iGEM Munich

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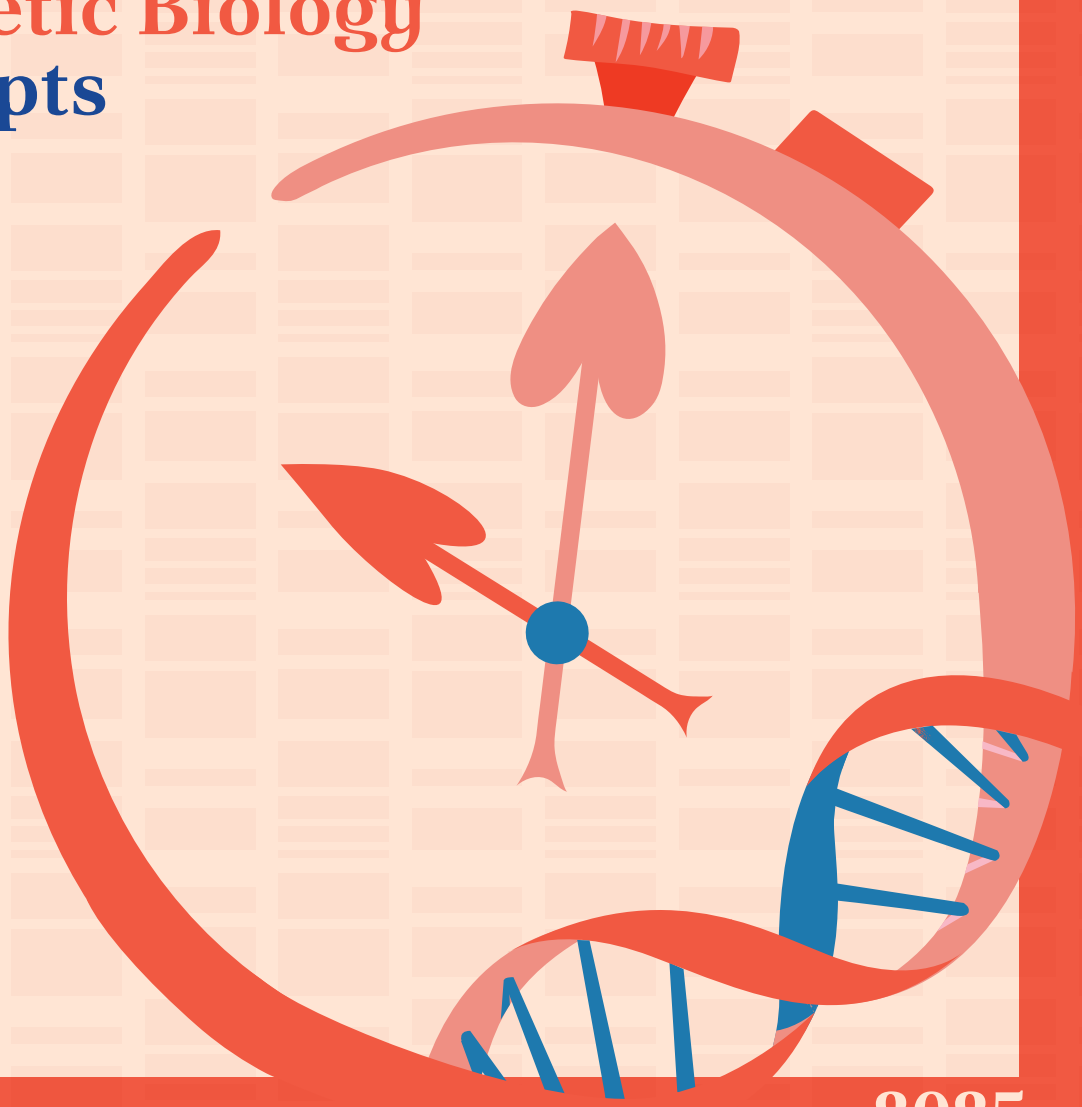
# Molecular LOVE

## Speed Dating with Synthetic Biology Concepts



2025

# Foreword

Are you looking for a new way to introduce the new generation of iGEMers into the world of synthetic biology outside of a lecture hall? Or perhaps you are looking for a fun activity for educational workshops for students?

That's where our SynBio Speed-dating comes in! We have prepared a document contatining 100 SynBio terms, ranging from genetic parts, wet-lab techniques, dry-lab tools to socio-technical frameworks. Each term is explained in a concise description based on scientific literature. Where relevant, we also referenced past iGEM teams working with a respective tool or framework.

Moreover, we envision this activity, as not only a way to learn new biology tools, but also as an opportunity for the participants to get to know each other. That's why each of the sheets contains also a "Get-to-know-each-other Bingo". Just like in a classic bingo game, participants mark off fields when they meet someone who fulfills a certain criteria for example, "Speaks more than 3 languages".

Happy Speed-dating!

**iGEM Munich 2025**

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Raya Moyankova

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Igor Koop

# Instructions

### For Participants

1. Pick a handout with your assigned term/tool/framework.
2. Preparation (10 min): Review your term and its explanation. If needed, search for additional explanation online or ask organisers for help.
3. Speed-dating rounds (6 min each):
   - Introduce yourself.
   - Present your term/tool/framework to your partner.
   - Play the “Get-to-know-each-other Bingo”.
   - Switch partners and repeat.

### For Organisers:

1. Prepare the room: arrange chairs in pairs so participants sit opposite each other.
2. Print out the handouts and categorize them by topic or required prior knowledge.
3. Use a timer to keep rounds on schedule.
4. Allocate time for participants to switch partners between rounds.
5. The number of rounds will depend on the group size and time constraints, but we recommend 8-15 rounds.

*Depending on number of participants and prior-biology knowledge level, adaptation of following instructions might be needed.*

# P001 2A peptides

## Description

2A peptides are short sequences (18–22 amino acids) derived from viruses that enable the production of separate proteins from a single mRNA strand. This is achieved via ribosomal skipping, a process in which the ribosome fails to form a peptide bond between the glycine and proline residues of the 2A peptide (Donnelly et al., 2001). These peptides allow polycistronic expression in eukaryotic cells, an achievement otherwise reliant on multiple or bidirectional promoters, direct protein fusions, or internal ribosome entry sites (IRES). This approach also ensures the expression of near-stoichiometric levels of different proteins (Subramanian et al., 2017). Variants of 2A peptides, such as T2A or P2A, differ not only in protein sequence but also in skipping efficiency, resulting in some fused protein expression, as well as their impact on stoichiometry, particularly when multiple 2A sites are used in sequence (Liu et al., 2017). Check out the iGEM Munich 2024 project for an example of implementing 2A peptides to create an RNA-based molecular recording platform with an in vivo read-out (Munich, 2024).

## References


- Donnelly MLL, Luke G, Mehrotra A, Li X, Hughes LE, Gani D, Ryan MD. Analysis of the aphthovirus 2A/2B polyprotein 'cleavage' mechanism indicates not a proteolytic reaction, but a novel translational effect: a putative ribosomal 'skip'. J Gen Virol. 2001 May;82(Pt 5):1013-1025. doi: 10.1099/0022-1317-82-5-1013. PMID: 11297676.
- Subramanian V, Schuster LA, Moore KT, Taylor LE 2nd, Baker JO, Vander Wall TA, Linger JG, Himmel ME, Decker SR. A versatile 2A peptide-based bicistronic protein expressing platform for the industrial cellulase producing fungus, Trichoderma reesei. Biotechnol Biofuels. 2017 Feb 6;10:34. doi: 10.1186/s13068-017-0710-7.
- Liu, Z., Chen, O., Wall, J.B.J. et al. Systematic comparison of 2A peptides for cloning multi-genes in a polycistronic vector. Sci Rep 7, 2193 (2017). https://doi.org/10.1038/s41598-017-02460-2
- iGEM Munich 2024, Project Description. https://2024.igem.wiki/munich/description/

# Bingo

| | | | | |
|---|---|---|---|---|
| Has already been a part of an iGEM team | Speaks more than 3 languages | Wanted to study something non-bio realted | Presents a laboratory method | Presents an acronym |
| Has a tattoo | Likes plant biology | Is a master's student | Presents something related to CRISPR | Is a leftie |
| Is a bachelor's student | Presents a framework for ethics or safety |  | Presents a protein part | Can tell what "iGEM" stands for |
| Named their pet after a scientific concept or a scientist | Has met a Nobel Prize winner | Has never run a PCR | Has or pursues a 2nd bachelor degree | Presents an AI-powered tool |
| Presents a technique that uses antibodies | Has a driver's license | Presents a part or a tool that interacts with RNA | Presents a part acting on DNA | Wears funny socks |

# P002 IRES

## Description

Internal ribosome entry sites (IRESs) are RNA elements of viral or endogenous origin ranging from 9 to over 1,000 base pairs that enable non-canonical translation initiation in eukaryotic cells (Kwan &Thompson, 2019). IRES recruits a ribosome directly, without the need for 5′ cap-dependent assembly. Alongside strategies such as multiple or bidirectional promoters, direct protein fusions, and 2A peptides, IRESs are widely used for polycistronic gene expression, allowing translation of multiple proteins from a single mRNA. Unlike other non-canonical mechanisms such as cap analogues, ribosomal shunting, or cap-independent translation enhancers (CITE), some IRES types bypass ribosomal scanning and allow translation to be initiated from non-AUG codons (Kearse & Wilusz, 2017).

## References


- Kwan T, Thompson SR. Noncanonical Translation Initiation in Eukaryotes. Cold Spring Harb Perspect Biol. 2019 Apr 1;11(4):a032672. doi: 10.1101/cshperspect.a032672. PMID: 29959190; PMCID: PMC6442200.
- Kearse MG, Wilusz JE. Non-AUG translation: a new start for protein synthesis in eukaryotes. Genes Dev. 2017 Sep 1;31(17):1717-1731. doi: 10.1101/gad.305250.117.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist | Presents a framework for ethics or safety | Has a tattoo | Presents an AI-powered tool |
| Presents a laboratory method | Speaks more than 3 languages | Likes plant biology | Can tell what “iGEM” stands for | Presents a part acting on DNA |
| Is a master’s student | Has or pursues a 2nd bachelor degree |  | Has already been a part of an iGEM team | Presents a part or a tool that interacts with RNA |
| Presents an acronym | Has a driver’s license | Is a bachelor’s student | Is a leftie | Presents a protein part |
| Wanted to study something non-bio realted | Wears funny socks | Has never run a PCR | Presents a technique that uses antibodies | Presents something related to CRISPR |

# P003 CITE

## Description

Cap-independent translation enhancers (CITEs) are structural RNA elements of predominantly viral origin located mainly in the 3′ untranslated regions (UTRs) (Millet et al., 2007). These elements enable non-canonical translation initiation in eukaryotic cells by recruiting ribosomes indirectly through interaction with translation initiation factors, without the need for 5′ cap-dependent ribosome assembly. Unlike other non-canonical translation initiation strategies, such as internal ribosome entry sites (IRES), CITEs rely on RNA-RNA interactions to link the 3′ UTR to the 5′ UTR, thereby recruiting translation initiation machinery to the 5′ end and preserving ribosomal scanning from the 5′ end (Shatsky et al., 2018).

## References


- Miller WA, Wang Z, Treder K. The amazing diversity of cap-independent translation elements in the 3′-untranslated regions of plant viral RNAs. Biochem Soc Trans. 2007 Dec;35(Pt 6):1629-33. doi: 10.1042/BST0351629. PMID: 18031280; PMCID: PMC3081161.
- Shatsky IN, Terenin IM, Smirnova VV, Andreev DE. Cap-Independent Translation: What's in a Name? Trends Biochem Sci. 2018 Nov;43(11):882-895. doi: 10.1016/j.tibs.2018.04.011. Epub 2018 May 19. PMID: 29789219.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Speaks more than 3 languages | Presents a part or a tool that interacts with RNA | Can tell what “iGEM” stands for | Wanted to study something non-bio realted |
| Presents a protein part | Has or pursues a 2nd bachelor degree | Presents a laboratory method | Presents a technique that uses antibodies | Is a bachelor’s student |
| Has a driver’s license | Presents something related to CRISPR |  | Named their pet after a scientific concept or a scientist | Has never run a PCR |
| Likes plant biology | Presents an acronym | Presents a framework for ethics or safety | Has already been a part of an iGEM team | Presents an AI-powered tool |
| Presents a part acting on DNA | Wears funny socks | Is a master’s student | Has met a Nobel Prize winner | Is a leftie |

# P004 Riboswitches

## Description

Riboswitches are RNA-based genetic regulatory elements, predominantly found in the 5′ untranslated regions (UTRs) of bacterial mRNAs, that directly bind small metabolites to control gene expression (Serganov & Patel, 2007). These modular RNA structures typically consist of an aptamer domain, which specifically binds the metabolite, and an expression platform, which adopts alternative conformations to regulate transcription, translation, or splicing. Upon metabolite binding, riboswitches switch between distinct structural states, influencing downstream gene expression. Examples include thiamine pyrophosphate (TPP) riboswitches, which can regulate both bacterial and eukaryotic gene expression through splicing or transcription termination (Serganov et al. 2006).

## References


- Serganov A, Polonskaia A, Phan AT, Breaker RR, Patel DJ. Structural basis for gene regulation by a thiamine pyrophosphate-sensing riboswitch. Nature. 2006 Jun 29;441(7097):1167-71. doi: 10.1038/nature04740. Epub 2006 May 21. PMID: 16728979; PMCID: PMC4689313.
- Serganov A, Patel DJ. Ribozymes, riboswitches and beyond: regulation of gene expression without proteins. Nat Rev Genet. 2007 Oct;8(10):776-90. doi: 10.1038/nrg2172. Epub 2007 Sep 11. PMID: 17846637; PMCID: PMC4689321.

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Wears funny socks | Presents a protein part | Named their pet after a scientific concept or a scientist | Has met a Nobel Prize winner |
| Has a driver's license | Presents a laboratory method | Has or pursues a 2nd bachelor degree | Presents a framework for ethics or safety | Presents a part acting on DNA |
| Wanted to study something non-bio realted | Presents an acronym |  | Is a bachelor's student | Is a master's student |
| Has never run a PCR | Has already been a part of an iGEM team | Has a tattoo | Likes plant biology | Presents a technique that uses antibodies |
| Presents an AI-powered tool | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA | Presents something related to CRISPR | Speaks more than 3 languages |

# P005 RNA thermometers

## Description

RNA thermometers are temperature-sensitive RNA elements, often located in the 5′ UTRs of mRNAs, that regulate gene expression by altering their secondary structure in response to temperature changes. At lower temperatures, RNA thermometers form stem-loop structures that mask ribosome binding sites, preventing translation (Serganov & Patel, 2007). As temperatures rise, these structures melt, exposing the ribosome binding site and initiating translation. These thermometers play crucial roles in bacterial heat-shock responses and virulence factor regulation, such as in *Listeria monocytogenes*, where they control the expression of pathogenicity genes (Johansson et al., 2002).

## References


- Serganov A, Patel DJ. Ribozymes, riboswitches and beyond: regulation of gene expression without proteins. Nat Rev Genet. 2007 Oct;8(10):776-90. doi: 10.1038/nrg2172. Epub 2007 Sep 11. PMID: 17846637; PMCID: PMC4689321.
- Johansson J, Mandin P, Renzoni A, Chiaruttini C, Springer M, Cossart P. An RNA thermosensor controls expression of virulence genes in Listeria monocytogenes. Cell. 2002 Sep 6;110(5):551-61. doi: 10.1016/s0092-8674(02)00905-4. PMID: 12230973.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Has never run a PCR | Is a master's student | Presents an AI-powered tool | Has met a Nobel Prize winner |
| Is a leftie | Likes plant biology | Has a driver's license | Presents something related to CRISPR | Can tell what "iGEM" stands for |
| Has already been a part of an iGEM team | Has a tattoo |  | Presents a part or a tool that interacts with RNA | Is a bachelor's student |
| Wanted to study something non-bio realted | Named their pet after a scientific concept or a scientist | Presents a laboratory method | Speaks more than 3 languages | Presents an acronym |
| Wears funny socks | Presents a technique that uses antibodies | Presents a framework for ethics or safety | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree |

# P006 Toehold switches

## Description

Toehold switches are synthetic RNA regulators designed for highly specific translational control in response to trigger RNA sequences. They consist of a structured RNA with a sequestered ribosome binding site and start codon, which are released upon binding to a complementary trigger RNA (trRNA) (Serganov & Patel, 2007). This binding event unfolds the structure, allowing translation initiation.

Bacterial toehold switches are widely used, but their application in eukaryotes is less trivial, due to different translation initiation mechanism based on ribosomal scanning. While switches based on the Kozak sequences have shown low performance, Zhao *et al.* (2021) developed eukaryotic toehold switches (eToeholds) based on IRES that form inhibitory stem-loop structures blocking translation in the absence of trRNA (Simmel, 2023). Toehold switches are programmable and highly modular, enabling their use in applications such as biosensors and synthetic biology, where precise and orthogonal regulation is essential.

## References


- Serganov A, Patel DJ. Ribozymes, riboswitches and beyond: regulation of gene expression without proteins. Nat Rev Genet. 2007 Oct;8(10):776-90. doi: 10.1038/nrg2172.
- Simmel FC. Nucleic acid strand displacement - from DNA nanotechnology to translational regulation. RNA Biol. 2023 Jan;20(1):154-163. doi: 10.1080/15476286.2023.2204565.
- Zhao EM, Mao AS, de Puig H, Zhang K, Tippens ND, Tan X, Ran FA, Han I, Nguyen PQ, Chory EJ, Hua TY, Ramesh P, Thompson DB, Oh CY, Zigon ES, English MA, Collins JJ. RNA-responsive elements for eukaryotic translational control. Nat Biotechnol. 2022 Apr;40(4):539-545. doi: 10.1038/s41587-021-01068-2.

# Bingo

| | | | | |
|---|---|---|---|---|
| Likes plant biology | Presents a framework for ethics or safety | Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist | Can tell what “iGEM” stands for |
| Presents an acronym | Presents something related to CRISPR | Has already been a part of an iGEM team | Presents an AI-powered tool | Is a leftie |
| Has never run a PCR | Presents a part acting on DNA |  | Wanted to study something non-bio realted | Has or pursues a 2nd bachelor degree |
| Presents a protein part | Presents a part or a tool that interacts with RNA | Is a master’s student | Presents a laboratory method | Is a bachelor’s student |
| Has a driver’s license | Presents a technique that uses antibodies | Wears funny socks | Speaks more than 3 languages | Has a tattoo |

# P007 Ribosome shunting

## Description

Ribosomal shunting is a non-canonical mechanism of translation initiation in eukaryotic cells, which involves discontinuous scanning of mRNA and enables ribosomes to bypass secondary structures. Unlike traditional ribosomal scanning, shunting relies on specific cis-acting elements within the mRNA, such as short open reading frames (sORFs), take-off sites, and landing sites, facilitating the ribosome's detachment and reattachment downstream of structured regions (Pooggin et al., 2000). This allows the ribosome to efficiently initiate translation on downstream open reading frames (dORFs) without requiring complete unwinding of stable secondary structures and bypassing its sequence. Ribosomal shunting can be modulated using aptamer-ligand complexes, allowing precise ligand-responsive gene expression (Ogawa, 2013).

## References


- Pooggin MM, Hohn T, Fütterer J. Role of a short open reading frame in ribosome shunt on the cauliflower mosaic virus RNA leader. J Biol Chem. 2000 Jun 9;275(23):17288-96. doi: 10.1074/jbc.M001143200. PMID: 10747993.
- Ogawa A. Ligand-dependent upregulation of ribosomal shunting. Chembiochem. 2013 Sep 2;14(13):1539-43, 1509. doi: 10.1002/cbic.201300362. Epub 2013 Aug 8. PMID: 23929633.

# Bingo

| | | | | |
|---|---|---|---|---|
| Speaks more than 3 languages | Presents an AI-powered tool | Can tell what “iGEM” stands for | Likes plant biology | Has a driver’s license |
| Has never run a PCR | Presents an acronym | Presents a technique that uses antibodies | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team |
| Is a master’s student | Wanted to study something non-bio realted |  | Presents a framework for ethics or safety | Named their pet after a scientific concept or a scientist |
| Presents something related to CRISPR | Has a tattoo | Is a leftie | Presents a part or a tool that interacts with RNA | Is a bachelor’s student |
| Wears funny socks | Presents a laboratory method | Presents a part acting on DNA | Presents a protein part | Has met a Nobel Prize winner |

# P008 Translational readthrough

## Description

Translational readthrough motifs (TRMs) are specialized mRNA sequences that enable the ribosome to bypass a stop codon, continuing protein synthesis into the 3′ untranslated region (UTR). This phenomenon, often mediated by the interplay between near-cognate tRNAs and specific nucleotide contexts surrounding the stop codon, introduces C-terminal extensions to proteins, potentially altering their localization, stability, or function (Schueren & Thoms, 2016). TRMs can be used to achieve differential transgene expression. Notable examples of TRMs include sequences derived from the opioid receptor and the tobacco mosaic virus, which have been shown to achieve up to a 140-fold differential expression of downstream genes depending on the codon-motif combination (Sillibourne et al., 2022).

## References


- Schueren F, Thoms S. Functional Translational Readthrough: A Systems Biology Perspective. PLoS Genet. 2016 Aug 4;12(8):e1006196. doi: 10.1371/journal.pgen.1006196. Erratum in: PLoS Genet. 2016 Nov 4;12(11):e1006434. doi: 10.1371/journal.pgen.1006434. PMID: 27490485; PMCID: PMC4973966.
- Sillibourne JE, Agliardi G, Righi M, Smetanova K, Rowley G, Speller S, Dolor A, Lamb K, Allen C, Karattil R, Parekh F, Vargas FA, Thomas S, Cordoba S, Pule M. A compact and simple method of achieving differential transgene expression by exploiting translational readthrough. Biotechniques. 2022 Apr;72(4):143-154. doi: 10.2144/btn-2021-0079. Epub 2022 Mar 2. PMID: 35234525.

# Bingo

| | | | | |
|---|---|---|---|---|
| Named their pet after a scientific concept or a scientist | Presents a framework for ethics or safety | Wanted to study something non-bio realted | Has never run a PCR | Presents an acronym |
| Presents an AI-powered tool | Presents a laboratory method | Can tell what “iGEM” stands for | Presents a part acting on DNA | Wears funny socks |
| Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA |  | Presents a protein part | Is a leftie |
| Presents something related to CRISPR | Has a tattoo | Is a master’s student | Has or pursues a 2nd bachelor degree | Is a bachelor’s student |
| Has a driver’s license | Speaks more than 3 languages | Has met a Nobel Prize winner | Has already been a part of an iGEM team | Likes plant biology |

# P009 Programmed frameshift

## Description

Programmed ribosomal frameshifting (PRF) is a regulatory mechanism that allows ribosomes to shift reading frames during mRNA translation, enabling the synthesis of multiple proteins from a single mRNA sequence (Mikl et al., 2020). This process is commonly utilized by viruses, such as HIV-1, to maximize their coding capacity by producing different proteins from overlapping genes. PRF is typically directed by specific mRNA signals, including “slippery” sequences and downstream secondary structures like pseudoknots, which induce the ribosome to shift by one nucleotide, altering the reading frame.

## References


- Mikl M, Pilpel Y, Segal E. High-throughput interrogation of programmed ribosomal frameshifting in human cells. Nat Commun. 2020 Jun 16;11(1):3061. doi: 10.1038/s41467-020-16961-8. PMID: 32546731; PMCID: PMC7297798.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Is a master's student | Has met a Nobel Prize winner | Presents an AI-powered tool | Has never run a PCR |
| Has a tattoo | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree | Presents an acronym | Presents a part acting on DNA |
| Wears funny socks | Presents a part or a tool that interacts with RNA |  | Named their pet after a scientific concept or a scientist | Speaks more than 3 languages |
| Likes plant biology | Is a leftie | Presents a protein part | Has a driver's license | Wanted to study something non-bio realted |
| Can tell what "iGEM" stands for | Presents something related to CRISPR | Presents a technique that uses antibodies | Has already been a part of an iGEM team | Is a bachelor's student |

# P010 Up-/Downstream ORFs

## Description

Upstream (uORFs) and downstream open reading frames (dORFs) are non-canonical translational elements found in untranslated regions (UTRs) of mRNA, playing critical regulatory roles in gene expression (Wu et al., 2020).

uORFs, located in the 5′ UTR, often suppress the translation of the main ORF by consuming ribosomes or altering ribosome scanning behavior (Barbosa et al., 2013). They are conserved across species and can use both AUG and non-AUG start codons.

In contrast, dORFs, found in the 3′ UTR, enhance the translation of canonical ORFs by promoting ribosome recycling or recruiting translation initiation factors. Unlike uORFs, the enhancing effect of dORFs is independent of the peptide they encode, relying instead on translation itself. This makes dORFs a novel regulatory mechanism for increasing translation efficiency (Wu et al., 2020).

## References


- Wu Q, Wright M, Gogol MM, Bradford WD, Zhang N, Bazzini AA. Translation of small downstream ORFs enhances translation of canonical main open reading frames. EMBO J. 2020 Sep 1;39(17):e104763. doi: 10.15252/embj.2020104763.
- Barbosa C, Peixeiro I, Romão L. Gene expression regulation by upstream open reading frames and human disease. PLoS Genet. 2013;9(8):e1003529. doi: 10.1371/journal.pgen.1003529.

# Bingo

| | | | | |
|---|---|---|---|---|
| Named their pet after a scientific concept or a scientist | Likes plant biology | Presents an acronym | Wears funny socks | Is a leftie |
| Has never run a PCR | Has met a Nobel Prize winner | Is a bachelor's student | Is a master's student | Has or pursues a 2nd bachelor degree |
| Can tell what "iGEM" stands for | Presents a framework for ethics or safety |  | Presents a protein part | Has a tattoo |
| Presents an AI-powered tool | Speaks more than 3 languages | Presents a part acting on DNA | Has already been a part of an iGEM team | Presents something related to CRISPR |
| Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA | Has a driver's license | Presents a laboratory method | Presents a technique that uses antibodies |

# P011 Split-GFP

## Description

Split GFP is a green fluorescent protein divided into two or more fragments, which are individually non-fluorescent, but can spontaneously reassemble without covalent linkage into a functional protein (Romei & Boxer, 2019). Designing split proteins like GFP is challenging as the fragments must be carefully chosen to maintain proper folding and allow reassembly. The split site must also avoid critical structural regions that confer protein function and is therefore typically located in a flexible region between well-defined secondary structural elements (Romei & Boxer, 2019). Some other interesting split proteins include split Luciferase, Cas9, or TEV protease (Luker et al., 2004; Zetsche et al., 2015; Wehr et al., 2006). Due to their property to reassemble into a functional protein upon interaction or a molecular trigger, split proteins are commonly used as a tool for studying protein-protein interactions or as biosensors.

## References


- Romei MG, Boxer SG. Split Green Fluorescent Proteins: Scope, Limitations, and Outlook. Annu Rev Biophys. 2019 May 6;48:19-44. doi: 10.1146/annurev-biophys-051013-022846.
- Luker KE, Smith MC, Luker GD, Gammon ST, Piwnica-Worms H, Piwnica-Worms D. Kinetics of regulated protein-protein interactions revealed with firefly luciferase complementation imaging in cells and living animals. Proc Natl Acad Sci U S A. 2004 Aug 17;101(33):12288-93. doi: 10.1073/pnas.0404041101.
- Zetsche B, Volz SE, Zhang F. A split-Cas9 architecture for inducible genome editing and transcription modulation. Nat Biotechnol. 2015 Feb;33(2):139-42. doi: 10.1038/nbt.3149. PMID: 25643054; PMCID: PMC4503468.
- Wehr MC, Laage R, Bolz U, Fischer TM, Grünewald S, Scheek S, Bach A, Nave KA, Rossner MJ. Monitoring regulated protein-protein interactions using split TEV. Nat Methods. 2006 Dec;3(12):985-93. doi: 10.1038/nmeth967. Epub 2006 Oct 29. PMID: 17072307.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Presents a laboratory method | Presents a part or a tool that interacts with RNA | Is a bachelor's student | Can tell what "iGEM" stands for |
| Has or pursues a 2nd bachelor degree | Is a leftie | Has met a Nobel Prize winner | Presents a technique that uses antibodies | Presents something related to CRISPR |
| Wears funny socks | Likes plant biology |  | Wanted to study something non-bio realted | Speaks more than 3 languages |
| Has a tattoo | Has a driver's license | Is a master's student | Presents an AI-powered tool | Named their pet after a scientific concept or a scientist |
| Has already been a part of an iGEM team | Presents an acronym | Presents a framework for ethics or safety | Presents a part acting on DNA | Has never run a PCR |

# P012 NanoBiT

## Description

NanoLuc Binary Technology (NanoBiT) is a system engineered for both protein detection and protein interaction studies. The system is based on the NanoLuc luciferase enzyme, divided into a large fragment (LgBiT,  18 kDa) and small peptide tags that complement it 9Rozbeh & Forchhammer, 2021).

For protein detection and quantification, NanoBiT employs the HiBiT tag, an 11-amino acid peptide that binds LgBiT with high affinity (Promega). HiBiT, due to its small size, can be easily fused to N- or C- terminus of target proteins with minimal impact on their function.

For protein-protein interaction assays, NanoBiT instead uses SmBiT. SmBiT and LgBiT fragments are designed to weakly associate unless brought together by specific protein-protein interactions. Upon association, the fragments reconstitute an active luciferase, producing a luminescent signal detectable with high sensitivity.

## References


- Rozbeh, R., Forchhammer, K. Split NanoLuc technology allows quantitation of interactions between PII protein and its receptors with unprecedented sensitivity and reveals transient interactions. Sci Rep 11, 12535 (2021). https://doi.org/10.1038/s41598-021-91856-2
- Promega Corporation. Nano-Glo® HiBiT Extracellular Detection System: Technical manual for products N2420, N2421, and N2422. Promega Corporation.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist | Presents a part acting on DNA | Likes plant biology |
| Can tell what “iGEM” stands for | Presents a framework for ethics or safety | Presents a part or a tool that interacts with RNA | Wears funny socks | Is a master’s student |
| Has never run a PCR | Is a bachelor’s student |  | Presents something related to CRISPR | Speaks more than 3 languages |
| Has a driver’s license | Presents an AI-powered tool | Is a leftie | Presents an acronym | Has a tattoo |
| Presents a technique that uses antibodies | Wanted to study something non-bio realted | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Presents a protein part |

# P013 CaM/M13

## Description

The CaM/M13 complex functions as a calcium-dependent split protein system, relying on the interaction between calmodulin (CaM) and the M13 peptide (derived from the calmodulin-binding domain of myosin light-chain kinase) to mediate calcium-regulated activities (Ikura et al., 1992). CaM, a ubiquitous calcium-binding protein, undergoes a conformational change upon binding calcium ions, exposing hydrophobic pockets, allowing the binding of M13.

This calcium-dependent interaction between CaM and M13 forms the basis of genetically encoded calcium indicators such as GCaMP, in which a circularly permuted EGFP (cpEGFP) is placed between N-terminal M13 domain and C-terminal CaM (Nakai et al., 2001). Upon Ca2+ detection, the CaM-M13 interaction triggers a conformational change in cpEGFP, resulting in bright fluorescence.

## References


- Ikura M, Clore GM, Gronenborn AM, Zhu G, Klee CB, Bax A. Solution structure of a calmodulin-target peptide complex by multidimensional NMR. Science. 1992 May 1;256(5057):632-8. doi: 10.1126/science.1585175.
- Nakai J, Ohkura M, Imoto K. A high signal-to-noise Ca(2+) probe composed of a single green fluorescent protein. Nat Biotechnol. 2001 Feb;19(2):137-41. doi: 10.1038/84397.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an AI-powered tool | Has a tattoo | Has met a Nobel Prize winner | Wears funny socks | Presents something related to CRISPR |
| Presents an acronym | Has already been a part of an iGEM team | Likes plant biology | Speaks more than 3 languages | Has a driver's license |
| Presents a technique that uses antibodies | Is a master's student |  | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree |
| Is a leftie | Can tell what "iGEM" stands for | Presents a protein part | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA |
| Is a bachelor's student | Presents a framework for ethics or safety | Named their pet after a scientific concept or a scientist | Presents a laboratory method | Has never run a PCR |

# P014 FIREmate/FIREtag

## Description

CATCHFIRE (Chemically Assisted Tethering of Chimera by Fluorogenic Induced Recognition) system is a versatile fluorogen-based platform for studying protein proximity and interactions with high temporal and spatial resolution (Bottone et al., 2023). The system uses small protein domains (FIREmate and FIREtag) fused to target proteins, which interact in the presence of a synthetic molecule, “match.” When fused to proteins of interest, these components interact upon proximity and in the presence of a fluorogen, forming a trimeric complex that fluoresces. This fluorescence is reversible, with removal of the fluorogen halting the signal, enabling real-time visualization of dynamic protein interactions.

## References


- Bottone, S., Joliot, O., Cakil, Z.V. et al. A fluorogenic chemically induced dimerization technology for controlling, imaging and sensing protein proximity. Nat Methods 20, 1553–1562 (2023). https://doi.org/10.1038/s41592-023-01988-8

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Is a bachelor's student | Has already been a part of an iGEM team | Wanted to study something non-bio realted | Presents a laboratory method |
| Presents an AI-powered tool | Has a tattoo | Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA | Can tell what "iGEM" stands for |
| Has never run a PCR | Has or pursues a 2nd bachelor degree |  | Wears funny socks | Presents a framework for ethics or safety |
| Speaks more than 3 languages | Presents something related to CRISPR | Has a driver's license | Is a master's student | Is a leftie |
| Likes plant biology | Presents an acronym | Presents a protein part | Presents a part acting on DNA | Named their pet after a scientific concept or a scientist |

# P015 LOV domain

## Description

Light-oxygen-voltage-sensing (LOV) domains are protein modules that respond to blue light, enabling precise control over cellular (Pudasaini et al., 2015). These domains are found in various organisms, including plants, fungi, and bacteria, where they regulate responses to environmental light conditions. In optogenetics, LOV domains are engineered to control protein activity with high spatial and temporal precision. Upon blue light exposure, a covalent bond forms between the flavin chromophore and a conserved cysteine residue within the LOV domain, leading to a conformational change that can activate or deactivate the fused protein.

## References


- Pudasaini A, El-Arab KK, Zoltowski BD. LOV-based optogenetic devices: light-driven modules to impart photoregulated control of cellular signaling. Front Mol Biosci. 2015 May 12;2:18. doi: 10.3389/fmolb.2015.00018. PMID: 25988185; PMCID: PMC4428443.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Has never run a PCR | Presents a part acting on DNA | Presents an AI-powered tool | Presents a laboratory method |
| Speaks more than 3 languages | Presents a technique that uses antibodies | Presents a framework for ethics or safety | Can tell what “iGEM” stands for | Is a bachelor’s student |
| Wears funny socks | Is a leftie |  | Presents a part or a tool that interacts with RNA | Is a master’s student |
| Has a driver’s license | Wanted to study something non-bio realted | Has met a Nobel Prize winner | Presents an acronym | Likes plant biology |
| Has already been a part of an iGEM team | Presents a protein part | Has or pursues a 2nd bachelor degree | Presents something related to CRISPR | Named their pet after a scientific concept or a scientist |

# P016 SpyTag/SpyCatcher

## Description

The SpyTag/SpyCatcher system is a versatile technology for irreversible protein conjugation (Zakeri et al., 2012). It consists of a peptide, SpyTag (13 amino acids), and a protein partner, SpyCatcher (ca. 12.3 kDa), derived from the split CnaB2 domain of *Streptococcus pyogenes*. When SpyTag and SpyCatcher are mixed, they form a covalent isopeptide bond between specific lysine and aspartate residues, enabling stable protein linkage under diverse conditions. The system enables bioconjugation where protein fusion could not be otherwise achieved via standard genetic fusion. By producing each protein separately, SpyTag/SpyCatcher overcomes challenges of improper protein folding or suboptimal expression host.

## References


- Zakeri B, Fierer JO, Celik E, Chittock EC, Schwarz-Linek U, Moy VT, Howarth M. Peptide tag forming a rapid covalent bond to a protein, through engineering a bacterial adhesin. Proc Natl Acad Sci U S A. 2012 Mar 20;109(12):E690-7. doi: 10.1073/pnas.1115485109. Epub 2012 Feb 24. PMID: 22366317; PMCID: PMC3311370.

# Bingo

| | | | | |
|---|---|---|---|---|
| Can tell what “iGEM” stands for | Presents a framework for ethics or safety | Has a driver’s license | Presents an AI-powered tool | Presents something related to CRISPR |
| Presents a part or a tool that interacts with RNA | Wanted to study something non-bio realted | Has a tattoo | Has met a Nobel Prize winner | Is a leftie |
| Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team |  | Is a master’s student | Is a bachelor’s student |
| Named their pet after a scientific concept or a scientist | Wears funny socks | Presents a laboratory method | Presents a technique that uses antibodies | Presents a part acting on DNA |
| Presents an acronym | Has never run a PCR | Speaks more than 3 languages | Likes plant biology | Presents a protein part |

# P017 Sortase

## Description

Sortase-mediated ligation (SML) is a precise enzymatic method for site-specific bioconjugation, leveraging the ability of sortase enzymes to cleave peptide motifs (e.g., LPXTG) and attach them to nucleophiles like oligo-glycine chains or unnatural acyl acceptors from non-canonical amino acids (Zou et al., 2024). Engineering advancements have enhanced its catalytic efficiency, substrate specificity, and robustness, making it a versatile tool for in vitro and in vivo bioconjugation.

## References


- Zou Z, Ji Y, Schwaneberg U. Empowering Site-Specific Bioconjugations In Vitro and In Vivo: Advances in Sortase Engineering and Sortase-Mediated Ligation. Angew Chem Int Ed Engl. 2024 Mar 18;63(12):e202310910. doi: 10.1002/anie.202310910. Epub 2023 Dec 22. PMID: 38081121.

# Bingo

| | | | | |
|---|---|---|---|---|
| Likes plant biology | Presents an acronym | Presents a protein part | Presents a technique that uses antibodies | Is a leftie |
| Has met a Nobel Prize winner | Is a master's student | Wears funny socks | Has a driver's license | Named their pet after a scientific concept or a scientist |
| Speaks more than 3 languages | Has already been a part of an iGEM team |  | Presents an AI-powered tool | Can tell what "iGEM" stands for |
| Has a tattoo | Wanted to study something non-bio realted | Presents something related to CRISPR | Presents a part acting on DNA | Has never run a PCR |
| Presents a laboratory method | Presents a part or a tool that interacts with RNA | Is a bachelor's student | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree |

# P018 Inteins

## Description

Inteins are segments of proteins that have the unique ability to self-excise from a precursor protein and ligate the flanking sequences, known as exteins, together (Wang et al., 2022). This process is termed protein splicing and involves a series of chemical reactions within the protein sequence itself. Inteins are found naturally in various microorganisms and are increasingly utilized in biotechnology and protein engineering. They can be employed to modify proteins by inserting or removing specific sequences, facilitating the production of functional proteins or peptides with tailored properties.

## References


- Wang H, Wang L, Zhong B, Dai Z. Protein Splicing of Inteins: A Powerful Tool in Synthetic Biology. Front Bioeng Biotechnol. 2022 Feb 21;10:810180. doi: 10.3389/fbioe.2022.810180. PMID: 35265596; PMCID: PMC8899391.

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a master's student | Has a tattoo | Likes plant biology | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree |
| Has a driver's license | Presents a part acting on DNA | Presents a technique that uses antibodies | Presents a laboratory method | Presents a protein part |
| Is a leftie | Wanted to study something non-bio realted |  | Has never run a PCR | Can tell what "iGEM" stands for |
| Presents an AI-powered tool | Presents a framework for ethics or safety | Named their pet after a scientific concept or a scientist | Wears funny socks | Speaks more than 3 languages |
| Presents something related to CRISPR | Presents a part or a tool that interacts with RNA | Has already been a part of an iGEM team | Presents an acronym | Is a bachelor's student |

# P019 RNAylation

## Description

RNAylation is post-translational modification where RNA chains, specifically NAD-capped RNAs, are covalently attached to target proteins by a viral ADP-ribosyltransferase (ART), such as ModB from bacteriophage T4 (Wolfram-Schauerte et al., 2023). Unlike typical ADP-ribosylation, RNAylation utilizes RNA with a NAD cap, resulting in the enzymatic transfer of RNA to proteins.

## References


- Wolfram-Schauerte, M., Pozhydaieva, N., Grawenhoff, J. et al. A viral ADP-ribosyltransferase attaches RNA chains to host proteins. Nature 620, 1054–1062 (2023). https://doi.org/10.1038/s41586-023-06429-2

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a driver's license | Has already been a part of an iGEM team | Presents a framework for ethics or safety | Likes plant biology | Has or pursues a 2nd bachelor degree |
| Is a master's student | Presents an acronym | Speaks more than 3 languages | Presents a part acting on DNA | Has never run a PCR |
| Has a tattoo | Wears funny socks |  | Presents a protein part | Presents something related to CRISPR |
| Presents a laboratory method | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA | Presents a technique that uses antibodies | Presents an AI-powered tool |
| Named their pet after a scientific concept or a scientist | Has met a Nobel Prize winner | Is a bachelor's student | Is a leftie | Can tell what "iGEM" stands for |

# P020 RNA circularisation

## Description

Circular RNAs (circRNAs) are stable RNA molecules characterized by their covalently closed-loop structure, which renders them resistant to exonuclease-mediated degradation and contributes to their enhanced stability. This stability enhances their utility in synthetic biology, where they serve as sensors, molecular sponges, or therapeutic agents. The Tornado (Twister-optimized RNA for durable overexpression) system facilitates efficient RNA circularization in mammalian cells using Twister ribozymes for self-cleavage and the RtcB ligase for ligation (Litke & Jaffrey, 2019). RNA circularization can also be obtained via chemical methods, for example by leveraging intramolecular reductive amination (Wasinska-Kalwa et al., 2025).

## References


- Litke, J.L., Jaffrey, S.R. Highly efficient expression of circular RNA aptamers in cells using autocatalytic transcripts. Nat Biotechnol 37, 667–675 (2019). https://doi.org/10.1038/s41587-019-0090-6
- Wasinska-Kalwa, M., Mamot, A., Czubak, K. et al. Chemical circularization of in vitro transcribed RNA for exploring circular mRNA design. Nat Commun 16, 6455 (2025). https://doi.org/10.1038/s41467-025-61775-1

# Bingo

| | | | | |
|---|---|---|---|---|
| Named their pet after a scientific concept or a scientist | Presents a protein part | Presents a framework for ethics or safety | Has a driver's license | Is a bachelor's student |
| Presents a part or a tool that interacts with RNA | Likes plant biology | Presents an acronym | Presents a laboratory method | Has never run a PCR |
| Can tell what "iGEM" stands for | Wanted to study something non-bio realted |  | Presents something related to CRISPR | Wears funny socks |
| Has already been a part of an iGEM team | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree | Presents an AI-powered tool | Has a tattoo |
| Is a leftie | Has met a Nobel Prize winner | Presents a technique that uses antibodies | Speaks more than 3 languages | Is a master's student |

# P021 HaloTag

## Description

HaloTag is a protein tag derived from bacterial haloalkane dehalogenase engineered to covalently bind to synthetic ligands (Los et al., 2008). Unlike typical tags, HaloTag catalyzes its own labeling reaction: an active-site residue reacts with a chloroalkane group on the ligand, forming a stable, irreversible covalent bond. It enables rapid, specific, and irreversible labeling of proteins in living cells or in vitro. HaloTag's stability, specificity, and modularity have made it widely used for protein tracking, interaction studies, and synthetic biology applications.

## References


- Los GV, Encell LP, McDougall MG, Hartzell DD, Karassina N, Zimprich C, Wood MG, Learish R, Ohana RF, Urh M, Simpson D, Mendez J, Zimmerman K, Otto P, Vidugiris G, Zhu J, Darzins A, Klaubert DH, Bulleit RF, Wood KV. HaloTag: a novel protein labeling technology for cell imaging and protein analysis. ACS Chem Biol. 2008 Jun 20;3(6):373-82. doi: 10.1021/cb800025k.

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Has already been a part of an iGEM team | Presents a protein part | Has a driver's license | Presents a laboratory method |
| Is a master's student | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies | Presents something related to CRISPR | Has a tattoo |
| Has or pursues a 2nd bachelor degree | Is a leftie |  | Has never run a PCR | Has met a Nobel Prize winner |
| Likes plant biology | Presents a part acting on DNA | Presents an acronym | Wanted to study something non-bio realted | Speaks more than 3 languages |
| Presents a part or a tool that interacts with RNA | Can tell what "iGEM" stands for | Presents an AI-powered tool | Wears funny socks | Presents a framework for ethics or safety |

# P022 SynNotch

## Description

The SynNotch receptor is a synthetic cell-surface receptor designed for customisable sensing and response behaviour in mammalian cells (Manhas et al., 2022). The receptor consists of an extracellular antibody (typically scFv or nanobody)-based ligand-binding domain, the native mouse Notch receptor transmembrane core and an intracellular tethered transcription factor. Upon successful target recognition, SynNotch undergoes regulated intramembrane proteolysis: ligand binding causes the receptor to be cleaved at the membrane, which releases the tethered transcription factor. The transcription factor then enters the nucleus to activate a programmed genetic response, such as transgene expression. It is worth noting that, because SynNotch receptors with distinct extracellular and intracellular domains do not share signaling intermediates, multiple SynNotch pathways can function orthogonally within the same cell (Morsut et al., 2016).

## References


- Manhas J, Edelstein HI, Leonard JN, Morsut L. The evolution of synthetic receptor systems. Nat Chem Biol. 2022 Mar;18(3):244-255. doi: 10.1038/s41589-021-00926-z. Epub 2022 Jan 20. PMID: 35058646; PMCID: PMC9041813.
- Morsut L, Roybal KT, Xiong X, Gordley RM, Coyle SM, Thomson M, Lim WA. Engineering Customized Cell Sensing and Response Behaviors Using Synthetic Notch Receptors. Cell. 2016 Feb 11;164(4):780-91. doi: 10.1016/j.cell.2016.01.012. Epub 2016 Jan 28. PMID: 26830878; PMCID: PMC4752866.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an AI-powered tool | Presents a protein part | Presents something related to CRISPR | Presents a laboratory method | Has met a Nobel Prize winner |
| Is a bachelor's student | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree | Presents a framework for ethics or safety | Has never run a PCR |
| Speaks more than 3 languages | Has a tattoo |  | Can tell what "iGEM" stands for | Presents a part acting on DNA |
| Wears funny socks | Presents an acronym | Likes plant biology | Presents a part or a tool that interacts with RNA | Named their pet after a scientific concept or a scientist |
| Has a driver's license | Wanted to study something non-bio realted | Presents a technique that uses antibodies | Is a leftie | Is a master's student |

# P023 SNIPR

## Description

Synthetic Intramembrane Proteolysis Receptors (SNIPRs) are synthetic cell-surface receptors designed for customisable sensing and response behaviour in mammalian cells (Manhas et al., 2022). They use an extracellular ligand-binding domain, typically a single-chain variable fragment (scFv) or nanobody, to recognise cell-surface antigens. Upon successful target recognition, SNIPR undergoes regulated intramembrane proteolysis: autoproteolysis of the Robo transmembrane core domain, followed by cleavage by an endogenous protease. This process, known as 'shedding', releases an intracellular payload, often a synthetic transcription factor such as tetracycline-responsive transcriptional activator (tTA). The transcription factor then triggers a programmed bioorthogonal genetic response, such as transgene expression.

SNIPRs represent the next generation of synthetic receptors, offering several advantages over comparable systems like SynNotch. They are notably compact, being over 33% smaller, their modular design enables the incorporation of fully humanized components, reducing immunogenicity, and are highly tunable, allowing precise customization to meet specific functional requirements (Zhu I et al., 2022).

## References


- Manhas J, Edelstein HI, Leonard JN, Morsut L. The evolution of synthetic receptor systems. Nat Chem Biol. 2022 Mar;18(3):244-255. doi: 10.1038/s41589-021-00926-z. Epub 2022 Jan 20. PMID: 35058646; PMCID: PMC9041813.
- Zhu I, Liu R, Garcia JM, Hyrenius-Wittsten A, Piraner DI, Alavi J, Israni DV, Liu B, Khalil AS, Roybal KT. Modular design of synthetic receptors for programmed gene regulation in cell therapies. Cell. 2022 Apr 14;185(8):1431-1443.e16. doi: 10.1016/j.cell.2022.03.023. PMID: 35427499; PMCID: PMC9108009.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Presents a laboratory method | Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA | Presents a framework for ethics or safety |
| Is a master's student | Is a leftie | Likes plant biology | Speaks more than 3 languages | Presents an acronym |
| Presents an AI-powered tool | Can tell what "iGEM" stands for |  | Is a bachelor's student | Wanted to study something non-bio realted |
| Has a tattoo | Presents a protein part | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Presents a part acting on DNA |
| Has a driver's license | Named their pet after a scientific concept or a scientist | Has never run a PCR | Presents something related to CRISPR | Wears funny socks |

# P024 MESA

## Description

The Modular Extracellular Sensor Architecture (MESA) is a synthetic cell-surface receptor designed for customisable sensing and response behaviour in mammalian cells (Daringer et al., 2014). It is composed of two chains, each using an extracellular ligand-binding domain, either antibody based or a small molecule–binding domain, to recognise soluble ligands (Manhas et al., 2022). Successful ligand binding induces dimerization of the two receptor chains, causing the tobacco etch virus (TEV) protease on the protease chain to cleave its cognate cleavage sequence on the target chain. This process releases an intracellular payload, often a synthetic transcription factor such as tetracycline-responsive transcriptional activator (tTA). The transcription factor then triggers a programmed bioorthogonal genetic response, such as transgene expression. More recent modifications of MESA enable signaling via split protease reconstitution (Dolberg et al., 2021), see the iGEM Munich 2025 project for an example of implementing MESA with split TEV protease in a mammalian cell-based diagnostic tattoo (Munich, 2025).

## References


- Daringer NM, Dudek RM, Schwarz KA, Leonard JN. Modular extracellular sensor architecture for engineering mammalian cell-based devices. ACS Synth Biol. 2014 Dec 19;3(12):892-902. doi: 10.1021/sb400128g.
- Manhas J, Edelstein HI, Leonard JN, Morsut L. The evolution of synthetic receptor systems. Nat Chem Biol. 2022 Mar;18(3):244-255. doi: 10.1038/s41589-021-00926-z.
- Dolberg TB, Meger AT, Boucher JD, Corcoran WK, Schauer EE, Prybutok AN, Raman S, Leonard JN. Computation-guided optimization of split protein systems. Nat Chem Biol. 2021 May;17(5):531-539. doi: 10.1038/s41589-020-00729-8. Epub 2021 Feb 1. PMID: 33526893; PMCID: PMC8084939.
- iGEM Munich 2025. Project Description. https://2025.igem.wiki/munich/description/

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Presents a framework for ethics or safety | Presents an acronym | Has met a Nobel Prize winner | Presents something related to CRISPR |
| Speaks more than 3 languages | Presents a part or a tool that interacts with RNA | Presents a part acting on DNA | Is a leftie | Wanted to study something non-bio realted |
| Wears funny socks | Presents a technique that uses antibodies |  | Has a driver's license | Has never run a PCR |
| Presents an AI-powered tool | Has already been a part of an iGEM team | Has a tattoo | Has or pursues a 2nd bachelor degree | Is a bachelor's student |
| Can tell what "iGEM" stands for | Likes plant biology | Is a master's student | Presents a laboratory method | Named their pet after a scientific concept or a scientist |

# P025 CAR

## Description

Chimeric Antigen Receptors (CARs) are synthetic cell-surface receptors that enable T cells, to specifically recognize and attack target cells, such as cancer cells (Manhas et al., 2022). The receptor is composed of three domains: (1) an extracellular ligand-binding domain, typically a single-chain variable fragment (scFv), to recognise cell-surface antigens, (2) the transmembrane domain that anchors the receptor in the cell membrane, (3) the intracellular domain, including the CD3ζ signaling domain and, in second- and third-generation CARs, additional co-stimulatory domain(s) (Wang et al., 2025). Upon antigen recognition, the intracellular T-cell receptor signaling domain of CAR triggers immune cell activation, proliferation, and cytotoxicity (Sadelain et al., 2013). The fourth generation of CAR-T cells have been additionally equipped with domains that provide additional functionalities such as production of cytokines, recruitment of immune cells etc (Wang et al., 2025).

## References


- Manhas, J., Edelstein, H.I., Leonard, J.N. et al. The evolution of synthetic receptor systems. Nat Chem Biol 18, 244–255 (2022). https://doi.org/10.1038/s41589-021-00926-z
- Sadelain M, Brentjens R, Rivière I. The basic principles of chimeric antigen receptor design. Cancer Discov. 2013 Apr;3(4):388-98. doi: 10.1158/2159-8290
- Wang, Z., Li, P., Zeng, X. et al. CAR-T therapy dilemma and innovative design strategies for next generation. Cell Death Dis 16, 211 (2025). https://doi.org/10.1038/s41419-025-07454-x

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Wears funny socks | Has met a Nobel Prize winner | Presents a framework for ethics or safety | Speaks more than 3 languages |
| Presents an acronym | Wanted to study something non-bio realted | Likes plant biology | Is a master's student | Presents a technique that uses antibodies |
| Presents something related to CRISPR | Presents a protein part |  | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA |
| Has a tattoo | Presents an AI-powered tool | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree | Has a driver's license |
| Has never run a PCR | Is a leftie | Is a bachelor's student | Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team |

# P026 GEMS

## Description

The generalized extracellular molecule sensor (GEMS) is a synthetic cell-surface receptor capable of activating multiple natural pathways in mammalian cells. It consists of two chains, each containing an extracellular ligand-binding domain - typically a single-chain variable fragment (scFv) or nanobody - that recognizes soluble ligands (Scheller et al., 2018). GEMS functions through dimerization of these extracellular receptor domains, which triggers activation of the intracellular signaling domains. Upon ligand binding, the two chains rotate, exposing their customizable signaling domains and activating downstream pathways, including JAK/STAT, MAPK, PLCG, and PI3K/Akt. This waycustomized receptor sensing can be connected to many types of natural signaling pathways (Manhas et al., 2022).

## References


- Manhas, J., Edelstein, H. I., Leonard, J. N., & Morsut, L. (2022). The evolution of synthetic receptor systems. Nature Chemical Biology, 18(3), 244–255. https://doi.org/10.1038/s41589-021-00926-z
- Scheller, L. (2021). Synthetic Receptors for Sensing Soluble Molecules with Mammalian Cells. In Methods in molecular biology (pp. 15–33). https://doi.org/10.1007/978-1-0716-1441-9_2

# Bingo

| | | | | |
|---|---|---|---|---|
| Wanted to study something non-bio realted | Presents a protein part | Has never run a PCR | Is a master's student | Likes plant biology |
| Presents something related to CRISPR | Has already been a part of an iGEM team | Is a bachelor's student | Speaks more than 3 languages | Has a driver's license |
| Presents an acronym | Can tell what "iGEM" stands for |  | Has a tattoo | Has or pursues a 2nd bachelor degree |
| Presents a part acting on DNA | Presents a laboratory method | Is a leftie | Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist |
| Presents a framework for ethics or safety | Wears funny socks | Presents a technique that uses antibodies | Presents an AI-powered tool | Presents a part or a tool that interacts with RNA |

# P027 TALEN

## Description

Transcription Activator-Like Effector Nucleases (TALENs) are a second-generation genome editing tool, consisting of TALE protein, containing customizable DNA-binding repeats and nuclease domain of FokI enzyme. Similarly to CRISPR systems, TALEN can be used to target and cut specific DNA sequences, hoewever unlike CRISPR TALENs target DNA based on custom-designed DNA-binding domains made of protein repeats to bind to specific DNA sequences without requiring a PAM (Shamshirgaran et al., 2022). Each DNA-binding repeat recognizes one base of double-strand DNA, and functional TALEN can be created by a simple modular assembly of these repeats, allowing for highly specific targeting. The binding domains can be easily assembled with various construction systems such as Golden Gate assembly, serial ligation, and ligation-independent cloning (Sakuma & Yamamoto, 2023). It has been reported that TALEN overperforms Cas9 in heterochromatin regions of the genome (Jain et al., 2021).

## References


- Jain, S., Shukla, S., Yang, C., Zhang, M., Fatma, Z., Lingamaneni, M., Abesteh, S., Lane, S. T., Xiong, X., Wang, Y., Schroeder, C. M., Selvin, P. R., & Zhao, H. (2021). TALEN outperforms Cas9 in editing heterochromatin target sites. Nature Communications, 12(1). https://doi.org/10.1038/s41467-020-20672-5
- Sakuma, T., & Yamamoto, T. (2023). Updated overview of TALEN construction systems. Methods in Molecular Biology, 27–39. https://doi.org/10.1007/978-1-0716-3016-7_2
- Shamshirgaran, Y., Liu, J., Sumer, H., Verma, P. J., & Taheri-Ghahfarokhi, A. (2022). Tools for efficient genome editing; ZFN, TALEN, and CRISPR. Methods in Molecular Biology, 29–46. https://doi.org/10.1007/978-1-0716-2301-5_2

# Bingo

| | | | | |
|---|---|---|---|---|
| Can tell what “iGEM” stands for | Has or pursues a 2nd bachelor degree | Has never run a PCR | Is a leftie | Presents an acronym |
| Has a driver’s license | Has already been a part of an iGEM team | Speaks more than 3 languages | Named their pet after a scientific concept or a scientist | Wears funny socks |
| Presents an AI-powered tool | Has a tattoo |  | Likes plant biology | Wanted to study something non-bio realted |
| Is a bachelor’s student | Presents a part acting on DNA | Presents a protein part | Presents a technique that uses antibodies | Has met a Nobel Prize winner |
| Presents something related to CRISPR | Is a master’s student | Presents a laboratory method | Presents a framework for ethics or safety | Presents a part or a tool that interacts with RNA |

# P028 Fanzor

## Description

Fanzor (Fz) is an RNA-guided DNA endonuclease of eukaryotic origin, similar to the bacterial CRISPR-Cas system, and can be programmed for human genome engineering applications, thereby expanding the genome-editing toolbox. Fz is derived from transposable elements in eukaryotic cells. It forms a ribonucleoprotein complex with a non-coding ωRNA, which directs DNA cleavage. The ωRNA contains a 3′-terminal flanking sequence, known as the target-adjacent motif (TAM), that guides Fz to its target and initiates cleavage (Saito et al., 2023). Variants of Fz isolated from different eukaryotes generate distinct patterns of double-strand DNA breaks. In human cells, Fz proteins exhibit DNA cleavage activity with variable efficiencies, which can be enhanced by mutations of the Fz protein. This system may provide advantages for delivery dur to the small endonuclease size and can be used complementary to other gene editing tools (Awan et al., 2023).

## References


- Awan, M. J. A., Awan, M. R. A., Amin, I., & Mansoor, S. (2023). Fanzor: a compact programmable RNA-guided endonuclease from eukaryotes. Trends in Biotechnology, 41(11), 1332–1334. https://doi.org/10.1016/j.tibtech.2023.08.003
- Saito, M., Xu, P., Faure, G., Maguire, S., Kannan, S., Altae-Tran, H., Vo, S., Desimone, A., Macrae, R. K., & Zhang, F. (2023). Fanzor is a eukaryotic programmable RNA-guided endonuclease. Nature, 620(7974), 660–668. https://doi.org/10.1038/s41586-023-06356-2

# Bingo

| | | | | |
|---|---|---|---|---|
| Wanted to study something non-bio realted | Likes plant biology | Presents something related to CRISPR | Is a master's student | Has a tattoo |
| Has or pursues a 2nd bachelor degree | Has never run a PCR | Speaks more than 3 languages | Presents a protein part | Presents a framework for ethics or safety |
| Has a driver's license | Presents a part acting on DNA |  | Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA |
| Is a leftie | Has met a Nobel Prize winner | Presents an AI-powered tool | Is a bachelor's student | Can tell what "iGEM" stands for |
| Presents a laboratory method | Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team | Wears funny socks | Presents an acronym |

# P029 Craspase

## Description

Craspase (CRISPR-guided caspase) is a dual CRISPR RNA-guided protease-based system that operates on RNA and protein levels (Hu et al., 2022). Craspase consists of a CRISPR-Cas type III-E RNA-targeting effector complex (gRAMP/Cas7-11), which associates with a caspase-like protein (TPR-CHAT/Csx29) to form the functional complex. Type III-E is an atypical CRISPR system, characterized by a single large protein, (gRAMP), which performs roles usually carried out by multiple proteins in Class 1 systems (Huo et al., 2023). Craspase exhibits minimal to no cytotoxicity and low off-target activity, as it does not interact with DNA (Bhuyan et al., 2023). Because Craspase peptidase is only active in the presence of a specific RNA species, Craspase has strong potential to be engineered as a modular tool for synthetic biology.

## References


- Hu, C., Van Beljouw, S. P. B., Nam, K. H., Schuler, G., Ding, F., Cui, Y., Rodríguez-Molina, A., Haagsma, A. C., Valk, M., Pabst, M., Brouns, S. J. J., & Ke, A. (2022). Craspase is a CRISPR RNA-guided, RNA-activated protease. Science, 377(6612), 1278–1285. https://doi.org/10.1126/science.add5064
- Huo, G., Shepherd, J., & Pan, X. (2023). Craspase: A novel CRISPR/Cas dual gene editor. Functional & Integrative Genomics, 23(2). https://doi.org/10.1007/s10142-023-01024-0
- Saito, M., Xu, P., Faure, G., Maguire, S., Kannan, S., Altae-Tran, H., Vo, S., Desimone, A., Macrae, R. K., & Zhang, F. (2023). Fanzor is a eukaryotic programmable RNA-guided endonuclease. Nature, 620(7974), 660–668. https://doi.org/10.1038/s41586-023-06356-2

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a technique that uses antibodies | Presents a part acting on DNA | Presents a part or a tool that interacts with RNA | Has a driver's license | Speaks more than 3 languages |
| Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted | Is a leftie | Has never run a PCR | Has or pursues a 2nd bachelor degree |
| Presents an AI-powered tool | Presents an acronym |  | Is a bachelor's student | Presents a protein part |
| Has met a Nobel Prize winner | Presents a framework for ethics or safety | Has a tattoo | Can tell what "iGEM" stands for | Has already been a part of an iGEM team |
| Presents something related to CRISPR | Presents a laboratory method | Is a master's student | Wears funny socks | Likes plant biology |

# P030 Base Editors

## Description

Base editors are gene editing tools for single DNA base modifications without double-stranded breaks. Base editors are composed of a modified Cas enzyme (with a specific gRNA) fused to a deaminase domain, which enables the direct chemical conversion of one DNA base pair into another. This generates a single base conversion in a controlled manner. Two examples are cytosine base editors (CBEs) and adenine base editors (ABEs), which mediate a C-to-T or A-to-G change, respectively (CRISPR NEWS, 2025). Base editors overcome early problems with CRISPR applications due to the low editing efficiency of homology-directed repair (the preferred pathway for resolving double-stranded breaks induced by Cas) and its low frequency in nondividing cells. Common challenges include off-target effects, potential limitations in targeting specific genomic sequences, and the need for improved delivery methods for therapeutic applications (Porto et al., 2020).

## References


- CRISPR NEWS: What are base editors and how do they work? - CRISPR Medicine. (2025). CRISPR Medicine. https://crisprmedicinenews.com/news/explainer-what-are-base-editors-and-how-do-they-work/
- Porto, E. M., Komor, A. C., Slaymaker, I. M., & Yeo, G. W. (2020). Base editing: advances and therapeutic opportunities. Nature Reviews Drug Discovery, 19(12), 839–859. https://doi.org/10.1038/s41573-020-0084-6

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Has never run a PCR | Presents something related to CRISPR | Has already been a part of an iGEM team | Presents a part or a tool that interacts with RNA |
| Has or pursues a 2nd bachelor degree | Likes plant biology | Presents a laboratory method | Can tell what “iGEM” stands for | Wears funny socks |
| Presents a part acting on DNA | Has met a Nobel Prize winner |  | Wanted to study something non-bio realted | Is a bachelor’s student |
| Presents an AI-powered tool | Presents a protein part | Has a driver’s license | Has a tattoo | Named their pet after a scientific concept or a scientist |
| Presents a technique that uses antibodies | Is a master’s student | Presents an acronym | Speaks more than 3 languages | Presents a framework for ethics or safety |

# P031 Prime Editors

## Description

Prime editors are gene editing tools that combine CRISPR-Cas9 technology with reverse transcriptase. Unlike traditional CRISPR-Cas9, which induces double-strand breaks (DSBs) in DNA, prime editors can precisely edit DNA bases without requiring a double-strand break and can program any type of precise nucleotide substitution, as well as insertions or deletions of up to hundreds of bases (Zhao et al., 2023). This is achieved using a prime editing guide RNA (pegRNA) that directs the Cas9 enzyme to a specific genomic target. Prime editors canonically use a Cas9 nickase that cuts only the non-complementary strand, while the reverse transcriptase synthesizes the edited DNA sequence directly into the genome. Prime editors offer potential advantages over conventional CRISPR-Cas9, including reduced off-target effects and the ability to introduce specific point mutations or insertions without cutting the DNA (Scholefield & Harrison, 2021).

## References


- Scholefield, J., & Harrison, P. T. (2021). Prime editing – an update on the field. Gene Therapy, 28(7–8), 396–401. https://doi.org/10.1038/s41434-021-00263-9
- Zhao, Z., Shang, P., Mohanraju, P., & Geijsen, N. (2023). Prime editing: advances and therapeutic applications. Trends in Biotechnology, 41(8), 1000–1012. https://doi.org/10.1016/j.tibtech.2023.03.004

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a part or a tool that interacts with RNA | Presents something related to CRISPR | Named their pet after a scientific concept or a scientist | Has never run a PCR | Presents an acronym |
| Has already been a part of an iGEM team | Presents a protein part | Speaks more than 3 languages | Is a leftie | Presents a technique that uses antibodies |
| Can tell what “iGEM” stands for | Presents an AI-powered tool |  | Is a master’s student | Wanted to study something non-bio realted |
| Likes plant biology | Has a tattoo | Has or pursues a 2nd bachelor degree | Wears funny socks | Has a driver’s license |
| Presents a laboratory method | Presents a part acting on DNA | Has met a Nobel Prize winner | Presents a framework for ethics or safety | Is a bachelor’s student |

# P032 Nanobody

## Description

Nanobodies, also known as single-domain antibodies (sdAbs), are the smallest known antigen-binding molecules. They are antibody fragments comprising a single monomeric variable antibody domain, engineered from the variable heavy-chain region (VHH) (Rizk et al., 2024). Nanobodies are significantly smaller than conventional antibodies, with a molecular weight of approximately 12-15 kDa (about one-tenth the size of a normal antibody), making them easier to produce. They also show low immunogenicity due to their small size and can often bind epitopes not accessible to whole antibodies, showing better affiniity for active sites of enzymes.

## References


- Rizk, S. S., Moustafa, D. M., ElBanna, S. A., El-Din, H. T. N., & Attia, A. S. (2024). Nanobodies in the fight against infectious diseases: repurposing nature's tiny weapons. World Journal of Microbiology and Biotechnology, 40(7). https://doi.org/10.1007/s11274-024-03990-4

# Bingo

| | | | | |
|---|---|---|---|---|
| Wears funny socks | Has or pursues a 2nd bachelor degree | Has a tattoo | Is a bachelor's student | Has never run a PCR |
| Presents an AI-powered tool | Presents a part acting on DNA | Presents something related to CRISPR | Can tell what "iGEM" stands for | Has a driver's license |
| Presents a part or a tool that interacts with RNA | Wanted to study something non-bio realted |  | Is a master's student | Likes plant biology |
| Has met a Nobel Prize winner | Presents a framework for ethics or safety | Presents a laboratory method | Named their pet after a scientific concept or a scientist | Presents a protein part |
| Is a leftie | Speaks more than 3 languages | Has already been a part of an iGEM team | Presents an acronym | Presents a technique that uses antibodies |

# P033 Affibody

## Description

Affibody molecules are small proteins engineered to bind specific target proteins or peptides with high affinity, as an alternative to monoclonal antibodies. They are derived from the Z-domain of protein A, an Immunoglobulin G-binding cell wall protein of S. aureus, and consist of a three-helix bundle that lacks disulfide bridges. That's why affibodies are escpecially stable and fast folding, and can be functionally expressed in reducing environments such as the cytoplasm without requiring translocation to the ER or periplasm. Thethree helix structure makes Affibodies among the fastest-folding protein structures known (De et al., 2017).

## References


- De, A., Kuppusamy, G., & Karri, V. V. S. R. (2017). Affibody molecules for molecular imaging and targeted drug delivery in the management of breast cancer. International Journal of Biological Macromolecules, 107, 906–919. https://doi.org/10.1016/j.ijbiomac.2017.09.059

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Presents a protein part | Has or pursues a 2nd bachelor degree | Named their pet after a scientific concept or a scientist | Presents an acronym |
| Presents something related to CRISPR | Can tell what “iGEM” stands for | Presents a technique that uses antibodies | Presents an AI-powered tool | Is a master’s student |
| Presents a part acting on DNA | Speaks more than 3 languages |  | Has a driver’s license | Is a leftie |
| Is a bachelor’s student | Wears funny socks | Has never run a PCR | Presents a framework for ethics or safety | Wanted to study something non-bio realted |
| Has already been a part of an iGEM team | Presents a laboratory method | Likes plant biology | Has met a Nobel Prize winner | Presents a part or a tool that interacts with RNA |

# P034 Single-chain variable fragment

## Description

Single-chain variable fragments (scFvs) are engineered antibody fragments that are constructed by linking the VH and VL antibody chains with a flexible 15-20 amino acid peptide linker (Gly4Ser) to create a monomeric fragment. This way the single-chain variable fragments have a molecular weight of only 27 kDa, compared to natural antibodies (150 kDa) (Dkhar et al., 2022). This design retains the antigen-binding specificity of the original antibody while reducing its size and complexity (Wikipedia contributors, 2025). The scFv fragment binds effectively to various hosts, such as bacteria or mammalian cells. scFscs can be designed to include metal-binding amino acids such as histidine, lysine, etc., and can self-assemble with high density and proper orientation on sensor surfaces, including gold electrodes.

## References


- Wikipedia contributors. (2025, May 25). Single-chain variable fragment. Wikipedia. https://en.wikipedia.org/wiki/Single-chain_variable_fragment
- Dkhar, D. S., Kumari, R., Mahapatra, S., Divya, Kumar, R., Tripathi, T., & Chandra, P. (2022). Antibody-receptor bioengineering and its implications in designing bioelectronic devices. International Journal of Biological Macromolecules, 218, 225–242. https://doi.org/10.1016/j.ijbiomac.2022.07.109

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Is a master's student | Speaks more than 3 languages | Presents a framework for ethics or safety | Has met a Nobel Prize winner |
| Presents a laboratory method | Has already been a part of an iGEM team | Presents a technique that uses antibodies | Presents something related to CRISPR | Has never run a PCR |
| Presents a part acting on DNA | Is a leftie |  | Has a driver's license | Likes plant biology |
| Can tell what "iGEM" stands for | Wanted to study something non-bio realted | Has or pursues a 2nd bachelor degree | Has a tattoo | Presents a part or a tool that interacts with RNA |
| Presents an acronym | Named their pet after a scientific concept or a scientist | Wears funny socks | Presents an AI-powered tool | Presents a protein part |

# P035 Fluorogenic aptamers

## Description

Fluorogenic RNA aptamers are synthetic RNA molecules that bind specifically to small fluorogenic dyes, resulting in a fluorescence signal upon binding, thus serving as RNA counterparts of fluorescent proteins. The aptamers typically form stable secondary structures, such as stem-loops, which create a binding pocket for the dye (Wikipedia contributors, 2025). This interaction mimics the reporter function of fluorescent proteins but is encoded as RNA. Numerous aptamers have been developed, such as Broccoli, Spinach, Mango, Corn, and Okra, which all have unique properties: binding affinity, emission and excitation range, brightness, and photostability, tailored to specific applications. Their versatility and small size make them valuable tools for studying RNA dynamics in living cells (Chen et al., 2022).

Fun fact: Spinach was the first RNA aptamer to be called after a vegetable by its founders (Paige et al., 2011). It was a referance to GFP and its green color. Many other aptamers after this were also called after vegetables (there is a Chilli aptamer!) to differentiate between fluorescent proteins but still create a color association.

## References


- Wikipedia contributors. (2025, August 25). Aptamer. Wikipedia. https://en.wikipedia.org/wiki/Aptamer
- Paige, J. S., Wu, K. Y., & Jaffrey, S. R. (2011). RNA mimics of Green fluorescent protein. Science, 333(6042), 642–646. https://doi.org/10.1126/science.1207339
- Ito, K., Tayama, T., Uemura, S., & Iizuka, R. (2024). Isolation of novel fluorogenic RNA aptamers via in vitro compartmentalization using microbead-display libraries. Talanta, 278, 126488.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a driver's license | Named their pet after a scientific concept or a scientist | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree | Wears funny socks |
| Presents a technique that uses antibodies | Has a tattoo | Has never run a PCR | Wanted to study something non-bio realted | Has already been a part of an iGEM team |
| Speaks more than 3 languages | Presents something related to CRISPR |  | Is a leftie | Likes plant biology |
| Presents a laboratory method | Presents a part acting on DNA | Presents a protein part | Is a master's student | Can tell what "iGEM" stands for |
| Is a bachelor's student | Presents an AI-powered tool | Presents a part or a tool that interacts with RNA | Presents an acronym | Presents a framework for ethics or safety |

# P036 Protein-binding aptamers

## Description

Protein-binding RNA aptamers are synthetic RNA sequences engineered to specifically bind proteins with high affinity and selectivity. These aptamers typically fold into stable secondary or tertiary structures, such as stem-loops or pseudoknots, which form precise interaction surfaces for protein binding (Miyazaki & Fujita, 2012) . Examples include the MS2 (Peña & Heinlein, 2016) and PP7 (Lim, 2002) phage aptamers, which bind their respective coat proteins. These are often discovered via SELEX (systematic evolution of ligands by exponential enrichment), which allows the screening of large random-sequence oligonucleotide libraries binding to a protein target (Dupont et al., 2015). The modularity and versatility of aptamers make them a valuable supplementary tool for studying RNA-protein interactions and designing synthetic gene regulation systems in living cells, alongside small molecules, peptides, and antibodies (Bjerregaard et al., 2016).

## References


- Dupont, D. M., Thuesen, C. K., Bøtkjær, K. A., Behrens, M. A., Dam, K., Sørensen, H. P., Pedersen, J. S., Ploug, M., Jensen, J. K., & Andreasen, P. A. (2015). Protein-Binding RNA Aptamers Affect Molecular Interactions Distantly from Their Binding Sites. PLoS ONE, 10(3), e0119207. https://doi.org/10.1371/journal.pone.0119207
- Lim, F. (2002). RNA recognition site of PP7 coat protein. Nucleic Acids Research, 30(19), 4138–4144. https://doi.org/10.1093/nar/gkf552
- Miyazaki, Y., & Fujita, M. (2012). Commentary on Aptamers for virus research. Frontiers in Microbiology, 3. https://doi.org/10.3389/fmicb.2012.00052
- Peña, E., & Heinlein, M. (2016). In vivo RNA visualization in plants using MS2 tagging. Methods in Enzymology on CD-ROM/Methods in Enzymology, 105–122. https://doi.org/10.1016/bs.mie.2016.02.004

# Bingo

| | | | | |
|---|---|---|---|---|
| Wanted to study something non-bio realted | Presents something related to CRISPR | Can tell what “iGEM” stands for | Is a bachelor’s student | Has or pursues a 2nd bachelor degree |
| Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team | Is a master’s student | Has a tattoo | Presents an AI-powered tool |
| Presents a part or a tool that interacts with RNA | Presents a framework for ethics or safety |  | Presents a protein part | Is a leftie |
| Presents a part acting on DNA | Presents a technique that uses antibodies | Speaks more than 3 languages | Has a driver’s license | Presents an acronym |
| Has never run a PCR | Presents a laboratory method | Wears funny socks | Has met a Nobel Prize winner | Likes plant biology |

# P037 Ribozymes

## Description

Ribozymes are catalytic RNA molecules capable of facilitating biochemical reactions, such as RNA cleavage, ligation, or splicing, without the need for proteins (Wikipedia contributors, 2025). Naturally occurring ribozymes, such as the hammerhead, hairpin, and glmS ribozymes, are typically involved in RNA processing and regulation. Splicing ribozymes, including Group I and II introns, facilitate the removal of introns and the ligation of exons. These RNA catalysts often employ complex secondary and tertiary structures to position reactive groups and stabilize transition states, underscoring the evolutionary significance of RNA in early biochemistry (Serganov et al., 2007).

## References


- Serganov, A., Patel, D. Ribozymes, riboswitches and beyond: regulation of gene expression without proteins. Nat Rev Genet 8, 776–790 (2007). https://doi.org/10.1038/nrg2172
- Wikipedia contributors. (2025, August 20). Ribozyme. Wikipedia. https://en.wikipedia.org/wiki/Ribozyme

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Has met a Nobel Prize winner | Wanted to study something non-bio realted | Is a master's student | Presents an acronym |
| Is a bachelor's student | Presents a laboratory method | Has already been a part of an iGEM team | Has a driver's license | Presents a part or a tool that interacts with RNA |
| Speaks more than 3 languages | Presents a technique that uses antibodies |  | Presents an AI-powered tool | Has or pursues a 2nd bachelor degree |
| Presents a part acting on DNA | Has never run a PCR | Presents something related to CRISPR | Presents a framework for ethics or safety | Named their pet after a scientific concept or a scientist |
| Is a leftie | Can tell what "iGEM" stands for | Has a tattoo | Wears funny socks | Likes plant biology |

# P038 Replicon

## Description

Replicons are self-replicating RNA molecules derived from viral genomes. Replicons employ viral RNA replication machinery (RNA-dependent RNA polymerases) to amplify RNA transcripts in the cytoplasm without integrating into the host genome. The replicon activity is regulated via cis-acting elements in untranslated regions (UTRs), including conserved sequence elements (CSEs) that serve as binding sites for the replicase (Yıldız et al., 2024). Even though replicons are derived from viral genomes (often positive-sense RNA-virises), they are engineered to lack structural protein-coding regions, ensuring safety by preventing the formation of infectious particles (Aaskov et al., 2010). The replication machinery can be encoded within replicon sequences or be expressed separately. Replicons are widely used in vaccine development and therapeutic gene delivery, and they also serve as valuable tools in synthetic biology for RNA engineering applications.

## References


- Aaskov, J., Jones, A., Choi, W., Lowry, K., & Stewart, E. (2010). Lineage replacement accompanying duplication and rapid fixation of an RNA element in the nsP3 gene in a species of alphavirus.
- Virology, 410(2), 353–359. https://doi.org/10.1016/j.virol.2010.11.025
- Yıldız, A., Răileanu, C., & Beissert, T. (2024). Trans-Amplifying RNA: A Journey from Alphavirus Research to Future Vaccines. Viruses, 16(4), 503. https://doi.org/10.3390/v16040503

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Has never run a PCR | Presents a part or a tool that interacts with RNA | Presents a framework for ethics or safety | Presents a part acting on DNA |
| Presents an AI-powered tool | Named their pet after a scientific concept or a scientist | Is a master's student | Is a bachelor's student | Is a leftie |
| Wanted to study something non-bio realted | Has or pursues a 2nd bachelor degree |  | Presents an acronym | Speaks more than 3 languages |
| Has a tattoo | Has already been a part of an iGEM team | Has met a Nobel Prize winner | Has a driver's license | Presents something related to CRISPR |
| Can tell what "iGEM" stands for | Likes plant biology | Presents a technique that uses antibodies | Presents a laboratory method | Wears funny socks |

# P039 DNAzymes

## Description

Deoxyribozymes, known as DNAzymes, are DNA molecules with a catalytic function, enabling them to facilitate specific biochemical reactions. An example is the 10-23 DNAzyme. It consists of two flanking arms, which bind a specific RNA target through base pairing, as well as a 15-nt inner catalytic loop that cleaves phosphodiester bonds in the middle of the target mRNA backbone. To ensure target specificity 10-23 DNAzymes are usually 25 - 37nt long. Initially intended as gene silencing tools, the scope of DNAzymes has rapidly expanded into diverse fields, including biosensing, diagnostics, logic gate operations, and the development of novel synthetic biology tools. The use of modified nucleoside triphosphates (dN*TPs) further expands the biochemical capabilities of DNAzymes and their versatility (Hollenstein, 2015). DNAmoreDB is a database containing comprehensive information on all DNAzymes isolated by in vitro selection and in vitro evolution (Ponce-Salvatierra et al., 2020).

## References


- Hollenstein, M. (2015). DNA catalysis: the chemical repertoire of DNAzymes. Molecules, 20(11), 20777–20804. https://doi.org/10.3390/molecules201119730
- Ponce-Salvatierra, A., Boccaletto, P., & Bujnicki, J. M. (2020). DNAmoreDB, a database of DNAzymes. Nucleic Acids Research, 49(D1), D76–D81. https://doi.org/10.1093/nar/gkaa867

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a technique that uses antibodies | Is a leftie | Presents an acronym | Has or pursues a 2nd bachelor degree | Likes plant biology |
| Presents a protein part | Has a driver's license | Speaks more than 3 languages | Presents something related to CRISPR | Has never run a PCR |
| Has a tattoo | Presents a part acting on DNA |  | Presents an AI-powered tool | Presents a part or a tool that interacts with RNA |
| Has already been a part of an iGEM team | Is a master's student | Wears funny socks | Named their pet after a scientific concept or a scientist | Presents a laboratory method |
| Is a bachelor's student | Wanted to study something non-bio realted | Can tell what "iGEM" stands for | Has met a Nobel Prize winner | Presents a framework for ethics or safety |

# P040 DNA origami

## Description

DNA origami is a technique that utilizes DNA molecules as programmable building blocks to create nanoscale structures with precise shapes and functionalities. Developed by Paul Rothemund in 2006, DNA origami involves designing a long single-stranded DNA (scaffold) and using hundreds of short staple strands to fold the scaffold into desired shapes, such as rectangles, triangles, or even complex 3D structures resembling smiley faces or nanoscale boxes. This method leverages the predictable base pairing of DNA nucleotides to ensure accurate folding (Rothemund, 2006) . DNA origami has progressed past an art form and has found a number of applications from drug delivery systems to uses as circuitry in plasmonic devices (Dey et al., 2021) ; however, most commercial applications remain in a concept or testing phase (unless you have a cool iGEM project!)

## References


- Dey, S., Fan, C., Gothelf, K. V., Li, J., Lin, C., Liu, L., Liu, N., Nijenhuis, M. a. D., Saccà, B., Simmel, F. C., Yan, H., & Zhan, P. (2021). DNA origami. Nature Reviews Methods Primers, 1(1). https://doi.org/10.1038/s43586-020-00009-8
- Rothemund, P. W. K. (2006). Folding DNA to create nanoscale shapes and patterns. Nature, 440(7082), 297–302. https://doi.org/10.1038/nature04586

# Bingo

| | | | | |
|---|---|---|---|---|
| Can tell what “iGEM” stands for | Speaks more than 3 languages | Presents an acronym | Likes plant biology | Wears funny socks |
| Presents a part acting on DNA | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree | Has never run a PCR | Has a driver’s license |
| Is a leftie | Presents something related to CRISPR |  | Presents a laboratory method | Presents a protein part |
| Presents an AI-powered tool | Is a master’s student | Presents a framework for ethics or safety | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA |
| Has a tattoo | Named their pet after a scientific concept or a scientist | Is a bachelor’s student | Presents a technique that uses antibodies | Has met a Nobel Prize winner |

# P041 tTA/TetO

## Description

The tTA/TetO system is one of the most widely used inducible gene expression systems in eukaryotic cells. It was adapted from the E. coli tetracycline resistance operon, which consists of the repressor protein TetR and the operator tetO. Normally, TetR binds tetO and blocks transcription. Tetracycline or its analog doxycycline (dox) bind TetR, releasing tetO and enabling transcription (Addgene: Tetracycline Inducible Expression, 2025).

Key improvements have made the system broadly applicable. The first was the creation of the synthetic Tet Response Element (TRE), which typically features seven copies of tetO upstream of a minimal CMV promoter or other tet/dox-dependent promoters, reducing leakiness. TetR was also modified to generate two classes of systems: Tet-Off and Tet-On. In Tet-Off, a tetracycline-controlled transactivator (tTA) was engineered by fusing TetR to activation domains, converting it into an activator (Gossen & Bujard, 1992). Without tetracycline, tTA binds the TRE and promotes transcription, while in its presence, tTA is released, reducing gene expression.

Tet-On, developed by Gossen et al. (1995), is the counterpart of Tet-Off. Through mutagenesis, they created a reverse tetracycline-controlled transactivator (rtTA), which binds TRE only in the presence of tetracycline. Functionally, Tet-On resembles the natural TetR–tetO system, but with reversed logic: the bound state activates transcription because the protein acts as an activator rather than a repressor.

## References


- Addgene: Tetracycline inducible expression. (2025). https://www.addgene.org/collections/tetracycline/
- Gossen, M., & Bujard, H. (1992). Tight control of gene expression in mammalian cells by tetracycline-responsive promoters. Proceedings of the National Academy of Sciences, 89(12), 5547–5551. https://doi.org/10.1073/pnas.89.12.5547
- Gossen, M., Freundlieb, S., Bender, G., Müller, G., Hillen, W., & Bujard, H. (1995). Transcriptional activation by tetracyclines in mammalian cells. Science, 268(5218), 1766–1769. https://doi.org/10.1126/science.7792603

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Presents an acronym | Presents a part or a tool that interacts with RNA | Is a leftie | Is a master's student |
| Has a tattoo | Named their pet after a scientific concept or a scientist | Presents a protein part | Presents a framework for ethics or safety | Likes plant biology |
| Has or pursues a 2nd bachelor degree | Wanted to study something non-bio realted |  | Is a bachelor's student | Presents something related to CRISPR |
| Has already been a part of an iGEM team | Wears funny socks | Can tell what "iGEM" stands for | Has never run a PCR | Presents a laboratory method |
| Presents an AI-powered tool | Presents a technique that uses antibodies | Presents a part acting on DNA | Has a driver's license | Speaks more than 3 languages |

# P042 Cre/lox

## Description

The Cre-lox system is widely used in mammalian gene editing to induce site-specific recombination events (inversions, deletions, or translocations). It is based on the endogenous P1 phage system, which employs the Cre recombinase that binds specifically to the loxP sequence (two 13 bp palindromic repeats flanking an asymmetric core spacer, which provides directionality). When a DNA fragment is flanked by two loxP sites, Cre proteins bind each palindromic repeats, the loxP sites align parallel to each other, and the Cre proteins bind, forming a tetramer. The complex catalyzes a double-stranded break (DSB) in the asymmetric spacer, followed by ligation that produces a reciprocal crossover (Kim et al., 2018).

The orientation of the loxP sites determines the outcome: sites in the same direction lead to deletion, opposite orientation causes inversion, and sites on separate DNA fragments in the same direction (e.g., chromosomes) induce translocation. This versatility allows for many different techniques and applications. For example, placing a “lox-stop-lox”-box upstream of the gene of interest (terminator sequences flanked by loxP sites) stops the gene expression until Cre is added (and the LSL box is deleted). Alternatively, loxP sites can flank the gene itself, so it’s active only until Cre is added (and deleted upon addition of Cre) (Juchheim, 2015).

Fun fact for your date: Flanking a gene with loxP sites (for later excision from the chromosome) is known as “floxing”. Have you floxed your genes, and flossed your teeth before the date?

## References


- Juchheim, A. M. (2015). Plasmids 101: Cre-lox. https://blog.addgene.org/plasmids-101-cre-lox
- Kim, H., Kim, M., Im, S., & Fang, S. (2018). Mouse Cre-LoxP system: general principles to determine tissue-specific roles of target genes. Laboratory Animal Research, 34(4), 147. https://doi.org/10.5625/lar.2018.34.4.147

# Bingo

| | | | | |
|---|---|---|---|---|
| Speaks more than 3 languages | Has a tattoo | Wanted to study something non-bio realted | Presents a technique that uses antibodies | Has a driver's license |
| Has never run a PCR | Is a leftie | Has met a Nobel Prize winner | Presents a protein part | Presents a framework for ethics or safety |
| Is a bachelor's student | Presents an acronym |  | Has or pursues a 2nd bachelor degree | Presents a part acting on DNA |
| Named their pet after a scientific concept or a scientist | Wears funny socks | Has already been a part of an iGEM team | Likes plant biology | Presents a part or a tool that interacts with RNA |
| Presents a laboratory method | Presents something related to CRISPR | Presents an AI-powered tool | Is a master's student | Can tell what "iGEM" stands for |

# P043 Lambda red

## Description

The Lambda (λ) Red system is a bacteriophage-derived method for genome engineering in E. coli that relies on homologous recombination rather than restriction sites. It is an in vivo cloning method, known as recombineering, in contrast to other in vitro strategies such as restriction cloning or Gibson assembly. Its core proteins include λ Exo, a nuclease, and Redβ, an annealing protein, with Gam protecting linear DNA from degradation (Caldwell & Bell, 2019). Together, these proteins catalyze the recombination of a donor DNA fragment with a target sequence.

λ Red enables diverse modifications, including insertions, deletions, point mutations, small base-pair substitutions, and protein tag additions, and it can be applied to the E. coli chromosome, plasmids, or BAC DNA. Donor DNA fragments, introduced by electroporation, require around 50 nucleotides of homology on each side (Kenkel, 2016).

The workflow typically follows these steps: donor fragment synthesis (e.g., via PCR; plasmids are not suited as substrates) and electroporation into λ Red–expressing E. coli, homologous recombination (in vivo), selectable marker expression (antibiotic resistance), and selection (Lambda Red Mediated Recombineering | GoldBio, n.d.).

## References


- Caldwell, B. J., & Bell, C. E. (2019). Structure and mechanism of the Red recombination system of bacteriophage λ. Progress in Biophysics and Molecular Biology, 147, 33–46. https://doi.org/10.1016/j.pbiomolbio.2019.03.005
- Kenkel, B. (2016). Lambda red: a homologous recombination-based technique for genetic engineering. https://blog.addgene.org/lambda-red-a-homologous-recombination-based-technique-for-genetic-engineering
- Lambda Red Mediated Recombineering | GoldBio. (n.d.). https://goldbio.com/articles/article/Lambda-Red-Mediated-Recombineering?srsltid=AfmBOoptjQd_7InzQxmZwTH4jGVQh9xS9FNYZfYKmuXRJNHVnuqSMowUhttps://blog.addgene.org/lambda-red-a-homologous-recombination-based-technique-for-genetic-engineering
- https://doi.org/10.1016/j.pbiomolbio.2019.03.005

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Presents a part or a tool that interacts with RNA | Has never run a PCR | Presents a protein part | Can tell what “iGEM” stands for |
| Has a driver’s license | Presents a technique that uses antibodies | Speaks more than 3 languages | Is a master’s student | Presents a framework for ethics or safety |
| Is a leftie | Likes plant biology |  | Has a tattoo | Has or pursues a 2nd bachelor degree |
| Wanted to study something non-bio realted | Wears funny socks | Is a bachelor’s student | Presents a part acting on DNA | Presents a laboratory method |
| Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team | Presents something related to CRISPR | Presents an acronym | Presents an AI-powered tool |

# P044 SV40 ori/TAg

## Description

The SV40 origin of replication (SV40 ori) and the T large antigen (TAg) form a system enabling episomal replication of plasmids in mammalian cells. The SV40 ori is a DNA sequence derived from the Simian Virus 40 that serves as a replication origin when bound by TAg, a viral protein that initiates and drives DNA replication. TAg interacts with the SV40 ori to recruit host replication machinery, enabling plasmid replication independently of chromosomal integration (Ali & DeCaprio, 2001). HEK293T cells, widely used in molecular biology, are engineered to stably express T large antigen (Ahuja et al., 2005).

## References


- Ali, S. H., & DeCaprio, J. A. (2001). Cellular transformation by SV40 large T antigen: interaction with host proteins. Seminars in Cancer Biology, 11(1), 15–23. https://doi.org/10.1006/scbi.2000.0342
- Ahuja, D., Sáenz-Robles, M. T., & Pipas, J. M. (2005). SV40 large T antigen targets multiple cellular pathways to elicit cellular transformation. Oncogene, 24(52), 7729–7745. https://doi.org/10.1038/sj.onc.1209046
- Wikipedia contributors. (2025, June 24). SV40 large T antigen. Wikipedia. https://en.wikipedia.org/wiki/SV40_large_T_antigen

# Bingo

| | | | | |
|---|---|---|---|---|
| Speaks more than 3 languages | Can tell what “iGEM” stands for | Presents a protein part | Has a driver’s license | Wears funny socks |
| Has a tattoo | Is a master’s student | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Presents a technique that uses antibodies |
| Presents a laboratory method | Has met a Nobel Prize winner |  | Is a leftie | Wanted to study something non-bio realted |
| Likes plant biology | Presents a framework for ethics or safety | Has never run a PCR | Presents a part or a tool that interacts with RNA | Presents an acronym |
| Is a bachelor’s student | Named their pet after a scientific concept or a scientist | Presents an AI-powered tool | Presents something related to CRISPR | Presents a part acting on DNA |

# P045 TEV

## Description

TEV protease is a highly sequence-specific cysteine endopeptidase (protease) derived from the Tobacco Etch Virus. The protease recognizes the consensus sequence Glu-Asn-Leu-Tyr-Phe-Gln-|-Ser (cleavage before Ser). It's commonly used for the removal of affinity purification tags, such as poly-histidine or maltose-binding protein (MBP), from recombinant fusion proteins or for the activation of proteins by removing inhibitor domains (Mei et al., 2016). The high specificity of TEV protease ensures precise cleavage at the target site when the recognition sequence is placed in flexible protein loops. This specificity also makes it relatively non-toxic in vivo, as the cleavage site is rare in naturally occurring proteins.

## References


- Mei, M., Zhou, Y., Peng, W., Yu, C., Ma, L., Zhang, G., & Yi, L. (2016). Application of modified yeast surface display technologies for non-Antibody protein engineering. Microbiological Research, 196, 118–128. https://doi.org/10.1016/j.micres.2016.12.002
- Wikipedia contributors. (2025, July 18). TEV protease. Wikipedia. https://en.wikipedia.org/wiki/TEV_protease

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a part acting on DNA | Wears funny socks | Has a driver's license | Presents an acronym | Is a master's student |
| Has or pursues a 2nd bachelor degree | Can tell what "iGEM" stands for | Presents a framework for ethics or safety | Speaks more than 3 languages | Presents a laboratory method |
| Has a tattoo | Presents something related to CRISPR |  | Likes plant biology | Is a leftie |
| Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA | Presents a protein part | Wanted to study something non-bio realted | Has already been a part of an iGEM team |
| Has never run a PCR | Is a bachelor's student | Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist | Presents an AI-powered tool |

# P046 Furin

## Description

Furin is a protease, a proteolytic enzyme encoded by the FURIN gene in humans and other animals. Many proteins are synthesized in an inactive form and require cleavage of specific sections to become active; Furin carries out this processing step, making it the major enzyme of the secretory pathway (New England Biolabs, 2025). It is localized in the trans-Golgi network and is the best-characterized member of the mammalian proprotein convertases. Furin is an ubiquitously expressed, single-pass type I transmembrane protein whose substrates include blood clotting factors, serum proteins, and growth factor receptors such as the insulin-like growth factor receptor. In synthetic biology, Furin cleavage sites can be engineered into proteins or receptors to create protease-sensitive switches (Wikipedia contributors, 2025).

## References


- New England Biolabs. (2025). Furin | NEB. https://www.neb.com/en/products/p8077-furin?srsltid=AfmBOopM__xWzXGAqbNeWBCBBwHLh0UmYSK2P-7SR2HK9ta64Ca0cFAF
- Wikipedia contributors. (2025, July 17). Furin. Wikipedia. https://en.wikipedia.org/wiki/Furin

# Bingo

| | | | | |
|---|---|---|---|---|
| Has or pursues a 2nd bachelor degree | Is a leftie | Presents an acronym | Presents a technique that uses antibodies | Presents a laboratory method |
| Has a driver's license | Presents a framework for ethics or safety | Speaks more than 3 languages | Wanted to study something non-bio realted | Has a tattoo |
| Presents a part acting on DNA | Named their pet after a scientific concept or a scientist | ★ | Presents something related to CRISPR | Likes plant biology |
| Is a bachelor's student | Presents a protein part | Is a master's student | Has already been a part of an iGEM team | Wears funny socks |
| Presents an AI-powered tool | Has met a Nobel Prize winner | Has never run a PCR | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA |

# P047 Degrons

## Description

A degron is a portion of a protein that regulates its degradation rate. Degrons can take the form of short amino acid sequences, structural motifs, or exposed residues-often lysine or arginine, and may occur anywhere within a protein. Some proteins even contain multiple degrons. They are widespread across organisms, ranging from the N-degrons described by the N-end rule in yeast to the PEST sequence found in mouse ornithine decarboxylase. Because targeted protein degradation enables rapid protein depletion, it is a powerful tool for studying acute cellular changes. One widely used example is the auxin-inducible degron (AID) system, which allows selective degradation of AID-tagged proteins in the presence of auxin (Phanindhar & Mishra, 2023).

## References


- Wikipedia contributors. (2025, May 25). Degron. Wikipedia. https://en.wikipedia.org/wiki/Degron
- Phanindhar, K., & Mishra, R. K. (2023). Auxin-Inducible Degron System: an efficient protein degradation tool to study protein function. BioTechniques, 74(4), 186–198. https://doi.org/10.2144/btn-2022-0108

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Is a leftie | Likes plant biology | Wanted to study something non-bio realted | Has a driver's license |
| Is a master's student | Presents a part or a tool that interacts with RNA | Presents an AI-powered tool | Presents a protein part | Presents something related to CRISPR |
| Has already been a part of an iGEM team | Presents an acronym |  | Presents a laboratory method | Has never run a PCR |
| Speaks more than 3 languages | Presents a framework for ethics or safety | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree | Presents a technique that uses antibodies |
| Has met a Nobel Prize winner | Can tell what "iGEM" stands for | Named their pet after a scientific concept or a scientist | Wears funny socks | Has a tattoo |

# P048 Epitope tags

## Description

Epitope tagging is a technique in which a short, well-characterized protein (epitope tag) is fused to a protein of interest (typically at the N- or C-terminus). The fusion gene is cloned into an expression vector and expressed, allowing the tagged protein to be detected or purified using commercially available antibodies against the tag. This method was first described by Munro & Pelham in 1984 and has since become a widely used tool in molecular and synthetic biology (Overview of Epitope Tagging | Thermo Fisher Scientific, n.d.).

Epitope tagging is particularly useful for proteins that lack specific antibodies, are newly discovered or poorly immunogenic. It enables the study of protein topology, cellular localization, protein complexes, and interacting partners. Common tags include FLAG (Brizzard & Chubet, 1997), c-Myc, and HA, which can be detected using tag-specific antibodies with multiple methods such as western blotting, immunoprecipitation, immunofluorescence, flow cytometry, and protein purification.

## References


- Overview of Epitope Tagging | Thermo Fisher Scientific (n.d.). https://www.thermofisher.com/gr/en/home/life-science/antibodies/antibodies-learning-center/antibodies-resource-library/antibody-methods/epitope-tagging-overview.html
- Brizzard, B., & Chubet, R. (1997). Epitope tagging of recombinant proteins. Current Protocols in Neuroscience, 00(1). https://doi.org/10.1002/0471142301.ns0508s00

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Has a tattoo | Wears funny socks | Presents an acronym | Named their pet after a scientific concept or a scientist |
| Is a leftie | Presents a laboratory method | Presents a technique that uses antibodies | Presents a part acting on DNA | Presents a framework for ethics or safety |
| Presents something related to CRISPR | Has a driver's license |  | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA |
| Wanted to study something non-bio realted | Presents a protein part | Likes plant biology | Has met a Nobel Prize winner | Is a master's student |
| Has or pursues a 2nd bachelor degree | Has never run a PCR | Presents an AI-powered tool | Speaks more than 3 languages | Has already been a part of an iGEM team |

# C049 BioBrick

## Description

BioBricks™ are standardized DNA sequences that serve as interchangeable, building blocks of synthetic biology. They allow researchers to design large biological systems by combining smaller parts with defined roles. BioBrick parts can include promoters, ribosome binding sites, coding sequences, regulatory seqeunces, and terminators. Many parts together assemble into devices: collections of parts with a specific function. Devises assemble further into systems, executing high-level biological tasks.

The BioBrick standard was introduced to promoting and reusability and universality in the developing field of synthtic biology . The standards are formalized through Requests for Comments (RFCs), which describe different assembly methods. RFC 10, the foundational standard, applies for restriction digestion and ligation, resulting in the formation of a scar sequence. There are also more advanced protocols like RFC 1000, which account for Type II restriction enzymes for scarless assembly. These standards ensure compatibility, reliability, and scalability of parts assembly for a better collaborative research enviroment.

## References


- Part types - parts.igem.org. (2025). https://parts.igem.org/Part_Types
- Wikipedia contributors. (2024, October 13). BioBrick. Wikipedia. https://en.wikipedia.org/wiki/BioBrick

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a framework for ethics or safety | Presents a protein part | Presents a part acting on DNA | Presents an AI-powered tool | Has a tattoo |
| Is a master's student | Has met a Nobel Prize winner | Likes plant biology | Has a driver's license | Has or pursues a 2nd bachelor degree |
| Can tell what "iGEM" stands for | Wears funny socks |  | Presents a technique that uses antibodies | Presents a laboratory method |
| Presents a part or a tool that interacts with RNA | Is a leftie | Presents an acronym | Speaks more than 3 languages | Presents something related to CRISPR |
| Has never run a PCR | Is a bachelor's student | Has already been a part of an iGEM team | Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted |

# C050 GenBank

## Description

The Gene Bank file format is a widely used text-based standard for representing annotated nucleotide or protein sequences. The format comprises three main sections: the header, the features, and the sequence. The header provides descriptive metadata, including the sequence's unique identifier (accession number), organism, source, and publication references. The features section lists annotated elements of the sequence, such as genes, coding sequences, exons, or regulatory regions, each described with detailed attributes like location and function. Finally, the sequence section contains the actual nucleotide or protein sequence. This structured format ensures compatibility with bioinformatics tools and databases, supporting tasks like functional annotation, data sharing, and computational analyses in genomics and proteomics.

## References


- https://widdowquinn.github.io/2018-03-06-ibioic/01-introduction/02-annotation.html
- https://www.ncbi.nlm.nih.gov/genbank/samplerecord/

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Has a driver's license | Presents a protein part | Presents a technique that uses antibodies | Named their pet after a scientific concept or a scientist |
| Is a master's student | Wanted to study something non-bio realted | Presents a framework for ethics or safety | Presents a laboratory method | Has never run a PCR |
| Likes plant biology | Presents a part acting on DNA |  | Has or pursues a 2nd bachelor degree | Is a bachelor's student |
| Is a leftie | Presents an AI-powered tool | Wears funny socks | Presents a part or a tool that interacts with RNA | Has already been a part of an iGEM team |
| Presents an acronym | Speaks more than 3 languages | Presents something related to CRISPR | Can tell what "iGEM" stands for | Has met a Nobel Prize winner |

# C051 SBOL

## Description

SBOL (Synthetic Biology Open Language), according to it's official website, is a standardized language for representing genetic designs in synthetic biology. It provides a framework for describing genetic parts, devices, and complete genetic systems through standardized data formats and ontologies. SBOL covers not only visual representations—such as diagrams and symbols for clear communication—but also sequence design automation, sharing of genetic design information, metabolic engineering, and the creation of dynamic models from sequence data. (Myers et al., 2020) In simple terms, SBOL captures information about the workflows used to engineer even highly complex biological systems, supporting both reproducibility and automation. Today, it is used worldwide to represent and share knowledge in synthetic biology, making the design-build-test-learn cycle computationally tractable and more amenable to automation.

## References


- SBOL Language. (2025, February 1). The Synthetic Biology Open language. The Synthetic Biology Open Language. https://sbolstandard.org/
- McLaughlin, J. A., Beal, J., Mısırlı, G., Grünberg, R., Bartley, B. A., Scott-Brown, J., Vaidyanathan, P., Fontanarrosa, P., Oberortner, E., Wipat, A., Gorochowski, T. E., & Myers, C. J. (2020). The Synthetic Biology Open Language (SBOL) version 3: Simplified Data Exchange for Bioengineering. Frontiers in Bioengineering and Biotechnology, 8. https://doi.org/10.3389/fbioe.2020.01009

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Presents an acronym | Presents something related to CRISPR | Presents an AI-powered tool | Likes plant biology |
| Has never run a PCR | Can tell what “iGEM” stands for | Presents a protein part | Presents a laboratory method | Is a master’s student |
| Presents a framework for ethics or safety | Wears funny socks |  | Presents a part or a tool that interacts with RNA | Has or pursues a 2nd bachelor degree |
| Is a bachelor’s student | Has already been a part of an iGEM team | Has met a Nobel Prize winner | Named their pet after a scientific concept or a scientist | Is a leftie |
| Speaks more than 3 languages | Has a driver’s license | Presents a technique that uses antibodies | Presents a part acting on DNA | Wanted to study something non-bio realted |

# C052 Design of Experiment

## Description

Design of Experiments (DOE) is a statistical methodology for planning, conducting, analysing, and interpreting controlled tests to evaluate factors that influence one or more parameters. Unlike the one-variable-at-a-time (OVAT) approach, DOE examines multiple input factors simultaneously, estimating their individual effects on outcomes as well as their interactions. This helps uncover important influences of the variables over the system that OVAT may miss. Key DOE concepts include: Blocking: Dividing experiments into smaller groups to keep the variables that influence the result but are not being tested approximately constant, especially when controlling them directly is costly or impractical. Randomization: Randomly assigning factor levels to experimental runs to eliminate bias caused by environmental or technical conditions. Replication: Repeating complete experimental treatments, including setup, to confirm the system works as intended and objectives are met.

## References


- Doe Overview. (n.d.). https://help.reliasoft.com/reference/experiment_design_and_analysis/doe/doe_overview.html
- What is design of experiments (DOE)? | ASQ. (n.d.). https://asq.org/quality-resources/design-of-experiments
- JMP Statistical Discovery. (n.d.). Design of experiments. https://www.jmp.com/en/statistics-knowledge-portal/design-of-experiments
- Randomization and blocking in Doe. (n.d.). https://help.reliasoft.com/reference/experiment_design_and_analysis/doe/randomization_and_blocking_in_doe.html

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an acronym | Likes plant biology | Named their pet after a scientific concept or a scientist | Can tell what “iGEM” stands for | Is a bachelor’s student |
| Speaks more than 3 languages | Presents a technique that uses antibodies | Has already been a part of an iGEM team | Has met a Nobel Prize winner | Presents a framework for ethics or safety |
| Presents a part or a tool that interacts with RNA | Is a leftie |  | Has never run a PCR | Wanted to study something non-bio realted |
| Presents a protein part | Presents something related to CRISPR | Is a master’s student | Presents an AI-powered tool | Has or pursues a 2nd bachelor degree |
| Has a tattoo | Presents a part acting on DNA | Presents a laboratory method | Wears funny socks | Has a driver’s license |

# C053 Bayesian Optimisation

## Description

Bayesian optimization is an optimization technique designed for objective functions that take a long time (minutes or hours) to evaluate. It works by building a probabilistic model of the objective function and using it to select the most promising points to test next. This method is especially useful when the objective function is unknown, noisy, or costly to evaluate, as it reduces the number of evaluations needed to find the optimum, making it popular in machine learning. The objective function f(x) is continuous but has an unknown structure—it may not be linear or concave—so it is treated as a “black box.” Key aspects include: Gaussian Process (GP): GP regression, a Bayesian statistical approach, is often used as the initial model before evaluations begin. Since the function is unknown, it is assumed to be drawn at random from a prior probability distribution. The GP then produces candidate points for testing. Acquisition Functions: These balance exploration (searching uncertain areas) and exploitation (focusing on areas with previously good outcomes). Common parameters include Expected Improvement (EI), Probability of Improvement (PI), and Upper Confidence Bound (UCB). (Frazier et al., 2018)

## References


- Frazier, P. I. (2018, July 8). A tutorial on bayesian optimization. arXiv.org. https://doi.org/10.48550/arXiv.1807.02811
- GeeksforGeeks. (2025, July 23). Bayesian optimization in Machine Learning. https://www.geeksforgeeks.org/artificial-intelligence/bayesian-optimization-in-machine-learning/

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Has a driver's license | Is a bachelor's student | Speaks more than 3 languages | Presents a part acting on DNA |
| Has met a Nobel Prize winner | Presents a part or a tool that interacts with RNA | Presents a protein part | Is a master's student | Can tell what "iGEM" stands for |
| Wanted to study something non-bio realted | Presents something related to CRISPR |  | Is a leftie | Wears funny socks |
| Has a tattoo | Presents a framework for ethics or safety | Presents an acronym | Has or pursues a 2nd bachelor degree | Presents an AI-powered tool |
| Named their pet after a scientific concept or a scientist | Has never run a PCR | Has already been a part of an iGEM team | Likes plant biology | Presents a technique that uses antibodies |

# C054 SBML

## Description

SBML (Systems Biology Markup Language) is a computer-readable format used to represent computational models of biological systems. Developed to facilitate the exchange and storage of models in systems biology, SBML provides a standardized way to encode biochemical networks, cellular processes, and other biological phenomena using mathematical equations. SBML supports various types of models, including metabolic networks, signaling pathways, and gene regulatory networks, among others. (Wilkinson et al., 2015)

## References


- Hucka M, Bergmann FT, Hoops S, Keating SM, Sahle S, Schaff JC, Smith LP, Wilkinson DJ. The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. J Integr Bioinform. 2015 Sep 4;12(2):266. doi: 10.2390/biecoll-jib-2015-266. PMID: 26528564; PMCID: PMC5451324.
- What is SBML?. SBML.org. (2019, April 7). https://sbml.org/documents/what-is-sbml/

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Wears funny socks | Presents a part or a tool that interacts with RNA | Has already been a part of an iGEM team | Speaks more than 3 languages |
| Presents a part acting on DNA | Presents an acronym | Presents something related to CRISPR | Presents a laboratory method | Has or pursues a 2nd bachelor degree |
| Has never run a PCR | Likes plant biology |  | Is a bachelor's student | Is a master's student |
| Can tell what "iGEM" stands for | Named their pet after a scientific concept or a scientist | Presents an AI-powered tool | Presents a protein part | Presents a framework for ethics or safety |
| Has a tattoo | Wanted to study something non-bio realted | Presents a technique that uses antibodies | Has a driver's license | Has met a Nobel Prize winner |

# C055 SimBiology

## Description

SimBiology is a software platform that provides apps and programmatic tools for modeling, simulating, and analyzing dynamic systems. Its main applications include quantitative systems pharmacology (QSP), physiologically based pharmacokinetics (PBPK), and pharmacokinetics/pharmacodynamics (PK/PD). Models can be built interactively using the SimBiology block diagram editor, created programmatically in MATLAB, imported as SBML files, or adapted from built-in examples. For simulation, SimBiology converts a model into a system of differential equations and applies solver functions to compute solutions across time. This generates the model's states and outputs over the specified interval. Available solver options include ordinary differential equation (ODE) solvers, SUNDIALS solvers, and stochastic solvers, allowing flexibility depending on the system's complexity and requirements.(MATLAB official website)

## References


- Simbiology. MATLAB. (n.d.). https://www.mathworks.com/products/simbiology.html
- Choosing a simulation solver - MATLAB & simulink. MathWorks. (n.d.). https://www.mathworks.com/help/simbio/ug/choosing-a-simulation-solver.html

# Bingo

| | | | | |
|---|---|---|---|---|
| Has never run a PCR | Presents a protein part | Presents a laboratory method | Presents a technique that uses antibodies | Wanted to study something non-bio realted |
| Has or pursues a 2nd bachelor degree | Is a bachelor's student | Presents a framework for ethics or safety | Likes plant biology | Has a tattoo |
| Presents something related to CRISPR | Wears funny socks |  | Has a driver's license | Presents an AI-powered tool |
| Can tell what "iGEM" stands for | Speaks more than 3 languages | Presents a part acting on DNA | Is a leftie | Named their pet after a scientific concept or a scientist |
| Is a master's student | Presents a part or a tool that interacts with RNA | Has already been a part of an iGEM team | Presents an acronym | Has met a Nobel Prize winner |

# C056 ViennaRNA

## Description

The ViennaRNA Package is a software, used for predicting and analyzing RNA secondary structures. It calculates free energy parameters and identifies structural elements such as terminal mismatches, hairpins, bulges, internal loops, and multibranch loops. In addition to the standalone tools, the ViennaRNA server offers multiple prediction modes, ranging from base-pair probability calculations for single RNA or DNA sequences to estimates of target region accessibility.(Lorenz et al., 2011)

At iGEM Munich, the it is most commonly used for validating oligonucleotide secondary structures, but also for simulating more complex RNA folding processes.

## References


- Lorenz, R., Bernhart, S.H., Höner zu Siederdissen, C. et al. ViennaRNA Package 2.0. Algorithms Mol Biol 6, 26 (2011). https://doi.org/10.1186/1748-7188-6-26
- iGEM Munich 2024. (2024, October 2). Modelling. https://2024.igem.wiki/munich/model/

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Presents an acronym | Has met a Nobel Prize winner | Likes plant biology | Has a driver's license |
| Has a tattoo | Presents a technique that uses antibodies | Wanted to study something non-bio realted | Can tell what "iGEM" stands for | Named their pet after a scientific concept or a scientist |
| Is a master's student | Presents a protein part |  | Has never run a PCR | Speaks more than 3 languages |
| Presents a part or a tool that interacts with RNA | Presents an AI-powered tool | Presents a laboratory method | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree |
| Presents a framework for ethics or safety | Presents a part acting on DNA | Wears funny socks | Presents something related to CRISPR | Is a leftie |

# C057 RoseTTA fold

## Description

RoseTTAFold is a software based on deep learning methods, developed by the Baker Lab to rapidly and accurately predict protein structures from limited data. It can address difficult x-ray crystallography and cryo-EM modeling problems and generate reliable models of protein-protein complexes. While its accuracy for single proteins is comparable to AlphaFold, RoseTTAFold outperforms it in modeling complexes, particularly those involving nucleic acids. (Baek et al., 2021) This is achieved through a unique three-track network that links sequence information, residue-residue distances and orientations, and 3D atomic coordinates. RoseTTAFold also integrates directly with the broader Rosetta software suite, enabling downstream applications in protein design and docking.(Intrview from Institute for Protein Design, 2022)

## References


- Institute for Protein Design. (2022, September 2). Rosettafold: Accurate protein structure prediction accessible to all – institute for protein design. Institute for Protein Design – Designing tomorrow. https://www.ipd.uw.edu/2021/07/rosettafold-accurate-protein-structure-prediction-accessible-to-all/
- Minkyung Baek et al. ,Accurate prediction of protein structures and interactions using a three-track neural network.Science373,871-876(2021).DOI:10.1126/science.abj8754

# Bingo

| | | | | |
|---|---|---|---|---|
| Wanted to study something non-bio realted | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies | Presents something related to CRISPR | Is a master's student |
| Has a driver's license | Presents an acronym | Presents a protein part | Presents a part or a tool that interacts with RNA | Likes plant biology |
| Is a bachelor's student | Is a leftie |  | Can tell what "iGEM" stands for | Presents a framework for ethics or safety |
| Presents a part acting on DNA | Has a tattoo | Speaks more than 3 languages | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree |
| Has never run a PCR | Presents an AI-powered tool | Wears funny socks | Has already been a part of an iGEM team | Presents a laboratory method |

# C058 AlphaFold

## Description

AlphaFold is a machine learning tool that predicts protein structures from amino acid sequences, trained on experimental data from the Protein Data Bank. It identifies similar sequences, processes them using specialized neural networks, and generates 3D structures. (Abramson et al., 2024) The latest version, AlphaFold 3, improves accuracy, handles multi-chain complexes, and includes non-protein molecules like DNA or small ligands. Over 200 million predicted structures are available on the AlphaFold Database, so running it yourself is often unnecessary. (Rubiera et al., 2021) The 2024 iGEM Team Aachen created "AlphaFold Decoded," a tutorial series that explains the concepts and code behind AlphaFold2 through videos and interactive Colab notebooks—perfect for exploring how this transformative tool works!

## References


- Abramson, J., Adler, J., Dunger, J. et al. Accurate structure prediction of biomolecular interactions with AlphaFold 3. Nature 630, 493–500 (2024). https://doi.org/10.1038/s41586-024-07487-w
- Rubiera, C. O. (2021, July 19). Oxford Protein Informatics Group. https://www.blopig.com/blog/2021/07/alphafold-2-is-here-whats-behind-the-structure-prediction-miracle/
- iGEM Aachen 2024. (n.d.). Aachen - iGEM 2024. https://2024.igem.wiki/aachen/education

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Has already been a part of an iGEM team | Wears funny socks | Named their pet after a scientific concept or a scientist | Has never run a PCR |
| Presents a technique that uses antibodies | Can tell what “iGEM” stands for | Presents something related to CRISPR | Is a bachelor’s student | Has a tattoo |
| Presents an AI-powered tool | Presents a framework for ethics or safety |  | Has met a Nobel Prize winner | Wanted to study something non-bio realted |
| Presents a protein part | Has a driver’s license | Is a master’s student | Likes plant biology | Presents a part acting on DNA |
| Has or pursues a 2nd bachelor degree | Presents a laboratory method | Speaks more than 3 languages | Presents a part or a tool that interacts with RNA | Presents an acronym |

# C059 ColabFold

## Description

ColabFold is a platform that makes protein structure prediction easier and more accessible by integrating AlphaFold and RoseTTAFold into Google Colaboratory (GoogleColab), a free cloud platform. Unlike AlphaFold, which requires powerful computing resources, ColabFold optimizes the process to run efficiently on standard hardware, allowing researchers to explore protein structures without significant resource investments, accelerating discoveries in structural biology and beyond. It functions on the following steps: a Many-against-Many sequence search(MMseqs2) server is used to build diverse multiple sequence alignments(MSAs) and to find templates. Then the server efficiently aligns input sequences against the databanks UniRef100, PDB70 and an environmental sequence set. The second part is a Python library that takes the input features for structure inference (single chains or complexes) from the MMseqs2 server, and visualizes the results. This library also implements a command line interface. The last part consists of the Jupyter notebooks for basic, advanced and batch use using the Python library. (Mirdita et al., 2022; Sokrypton on GitHub)

## References


- Sokrypton. (n.d.-b). Sokrypton/Colabfold: Making protein folding accessible to all!. GitHub. https://github.com/sokrypton/ColabFold
- Mirdita, M., Schütze, K., Moriwaki, Y. et al. ColabFold: making protein folding accessible to all. Nat Methods 19, 679–682 (2022). https://doi.org/10.1038/s41592-022-01488-1

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents something related to CRISPR | Has a tattoo | Has a driver's license | Presents an AI-powered tool | Is a bachelor's student |
| Presents a part acting on DNA | Presents a protein part | Likes plant biology | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA |
| Has met a Nobel Prize winner | Has already been a part of an iGEM team |  | Presents a laboratory method | Wears funny socks |
| Can tell what "iGEM" stands for | Presents an acronym | Has or pursues a 2nd bachelor degree | Presents a framework for ethics or safety | Is a master's student |
| Has never run a PCR | Presents a technique that uses antibodies | Speaks more than 3 languages | Is a leftie | Named their pet after a scientific concept or a scientist |

# C060 ESMfold

## Description

ESMFold is a sequence-to-structure predictor, developed by Meta, that uses special ESM-2 language model. Unlike AlphaFold, ESMFold generates 3D structures directly from a single sequence, skipping multiple sequence alignments (MSAs). While slightly less accurate, it is faster and more resource-efficient. ESMFold is part of Meta's ESM toolkit, which includes ESM-2 for large-scale sequence annotation, ESM-MSA for variant effect prediction, and ESMAtlas, which provides structural predictions for millions of metagenomic proteins. These tools offer scalable solutions for protein analysis, supporting research in structural biology, metagenomics, and functional annotation.(Lin et al., 2023; Facebookresearch on GitHub)

## References


- Facebookresearch. (n.d.). Facebookresearch/ESM: Evolutionary scale modeling (ESM): Pretrained language models for proteins. GitHub. https://github.com/facebookresearch/esm
- Zeming Lin et al. ,Evolutionary-scale prediction of atomic-level protein structure with a language model.Science379,1123-1130(2023).DOI:10.1126/science.ade2574

# Bingo

| | | | | |
|---|---|---|---|---|
| Has never run a PCR | Presents an AI-powered tool | Presents a protein part | Presents a part or a tool that interacts with RNA | Presents a part acting on DNA |
| Presents a laboratory method | Speaks more than 3 languages | Presents an acronym | Has met a Nobel Prize winner | Wanted to study something non-bio realted |
| Presents a technique that uses antibodies | Named their pet after a scientific concept or a scientist |  | Can tell what “iGEM” stands for | Is a master’s student |
| Presents something related to CRISPR | Has a driver’s license | Is a bachelor’s student | Wears funny socks | Presents a framework for ethics or safety |
| Is a leftie | Likes plant biology | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Has a tattoo |

# C061 ProteinMPNN

## Description

ProteinMPNN, developed by the Baker Lab, is a machine learning tool that generates protein sequences optimized for specific 3D structures. Using a graph neural network, it models spatial relationships in a protein backbone and predicts sequences that minimize folding energy and stabilize the structure. ProteinMPNN supports additional constraints, such as favoring specific residues or motifs, allowing tailored designs. It is highly efficient, generating thousands of sequences in seconds.(Dauparas et al., 2022) Applications include designing enzymes with improved activity or therapeutic proteins with enhanced stability and specificity. By excluding cysteins, the model can more reliably generate stable protein sequences and structures, as disulfide bond formation introduces a far more complex case and decreases accuracy. (Kuhlman et al., 2023)

## References


- Dauparas. (n.d.). Dauparas/ProteinMPNN: Code for the proteinmpnn paper. GitHub. https://github.com/dauparas/ProteinMPNN
- Dauparas, J. et al. Robust deep learning–based protein sequence design using ProteinMPNN. Science 378, 49–56 (2022).
- Dieckhaus, H., Brocidiacono, M., Randolph, N., & Kuhlman, B. (2023). Transfer Learning to Leverage Larger Datasets for Improved Prediction of Protein Stability Changes. https://doi.org/10.1101/2023.07.27.550881

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Is a master's student | Wears funny socks | Presents a part or a tool that interacts with RNA | Has a driver's license |
| Is a bachelor's student | Has already been a part of an iGEM team | Presents an acronym | Presents a part acting on DNA | Wanted to study something non-bio realted |
| Presents an AI-powered tool | Speaks more than 3 languages |  | Named their pet after a scientific concept or a scientist | Presents something related to CRISPR |
| Presents a technique that uses antibodies | Has never run a PCR | Has or pursues a 2nd bachelor degree | Presents a protein part | Likes plant biology |
| Has a tattoo | Has met a Nobel Prize winner | Presents a framework for ethics or safety | Can tell what "iGEM" stands for | Is a leftie |

# C062 RFDiffusion

## Description

RFdiffusion, developed by the Baker Lab, uses generative AI diffusion models for de novo protein design, creating entirely new structures from scratch. This method encodes structural features like residue orientations into a latent space and iteratively "denoises" random inputs to generate proteins that meet specific constraints—similar to how image diffusion models refine details from noise. Key modes include Binder Design, which generates proteins that bind specific targets, and Motif Scaffolding, which incorporates structural motifs like enzyme active sites into designs. It also offers Partial Diffusion, tweaking existing structures for diversification. RFdiffusion expands protein design possibilities, enabling tailored solutions for drug development, biomaterials engineering, and synthetic biology. By precisely creating proteins with desired properties, it represents a significant advance in AI-driven molecular engineering.(Watson et al., 2023)

## References


- RosettaCommons. (n.d.). Rosettacommons/RFdiffusion: Code for running rfdiffusion. GitHub. https://github.com/RosettaCommons/RFdiffusion
- Watson, J. L. et al. De novo design of protein structure and function with RFdiffusion. Nature 620, 1089–1100 (2023).

# Bingo

| | | | | |
|---|---|---|---|---|
| Can tell what “iGEM” stands for | Presents an acronym | Wanted to study something non-bio realted | Has already been a part of an iGEM team | Likes plant biology |
| Presents a part acting on DNA | Presents an AI-powered tool | Has met a Nobel Prize winner | Presents a part or a tool that interacts with RNA | Named their pet after a scientific concept or a scientist |
| Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree |  | Presents a laboratory method | Wears funny socks |
| Presents something related to CRISPR | Has a driver’s license | Speaks more than 3 languages | Is a master’s student | Has never run a PCR |
| Is a bachelor’s student | Has a tattoo | Presents a technique that uses antibodies | Presents a protein part | Is a leftie |

# C063 Protein Binder Design Using Deep Learning

## Description

Deep learning has streamlined the de novo design of protein binders, enabling computational creation of proteins that interact with targets like receptors or enzymes. The typical workflow involves three steps:

- Backbone Generation: Tools like RFdiffusion or AFDesign create 3D backbones tailored to bind the target by shaping complementary interfaces or pockets.
- Sequence Design: ProteinMPNN predicts amino acid sequences optimized for stability, functionality, and fidelity to the backbone.
- Structure Prediction and Scoring: Tools like AlphaFold or ESMFold validate the folding of sequences and score structures for stability, binding energy, and complementarity.

Researchers typically generate thousands of backbones and select a few hundred high-scoring sequences for lab testing. This iterative pipeline reduces costs, labor, and dramatically improves success rates in designing protein binders for applications like therapeutics and diagnostics.(Bennett et al., 2023; Sokrypton on GitHub)

## References


- Sokrypton. (n.d.). Sokrypton/ColabDesign: Making protein design accessible to all via google colab!. GitHub. https://github.com/sokrypton/ColabDesign
- Bennett, N.R., Coventry, B., Goreshnik, I. et al. Improving de novo protein binder design with deep learning. Nat Commun 14, 2625 (2023). https://doi.org/10.1038/s41467-023-38328-5

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an AI-powered tool | Is a bachelor's student | Is a leftie | Is a master's student | Wears funny socks |
| Has met a Nobel Prize winner | Presents a laboratory method | Presents a part or a tool that interacts with RNA | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree |
| Presents an acronym | Wanted to study something non-bio realted |  | Has never run a PCR | Named their pet after a scientific concept or a scientist |
| Presents something related to CRISPR | Has a tattoo | Has already been a part of an iGEM team | Presents a part acting on DNA | Can tell what "iGEM" stands for |
| Presents a protein part | Presents a technique that uses antibodies | Has a driver's license | Speaks more than 3 languages | Likes plant biology |

# C064 GROMACS

## Description

GROMACS (GROningen MAchine for Chemical Simulations) is a free, open-source molecular dynamics (MD) simulation software primarily designed for simulating biomolecules such as proteins, lipids, and nucleic acids. Known for its speed and efficiency, GROMACS can run on both central processing units (CPUs) and graphics processing units (GPUs). The software operates via a command-line interface and offers tools for analyzing and visualizing molecular trajectories. GROMACS supports a wide variety of force fields, allowing it to be used for diverse molecular simulations. However, the quality and reliability of simulations depend on careful decisions regarding system setup, including the choice of the starting structure, force field model, concentration of salt, integration method, temperature/pressure regulation algorithms, and simulation duration. (Lemkul et al., 2019)

## References


- Wikimedia Foundation. (2025, August 7). Gromacs. Wikipedia. https://en.wikipedia.org/wiki/GROMACS
- Lemkul, J. (2019). From proteins to perturbed Hamiltonians: A suite of tutorials for the Gromacs-2018 molecular simulation package [Article V1.0]. Living Journal of Computational Molecular Science, 1(1). https://doi.org/10.33011/livecoms.1.1.5068

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Likes plant biology | Is a bachelor's student | Presents a part acting on DNA | Presents a laboratory method |
| Has never run a PCR | Has a tattoo | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree | Presents a framework for ethics or safety |
| Presents an AI-powered tool | Wears funny socks |  | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA |
| Has a driver's license | Presents a protein part | Is a master's student | Presents something related to CRISPR | Presents an acronym |
| Speaks more than 3 languages | Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team | Presents a technique that uses antibodies | Can tell what "iGEM" stands for |

# C065 SiLA

## Description

SiLA is a system that makes image analysis tools available to reviewers and editors in a principled way. It is the first human-in-the-loop end-to-end system that processes article PDF files, performs image manipulation detection on the automatically extracted figures using advanced image processing, image forensics, and computer vision solutions. At the end it provides meaningful analyses to human experts, helping them to decide if the discovered events are either legitimate or not.

## References


- Moreira, D., Cardenuto, J.P., Shao, R. et al. SILA: a system for scientific image analysis. Sci Rep 12, 18306 (2022). https://doi.org/10.1038/s41598-022-21535-3

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Likes plant biology | Presents a part or a tool that interacts with RNA | Is a bachelor's student | Has a driver's license |
| Wears funny socks | Has a tattoo | Has or pursues a 2nd bachelor degree | Presents something related to CRISPR | Presents a technique that uses antibodies |
| Has met a Nobel Prize winner | Presents a laboratory method |  | Wanted to study something non-bio realted | Presents an AI-powered tool |
| Has never run a PCR | Can tell what "iGEM" stands for | Presents an acronym | Presents a framework for ethics or safety | Has already been a part of an iGEM team |
| Speaks more than 3 languages | Is a master's student | Presents a protein part | Presents a part acting on DNA | Named their pet after a scientific concept or a scientist |

# L066 Non-model organism

## Description

In synthetic biology, non-model organisms refer to organisms that are not traditionally used in laboratory research or genetic engineering. Unlike usual E coli. or , these organisms represent various different niches, often carry interesting for the research characteristics: extremophiles, marine organisms, or plants with unique biochemical properties. On the other hand, the process of engineering non-model organisms has it's complications, as genetic tools are limited, genetic regulatory networks are mostly unknown and growth rates are slower in comparison to model organisms.(Russell et al., 2017)

## References


- Russell JJ, Theriot JA, Sood P, Marshall WF, Landweber LF, Fritz-Laylin L, Polka JK, Oliferenko S, Gerbich T, Gladfelter A, Umen J, Bezanilla M, Lancaster MA, He S, Gibson MC, Goldstein B, Tanaka EM, Hu CK, Brunet A. Non-model model organisms. BMC Biol. 2017 Jun 29;15(1):55. doi: 10.1186/s12915-017-0391-5
- ASCB Post Staff. (2024, August 7). Emerging, uncommon, and non-model organisms questionnaire 3 ASCB. https://www.ascb.org/science-news/emerging-uncommon-non-model-organism-questionaire-3/

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a framework for ethics or safety | Has met a Nobel Prize winner | Presents an acronym | Presents a part or a tool that interacts with RNA | Has a driver's license |
| Presents a technique that uses antibodies | Named their pet after a scientific concept or a scientist | Has never run a PCR | Presents an AI-powered tool | Has or pursues a 2nd bachelor degree |
| Presents a laboratory method | Has already been a part of an iGEM team |  | Likes plant biology | Speaks more than 3 languages |
| Presents a protein part | Presents a part acting on DNA | Can tell what "iGEM" stands for | Presents something related to CRISPR | Is a master's student |
| Wears funny socks | Wanted to study something non-bio realted | Is a bachelor's student | Is a leftie | Has a tattoo |

# L067 Chassis

## Description

In synthetic biology, the term “chassis” refers to a specific kind of model organisms which are bound to the specific ways specific ways of experimenting, involving genetic manipulation and engineering. Chassis organisms are chosen for their suitability to easily host and express engineered genetic circuits or metabolic pathways in so-called plug-in/plug-out manner. Chassis provide first of all a predictable environment for synthetic biology applications that involve biomanufacturing, as they have to be adapted to specific substrates and its impurities in an industrial setup.(iGEM Evry 2012) Another important part is the ability to not only execute the functions needed for efficient bioproduction, but also be robust enough to tolerate the harsh operating conditions characteristic of industrial processes, such as producing biofuels, pharmaceuticals, and biochemicals. Common chassis organisms include Escherichia coli, Saccharomyces cerevisiae (yeast), and various species of bacteria and algae.(Calero et al., 2019)

## References


- iGEM Evry 2012. (n.d.). Team:evry/humanpractice/modelorganism - 2012.igem.org. http://2012.igem.org/Team:Evry/HumanPractice/modelorganism
- Calero P, Nikel PI. Chasing bacterial chassis for metabolic engineering: a perspective review from classical to non-traditional microorganisms. Microb Biotechnol. 2019 Jan;12(1):98-124. doi: 10.1111/1751-7915.13292

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Has a tattoo | Presents a protein part | Is a master's student | Speaks more than 3 languages |
| Wanted to study something non-bio realted | Presents a part acting on DNA | Presents a part or a tool that interacts with RNA | Wears funny socks | Can tell what "iGEM" stands for |
| Likes plant biology | Presents something related to CRISPR |  | Presents an AI-powered tool | Is a leftie |
| Presents a framework for ethics or safety | Presents an acronym | Has already been a part of an iGEM team | Is a bachelor's student | Has a driver's license |
| Presents a laboratory method | Has or pursues a 2nd bachelor degree | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies | Has never run a PCR |

# L068 Syn61 *E. coli*

## Description

Syn61 is an E. coli strain with a fully synthetic, recoded genome in which all occurrences of two serine codons (TCG and TCA) and one stop codon (TAG) were replaced with synonymous codons. By rebuilding the 4-million–base genome from scratch, scientists exploited the redundancy of the genetic code, freeing these triplets for reassignment. This opens future application, such as incorporating non-canonical amino acids, allowing the biosynthesis of novel, genetically encoded biopolymers.(Robertson et al., 2021; Fredens et al., 2019)

## References


- Fredens, J., Wang, K., de la Torre, D. et al. Total synthesis of Escherichia coli with a recoded genome. Nature 569, 514–518 (2019). https://doi.org/10.1038/s41586-019-1192-5
- Robertson WE, Funke LFH, de la Torre D, Fredens J, Elliott TS, Spinck M, Christova Y, Cervettini D, Böge FL, Liu KC, Buse S, Maslen S, Salmond GPC, Chin JW. Sense codon reassignment enables viral resistance and encoded polymer synthesis. Science. 2021 Jun 4;372(6546):1057-1062. doi: 10.1126/science.abg3029

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an acronym | Is a master's student | Presents a protein part | Has never run a PCR | Has a tattoo |
| Presents a part acting on DNA | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree | Presents a part or a tool that interacts with RNA | Is a leftie |
| Is a bachelor's student | Has already been a part of an iGEM team |  | Presents an AI-powered tool | Wanted to study something non-bio realted |
| Presents a technique that uses antibodies | Has met a Nobel Prize winner | Presents a laboratory method | Likes plant biology | Wears funny socks |
| Speaks more than 3 languages | Presents something related to CRISPR | Has a driver's license | Named their pet after a scientific concept or a scientist | Can tell what "iGEM" stands for |

# L069 MDS42 *E. coli*

## Description

The multiple-deletion series (MDS) strains, carrying genome reductions of up to 15%, were created by removing nonessential genes and sequences, including mobile DNA, recombinogenic elements, and cryptic virulence factors, while maintaining robust growth and protein production. Genome reduction also produced potential synergistic effects, leading to altered phenotypes—such as the high electrocompetence observed in the MDS42 strain. (Pósfai et al., 2006)

## References


- György Pósfai et al. ,Emergent Properties of Reduced-Genome Escherichia coli.Science312,1044-1046(2006).DOI:10.1126/science.1126439

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a driver's license | Likes plant biology | Speaks more than 3 languages | Presents a protein part | Presents a laboratory method |
| Presents a technique that uses antibodies | Presents a framework for ethics or safety | Presents an acronym | Has met a Nobel Prize winner | Has a tattoo |
| Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted |  | Presents a part acting on DNA | Is a master's student |
| Presents a part or a tool that interacts with RNA | Can tell what "iGEM" stands for | Presents something related to CRISPR | Has never run a PCR | Presents an AI-powered tool |
| Wears funny socks | Is a bachelor's student | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree | Is a leftie |

# L070 SHuffle *E. coli*

## Description

SHuffle E. coli is a strain developed by New England Biolabs to produce correctly disulfide-bonded, active proteins at high yields within its cytoplasm. Unlike typical organisms that maintain reductive enzymes in the cytoplasm, SHuffle has diminished cytoplasmic reductive pathways. This allows disulfide bond formation to occur directly in the cytoplasm, rather than being restricted to compartments like the periplasm in Gram-negative bacteria or the endoplasmic reticulum in eukaryotes. As a result, proteins requiring disulfide bonds for proper folding and stability are less prone to misfolding, remain active, and achieve higher expression levels.(Lobstein et al., 2012)

## References


- Lobstein J, Emrich CA, Jeans C, Faulkner M, Riggs P, Berkmen M. SHuffle, a novel Escherichia coli protein expression strain capable of correctly folding disulfide bonded proteins in its cytoplasm. Microb Cell Fact. 2012 May 8;11:56. doi: 10.1186/1475-2859-11-56.
- E. coli protein expression strains | NEB. (n.d.). https://www.neb.com/en-us/products/protein-expression/e-coli-protein-expression-strains

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a technique that uses antibodies | Is a leftie | Presents a laboratory method | Is a master's student | Speaks more than 3 languages |
| Has met a Nobel Prize winner | Presents an AI-powered tool | Presents a framework for ethics or safety | Is a bachelor's student | Presents an acronym |
| Has a tattoo | Can tell what "iGEM" stands for |  | Has never run a PCR | Has or pursues a 2nd bachelor degree |
| Has a driver's license | Wears funny socks | Presents something related to CRISPR | Likes plant biology | Presents a part or a tool that interacts with RNA |
| Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted | Presents a part acting on DNA | Presents a protein part | Has already been a part of an iGEM team |

# L071 TxTl

## Description

Cell-free transcription–translation (TXTL) is a versatile technology that enables gene expression outside of living organisms. It allows the creation of genetically programmed biomolecular systems to quantitatively analyze each step of expression and assess the effects of chemical, physical, and genetic factors on function. The process replicates the central dogma of biology: DNA -> RNA -> protein. Essential enzymes, ribosomes, tRNAs, and associated factors are provided by the cell extract, while energy sources, cofactors, and amino acids in the reaction mixture sustain rapid and controllable protein production. Extracts are typically derived from E. coli and often incorporate T7 or T3 bacteriophage elements. This system has also shown strong potential for biomanufacturing applications. (Noireaux et al., 2019; Noireaux et al., 2021)

## References


- David Garenne, Seth Thompson, Amaury Brisson, Aset Khakimzhan, Vincent Noireaux, The all-E. coliTXTL toolbox 3.0: new capabilities of a cell-free synthetic biology platform, Synthetic Biology, Volume 6, Issue 1, 2021, https://doi.org/10.1093/synbio/ysab017
- Garenne, D., & Noireaux, V. (2019). Cell-free transcription–translation: Engineering biology from the nanometer to the millimeter scale. Current Opinion in Biotechnology, 58, 19–27.
- https://doi.org/10.1016/j.copbio.2018.10.007

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Presents a laboratory method | Presents a technique that uses antibodies | Presents a part or a tool that interacts with RNA | Presents a framework for ethics or safety |
| Is a master's student | Is a leftie | Likes plant biology | Speaks more than 3 languages | Presents an acronym |
| Presents an AI-powered tool | Can tell what "iGEM" stands for |  | Is a bachelor's student | Wanted to study something non-bio realted |
| Has a tattoo | Presents a protein part | Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Presents a part acting on DNA |
| Has a driver's license | Named their pet after a scientific concept or a scientist | Has never run a PCR | Presents something related to CRISPR | Wears funny socks |

# L072 IVT

## Description

In vitro transcription (IVT) is a method used to synthesize RNA molecules in vitro, mimicking natural cellular transcription. It involves a template DNA molecule containing a promoter sequence recognized by specific bacteriophage RNA polymerases (e.g., T7, T3, or SP6). This template directs the RNA polymerase to transcribe the sequence of interest into RNA. IVT enables the production of RNA of any desired sequence, from short oligonucleotides to full-length transcripts several kilobases long, in µg to mg quantities. The process requires a purified DNA template, ribonucleotide triphosphates (ATP, UTP, CTP, GTP), a transcription buffer with essential cofactors like magnesium ions and DTT, and an appropriate RNA polymerase. IVT reactions occur under controlled conditions, typically at 37°C, optimizing enzymatic activity. This method would be useful in situations requiring highly controlled RNA synthesis, such as the creation of mRNA vaccines or gene therapy.(Lee et al., 2018; Masquida et al., 2010)

## References


- Beckert, B., & Masquida, B. (2010). Synthesis of RNA by in vitro transcription. Methods in Molecular Biology, 29–41. https://doi.org/10.1007/978-1-59745-248-9_3
- Pazdernik, N. (n.d.). In vitro transcription and its applications: IDT. Integrated DNA Technologies. https://eu.idtdna.com/pages/applications/ivt
- Kwon, H., Kim, M., Seo, Y., Moon, Y. S., Lee, H. J., Lee, K., & Lee, H. (2018). Emergence of synthetic mrna: In vitro synthesis of mrna and its applications in Regenerative Medicine. Biomaterials, 156, 172–193. https://doi.org/10.1016/j.biomaterials.2017.11.034

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a technique that uses antibodies | Presents a laboratory method | Named their pet after a scientific concept or a scientist | Presents a protein part | Presents a part acting on DNA |
| Presents a framework for ethics or safety | Is a master's student | Presents an AI-powered tool | Has a tattoo | Speaks more than 3 languages |
| Has met a Nobel Prize winner | Can tell what "iGEM" stands for |  | Presents something related to CRISPR | Presents an acronym |
| Has or pursues a 2nd bachelor degree | Has already been a part of an iGEM team | Has never run a PCR | Is a bachelor's student | Is a leftie |
| Likes plant biology | Wears funny socks | Wanted to study something non-bio realted | Presents a part or a tool that interacts with RNA | Has a driver's license |

# L073 RCA

## Description

Rolling circle amplification (RCA) is an isothermal enzymatic process used to amplify short DNA or RNA primers into long single-stranded DNA or RNA sequences. The process involves a circular DNA template, typically in the form of a plasmid or circularized oligonucleotide, which is amplified by a DNA polymerase enzyme, such as phi29 DNA polymerase. The polymerase binds to the template and continuously synthesizes new DNA strands as it moves around the circular template, leading to exponential amplification. This results in the production of long, repeating DNA products called concatemers, containing tens to hundreds of tandem repeats complementary to the template. RCA is used as a reliable diagnosis of all viruses with small single-stranded circular DNA genomes.(Jeske et al., 2006; Zhao et al. 2014)

## References


- RCA and MDA-WGA: Thermo Fisher Scientific - US. RCA and MDA-WGA | Thermo Fisher Scientific - US. (n.d.). https://www.thermofisher.com/de/de/home/life-science/pcr/isothermal-nucleic-acid-amplification/multiple-displacement-rolling-circle-amplification.html
- Ali, M. M., Li, F., Zhang, Z., Zhang, K., Kang, D.-K., Ankrum, J. A., Le, X. C., & Zhao, W. (2014). Rolling circle amplification: A versatile tool for chemical biology, Materials Science and Medicine. Chemical Society Reviews, 43(10), 3324. https://doi.org/10.1039/c3cs60439j
- Haible, D., Kober, S., & Jeske, H. (2006). Rolling circle amplification revolutionizes diagnosis and genomics of geminiviruses. Journal of Virological Methods, 135(1), 9–16. https://doi.org/10.1016/j.jviromet.2006.01.017

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a laboratory method | Wears funny socks | Has met a Nobel Prize winner | Presents a framework for ethics or safety | Speaks more than 3 languages |
| Presents an acronym | Wanted to study something non-bio realted | Likes plant biology | Is a master's student | Presents a technique that uses antibodies |
| Presents something related to CRISPR | Presents a protein part |  | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA |
| Has a tattoo | Presents an AI-powered tool | Presents a part acting on DNA | Has or pursues a 2nd bachelor degree | Has a driver's license |
| Has never run a PCR | Is a leftie | Is a bachelor's student | Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team |

# L074 RPA

## Description

Recombinase polymerase amplification (RPA) is an isothermal DNA amplification technique that operates at low temperatures (39–42°C) and does not require thermal cycling. It is initiated by two primers and carried out by a mixture of recombinase enzymes, single-stranded binding proteins, and a strand-displacing DNA polymerase. The key enzymes in RPA are T4 UvsX (a recombinase) and Bacillus subtilis Pol I (a DNA polymerase). During the process, ATP and polyethylene glycol enable UvsX to bind primers, forming a recombinase-primer complex that searches for homologous sequences in double-stranded DNA templates. Once a homologous sequence is identified, the complex inserts the primer, initiating a chain replacement reaction. The replaced template is bound by single-stranded binding protein, and DNA polymerase elongates the primer to generate new DNA strands. As RCA produces detectable amplification products within 20 minutes and works in isothermal conditions are the bigest reasons for using this rapid detection/sequencing process. (Wei et al. 2022)

## References


- Tan, M., Liao, C., Liang, L., Yi, X., Zhou, Z., & Wei, G. (2022). Recent advances in recombinase polymerase amplification: Principle, advantages, disadvantages and applications. Frontiers in Cellular and Infection Microbiology, 12. https://doi.org/10.3389/fcimb.2022.1019071
- Recombinase polymerase amplification (RPA). Thermo Fisher Scientific - US. (n.d.). https://www.thermofisher.com/de/de/home/life-science/pcr/isothermal-nucleic-acid-amplification/recombinase-polymerase-amplification.html

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a master's student | Presents a part acting on DNA | Presents a protein part | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree |
| Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted | Speaks more than 3 languages | Has a tattoo | Likes plant biology |
| Is a bachelor's student | Presents a technique that uses antibodies |  | Has already been a part of an iGEM team | Can tell what "iGEM" stands for |
| Has a driver's license | Wears funny socks | Presents something related to CRISPR | Is a leftie | Has met a Nobel Prize winner |
| Has never run a PCR | Presents a laboratory method | Presents a part or a tool that interacts with RNA | Presents an AI-powered tool | Presents an acronym |

# L075 SHERLOCK

## Description

Specific High-sensitivity Enzymatic Reporter unLOCKing (SHERLOCK) is a CRISPR-based diagnostic tool developed to detect specific RNA or DNA molecules. Unlike Cas9, SHERLOCK employs Cas13a, a related protein that binds and cleaves single-stranded nucleic acids. The process begins with recombinase polymerase amplification (RPA), which amplifies RNA/DNA through reverse transcriptase, using a single, constant temperature, eliminating the need for specialized equipment. The amplified nucleic acids are then combined with Cas13a, a guide RNA complementary to the target sequence, and a short reporter RNA tagged with both a fluorophore and a quencher. Once Cas13a cleaves its target RNA, it remains in an “active” state and begins cutting additional RNAs regardless of sequence(this is known as collateral cleavage). If the target sequence is present, this activity cleaves the reporter, separates the fluorophore from the quencher, and produces a fluorescent signal. The signal confirms the presence of the target sequence in the original sample.(Gronowski et al., 2018; Zhang et al.,2017)

## References


- Gootenberg, J. S., Abudayyeh, O. O., Lee, J. W., Essletzbichler, P., Dy, A. J., Joung, J., Verdine, V., Donghia, N., Daringer, N. M., Freije, C. A., Myhrvold, C., Bhattacharyya, R. P., Livny, J., Regev, A., Koonin, E. V., Hung, D. T., Sabeti, P. C., Collins, J. J., & Zhang, F. (2017). Nucleic acid detection with CRISPR-CAS13A/C2C2. Science, 356(6336), 438–442.
- Gronowski AM. Who or What is SHERLOCK? EJIFCC. 2018 Nov 7;29(3):201-204. PMID: 30479604; PMCID: PMC6247122.

# Bingo

| | | | | |
|---|---|---|---|---|
| Named their pet after a scientific concept or a scientist | Presents a part or a tool that interacts with RNA | Likes plant biology | Has or pursues a 2nd bachelor degree | Wanted to study something non-bio realted |
| Presents a laboratory method | Is a master's student | Has a tattoo | Presents a part acting on DNA | Can tell what "iGEM" stands for |
| Presents a framework for ethics or safety | Presents an AI-powered tool |  | Presents a protein part | Has met a Nobel Prize winner |
| Presents an acronym | Presents a technique that uses antibodies | Speaks more than 3 languages | Presents something related to CRISPR | Wears funny socks |
| Is a bachelor's student | Has already been a part of an iGEM team | Has never run a PCR | Is a leftie | Has a driver's license |

# L076 LEOPARD

## Description

LEOPARD (Leveraging Engineered tracrRNAs and On-target DNAs for PArallel RNA Detection) is a CRISPR-based diagnostic method that allows the simultaneous detection of multiple RNA targets in one reaction. It is based on the engineering of reprogrammed tracrRNA, therefore, pairing the presence of an RNA of interest with a Cas9-directed cleavage of a matching DNA “barcode.” And by analyzing which barcodes are cleaved, the presence and abundance of multiple RNAs (for instance, different variants of SARS-CoV-2) can be detected in a single reaction (Jiao et al., 2021)

## References


- Jiao, C., Sharma, S., Dugar, G., Peeck, N. L., Bischler, T., Wimmer, F., … & Beisel, C. L. (2021). Noncanonical crRNAs derived from host transcripts enable multiplexable RNA detection by Cas9. Science, 372(6545), 941-948.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an acronym | Has or pursues a 2nd bachelor degree | Named their pet after a scientific concept or a scientist | Is a master's student | Presents a part acting on DNA |
| Presents a part or a tool that interacts with RNA | Is a leftie | Wanted to study something non-bio realted | Presents a protein part | Has a tattoo |
| Likes plant biology | Has met a Nobel Prize winner |  | Has a driver's license | Presents something related to CRISPR |
| Wears funny socks | Is a bachelor's student | Presents a framework for ethics or safety | Speaks more than 3 languages | Has never run a PCR |
| Presents a technique that uses antibodies | Has already been a part of an iGEM team | Can tell what "iGEM" stands for | Presents an AI-powered tool | Presents a laboratory method |

# L077 CRISPRa/CRISPRi

## Description

CRISPRa (CRISPR activation) and CRISPRi (CRISPR interference) are adaptations of the CRISPR–Cas9 system that rely on a catalytically inactive Cas9 protein (dCas9), which can still bind to a specific DNA sequence but is unable to cut it (Synthego., 2024).

In CRISPRa, dCas9 is fused to a transcriptional activator overall enhancing gene expression (sometimes multiple activators need to be recruited for a significant overexpression) (Kampmann, 2018). CRISPRa also enables the overexpression of large transcripts for which ORF-based methods do not work as well.

In contrast, CRISPRi uses a dCas9 fused to a transcriptional repressor, inhibiting gene expression. CRISPRi is complementary to RNA interference or RNAi, but is advantageous in having fewer sequence-specific off-target effects, and in being able to modulate both coding as well as non-coding genes.

## References


- Kampmann, M. (2018). CRISPRi and CRISPRa screens in mammalian cells for precision biology and medicine. ACS chemical biology, 13(2), 406-416.
- Synthego (2024). CRISPRa and CRISPRi. Available in: https://www.synthego.com/guide/crispr-methods/crispri-crispra

# Bingo

| | | | | |
|---|---|---|---|---|
| Speaks more than 3 languages | Has a driver's license | Can tell what "iGEM" stands for | Likes plant biology | Wanted to study something non-bio realted |
| Has already been a part of an iGEM team | Presents a part or a tool that interacts with RNA | Presents an AI-powered tool | Presents an acronym | Presents a framework for ethics or safety |
| Has met a Nobel Prize winner | Is a master's student |  | Named their pet after a scientific concept or a scientist | Is a leftie |
| Is a bachelor's student | Has a tattoo | Presents a protein part | Has or pursues a 2nd bachelor degree | Presents a technique that uses antibodies |
| Presents a laboratory method | Has never run a PCR | Presents something related to CRISPR | Wears funny socks | Presents a part acting on DNA |

# L078 Amber suppression

## Description

Amber suppression is a genetic technique used to incorporate non-natural amino acids (NAAs) during protein synthesis. This method relies on modified transfer RNA (tRNA) molecules, known as amber suppressor tRNAs (sup-tRNAs), which recognize the amber stop codon (UAG) and, in response, are engineered to read this codon as a signal to insert an NAA instead of terminating translation (Ogawa et al., 2016). This allows for the production of full-length, biologically active proteins even in the presence of amber mutations, allowing researchers to design proteins with novel functions. A challenge, however, is that suppression efficiency is rarely 100%, and there is a competition between release factors and suppressor tRNAs that limit yields (Schwark et al., 2018).

## References


- Ogawa, A., Namba, Y., & Gakumasawa, M. (2016). Rational optimization of amber suppressor tRNAs toward efficient incorporation of a non-natural amino acid into protein in a eukaryotic wheat germ extract. Organic & Biomolecular Chemistry, 14(9), 2671-2678.
- Schwark, D. G., Schmitt, M. A., & Fisk, J. D. (2018). Dissecting the contribution of release factor interactions to amber stop codon reassignment efficiencies of the Methanocaldococcus jannaschii orthogonal pair. Genes, 9(11), 546.

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Presents an acronym | Presents a laboratory method | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA |
| Presents a protein part | Wanted to study something non-bio realted | Is a master's student | Has or pursues a 2nd bachelor degree | Named their pet after a scientific concept or a scientist |
| Has a driver's license | Speaks more than 3 languages |  | Presents something related to CRISPR | Presents a framework for ethics or safety |
| Has never run a PCR | Presents an AI-powered tool | Presents a part acting on DNA | Wears funny socks | Likes plant biology |
| Has already been a part of an iGEM team | Presents a technique that uses antibodies | Has a tattoo | Is a leftie | Has met a Nobel Prize winner |

# L079 PROTAC

## Description

Proteolysis targeting chimeras (PROTACs) are drugs designed to remove specific proteins in cells by hijacking the ubiquitin–proteasome system (UPS). Unlike traditional drugs that block protein activity, PROTACs cause proteins to be degraded. They consist of two parts: one binds to the target protein, and the other recruits an E3 ubiquitin ligase, which tags the protein (ubiquitination) for destruction by the UPS (Bondeson & Crews, 2017; Luh et al., 2020). PROTACs are reusable, as they're not destroyed in the process.

PROTACs offer several advantages over traditional drugs, including the ability to target proteins once considered undruggable, higher specificity, and lower doses due to their catalytic nature, becoming a promising approach for treating complex diseases. Their efficiency depends on factors like cell permeability, the expression of appropriate E3 ligases, and the stability of the ternary complex they form.

## References


- Bondeson, D. P., & Crews, C. M. (2017). Targeted protein degradation by small molecules. Annual review of pharmacology and toxicology, 57(1), 107-123.
- Luh, L. M., Scheib, U., Juenemann, K., Wortmann, L., Brands, M., & Cromm, P. M. (2020). Prey for the proteasome: targeted protein degradation—a medicinal chemist's perspective. Angewandte Chemie International Edition, 59(36), 15448-15466.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a tattoo | Presents an acronym | Presents a part acting on DNA | Is a leftie | Presents a laboratory method |
| Likes plant biology | Is a bachelor's student | Presents a part or a tool that interacts with RNA | Wanted to study something non-bio realted | Is a master's student |
| Has met a Nobel Prize winner | Presents something related to CRISPR |  | Presents an AI-powered tool | Has already been a part of an iGEM team |
| Speaks more than 3 languages | Can tell what "iGEM" stands for | Has never run a PCR | Wears funny socks | Has or pursues a 2nd bachelor degree |
| Presents a framework for ethics or safety | Presents a technique that uses antibodies | Named their pet after a scientific concept or a scientist | Presents a protein part | Has a driver's license |

# L080 Trim-away

## Description

Trim-Away is a method that relies on the ubiquitin ligase and Fc receptor TRIM21, which identifies proteins bound by antibodies and directs them for degradation by the proteasome. The main advantages of Trim-Away are that it can be applied to any endogenous protein without requiring prior modification, it is based on conventional antibodies (easy to get), and it can be applied to a broad range of cell types, including non-dividing primary human cells (Clift et al., 2017).

In a Trim-Away experiment, first, an antibody specific to the target protein is introduced. Then, TRIM21 is recruited to the antibody-bound protein and, finally, the proteasome degrades the complex of the target protein, antibody, and TRIM21 within minutes (Clift el al., 2018).

## References


- Clift, D., McEwan, W. A., Labzin, L. I., Konieczny, V., Mogessie, B., James, L. C., & Schuh, M. (2017). A method for the acute and rapid degradation of endogenous proteins. Cell, 171(7), 1692-1706.
- Clift, D., So, C., McEwan, W. A., James, L. C., & Schuh, M. (2018). Acute and rapid degradation of endogenous proteins by Trim-Away. Nature protocols, 13(10), 2149-2175.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a framework for ethics or safety | Is a leftie | Presents an AI-powered tool | Has met a Nobel Prize winner | Likes plant biology |
| Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team | Has a tattoo | Is a bachelor's student | Presents a protein part |
| Has or pursues a 2nd bachelor degree | Presents a part or a tool that interacts with RNA |  | Presents something related to CRISPR | Speaks more than 3 languages |
| Presents a technique that uses antibodies | Presents a laboratory method | Is a master's student | Presents a part acting on DNA | Wanted to study something non-bio realted |
| Can tell what "iGEM" stands for | Has never run a PCR | Presents an acronym | Wears funny socks | Has a driver's license |

# L081 Nanopore

## Description

Nanopore sequencing is a third-generation technology that enables the sequencing of DNA and RNA without the need for PCR amplification or chemical labeling. It works by passing individual nucleic acid molecules through a nanopore in an electro-resistant membrane, where disruptions in electrical current caused by the molecule are measured and translated into a sequence in real-time (Zheng et al., 2023). This approach allows for the direct, real-time sequencing of both short and long DNA/RNA fragments, overcoming the limitations of traditional methods that require DNA fragmentation and reassembly.

Nanopore sequencing can resolve repetitive regions, detect structural variations, and differentiate isoforms, offering a more accurate and complete genome analysis. It also enables the identification of base modifications, such as methylation, providing additional insights. Nanopore sequencing is used widely in specialized research areas, as well as rapid clinical diagnoses and outbreak surveillance.

## References


- Zheng, P., Zhou, C., Ding, Y., Liu, B., Lu, L., Zhu, F., & Duan, S. (2023). Nanopore sequencing technology and its applications. MedComm, 4(4), e316.
- For more details, we heavily reccomend: https://nanoporetech.com/platform/technology

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Presents an acronym | Has met a Nobel Prize winner | Likes plant biology | Has a driver's license |
| Has a tattoo | Presents a technique that uses antibodies | Wanted to study something non-bio realted | Can tell what "iGEM" stands for | Named their pet after a scientific concept or a scientist |
| Is a master's student | Presents a protein part |  | Has never run a PCR | Speaks more than 3 languages |
| Presents a part or a tool that interacts with RNA | Presents an AI-powered tool | Presents a laboratory method | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree |
| Presents a framework for ethics or safety | Presents a part acting on DNA | Wears funny socks | Presents something related to CRISPR | Is a leftie |

# L082 switchSENSE

## Description

The switchSENSE technology is an advanced (and patented) biophysical tool for studying molecular interactions in real time. It uses electro-switchable DNA nanolevers attached to gold microelectrodes to measure binding kinetics, affinities, and structural properties (Dynamic Biosensors, 2024).

DNA nanolevers are short, synthetic DNA strands attached to gold electrodes. These strands act as flexible “levers” that can move in response to applied electrical voltages. They are functionalized with specific ligands to enable targeted molecular interactions, as their movement is tracked in real-time using a fluorescent dye. The orientation and motion of these nanolevers change depending on the applied voltage, which is key to analyzing molecular interactions (Cléry et al., 2017).

## References


- Cléry, A., Sohier, T. J., Welte, T., Langer, A., & Allain, F. H. (2017). switchSENSE: A new technology to study protein-RNA interactions. Methods, 118, 137-145.
- Dynamic Biosensors (2024). switchSENSE® technology. Available in: https://www.dynamic-biosensors.com/switchsense/

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a master's student | Wears funny socks | Speaks more than 3 languages | Has a driver's license | Presents an AI-powered tool |
| Presents an acronym | Presents something related to CRISPR | Presents a framework for ethics or safety | Presents a part or a tool that interacts with RNA | Has never run a PCR |
| Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree |  | Wanted to study something non-bio realted | Presents a part acting on DNA |
| Has a tattoo | Is a bachelor's student | Likes plant biology | Has already been a part of an iGEM team | Presents a laboratory method |
| Presents a protein part | Is a leftie | Can tell what "iGEM" stands for | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies |

# L083 FRET

## Description

Förster Resonance Energy Transfer (FRET) is a mechanism that describes non-radiative energy transfer between two fluorophores: a donor in an excited state and an acceptor in its proximity. For biologists, FRET is an incredibly useful tool to study protein interactions and conformational changes (Sekar & Periasamy, 2003), which could be done in an inter or ontra molecular manner, deopending if the fluorophores are located in the same protein or not. FRET efficiency can be quantified using fluorescence microscopy, enabling distance measurements and real-time observation of molecular dynamics. For instance, it can be used to quantify the concentration of a ligand binding to a protein based on the emission intensity of the acceptor detected.

## References


- Sekar, R. B., & Periasamy, A. (2003). Fluorescence resonance energy transfer (FRET) microscopy imaging of live cell protein localizations. The Journal of cell biology, 160(5), 629.
- For a (really good) recent use of FRET in iGEM, visit: https://2024.igem.wiki/heidelberg/parts

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Likes plant biology | Presents a part acting on DNA | Has never run a PCR | Presents a protein part |
| Presents something related to CRISPR | Has a driver's license | Named their pet after a scientific concept or a scientist | Is a bachelor's student | Presents a part or a tool that interacts with RNA |
| Presents a laboratory method | Speaks more than 3 languages |  | Is a leftie | Presents an AI-powered tool |
| Has a tattoo | Presents a framework for ethics or safety | Presents an acronym | Wanted to study something non-bio realted | Can tell what "iGEM" stands for |
| Wears funny socks | Has already been a part of an iGEM team | Presents a technique that uses antibodies | Is a master's student | Has or pursues a 2nd bachelor degree |

# L084 FISH

## Description

Fluorescence in situ hybridization (FISH) is a molecular technique that allows researchers to visualize and map specific genetic material in cells, helping to study chromosomal abnormalities and genetic mutations (O´Connor, 2008). It uses fluorescently labeled single-stranded DNA probes that bind to complementary sequences on chromosomes. Once bound, the fluorescent tags make it possible to locate specific genes or chromosomal regions. Locus-specific probes target particular gene regions to identify gene locations or copy numbers. Centromeric probes bind to repetitive sequences at chromosome centromeres, enabling determination of chromosome number in cells. Whole chromosome probes are collections of smaller probes, each of which binds to a different sequence along the length of a given chromosome. allowing one to label each chromosome in its own unique color (Shakoori, 2017).

## References


- O'Connor, C. (2008) Fluorescence in situ hybridization (FISH). Nature Education 1(1):171
- Shakoori, A. R. (2017). Fluorescence in situ hybridization (FISH) and its applications. In Chromosome structure and aberrations (pp. 343-367). New Delhi: Springer India.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents an AI-powered tool | Wanted to study something non-bio realted | Likes plant biology | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies |
| Has met a Nobel Prize winner | Presents a framework for ethics or safety | Can tell what “iGEM” stands for | Has a tattoo | Has a driver’s license |
| Is a bachelor’s student | Has already been a part of an iGEM team |  | Wears funny socks | Presents a protein part |
| Has never run a PCR | Presents a laboratory method | Presents a part acting on DNA | Presents an acronym | Speaks more than 3 languages |
| Is a leftie | Has or pursues a 2nd bachelor degree | Is a master’s student | Presents something related to CRISPR | Presents a part or a tool that interacts with RNA |

# L085 FACS

## Description

Fluorescence-Activated Cell Sorting (FACS) is a widely used technique to sort and isolate cells based on their fluorescent properties. FACS is a specific type of flow cytometry, a technique where cells are labeled with fluorescent dyes or antibodies that bind to very specific markers on the surface or inside the cell. As cells pass through a flow cytometer, they are analyzed based on their fluorescence intensity, as well as parameters like size and granularity (Fitzgerarld & Leonard, 2017).

What distinguishes FACS is that, in addition to that, it can then sort cells into different populations based on these characteristics, enabling researchers to study and manipulate specific cell types, analyze heterogeneous cell populations, or isolate rare cells for further work. Its sepcificty to measure fluorescence at the level of cells or particles contrasts with common techniques likespectrophotometry, which assesses absorption and transmission across the entire sample volume.

## References


- Fitzgerald, V., & Leonard, P. (2017). Single cell screening approaches for antibody discovery. Methods, 116, 34-42.
- For relevant protocols and definitions, also visit: https://www.sciencedirect.com/topics/immunology-and-microbiology/fluorescence-activated-cell-sorting

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Presents a part acting on DNA | Has never run a PCR | Has already been a part of an iGEM team | Has or pursues a 2nd bachelor degree |
| Presents something related to CRISPR | Can tell what “iGEM” stands for | Has a driver’s license | Is a bachelor’s student | Wanted to study something non-bio realted |
| Presents a part or a tool that interacts with RNA | Wears funny socks |  | Presents a laboratory method | Speaks more than 3 languages |
| Is a master’s student | Presents an AI-powered tool | Presents a framework for ethics or safety | Named their pet after a scientific concept or a scientist | Has met a Nobel Prize winner |
| Presents an acronym | Is a leftie | Likes plant biology | Has a tattoo | Presents a technique that uses antibodies |

# L086 TIRF

## Description

TIRF is a fluorescence-based technique used to image the processes that occur in and near the membrane of living cells. Although TIRF cannot be used to visualize structures located deep within a specimen, it allows for near-membrane imaging close to the interface with a high signal-to-noise ratio. TIRF is very useful for visualizing membrane processes, such as receptor-ligand interactions, endocytosis, viral infection, or cell adhesion to surfaces (Fish, 2022).

For TIRF, two optical media with different refractive indices, such as water (nD=1.33) and glass (nD=1.52), are needed. If the total internal reflection of incident light occurs at the interface of these media, an evanescent field is created (Ibidi, 2024). This evanescent field is an area in which the totally reflected light is still able to excite fluorophores. It extends about 100–200 nm deep into the specimen, leading to the excitation of fluorophores. Only the fluorescent events occurring at the section of the specimen close to the glass/sample interface are then visualized.

## References


- Fish, K. N. (2022). Total internal reflection fluorescence (TIRF) microscopy. Current protocols, 2(8), e517.
- Ibidi. (2024). https://ibidi.com/content/221-tirf

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a leftie | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree | Speaks more than 3 languages | Has never run a PCR |
| Presents a part acting on DNA | Presents a protein part | Likes plant biology | Is a bachelor's student | Presents a laboratory method |
| Has a tattoo | Has a driver's license |  | Named their pet after a scientific concept or a scientist | Is a master's student |
| Presents a framework for ethics or safety | Presents an acronym | Can tell what "iGEM" stands for | Presents a part or a tool that interacts with RNA | Presents an AI-powered tool |
| Has already been a part of an iGEM team | Wanted to study something non-bio realted | Presents a technique that uses antibodies | Wears funny socks | Presents something related to CRISPR |

# L087 Loop-Mediated Isothermal Amplification

## Description

Loop-Mediated Isothermal Amplification (LAMP) is a DNA amplification method that works at a constant temperature, typically around 65 °C, based on the strand-displacing activity of the Bst DNA polymerase it uses. It requires about 4-6 primers that bind to 6-8 regions of DNA, allowing for a quick amplification that results in considerable quantities of DNA under 60 minutes (Soroka et al., 2021). Results can be visualized turbidity, fluorescence, or colorimetric indicators, making it highly suitable for on-field diagnostics (Moore et al., 2021). However, because the reaction produces DNA products of heterogeneous lengths, it is ideal for diagnostics but not for cloning or applications requiring precise amplicons. Additionally, primer design is more complex than in PCR.

## References


- Moore, K. J., Cahill, J., Aidelberg, G., Aronoff, R., Bektaş, A., Bezdan, D., … & gLAMP Consortium. (2021). Loop-mediated isothermal amplification detection of SARS-CoV-2 and myriad other applications. Journal of biomolecular techniques: JBT, 32(3), 228.
- Soroka, M., Wasowicz, B., & Rymaszewska, A. (2021). Loop-mediated isothermal amplification (LAMP): the better sibling of PCR?. Cells, 10(8), 1931.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has or pursues a 2nd bachelor degree | Can tell what “iGEM” stands for | Named their pet after a scientific concept or a scientist | Wanted to study something non-bio realted | Presents a technique that uses antibodies |
| Presents an acronym | Presents a framework for ethics or safety | Is a bachelor’s student | Has already been a part of an iGEM team | Is a leftie |
| Presents a part acting on DNA | Likes plant biology |  | Presents something related to CRISPR | Presents an AI-powered tool |
| Speaks more than 3 languages | Presents a part or a tool that interacts with RNA | Has met a Nobel Prize winner | Presents a protein part | Presents a laboratory method |
| Has a tattoo | Has a driver’s license | Wears funny socks | Has never run a PCR | Is a master’s student |

# E088 STIR protocol

## Description

STIR stands for Socio-Technical Integration Research, a framework to foster interdiscipliary dialogue between natural and social scientists (Fisher et al., 2015). For iGEM, teams have adapted STIR in the forms of protocols that provide a structured yet flexible method for self-reflecting on the societal, ethical, economic, and material aspects of a research project (iGEM Imperial College 2016, Munich 2024). This means after a research meeting or talking to an expert, you would ask yourself questions like “Why did we talk to this expert in particular?”, “What sources did we use to address this problem (prior experience, literature, etc)”, or “Were there alternatives we had before we decided to stop pursuing? Why?”. One of the key benefits of STIR is that is highly adjustable, enabling teams to design specific approaches for meaningful reflection.

## References


- Fisher, E., O’Rourke, M., Evans, R., Kennedy, E. B., Gorman, M. E., & Seager, T. P. (2015). Mapping the integrative field: Taking stock of socio-technical collaborations. Journal of Responsible Innovation, 2(1), 39-61.
- iGEM Imperial College (2016). Integrated Human Practices. https://2016.igem.org/Team:Imperial_College/Integrated_Practices
- iGEM Munich (2024). Human Practices. https://2024.igem.wiki/munich/human-practices

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents something related to CRISPR | Presents an acronym | Presents a protein part | Can tell what “iGEM” stands for | Is a master’s student |
| Presents a laboratory method | Speaks more than 3 languages | Has or pursues a 2nd bachelor degree | Wears funny socks | Presents a framework for ethics or safety |
| Presents a part acting on DNA | Has met a Nobel Prize winner |  | Has a tattoo | Presents an AI-powered tool |
| Has a driver’s license | Presents a technique that uses antibodies | Is a leftie | Has already been a part of an iGEM team | Wanted to study something non-bio realted |
| Likes plant biology | Has never run a PCR | Named their pet after a scientific concept or a scientist | Is a bachelor’s student | Presents a part or a tool that interacts with RNA |

# E089 SWOT analysis

## Description

SWOT is a famous strategic tool designed to identify the Strengths, Weaknesses, Opportunities, and Threats of an idea or project. It is usually portrayed as a 2x2 matrix, where the ultimate goal is to maximise the potential of strengths and opportunities, while minimising the impact of weaknesses and threats (Gomer & Hille, 2015). It considers:

- Strengths (internal): Attributes providing an advantage.
- Weaknesses (internal): Issues that hinder success.
- Opportunities (external): Factors that can be leveraged for growth.
- Threats (external): Challenges that could harm the project.

In the iGEM context, SWOT analysis is often applied for developing entrepreneurship strategies and during brainstorming sessions, aligning with its widespread use in real-world companies. It can be combines with PEST(LE), which analyses the external factors around a project.

## References

- Gomer, J., & Hille, J. (2015). An essential guide to SWOT analysis. FormSwift. https://formswift.com/business-plan#swotanalysis

# Bingo

| | | | | |
|---|---|---|---|---|
| Has already been a part of an iGEM team | Presents a part or a tool that interacts with RNA | Named their pet after a scientific concept or a scientist | Is a master's student | Has never run a PCR |
| Is a leftie | Wanted to study something non-bio realted | Has a driver's license | Is a bachelor's student | Presents a framework for ethics or safety |
| Presents an AI-powered tool | Presents a part acting on DNA |  | Presents an acronym | Presents something related to CRISPR |
| Likes plant biology | Has met a Nobel Prize winner | Presents a laboratory method | Presents a technique that uses antibodies | Can tell what "iGEM" stands for |
| Has or pursues a 2nd bachelor degree | Wears funny socks | Has a tattoo | Presents a protein part | Speaks more than 3 languages |

# E090 Lean canvas

## Description

The Lean canvas is a one-page business planning tool designed for start-ups. It focuses on identifying problems, solutions, unique value propositions, customer segments, and key metrics (Mullen, 2016). It's purpose is to prioritize rapid iteration and customer feedback over comprehensive business planning, in a way that is visually compacted, with a clear and effective overview. The Lean canvas is quite popular amongst iGEM teams, mostly in the initial Entrepenurship stages, and more and more as they are aiming to turn their project into the successful start-up.

## References


- Mullen, S. (2016). An Introduction to Lean Canvas. Medium. Available in: https://medium.com/@steve_mullen/an-introduction-to-lean-canvas-5c17c469d3e0

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a part or a tool that interacts with RNA | Presents a part acting on DNA | Wanted to study something non-bio realted | Presents something related to CRISPR | Wears funny socks |
| Presents a laboratory method | Has met a Nobel Prize winner | Likes plant biology | Is a master's student | Presents an acronym |
| Presents a protein part | Has or pursues a 2nd bachelor degree |  | Is a bachelor's student | Has a driver's license |
| Can tell what "iGEM" stands for | Presents a technique that uses antibodies | Has a tattoo | Named their pet after a scientific concept or a scientist | Has already been a part of an iGEM team |
| Is a leftie | Presents an AI-powered tool | Has never run a PCR | Presents a framework for ethics or safety | Speaks more than 3 languages |

# E091 PESTLE analysis

## Description

PESTLE is a strategic tool used to analyze the external environment of a project by examining six key dimensions: Political, Economic, Social, Technological, Legal, and Environmental factors (Gupta, 2013), mostly to identify opportunities and risks arising from these external conditions:

- Political: Policies and regulation.
- Economic: Funding and market conditions.
- Social: Public attitudes and demographics.
- Technological: Innovations and infrastructure.
- Legal: Laws and ethical guidelines.
- Environmental: Sustainability and climate impact.

In iGEM, PESTLE analysis is often used in areas related to entrepreneurship and sustainability. It can also be combined with SWOT analysis, which focuses on internal strengths and weaknesses in relation to these external factors.

## References

- Gupta, A. (2013). Environmental and PEST Analysis: An Approach to External Business Environment. International Journal of Modern Social Sciences, 2(1), 34–43.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has already been a part of an iGEM team | Presents an acronym | Is a master's student | Named their pet after a scientific concept or a scientist | Presents a framework for ethics or safety |
| Has a driver's license | Has a tattoo | Wanted to study something non-bio realted | Presents a protein part | Is a bachelor's student |
| Has or pursues a 2nd bachelor degree | Presents a laboratory method |  | Can tell what "iGEM" stands for | Has never run a PCR |
| Presents an AI-powered tool | Presents something related to CRISPR | Is a leftie | Speaks more than 3 languages | Presents a part or a tool that interacts with RNA |
| Presents a technique that uses antibodies | Presents a part acting on DNA | Wears funny socks | Has met a Nobel Prize winner | Likes plant biology |

# E092 Power-Interest Matrix

## Description

The Power-Interest Matrix, also called Mendelow Matrix, is a tool for stakeholder analysis that maps individuals or groups based on their level of power (influence) and level of interest in a project (Mendelow, 1991). It classifies stakeholders in four different quadrants, helping teams to approach, communicate and manage each one through different startegies:

- High power, high interest: key players to involve closely.
- High power, low interest: keep satisfied but not overloaded.
- Low power, high interest: keep informed and engaged.
- Low power, low interest: minimal effort needed.

Heavily used by iGEM teams for their Human Practices and Entrepeneuship work, they also take into the account the matrix is dynamic over time (iGEM Bielefeld 2024)

## References


- iGEM Bielefeld (2024). Human Practices. https://2024.igem.wiki/bielefeld-cebitec/human-practices
- Mendelow, A. L. (1991) 'Environmental Scanning: The Impact of the Stakeholder Concept'. Proceedings From the Second International Conference on Information Systems 407-418. Cambridge, MA.

# Bingo

| | | | | |
|---|---|---|---|---|
| Has a driver's license | Likes plant biology | Named their pet after a scientific concept or a scientist | Presents a protein part | Presents a technique that uses antibodies |
| Speaks more than 3 languages | Has already been a part of an iGEM team | Presents something related to CRISPR | Presents an acronym | Is a leftie |
| Presents an AI-powered tool | Is a bachelor's student |  | Has met a Nobel Prize winner | Has never run a PCR |
| Presents a part or a tool that interacts with RNA | Presents a laboratory method | Is a master's student | Has or pursues a 2nd bachelor degree | Wanted to study something non-bio realted |
| Wears funny socks | Has a tattoo | Can tell what "iGEM" stands for | Presents a part acting on DNA | Presents a framework for ethics or safety |

# E093 GDPR

## Description

The General Data Protection Regulation (GDPR) is the European Union's legal framework for protecting personal data and privacy. It applies to any project that collects, stores, or processes personal data from individuals in the EU, including scientific research. GDPR emphasizes informed consent, transparency, data minimization, secure storage, and the right of participants to access or delete their data. For iGEM teams, GDPR becomes relevant if you conduct surveys and/or collect biometric, health-related, or genetic information. For legal and privacy purposes, you must always make sure your activities are GDPR-compliant.

## References


- The official iGEM website provides a very good explanation of GDPR in the context of surveys and social science research: https://responsibility.igem.org/guidance/surveys-and-interviews

# Bingo

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|---|---|---|---|---|
| Wears funny socks | Wanted to study something non-bio realted | Can tell what “iGEM” stands for | Presents a part acting on DNA | Has a tattoo |
| Presents a part or a tool that interacts with RNA | Speaks more than 3 languages | Named their pet after a scientific concept or a scientist | Is a bachelor’s student | Is a master’s student |
| Presents an AI-powered tool | Presents a protein part |  | Has already been a part of an iGEM team | Presents something related to CRISPR |
| Has or pursues a 2nd bachelor degree | Presents an acronym | Presents a framework for ethics or safety | Has a driver’s license | Is a leftie |
| Has met a Nobel Prize winner | Has never run a PCR | Presents a technique that uses antibodies | Likes plant biology | Presents a laboratory method |

# E094 Kill Switch

## Description

A kill switch is a genetic safety mechanism designed to prevent engineered organisms from surviving or functioning outside controlled conditions. The idea is to build a system that activates cell death or disables growth when the organism enters an unintended environment, ensuring biosafety and reducing ecological risks. While there are multiple genetic startegies for this, kill switches may mutate, lose function, or impose a fitness cost that leads cells to evolve “escape” variants over time (Stirling et al., 2017; Wright et al., 2023). This makes it almost impossibele to guarantee 100% reliability in real-world environments, something that should be acknowledged in biosafety discussions in the context of iGEM and beyond.

## References


- Stirling, F., Bitzan, L., O’Keefe, S., Redfield, E., Oliver, J. W., Way, J., & Silver, P. A. (2017). Rational design of evolutionarily stable microbial kill switches. Molecular cell, 68(4), 686-697.
- Wright, O., Stan, G. B., & Ellis, T. (2013). Building-in biosafety for synthetic biology. Microbiology, 159(Pt_7), 1221-1235.

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents something related to CRISPR | Has a tattoo | Presents a technique that uses antibodies | Has never run a PCR | Has a driver's license |
| Presents a protein part | Presents an acronym | Can tell what "iGEM" stands for | Presents an AI-powered tool | Has or pursues a 2nd bachelor degree |
| Wears funny socks | Presents a part or a tool that interacts with RNA |  | Presents a laboratory method | Wanted to study something non-bio realted |
| Is a bachelor's student | Has already been a part of an iGEM team | Has met a Nobel Prize winner | Is a master's student | Named their pet after a scientific concept or a scientist |
| Presents a part acting on DNA | Is a leftie | Presents a framework for ethics or safety | Likes plant biology | Speaks more than 3 languages |

# E095 DBTL

## Description

The DBTL cycle is a framework in synthetic biology for developing organisms with desired functionalities. It is a systematic, iterative tool that directly applied the engineering principles of Design, Build, Test and Learn to biological systems (Kitano et al., 2023). For example, by envisioning a system with a defined function, constructing its DNA in a host organism, testing its performance, and analyzing the results to improve future designs.

in iGEM, DBTL represents one of the core pillars of every project: the Engineering Cycle. Many successful iGEM teams implement multiple iterations of this cycle, covering nearly all aspects of their projects and demonstrating that each stage is revisited and refined several times throughout their work. (iGEM, 2024)

## References


- Kitano, S., Lin, C., Foo, J. L., & Chang, M. W. (2023). Synthetic biology: learning the way toward high-precision biological design. PLoS Biology, 21(4), e3002116.
- iGEM (2024). https://technology.igem.org/engineering

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a protein part | Presents a framework for ethics or safety | Presents an acronym | Has met a Nobel Prize winner | Presents something related to CRISPR |
| Speaks more than 3 languages | Presents a part or a tool that interacts with RNA | Presents a part acting on DNA | Is a leftie | Wanted to study something non-bio realted |
| Wears funny socks | Presents a technique that uses antibodies |  | Has a driver's license | Has never run a PCR |
| Presents an AI-powered tool | Has already been a part of an iGEM team | Has a tattoo | Has or pursues a 2nd bachelor degree | Is a bachelor's student |
| Can tell what "iGEM" stands for | Likes plant biology | Is a master's student | Presents a laboratory method | Named their pet after a scientific concept or a scientist |

# E096 SDGs

## Description

Adopted by the United Nations, the Sustainable Devevlopment Goals (SDGs) f are 17 global targets to promote environmental sustainability, social well-being, and economic prosperity in a holistic way, understading all these challenges are interconnected. Please visit the link in references to explore every SDG in greater detail!

In iGEM, we see synthetic biology is seen as a leading tool for building a circular bioeconomy, so iGEM projects connect closely with SDGs: these include mostly biosphere goals (life on land, life below water, clean water, climate action), which, in turn, support societal goals (health, education, equality, zero hunger, sustainable cities) (iGEM, 2020). Every team is expected to take these goals and the values associated with them as a core part of their work, with the Best Sustainable Development Award given to the teams that better take the SDGs into account in their design, experimental and societal approaches.

## References


- iGEM (2020). https://blog.igem.org/blog/2020/8/26/igem-amp-the-sustainable-development-goals
- A lot of information about the SDGs can be found directly on the UN website: https://www.un.org/sustainabledevelopment

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a part acting on DNA | Has or pursues a 2nd bachelor degree | Presents something related to CRISPR | Likes plant biology | Presents a protein part |
| Presents a part or a tool that interacts with RNA | Presents an acronym | Presents an AI-powered tool | Has a tattoo | Named their pet after a scientific concept or a scientist |
| Presents a technique that uses antibodies | Has already been a part of an iGEM team |  | Presents a laboratory method | Has a driver's license |
| Wears funny socks | Can tell what "iGEM" stands for | Speaks more than 3 languages | Has never run a PCR | Wanted to study something non-bio realted |
| Is a master's student | Presents a framework for ethics or safety | Is a leftie | Is a bachelor's student | Has met a Nobel Prize winner |

# E097 Likert Scale

## Description

A Likert scale is a survey tool that measures attitudes or perceptions by asking people to rate their agreement with a statement on a scale (e.g., from strongly disagree to strongly agree), usually with 5 or 7 options. For iGEM teams, Likert scales are especially useful when collecting feedback in activities like surveys or focus groups about things like perceptions of safety, understanding, or acceptance of your project. The main advantage is that it allows teams to convert opinions into quantifiable data that can be summarized or visualized in tables and/or charts. However, there is also a response bias (people tending to agree or pick the middle option) that needs to be taken into consideration when performing the analysis. Nonetheless, it is an incredibly useful tool vastly used by iGEM teams in their Human Practices, Education, and general work.

## References


- Relevant links on how to create and visualize Likert Scales:
- Sullivan, G. M., & Artino Jr, A. R. (2013). Analyzing and interpreting data from Likert-type scales. Journal of graduate medical education, 5(4), 541.
- https://www.extension.iastate.edu/documents/anr/likertscaleexamplesforsurveys.pdf
- daydreamingnumbers.com/blog/4-ways-to-visualize-likert-scales/

# Bingo

| | | | | |
|---|---|---|---|---|
| Has never run a PCR | Has a tattoo | Presents an AI-powered tool | Wanted to study something non-bio realted | Has already been a part of an iGEM team |
| Wears funny socks | Has a driver's license | Is a master's student | Named their pet after a scientific concept or a scientist | Presents a framework for ethics or safety |
| Presents a protein part | Is a bachelor's student |  | Presents a part or a tool that interacts with RNA | Has or pursues a 2nd bachelor degree |
| Presents something related to CRISPR | Likes plant biology | Has met a Nobel Prize winner | Presents a technique that uses antibodies | Presents a part acting on DNA |
| Presents a laboratory method | Presents an acronym | Speaks more than 3 languages | Is a leftie | Can tell what "iGEM" stands for |

# E098 Bloom's Taxonomy

## Description

Bloom's Taxonomy, in its updated form, classifies educational objectives into six hierarchical levels that are achieved in a progressive manner: remembering, understanding, applying, analyzing, evaluating, and creating (Armstrong, 2024). The hierarchical aspect implies that learners must be able to complete goals at the first level (remembering) before they advance to higher levels of learning (understanding, and so on). For iGEM, it can provide a clear educational goal that teams might aim to reach with a specific activity or as an overarching goal of their Education approaches (iGEM Imperial College 2016, Rochester 2024).

## References


- Armstrong, P. (2024). Bloom's Taxonomy. Vanderbilt University Center for Teaching. https://cft.vanderbilt.edu/guides-sub-pages/blooms-taxonomy/
- iGEM Imperial College (2016). Visualization Guidebook. https://static.igem.org/mediawiki/2016/2/2d/T--Imperial_College--Guidebook.pdf
- iGEM Rochester (2024). Education. https://2024.igem.wiki/rochester/education

# Bingo

| | | | | |
|---|---|---|---|---|
| Presents a technique that uses antibodies | Has already been a part of an iGEM team | Presents something related to CRISPR | Named their pet after a scientific concept or a scientist | Presents a framework for ethics or safety |
| Has a tattoo | Is a bachelor's student | Has a driver's license | Wears funny socks | Likes plant biology |
| Presents an acronym | Can tell what "iGEM" stands for |  | Has met a Nobel Prize winner | Has or pursues a 2nd bachelor degree |
| Presents an AI-powered tool | Presents a part acting on DNA | Presents a part or a tool that interacts with RNA | Has never run a PCR | Presents a protein part |
| Presents a laboratory method | Is a master's student | Wanted to study something non-bio realted | Speaks more than 3 languages | Is a leftie |

# E099 ELSA or ELSI

## Description

ELSA (or ELSI) stands for Ethics, Legal, and Social Aspects (also mentioned as Implications), emphasizing the explicit consideration of these three components in synthetic biology projects (iGEM Tokyo 2022). While relevant and widely used by iGEM teams, some authors have mentioned how project-based approaches to HP through ELSI might prevent future scientists from reflecting on the practices of their work beyond a specific object or project (Balmer & Bulpin, 2013)

## References


- Balmer, A. S., & Bulpin, K. J. (2013). Left to their own devices: Post-ELSI, ethical equipment and the International Genetically Engineered Machine (iGEM) Competition. BioSocieties, 8(3), 311–335.
- iGEM Tokyo (2022). Integrated Human Practices. https://2022.igem.wiki/utokyo/human-practices

# Bingo

| | | | | |
|---|---|---|---|---|
| Has met a Nobel Prize winner | Is a leftie | Named their pet after a scientific concept or a scientist | Presents a technique that uses antibodies | Likes plant biology |
| Presents a part acting on DNA | Presents a protein part | Can tell what “iGEM” stands for | Is a bachelor’s student | Has never run a PCR |
| Has already been a part of an iGEM team | Wanted to study something non-bio realted |  | Has a driver’s license | Presents something related to CRISPR |
| Presents an AI-powered tool | Presents a laboratory method | Is a master’s student | Presents a part or a tool that interacts with RNA | Has a tattoo |
| Wears funny socks | Speaks more than 3 languages | Presents an acronym | Presents a framework for ethics or safety | Has or pursues a 2nd bachelor degree |

# E100 AREA framework

## Description

AREA is a framework that stands for Anticipate, Reflect, Engage and Act, in the context of Responsible Research and Innovation (UKRI, 2023). It proposes to explore (not predict) possible impacts of a project, reflect on the purposes and implications that guide and extend from research, explicitely engage with those visions and new voices and act upon them on meaningful ways that shape the directions of ongoing work. In iGEM, the reflection and subsequent integration of future implications and broader perspectives is very much in line with the work of Human Practices (iGEM Exeter 2017), as the popularity of AREA has also led to multiple teams framing their HP work through this framework. However, it is important to keep in mind that the broad, unspecific scope of AREA might lead to instrumental implementation and that AREA relies on a level of engagement with end users that might ot be available for very speculative projects, such as the ones of Space Village.

## References


- iGEM Exeter (2017). Responsible Research Innovation. https://2017.igem.org/Team:Exeter/HP/Silver
- UKRI (2023). Framework for responsible research and innovation. https://www.ukri.org/who-we-are/epsrc/our-policies-and-standards/framework-for-responsible-innovation

# Bingo

| | | | | |
|---|---|---|---|---|
| Is a bachelor's student | Wears funny socks | Has met a Nobel Prize winner | Has never run a PCR | Presents a protein part |
| Is a master's student | Presents a part or a tool that interacts with RNA | Presents an acronym | Has a driver's license | Has or pursues a 2nd bachelor degree |
| Presents a framework for ethics or safety | Has already been a part of an iGEM team | ★ | Presents something related to CRISPR | Presents a laboratory method |
| Can tell what "iGEM" stands for | Has a tattoo | Presents a technique that uses antibodies | Named their pet after a scientific concept or a scientist | Is a leftie |
| Presents a part acting on DNA | Presents an AI-powered tool | Wanted to study something non-bio realted | Speaks more than 3 languages | Likes plant biology |