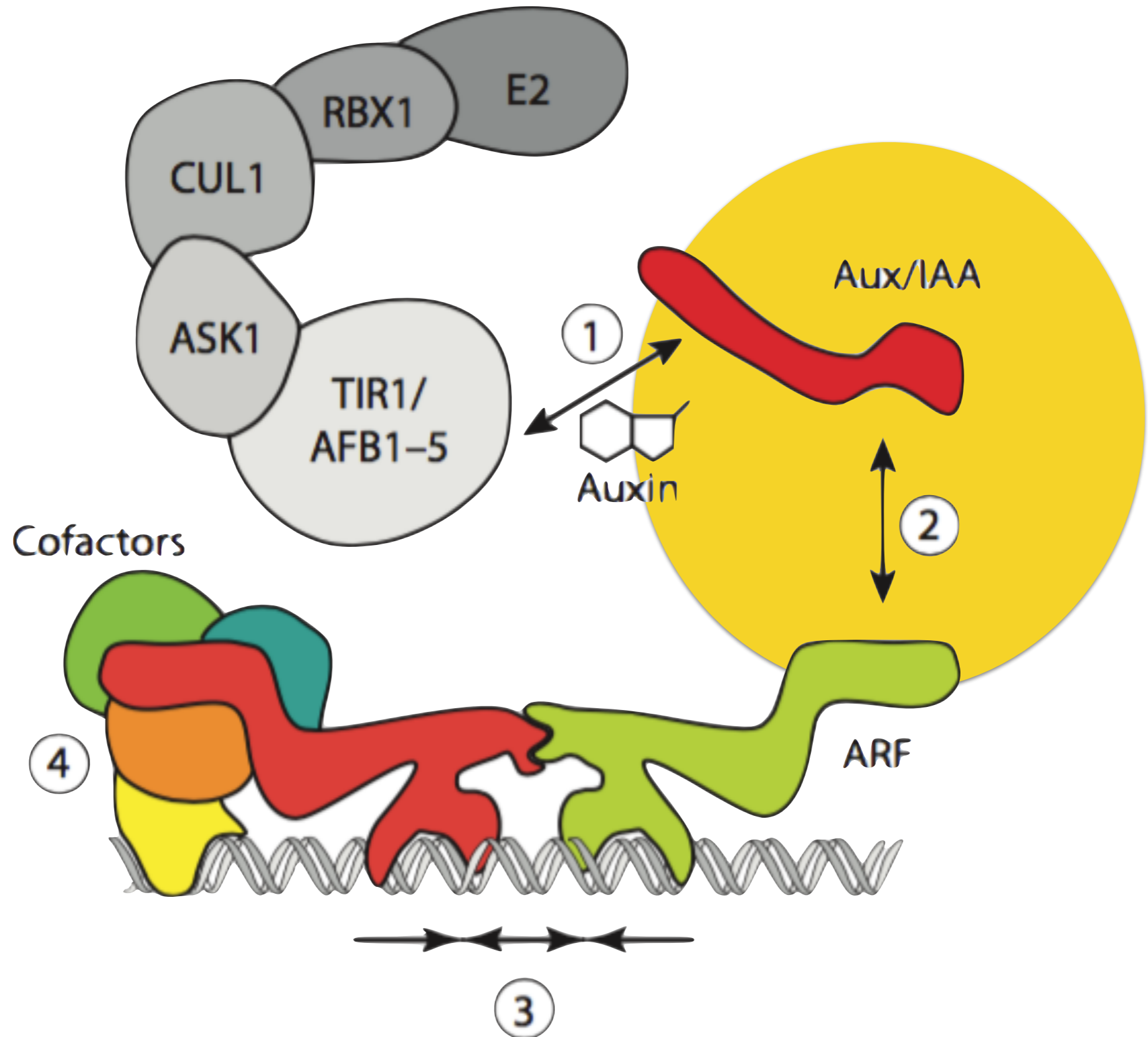
Figure 2

Auxin perception by the F-box protein TIR1. (a) Structure of TIR1 (gray) in complex with ASK1 (dark blue), indole-3-acetic acid (IAA) (green), Aux/IAA domain II peptide (orange), and inositol hexakisphosphate (red). (b) Close-up of the auxin-binding pocket occupied by IAA (green). Surrounding TIR1 residues are shown in yellow. Dashed pink lines indicate hydrogen bonds between the carboxyl group of IAA and conserved R403. (c) Surface view of TIR1 in complex with IAA (green) and domain II peptide (orange).

TIR1-mediated ubiquitination of AUX/IAA proteins



2. Targeted degradation of AUX/IAA repressors



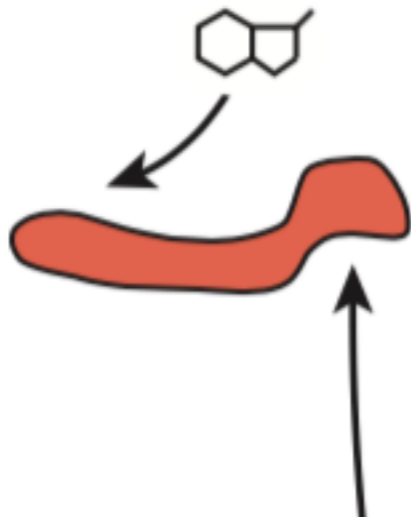
a TIR1/AFB



Tethering to SCF complex

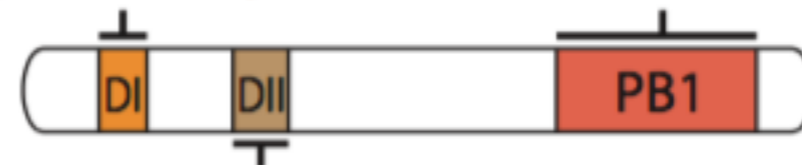
Auxin and Aux/IAA interaction

b Aux/IAA

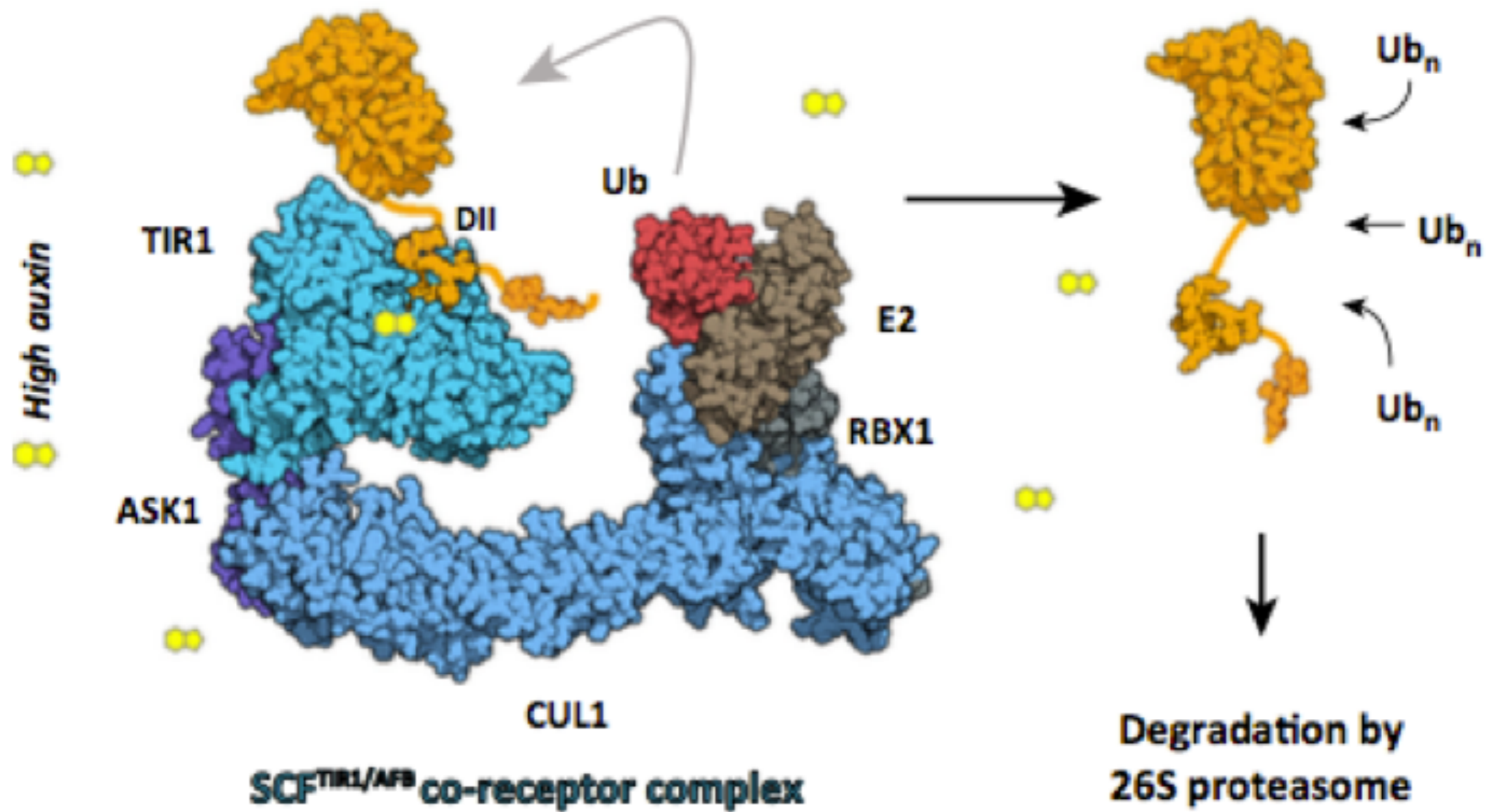


EAR domain
(Δ in IAA33)

ARF and Aux/IAA Interaction



Degron: GWPP(V/I)
(Δ in IAA20 and -30-34)
TIR1-auxin interaction



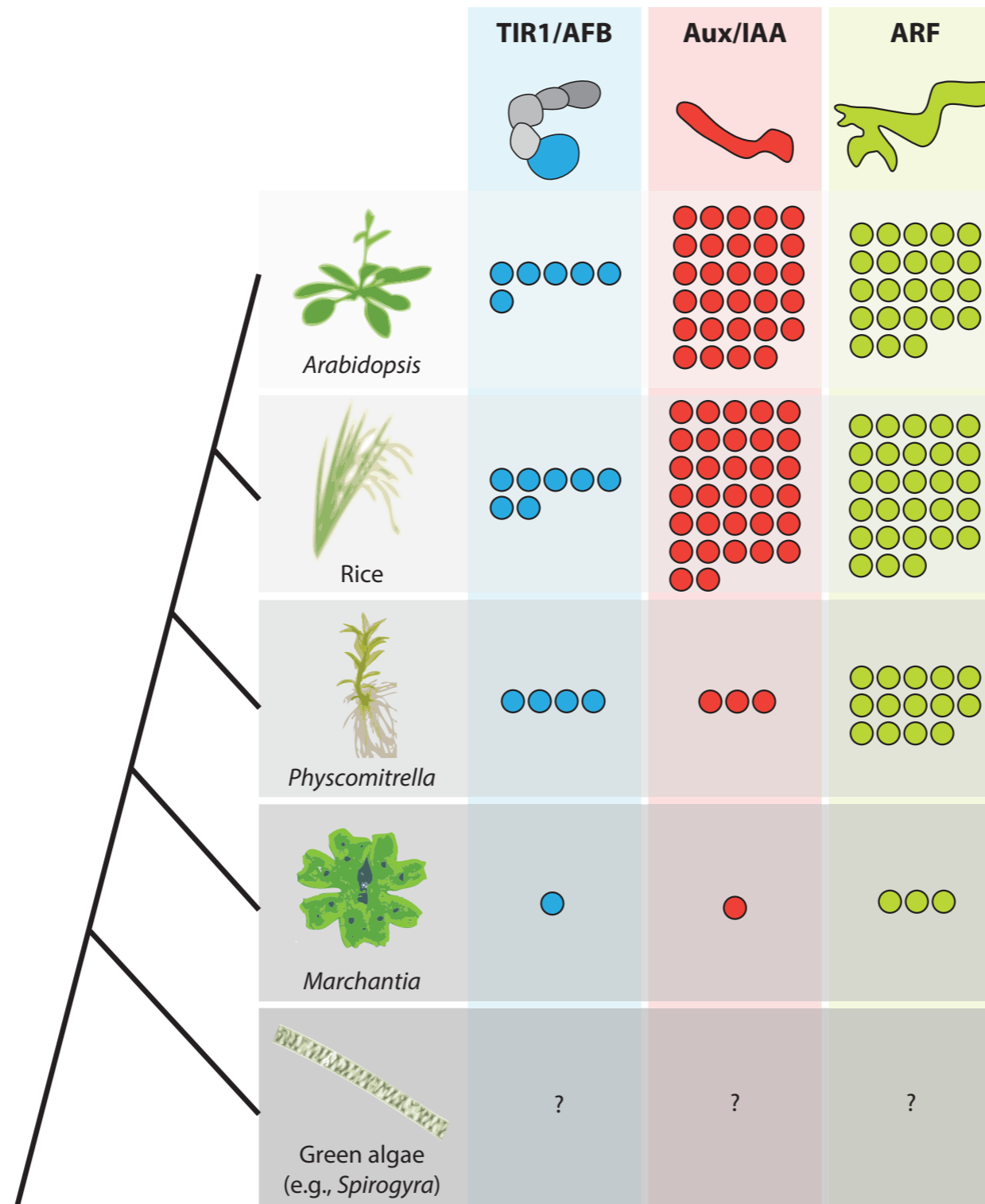
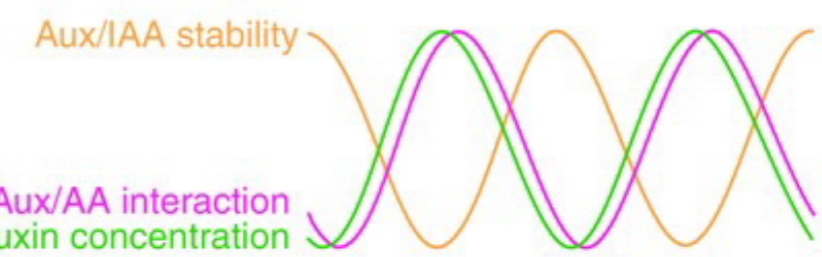
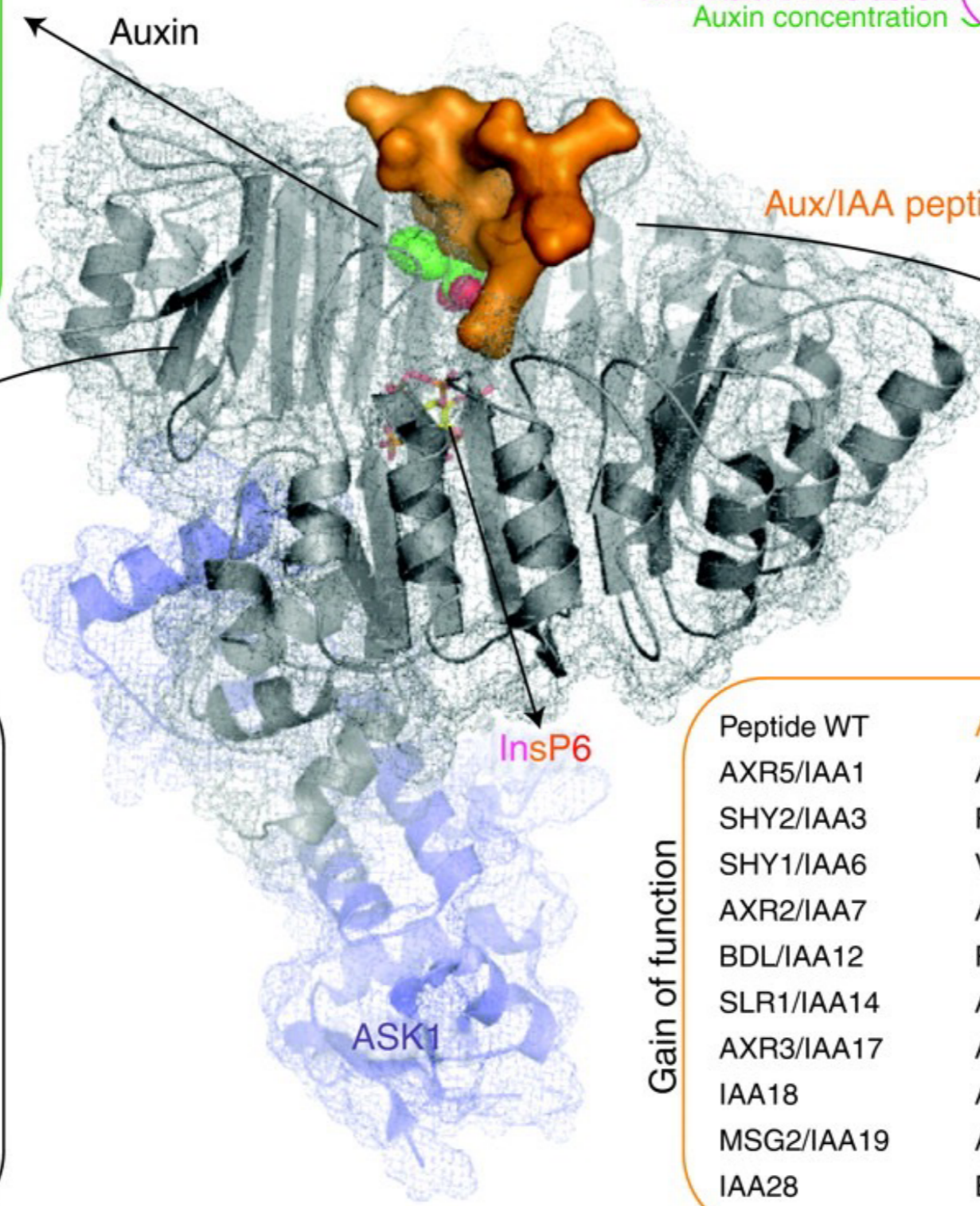
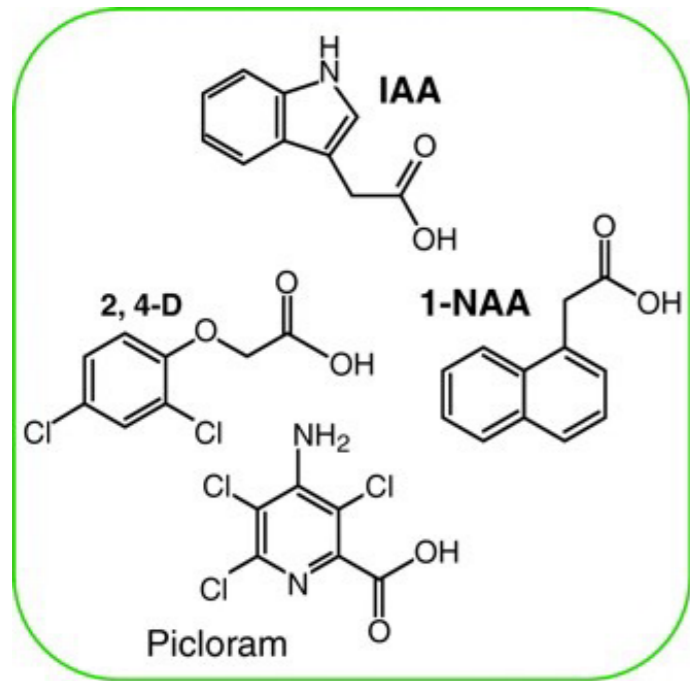
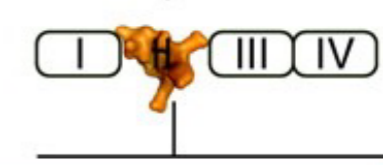


Figure 7

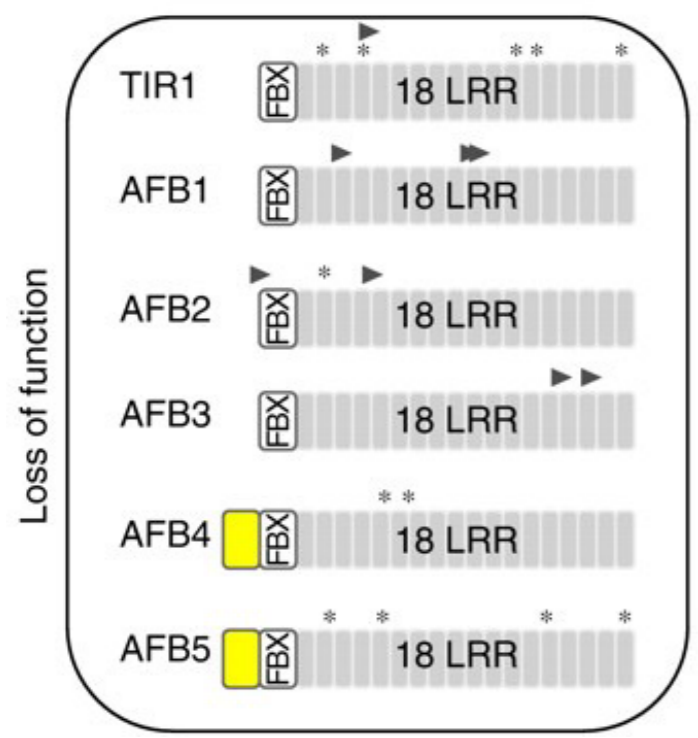
The evolution of the auxin response pathway, showing the distribution of genes encoding TIR1/AFB, Aux/IAA, and ARF proteins in published plant genomes for several plant species. These species represent eudicots (*Arabidopsis*), monocots (rice), mosses (*Physcomitrella*), liverworts (*Marchantia*), and green algae (*Spirogyra*, as an example of charophytes). The tree on the left-hand side indicates the divergence order but is not drawn to scale. Protein abbreviations: ARF, AUXIN RESPONSE FACTOR; Aux/IAA, AUXIN/INDOLE-3-ACETIC ACID; TIR1/AFB, TRANSPORT INHIBITOR RESISTANT 1/AUXIN SIGNALING F-BOX.



Aux/IAA peptide



TIR1/AFBs



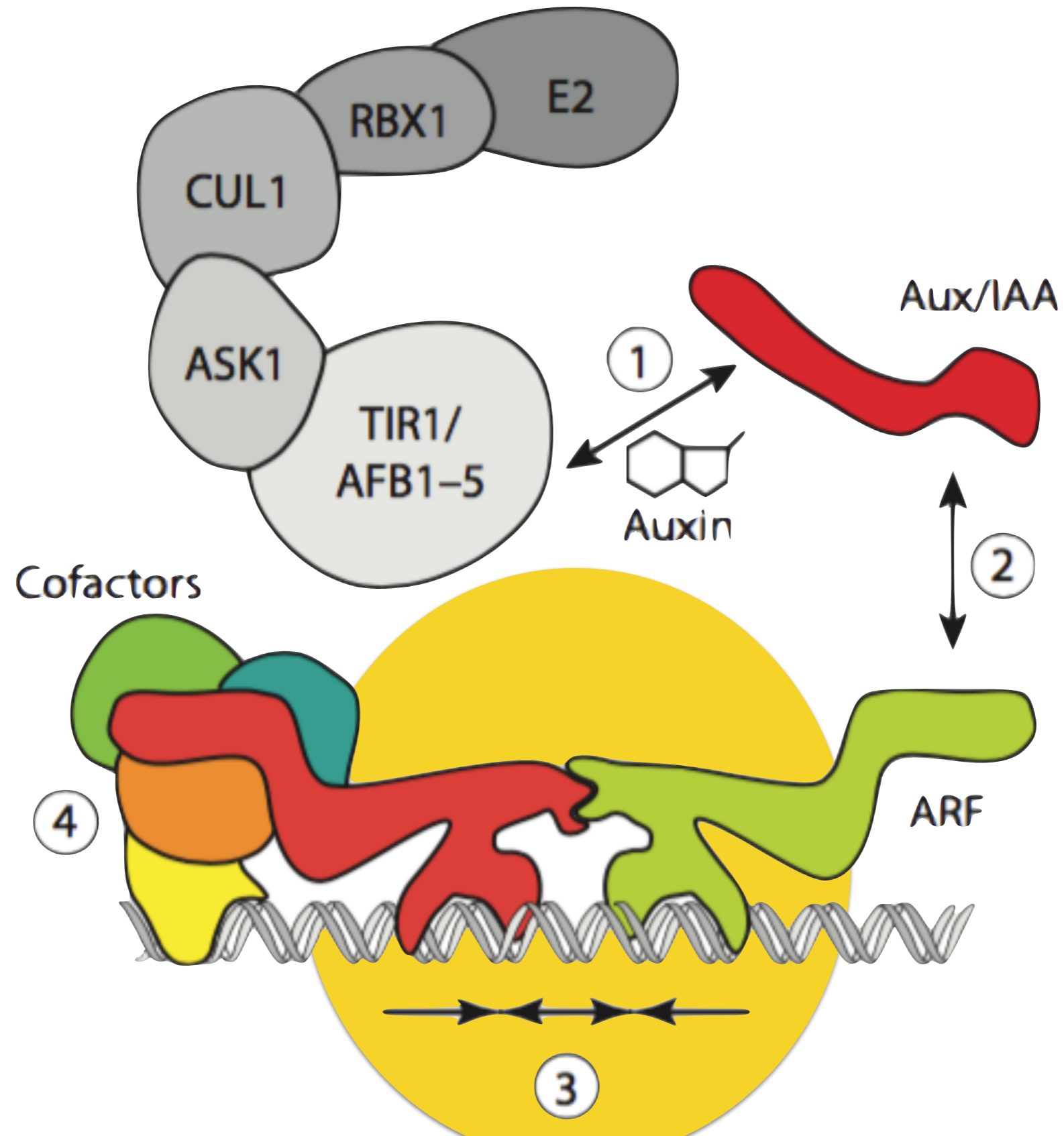
InsP6

ASK1

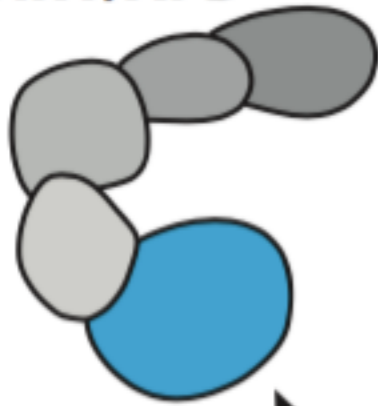
Gain of function

Peptide WT	AKAQVVGWPPVRNYRKN
AXR5/IAA1	AKTQIVGWPPVRSNRKN
SHY2/IAA3	RKAQIVGWPPVRSYRKN
SHY1/IAA6	VKSQAVGWPPVCSYRRK
AXR2/IAA7	AKAQVVGWPPVRNYRKN
BDL/IAA12	RSSQVVGWPPIGLHRMN
SLR1/IAA14	AKAQVVGWPPVRNYRKN
AXR3/IAA17	AKAQVVGWPPVRSYRKN
IAA18	APGPVVGWPPVRSFRKN
MSG2/IAA19	AKSFQVVGWPPVCSYRKK
IAA28	EVAPVVGWPPVRSSRRN

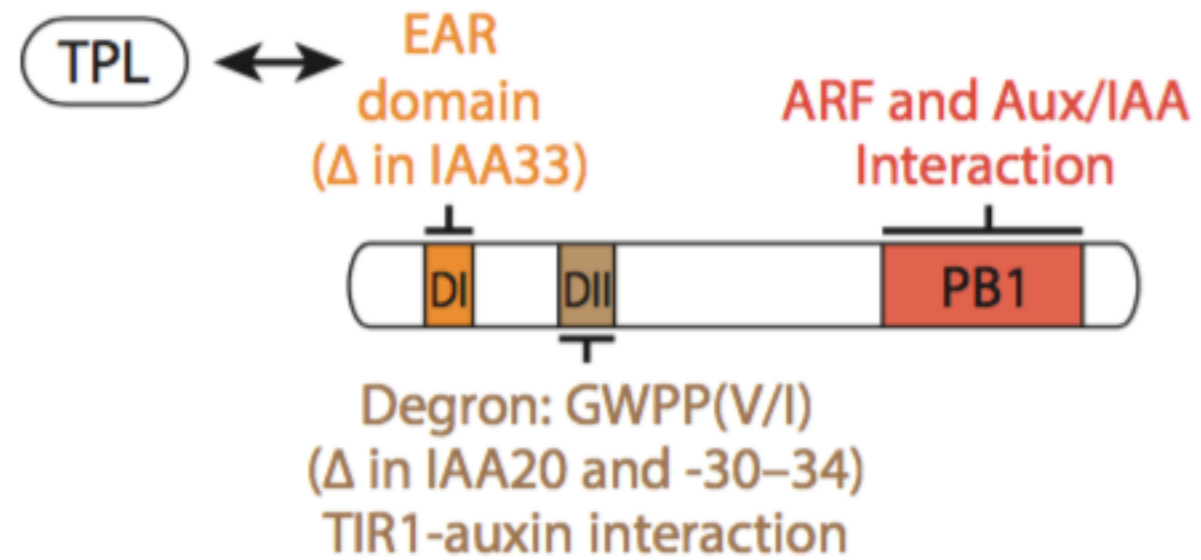
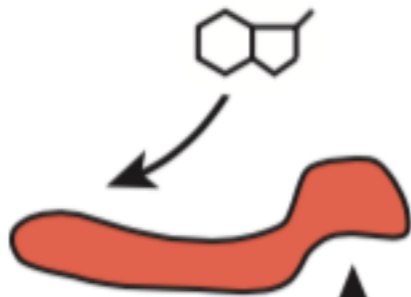
3. Selective activation of genes by ARF binding to auxin responsive promoters



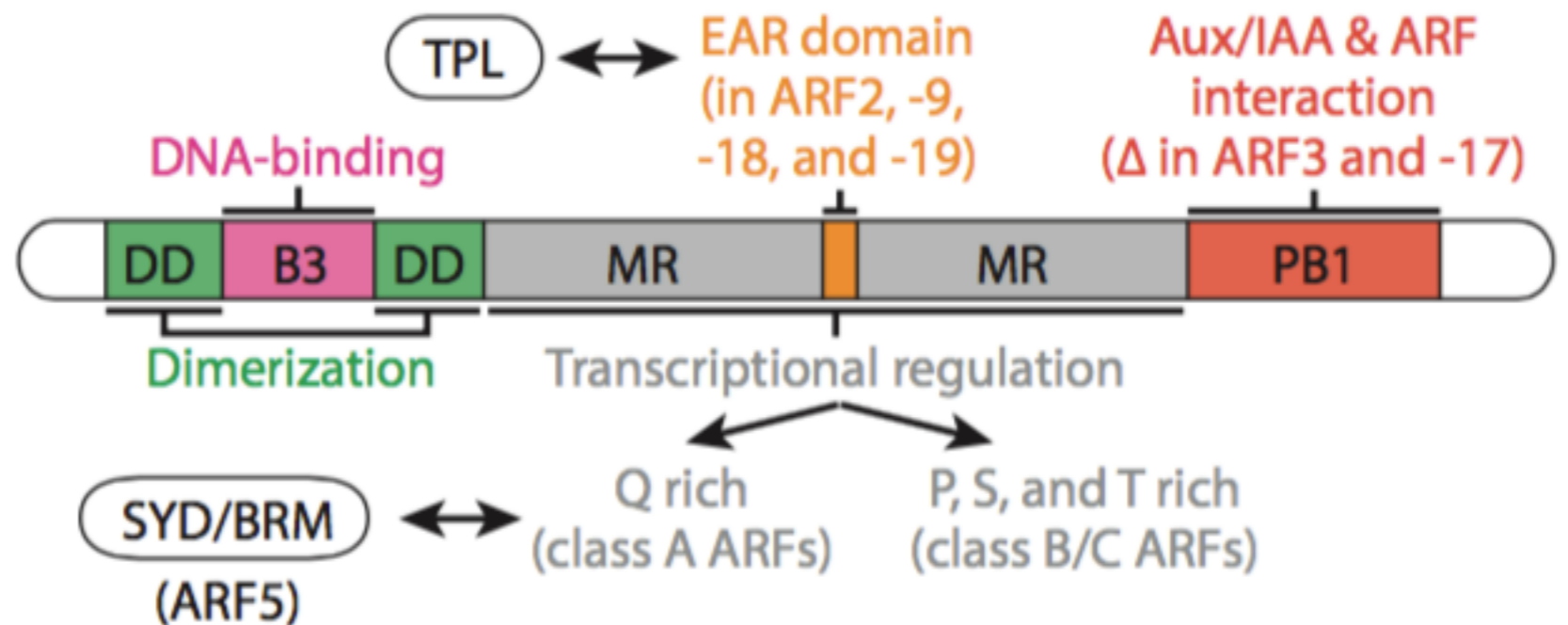
a TIR1/AFB

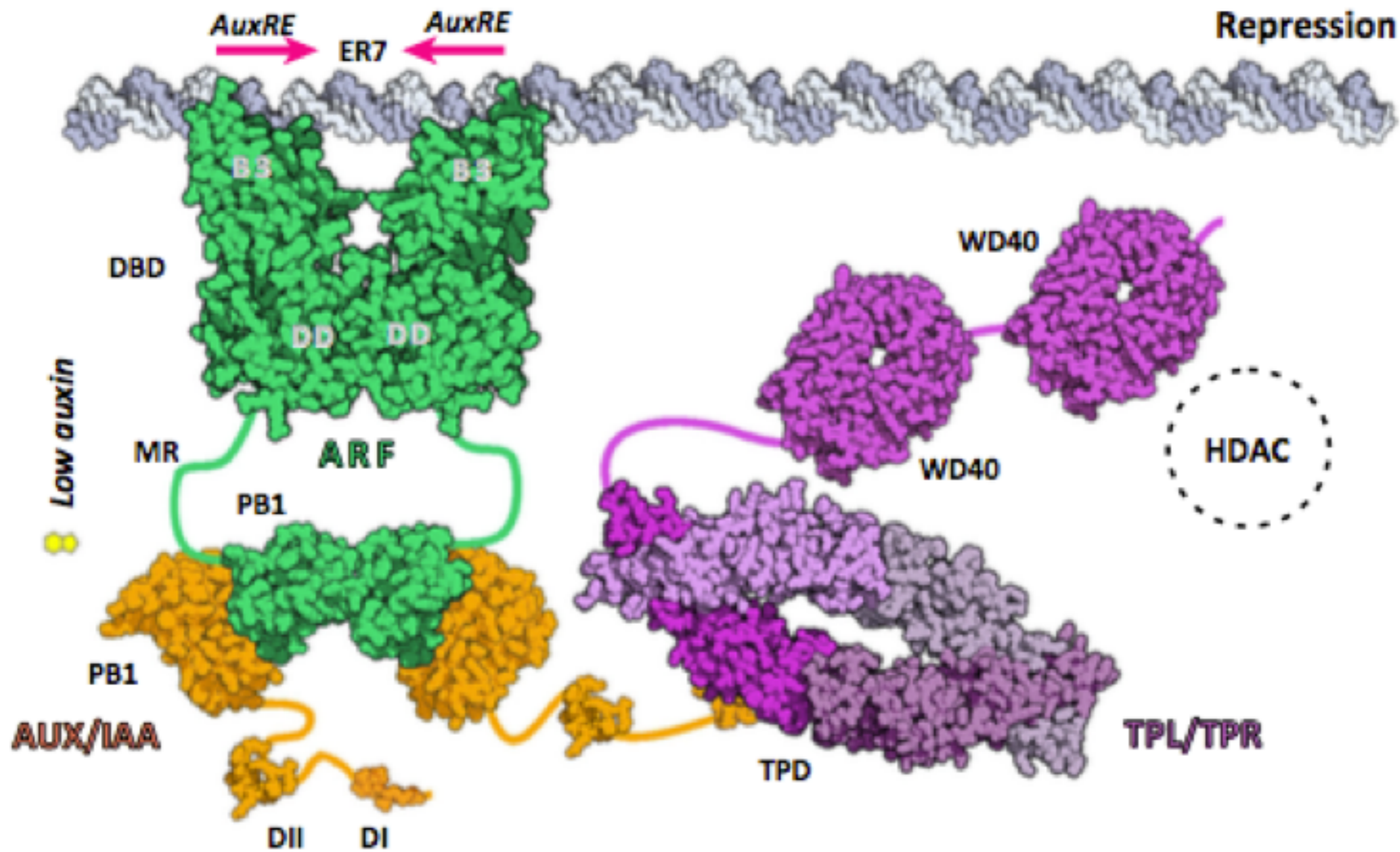


b Aux/IAA



c ARF

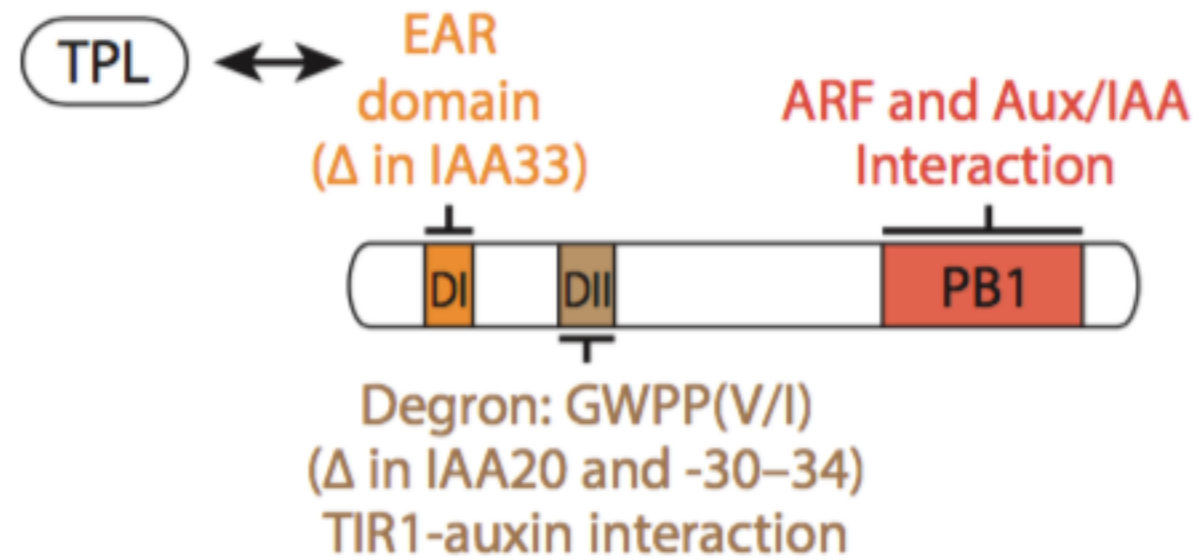
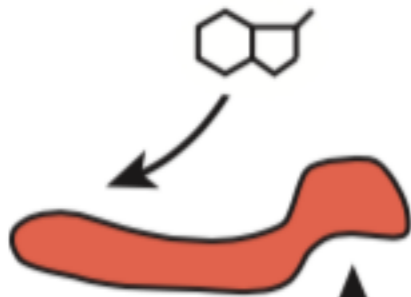




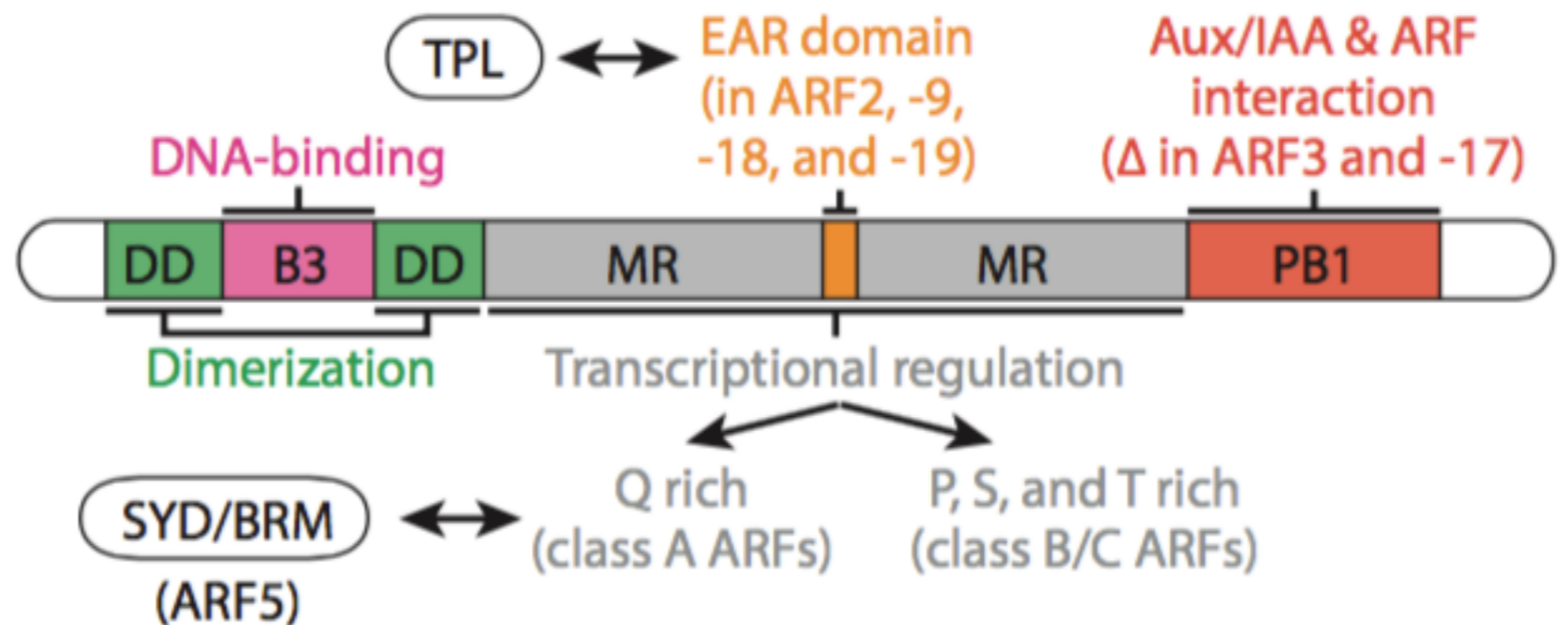
a TIR1/AFB

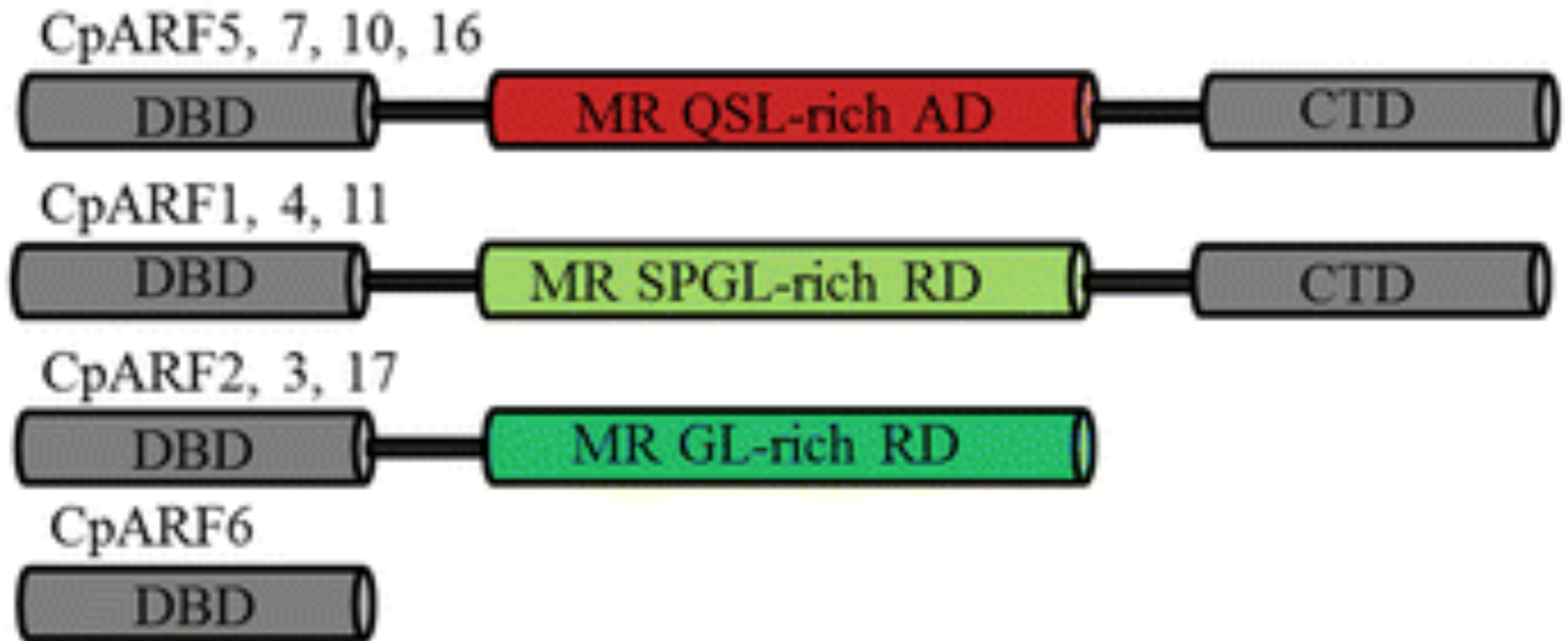


b Aux/IAA



c ARF

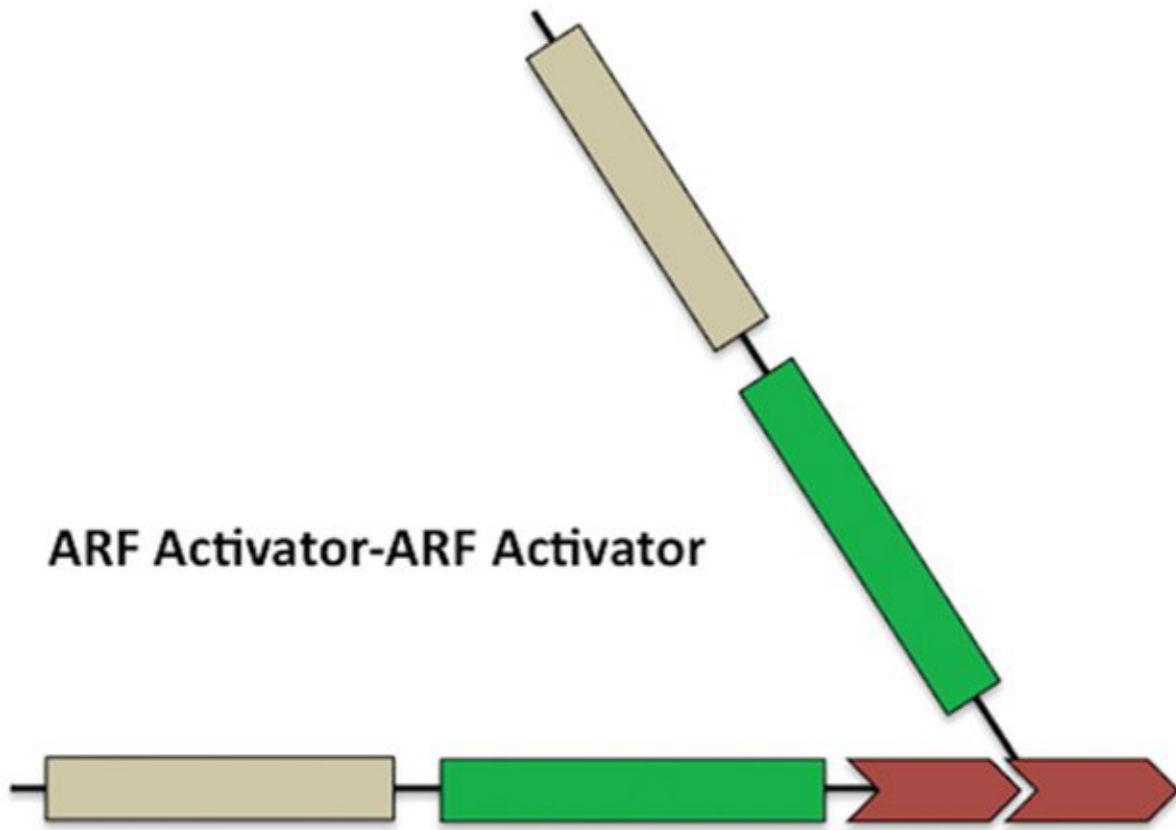




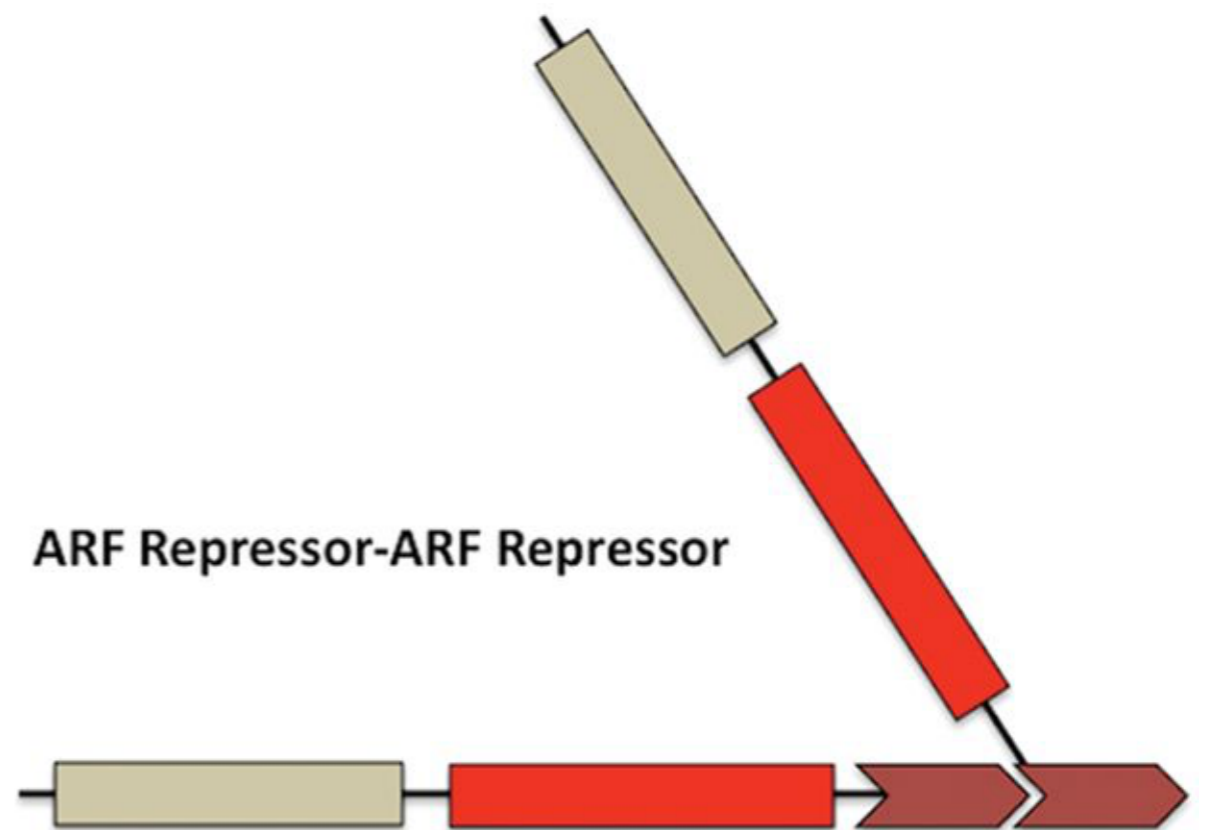
The protein structure of ARFs.

DBD, DNA-binding domain; CTD, C-terminal dimerization domain; MR, middle region; RD, repression domain; AD, activation domain;

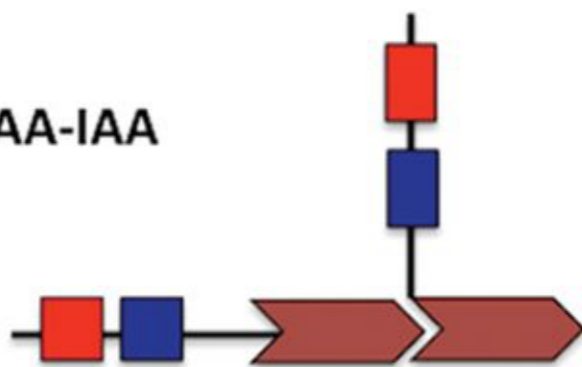
ARF Activator-ARF Activator



ARF Repressor-ARF Repressor



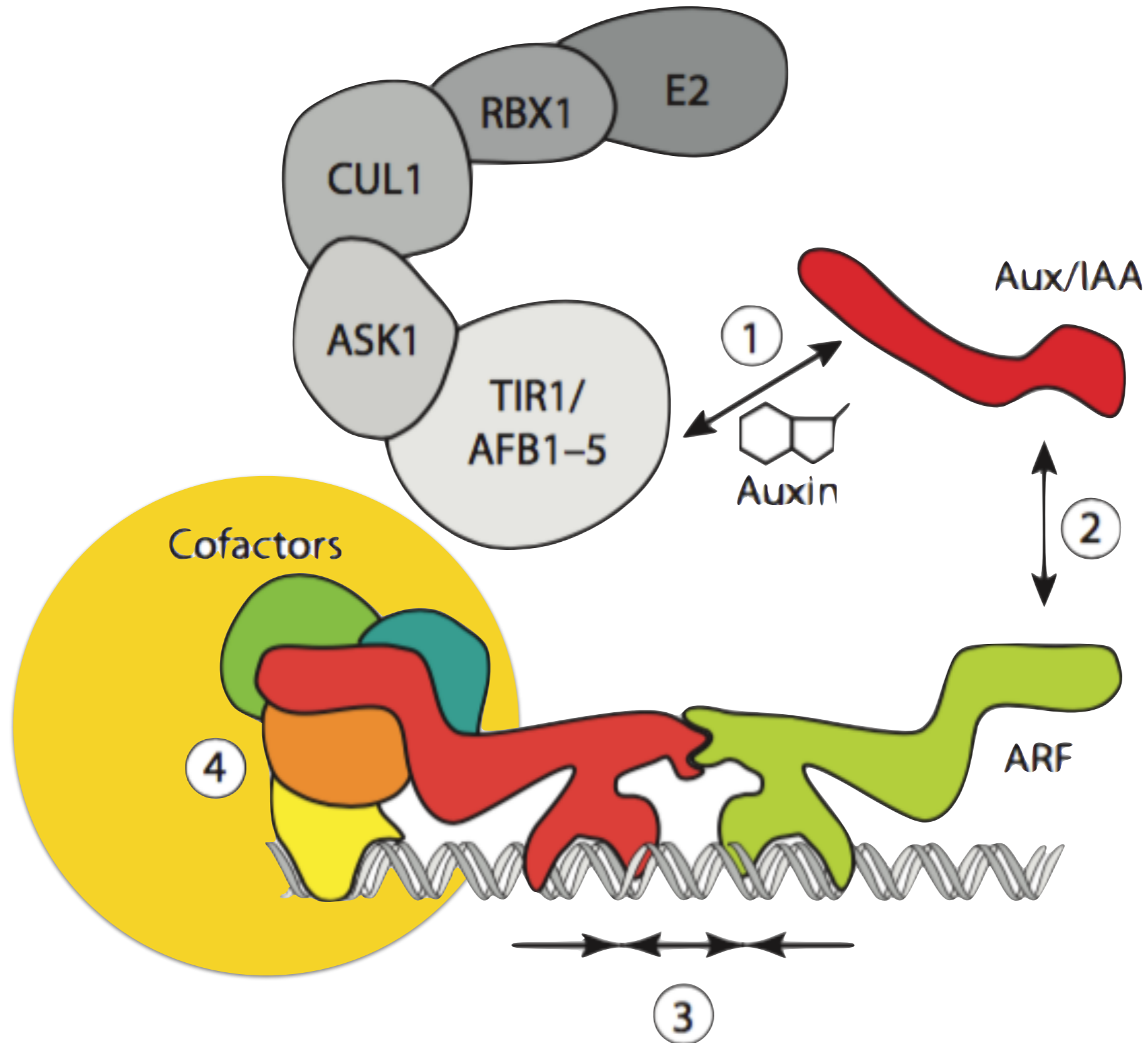
IAA-IAA

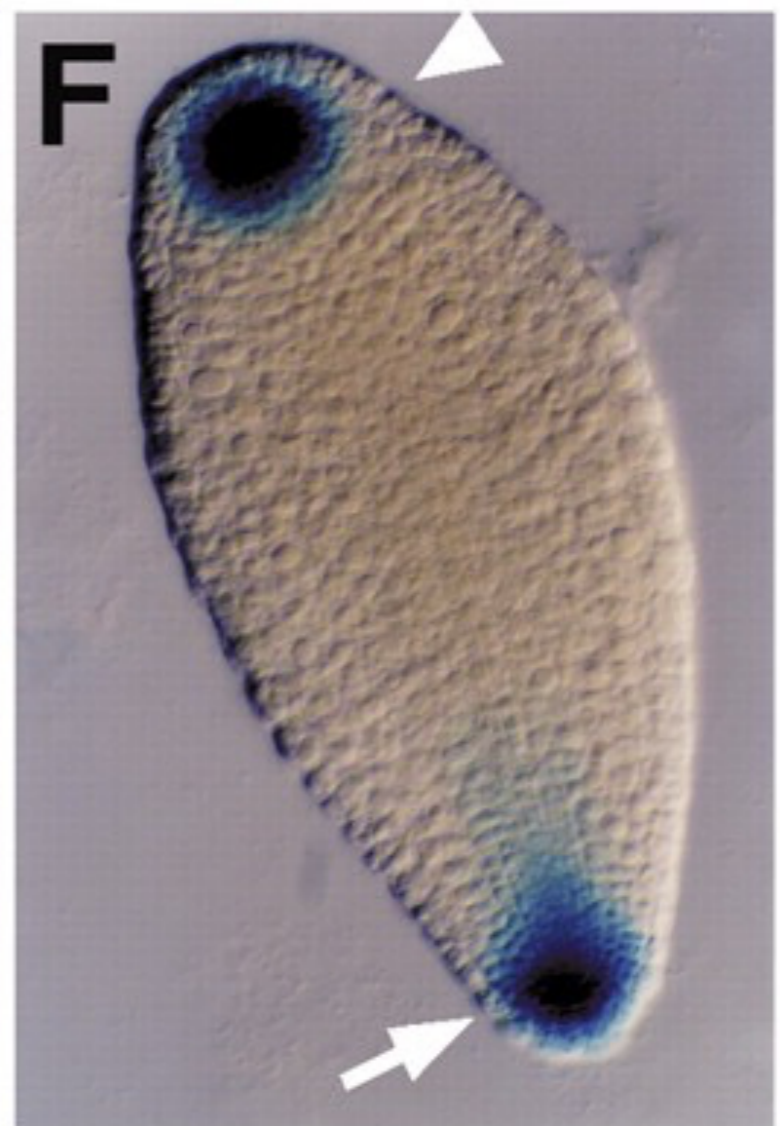
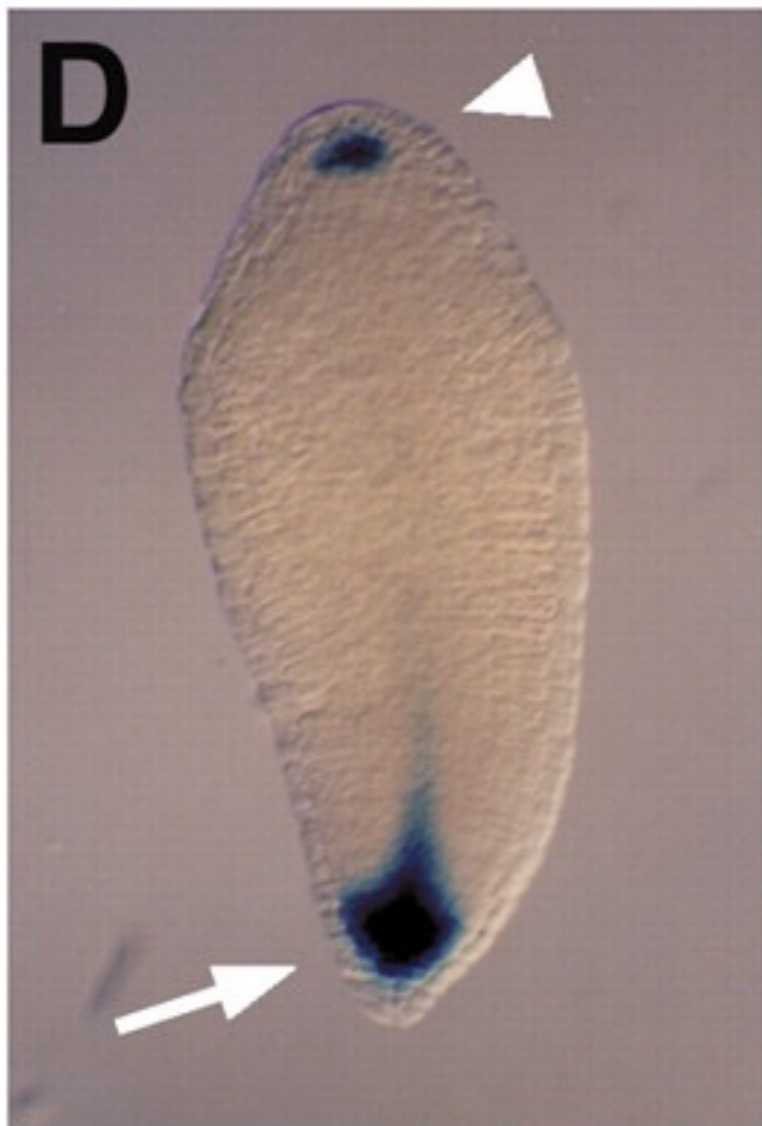
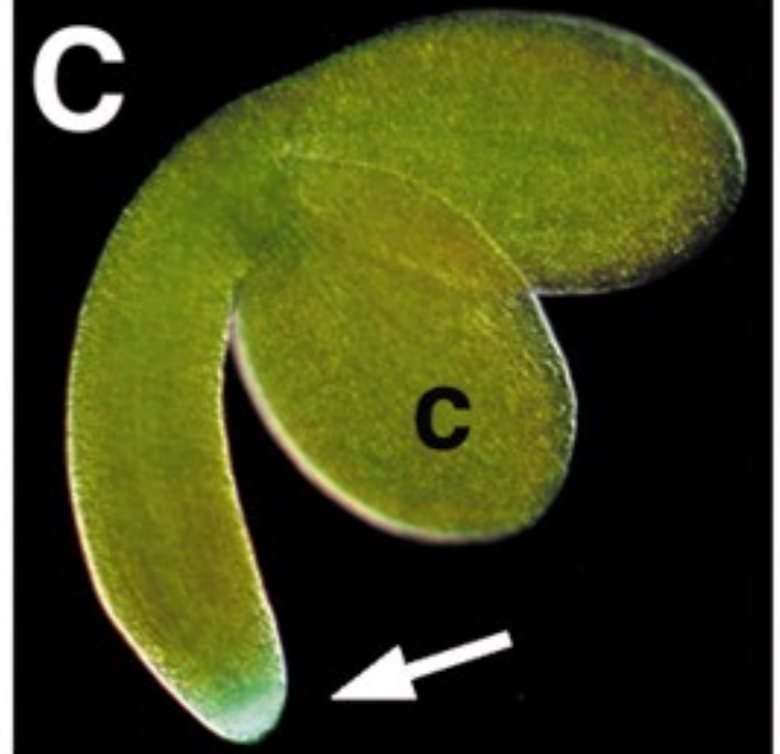
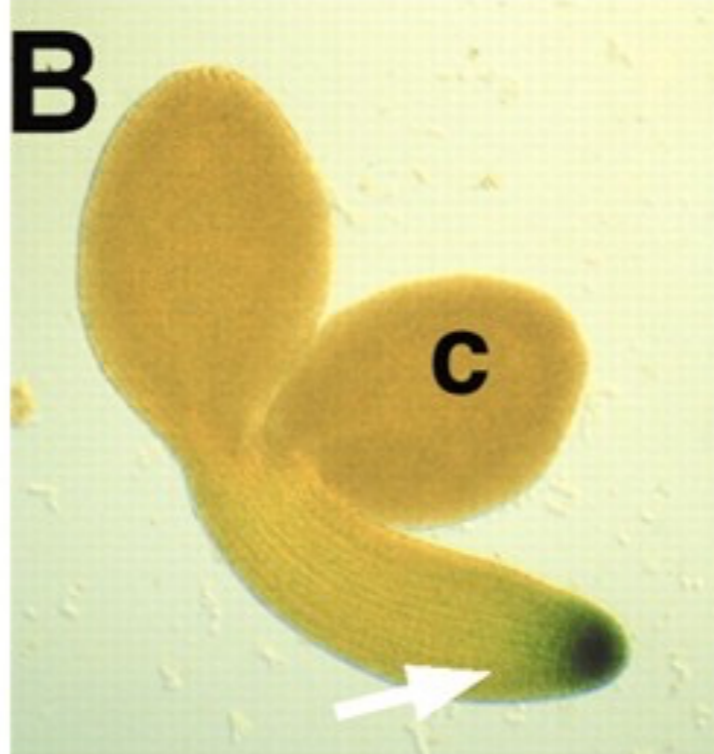
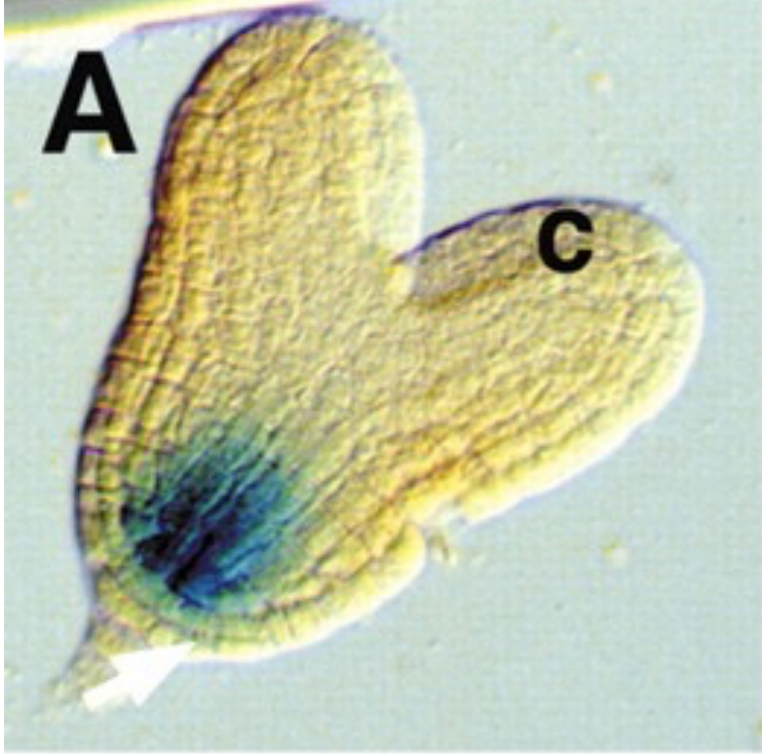


ARF Activator-IAA

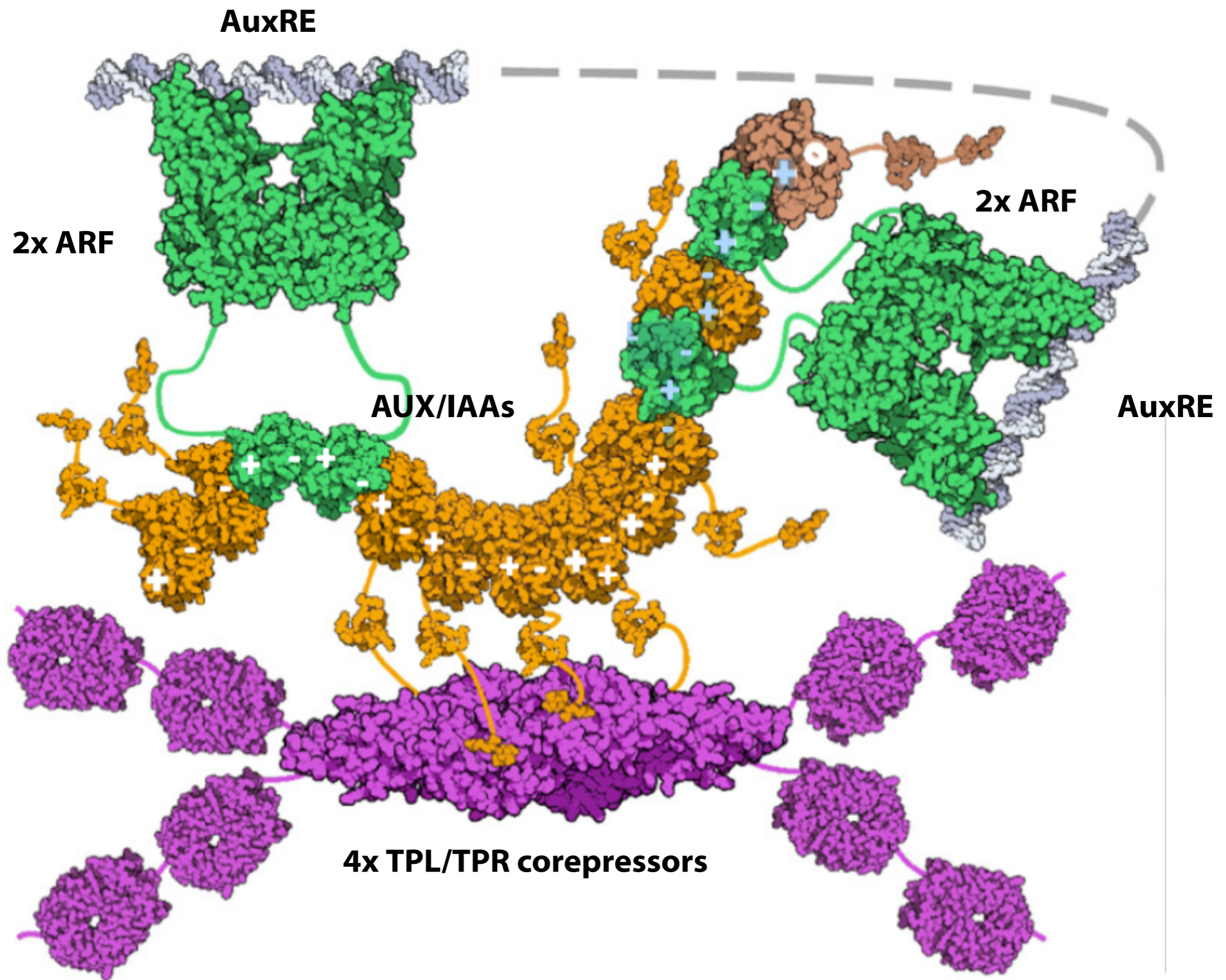


4. Recruitment of protein co-factors for maintenance of gene expression



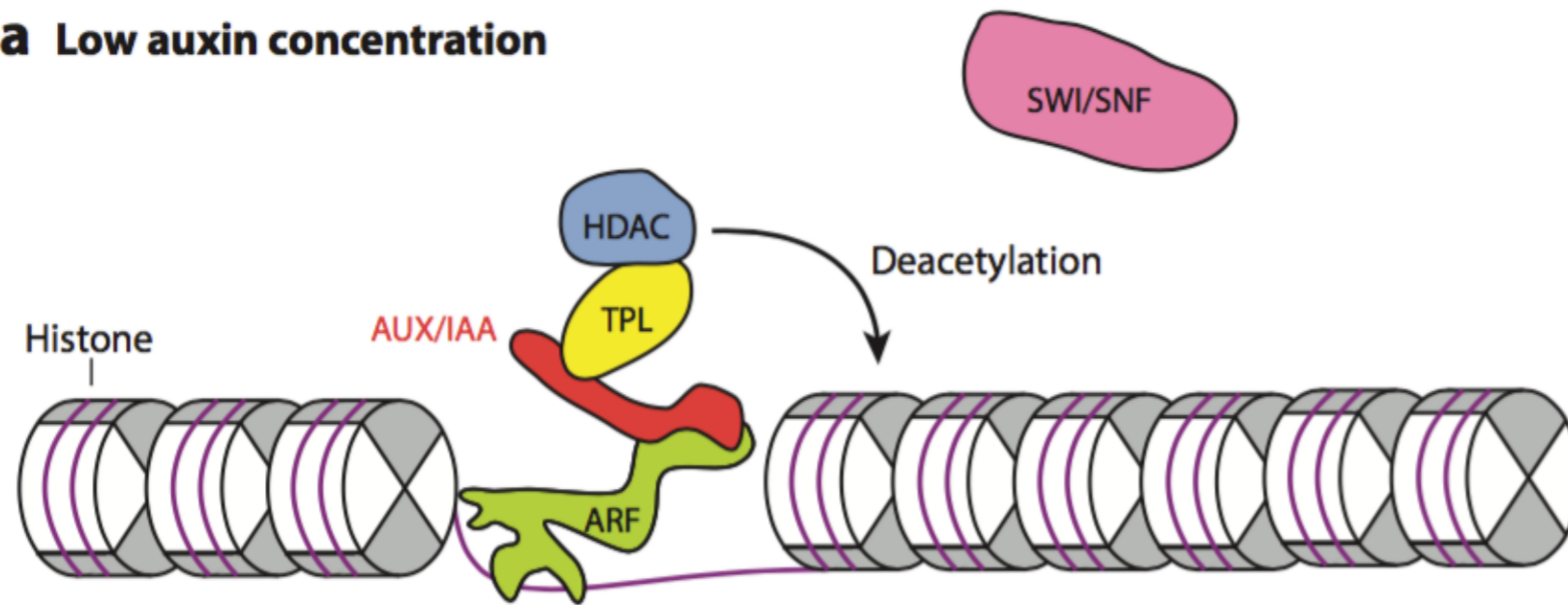


***topless (tpl)* mutant**

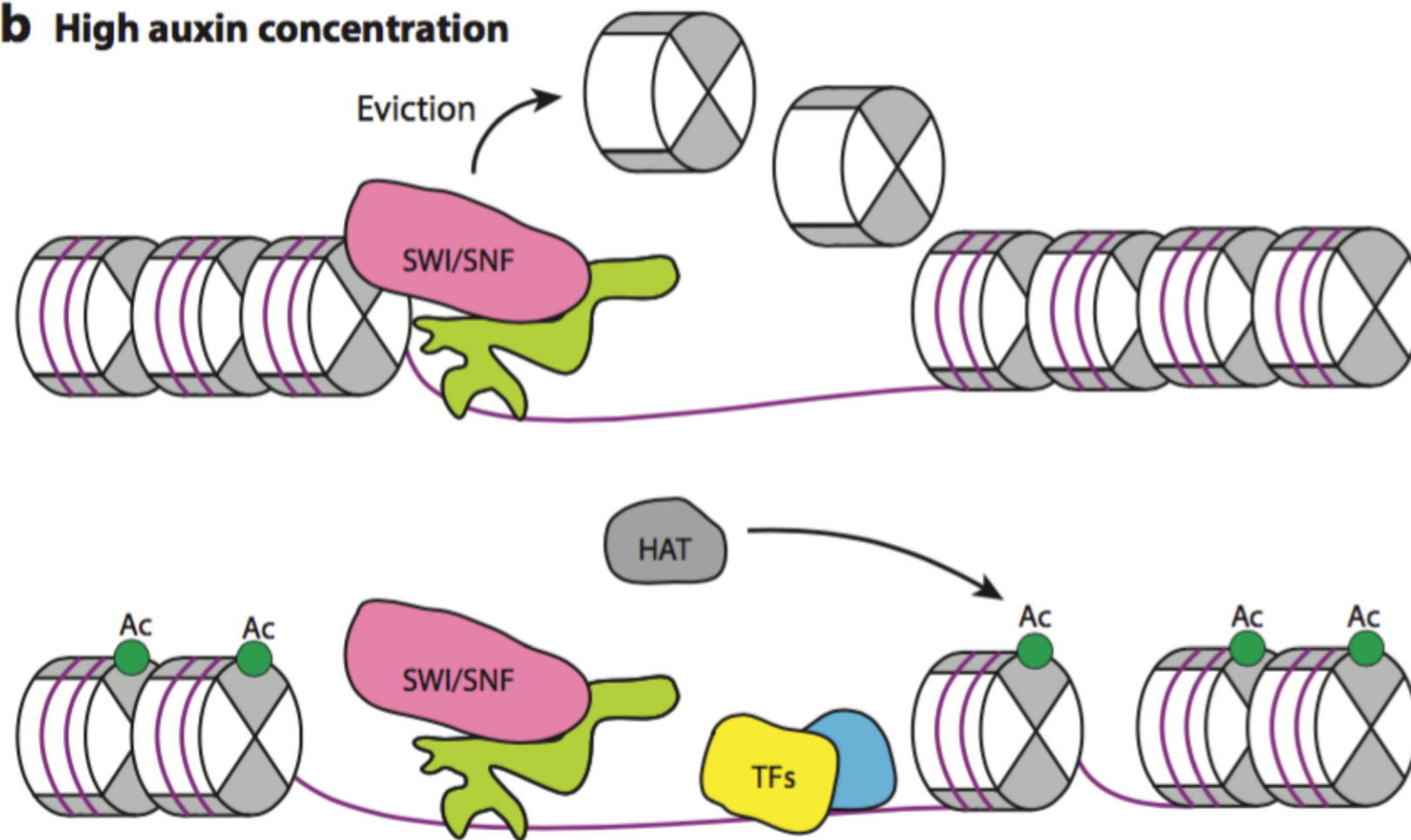


Recognition of composite AuxREs and recruitment of tetrameric TPL/TPR corepressors

a Low auxin concentration



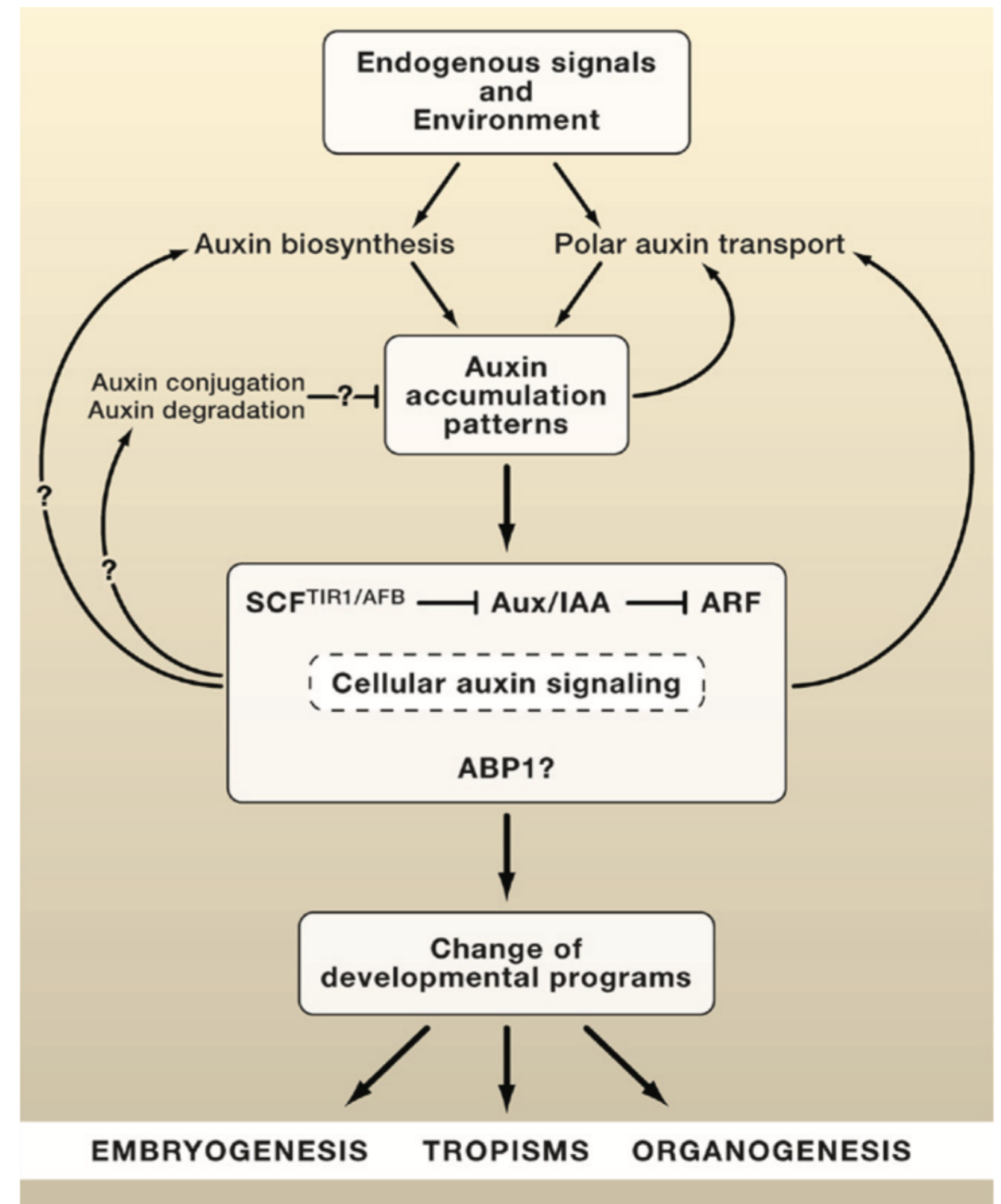
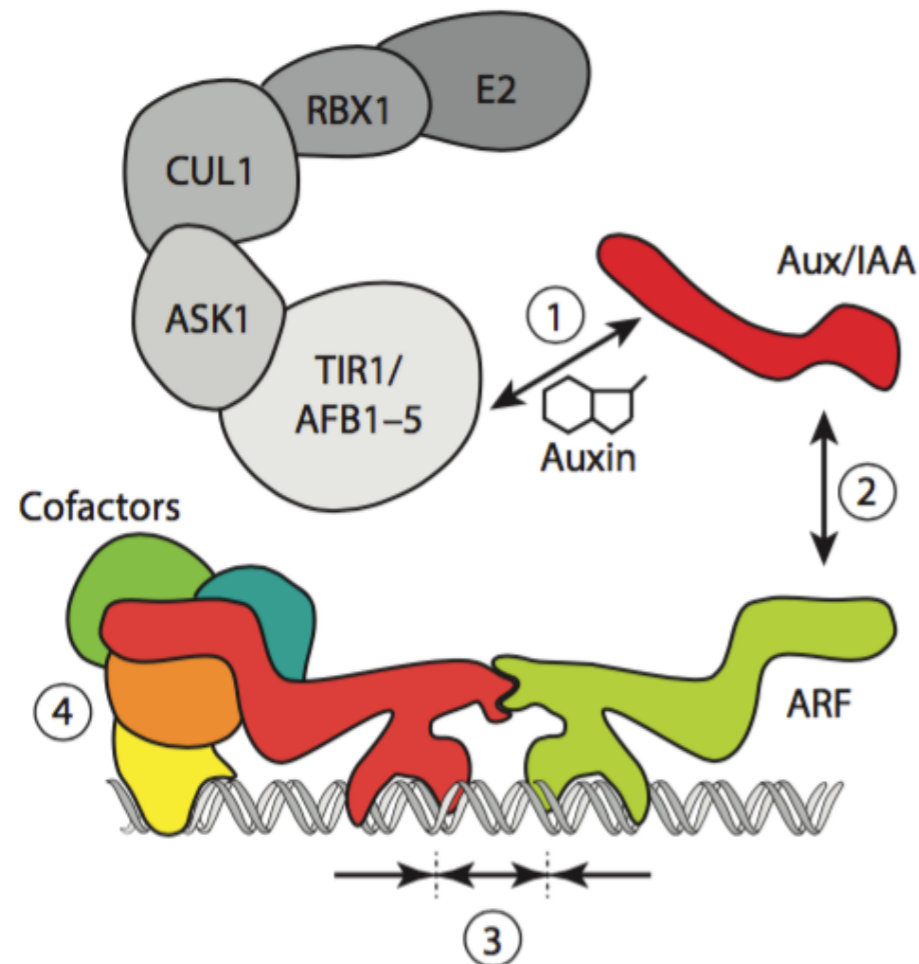
b High auxin concentration

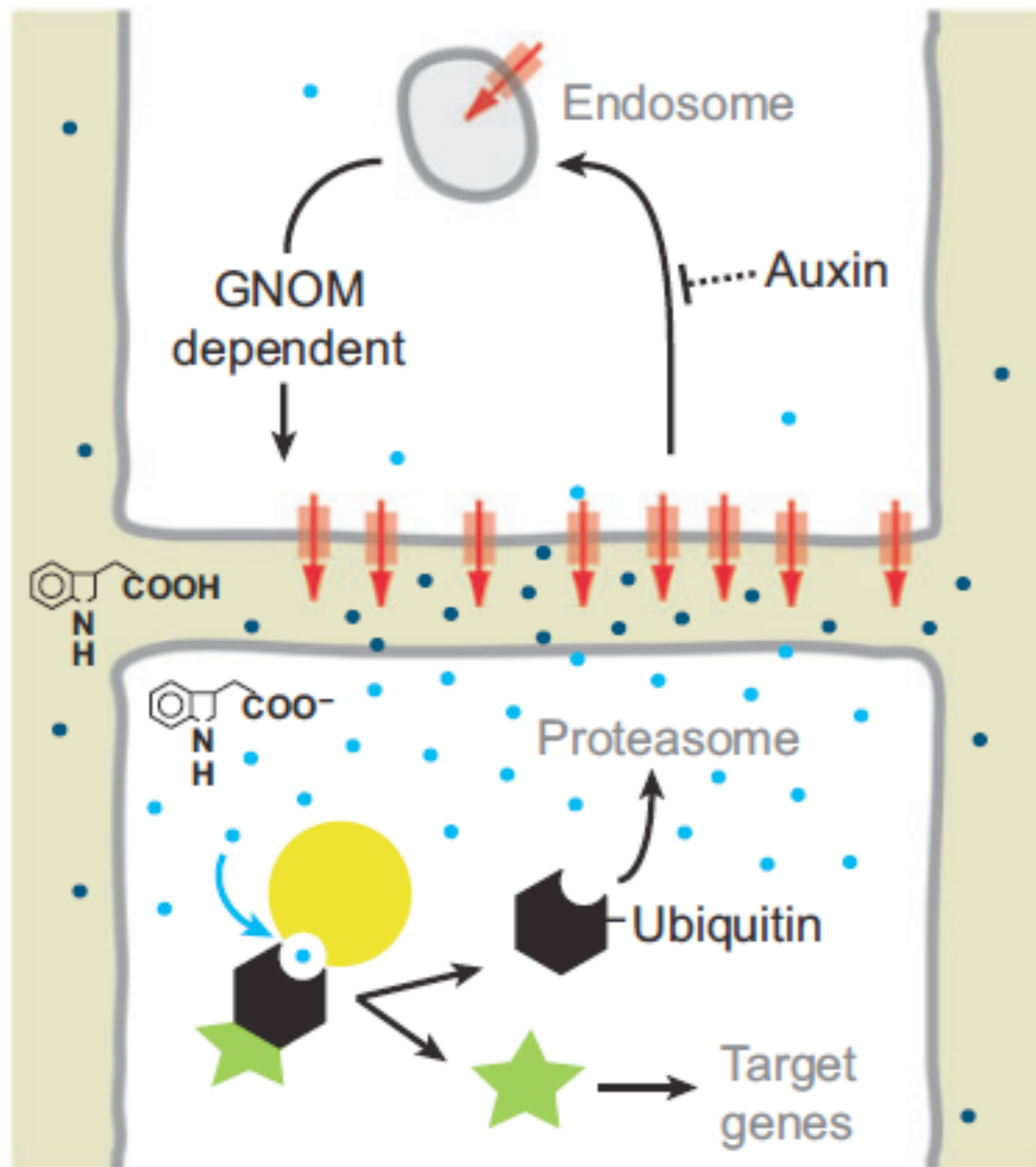


Recruitment of Switch/Sucrose Non-Fermenting (SWI/SNF) and Histone Acetyltransferase (HAT) complexes for remodelling chromatin

Regulation of gene expression by auxin

1. Intracellular binding of auxin
2. Targeted degradation of Aux/IAA repressors
3. Selective activation of genes by ARF binding to auxin responsive promoter elements
4. Recruitment of protein co-factors for maintenance of gene expression
5. Cell-cell communication





- Protonated IAA
- Dissociated IAA
- ↓ PIN efflux carrier
- SCF-TIR ubiquitin ligase
- Aux/IAA protein
- ★ Auxin response factor