

# STUDENTS' PPT PRESENTATION

## Your seminars: 60-70min:

1. **First part of seminar** (max. 20 min): general introduction into the topic using the selected reviews (**10- 15 powerpoint slides**).
2. **Second part of the seminar** (ca. 40 min): Students present the results of a key scientific publication on the topic (**25- 35 powerpoint slides**)  
Publications to be selected are available on MSTeams
3. **Third part** (max. 5 min): **Integrative model of research paper, put into a larger contex (1-2 powerpoint slides)**
4. **Fourth part of the seminar** (min. 15 min): **Discussion: question by colleagues. Important: 3 other student groups have to prepare at least 3 questions for the discussion (Total 9 questions + questions from other students)**
5. The use of **artificial intelligence tools** for the designing the introduction and analysing additional research papers is encouraged (For example »Solve any biology problem»: <https://bgpt.pro/>) Indicate what AI tools used and for what tasks AI was used

### IMPORTANT:

Seminars need to be prepared **in collaboration** – not as separate fragments put together

Students of a group needs to cover the **same amount of presentation time**

**Note: The use of artificial intelligence tools for the designing the introduction and analysing additional research papers is encouraged.** For example »Solve any biology problem»: <https://bgpt.pro/>

PS: an example of a good seminar ppt will be available online on MSTeams

# ncRNA Biology –SEMINARS

## Some comments on the use of AI for preparation of scientific data to an audience of experts

AI is used as a tool for our work but it's the **presenter's responsibility to provide audience with correct information**

AI tools can help to identify key points of a topic

AI tools can help to screen a higher number of papers and allow to efficiently summarize the information and relevance

AI tools can help you to improve scientific language and make a text more efficient

AI tools can help you creating images or graphs

AI tools can help get fast information on details on a method/topic/basic knowledge

**...BUT: AI tools may use sources that can also not be trusted**

**...The professional use of AI requires the validation of obtained information (open link to reference information, read related reviews or papers)**

### **SYNERGY TASK:**

**Students can search and test AI tools and integrate the tools into the work of seminar preparation**

**At end of lecture: EXCHANGE OF EXPERIENCES BETWEEN COLLEAGUES**

# ncRNA Biology – EXAM – SEMINAR EVALUATION

## Evaluation seminar (for entire group, max. 16 points):

- Introduction: clearness, biological/scientific importance, quality of slides; prepares colleagues for scientific paper?
- Research paper: important data shown, quality of slides, clear structure of data presentation (Why?, How?, Result? Conclusion?)
- Summary and Outlook: quality of summary and conclusion, explanation or relevance, future outlook
- Discussion session: ability to answer questions; flexibility (all group members should give answers)
- Overall level of preparation for the seminar and motivation

Note: Quality of English will be not evaluated

## Oral exam (evaluation: max. 15 points):

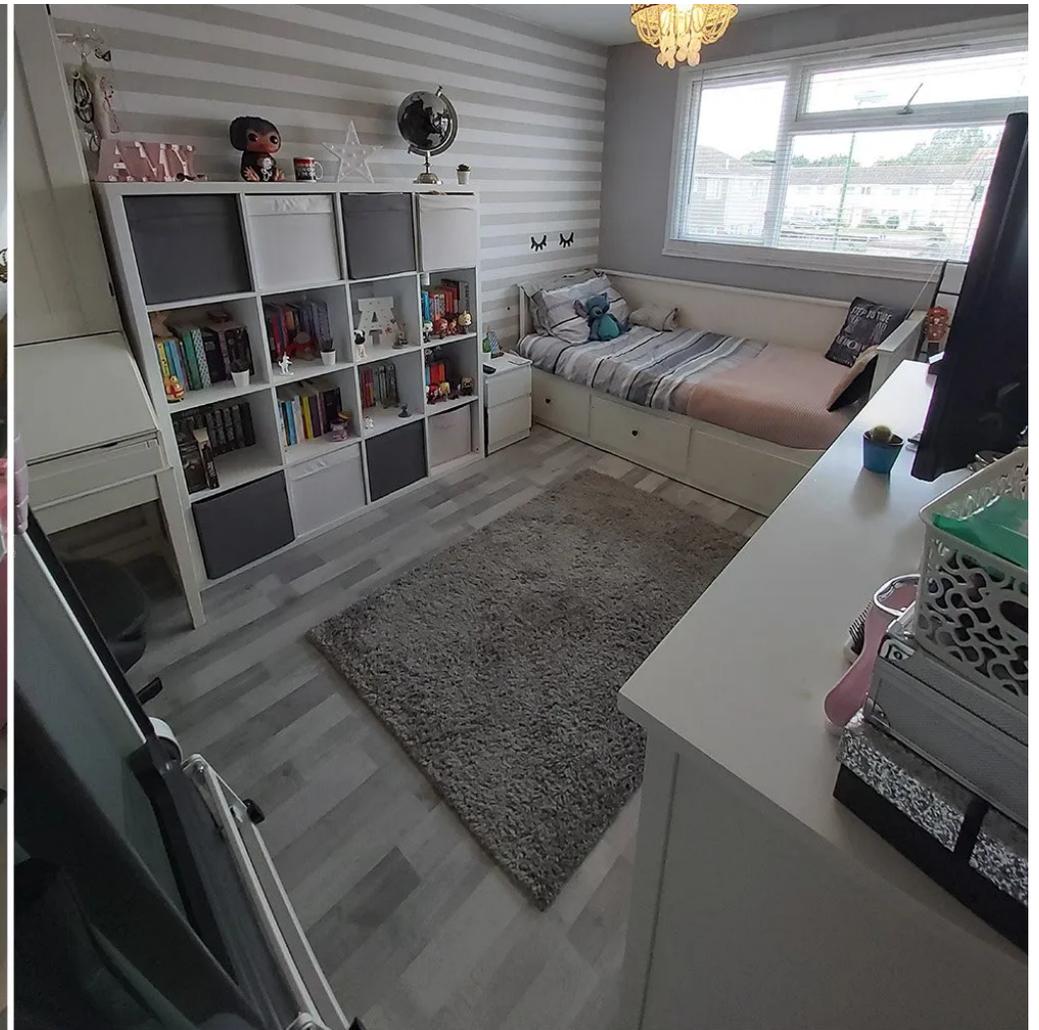
- An inscription into an “Appello” on Esse3 is necessary to perform the oral exam, participation only after completed seminar presentation
- → 1 question about own seminar presented
- → 1 question on seminar of colleagues
- → 1 question of Prof’s lectures
- → Students need to show general knowledge on individual topics and discuss experimental approaches on how to address a particular problem related to the topics (scientific question – experimental approach chosen – result – interpretation)
- → Duration: 20-30 min per exam
- → Books, electronic devices or scripts are not allowed during the exam.

## Final grade (voto finale): max 31 = 30L

- Points Student’s lecture + Points oral exam

## Most important thing:

- Avoid confusion
- Provide clear picture to audience that lists to results the first time



# HOW TO STRUCTURE A SEMINAR – classic approach

## 1° page:

- **Who and What?**
- Hosting institute affiliation
- Name of presenter
- Title of presentation
- Eventualluy graphical image – not overloading



UNIVERSITÀ  
DEGLI STUDI  
DI TRIESTE



Dipartimento di  
**Scienze della Vita**

## **Nucleolar RNA polymerase II drives ribosome biogenesis**

Biz Giulia, Rinaldin Mirko

### **Nucleolar RNA polymerase II drives ribosome biogenesis**

<https://doi.org/10.1038/s41586-020-2497-0>

Received: 19 December 2018

Accepted: 21 April 2020

Published online: 15 July 2020

Check for updates

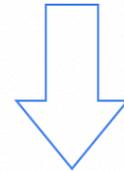
Karan J. Abraham<sup>1†</sup>, Negin Khosraviani<sup>1†</sup>, Janet N. Y. Chan<sup>1</sup>, Aparna Gorthi<sup>2</sup>, Anas Samman<sup>1</sup>, Dorothy Y. Zhao<sup>3,4</sup>, Miling Wang<sup>5</sup>, Michael Bokros<sup>5</sup>, Elva Vidya<sup>1</sup>, Lauren A. Ostrowski<sup>1</sup>, Roxanne Oshidari<sup>1</sup>, Violena Pietrobon<sup>1</sup>, Parasvi S. Patel<sup>6</sup>, Arash Algouneh<sup>1,6</sup>, Rajat Singhania<sup>6</sup>, Yupeng Liu<sup>1</sup>, V. Talya Yertici<sup>1</sup>, Daniel D. De Carvalho<sup>6</sup>, Michael Ohh<sup>1,7</sup>, Brendan C. Dickson<sup>1,8</sup>, Razq Hakem<sup>6</sup>, Jack F. Greenblatt<sup>3,4</sup>, Stephen Lee<sup>5</sup>, Alexander J. R. Bishop<sup>2,9</sup> & Karim Mekhail<sup>1,10,✉</sup>

# HOW TO STRUCTURE A SEMINAR – classic approach

## 2° page:

- **Provide overview on the structure of your talk**
- Introduction = background to understand the scientific paper
- Scientific publication with experimental data
- Discussion
- Conclusion

## Outline



- Nucleolar localisation of Pol II;
- Pol II operates directly at the level of IGS by generating asyncRNA;
- Pol II forms an antisense R-loop that restricts the synthesis of Pol-I-dependent syncRNAs;
- SyncRNA accumulation drives nucleolar disorganisation;
- Senatassin supports the R-loop shield;

# HOW TO STRUCTURE A SEMINAR – classic approach

## Introductory slides

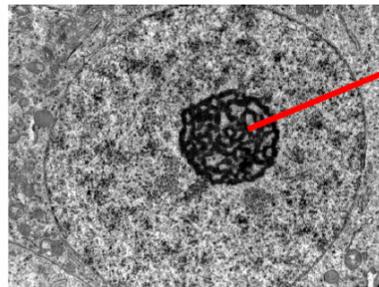
- Make clear in which part of the presentation you are....(Intro)
- Clear title for different pieces of introductory information
- Preferred use of bullet point
- Few but clear images



## Ribosome biogenesis: the nucleolus

Main components of the **nucleolus**:

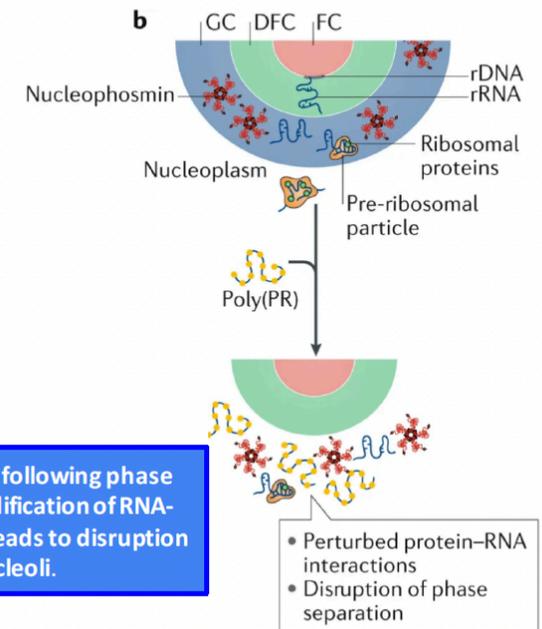
- **Fibrillary center (FC)**: involved in the transcription of rRNA genes;
- **Dense fibrillar component (DFC)**: contains the rRNA processing machinery;
- **Granular component (GC)**: Accumulation site of ribonucleoprotein particles involved in the ribosomal assembly process.



nucleolus

The nucleolus arises following phase separation: the modification of RNA-protein interactions leads to disruption of the nucleoli.

Fig.1 Histological representation of the nucleolus



# HOW TO STRUCTURE A SEMINAR – classic approach

## Last introductory slides

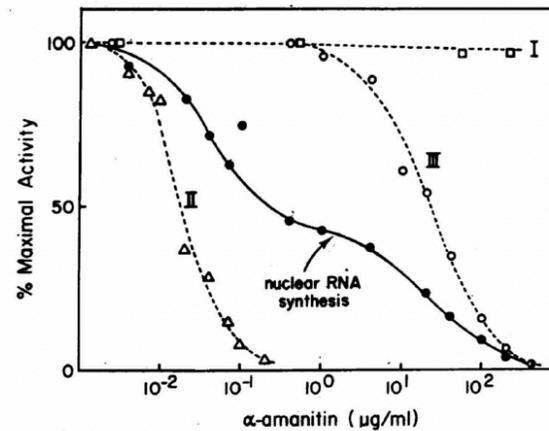
- place a strong scientific question as starting point for experimental part
- If possible provide a «wake up» information that stimulates the audience....

The study uses RNA Pol II inhibitors....

Alpha amanitin is produced by fungus

Effect in nucleoli → a subnuclear region defined by strong RNA Pol I activity

## Experimental observation



RNAPII inhibition by the fungal venom  $\alpha$ -amanitin destroys nucleoli, although RNAPI activity is not affected by the drug.



Fig.13 Effect of  $\alpha$ -amanitin concentration on purified RNA polymerases and on endogenous RNA polymerase activity in isolated nuclei.  
(Oliver H. Lowry, May 22, 1974)

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

- Screenshot of paper title
- Authors
- Laboratory
- Journal where work was published

## Nucleolar RNA polymerase II drives ribosome biogenesis

<https://doi.org/10.1038/s41586-020-2497-0>

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Karan J. Abraham<sup>1,11</sup>, Negin Khosraviani<sup>1,11</sup>, Janet N. Y. Chan<sup>1</sup>, Aparna Gorthi<sup>2</sup>, Anas Samman<sup>1</sup>, Dorothy Y. Zhao<sup>3,4</sup>, Miling Wang<sup>5</sup>, Michael Bokros<sup>5</sup>, Elva Vidya<sup>1</sup>, Lauren A. Ostrowski<sup>1</sup>, Roxanne Oshidari<sup>1</sup>, Violena Pietrobon<sup>1</sup>, Parasvi S. Patel<sup>6</sup>, Arash Algouneh<sup>1,6</sup>, Rajat Singhania<sup>6</sup>, Yupeng Liu<sup>1</sup>, V. Talya Yerlici<sup>1</sup>, Daniel D. De Carvalho<sup>6</sup>, Michael Ohh<sup>1,7</sup>, Brendan C. Dickson<sup>1,8</sup>, Razq Hakem<sup>6</sup>, Jack F. Greenblatt<sup>3,4</sup>, Stephen Lee<sup>5</sup>, Alexander J. R. Bishop<sup>2,9</sup> & Karim Mekhail<sup>1,10</sup>✉

Proteins are manufactured by ribosomes—macromolecular complexes of protein and RNA molecules that are assembled within major nuclear compartments called nucleoli<sup>1,2</sup>. Existing models suggest that RNA polymerases I and III (Pol I and Pol III) are the only enzymes that directly mediate the expression of the ribosomal RNA (rRNA) components of ribosomes. Here we show, however, that RNA polymerase II (Pol II) inside human nucleoli operates near genes encoding rRNAs to drive their expression. Pol II, assisted by the neurodegeneration-associated enzyme senataxin, generates a shield comprising triplex nucleic acid structures known as R-loops at intergenic spacers flanking nucleolar rRNA genes. The shield prevents Pol I from producing sense intergenic noncoding RNAs (sincRNAs) that can disrupt nucleolar organization and rRNA expression. These disruptive sincRNAs can be unleashed by Pol II inhibition, senataxin loss, Ewing sarcoma or locus-associated R-loop repression through an experimental system involving the proteins RNaseH1, eGFP and dCas9 (which we refer to as ‘red laser’). We reveal a nucleolar Pol-II-dependent mechanism that drives ribosome biogenesis, identify disease-associated disruption of nucleoli by noncoding RNAs, and establish locus-targeted R-loop modulation. Our findings revise theories of labour division between the major RNA polymerases, and identify nucleolar Pol II as a major factor in protein synthesis and nuclear organization, with potential implications for health and disease.

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

### Option 1:

- Separate experimental part into main scientific question



**QUESTION 1 : Is the nucleolar disruption, established with  $\alpha$ -amanitin, due to an actual presence of Pol II at the level of nucleoli?**

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

### Option 1:

- Separate experimental part into main scientific question

1. What method used to address the question
2. What are the results
3. Conclusion of experiment



### Experimental approach

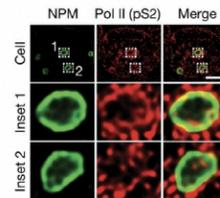
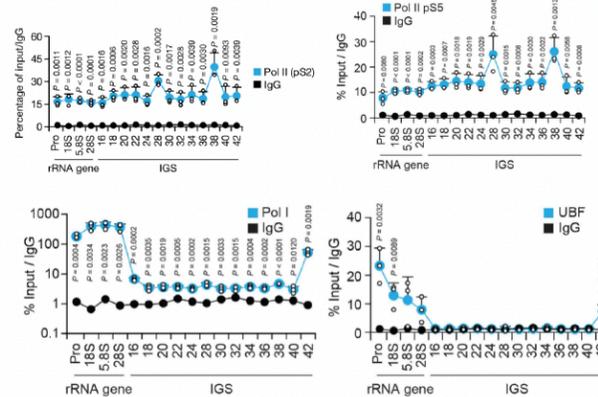


Fig.14 Immunofluorescence coupled with super-resolution microscopy to detect NPM and Pol II (pS2).



It was observed that within the nucleoli, delineated by nucleophosmin (NPM), there are foci corresponding to active Pol II (pS2)



Observations following chromatin immunoprecipitation (ChIP):

- Pol II (pS2) and Pol II (pS5) are enriched throughout the rDNA, with the highest levels at IGS28 and IGS38.
- Pol I and its initiation factor (UPF) are mainly located in rRNA genes, although low levels of Pol I exist in all IGS.
- Pol II was overrepresented compared with Pol I only within IGSs.

Results: These data suggest that rDNA loci are cohabited by Pol I and Pol II.

Fig.15. Pol I and Pol II localize to rDNA IGSs.

(my comment: too much text)

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

### Option 1:

- Separate experimental part into main scientific question



**QUESTION 2: Is Pol II activity directly involved in rRNA expression?**

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

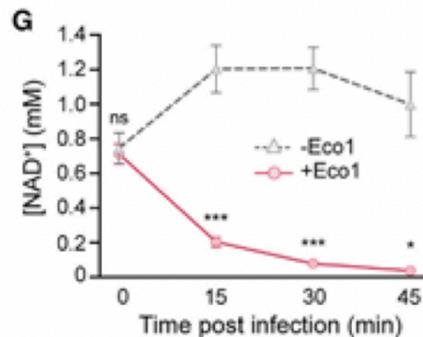
### Option 2:

- Write conclusion already into title

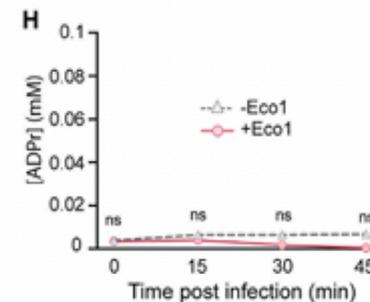
1. What method used to address the problem
2. What are the results
3. Conclusion of experiment

- Write scientific question on the bottom of the slide to guide into next slide...

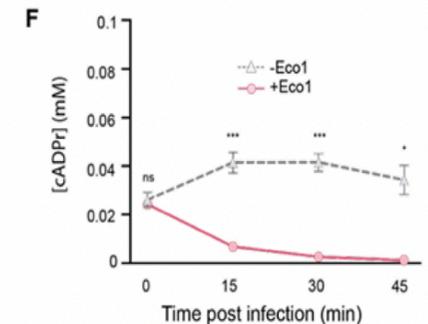
## Retron-Eco1 activity during active infection causes NAD<sup>+</sup> depletion in bacterial cells



Retron-Eco1 containing cells show a **decrease in cellular NAD<sup>+</sup> concentration** during infection



Interestingly, neither of the two ADPr or cyclic ADP ribose were detected → **ADPr and its metabolites are further processed or transferred to other molecules.**



Comment: here there should be the question that guides to the next slide

# HOW TO STRUCTURE A SEMINAR – classic approach

## Experimental part – Scientific paper

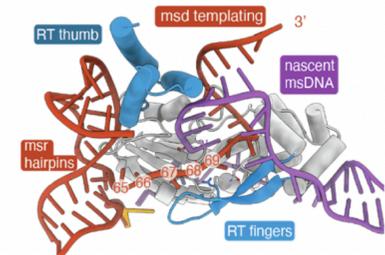
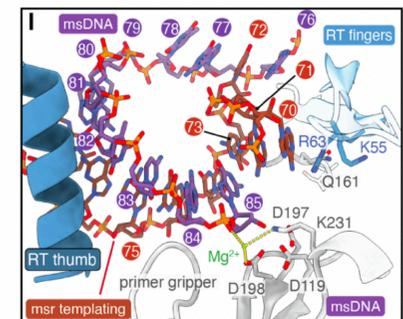
### ADDITIONAL OPTION IF A SECTION OF A PAPER CONTAINS A LOT OF EXPERIMENTS AND DATA

- Summarize key points

- Then move to next section

## Key points – RT and reverse transcription termination

1. The RT is present in a post-catalytic state
2. Reverse transcription termination likely occurs for two reasons:
  - Flipping and stabilization of the U72 residue
  - Finger dislocation
3. Reverse transcription termination is essential to allow the correct production of msDNA
4. Mutants with additional retro-transcribed nucleotides produce msDNA less efficiently and lose immunity against phages



# HOW TO STRUCTURE A SEMINAR – classic approach

## Conclusions – Future outlook

- Offer a graphical image (movie) of a working model that summarizes the biological process unraveled
- Explain clearly the working model

## Conclusion – Future outlook



### Discussion

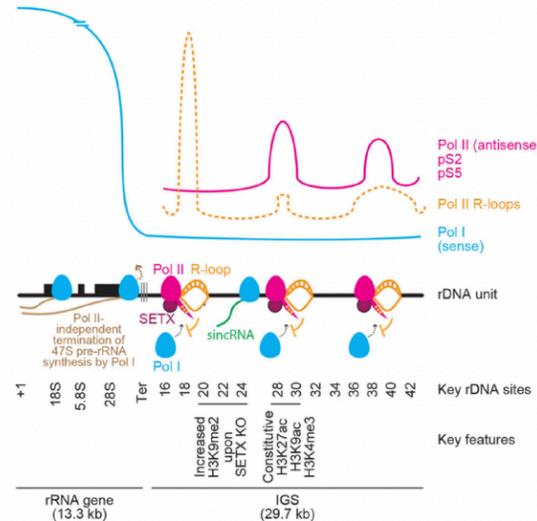


Fig.34 Detailed model illustrating how nucleolar Pol-II-dependent R-loops shield the IGS from sincRNA synthesis by Pol I.

Together these results demonstrate that **Pol II constitutively represses several Pol-I-dependent sincRNAs to prevent unscheduled nucleolar phase transitions and to maintain endogenous nucleolar condensates, which are essential for rRNA biogenesis.**

The data indicate that **SETX is co-enriched with Pol II IGS and supports it in repressing a subset of Pol-I-dependent sincRNAs that can disrupt nucleolar organisation and function. SETX could achieve this effect by promoting efficient loading and release of Pol II in an intergenic promoter of IGS28.**

# HOW TO STRUCTURE A SEMINAR – classic approach

## Conclusions – Future outlook

- **Provide conclusions (ideally in bullet points)**
- **Why are the findings relevant**
- **What can be done in future research**
- **What is the clinical relevance**
- **What is the scientific progress made**



## Conclusion

- Nucleolar organization, which is intimately linked to cell growth and viability, can be an aid in the diagnosis and treatment of some tumors.
- Nucleolar disruption following Pol II dysregulation is similar to constitutive disorganization of nucleoli in human Ewing sarcoma tumors.
- EWS cells showed increased levels of ncRNA and R-loops in all IGS.
- The natural increase in syncRNA levels may explain the aberrant nucleolar morphologies commonly observed in cancer.
- The increase in R-loops in this context may reflect the selection of cells that have compensated for the increased syncRNA levels.

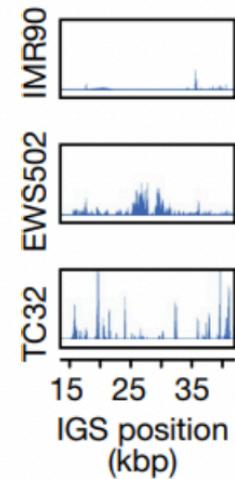


Fig.35 RNA-seq data indicate increased ncRNA levels at the IGSs of EWS502 and TC32 cells, as compared with IMR90 control cells

## HOW TO STRUCTURE A SEMINAR – classic approach

**Discussion:**

**ACTIVE PARTECIPATION BY ALL STUDENTS**