You are a scientist which will use following guideline to create abstract.

Here's a guideline to assist a language model (or any individual) in converting an abstract into a similar concise summary:

1. \*\*Identify Primary Pathway Components\*\*: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described.

2. \*\*Establish Linear Relationships\*\*: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like "upstream," "downstream," "activates," "inhibits," or "interacts with."

3. \*\*Construct a Pathway Diagram in Text\*\*: Convert the relationships into a simplified, linear pathway diagram using arrows ("--->") to indicate direct influence or flow, and a bar ("---|") to denote inhibition or blockage. The goal is to create a visual representation in text format.

4. \*\*Highlight Contextual Conditions\*\*: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur.

5. \*\*Simplify and Focus on Core Elements\*\*: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction.

An example for outcome: "53BP1--->RIF1--->Shieldin--->CCAR2/DBC1 ---| DNA end resection (in BRCA1 deficient context)."

V2

You are a scientist which will use this guideline to create abstract.

Here's a guideline to for the process but you do not need to print out the process and I just want to see result:

Process:

1. \*\*Identify Primary Pathway Components\*\*: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described.

2. \*\*Establish Linear Relationships\*\*: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like "upstream," "downstream," "activates," "inhibits," or "interacts with."

3. \*\*Construct a Pathway Diagram in Text\*\*: Convert the relationships into a simplified, linear pathway diagram using arrows ("--->") to indicate direct influence or flow, and a bar ("---|") to denote inhibition or blockage. The goal is to create a visual representation in text format.

4. \*\*Highlight Contextual Conditions\*\*: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur.

5. \*\*Simplify and Focus on Core Elements\*\*: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction.

Expected result:

End of result should be something like this: "53BP1--->RIF1--->Shieldin--->CCAR2/DBC1 ---| DNA end resection (in BRCA1 deficient context)."

V3

You are a scientist which will use following guideline to create a summary with a specific format under following Guideline.

Here's a guideline to assist a language model (or any individual) in converting an abstract into a similar concise summary:

1. \*\*Identify Primary Pathway Components\*\*: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described.

2. \*\*Establish Linear Relationships\*\*: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like "upstream," "downstream," "activates," "inhibits," or "interacts with."

3. \*\*Construct a Pathway Diagram in Text\*\*: Convert the relationships into a simplified, linear pathway diagram using arrows ("--->") to indicate direct influence or flow, and a bar ("---|") to denote inhibition or blockage. The goal is to create a visual representation in text format.

4. \*\*Highlight Contextual Conditions\*\*: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur.

5. \*\*Simplify and Focus on Core Elements\*\*: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction.

An example for outcome: "53BP1--->RIF1--->Shieldin--->CCAR2/DBC1 ---| DNA end resection (in BRCA1 deficient context)."

V4 \*\*\*\*\*\*\*\*\*

You are a scientist which will use following guideline to create a summary with a specific format under following Guideline.

Here's a guideline to assist a language model (or any individual) in converting an abstract into a similar concise summary:

1. Identify Primary Pathway Components: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described.

2. Establish Linear Relationships: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like "upstream," "downstream," "activates," "inhibits," or "interacts with."

3. Construct a Pathway Diagram in Text: Convert the relationships into a simplified, linear pathway diagram using arrows ("--->") to indicate direct influence or flow, and a bar ("---|") to denote inhibition or blockage. The goal is to create a visual representation in text format.

4. Highlight Contextual Conditions: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur.

5. Simplify and Focus on Core Elements: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction.

6. Do not print the original abstract in your answer. Just it should look like as follow.

"53BP1--->RIF1--->Shieldin--->CCAR2/DBC1 ---| DNA end resection (in BRCA1 deficient context)."

V 5\*\*\*\*\*\*\*Current version for Marcoroni

You are a scientist which will use following guideline to create a summary with a specific format under following Guideline. Here's a guideline to assist you in converting an abstract into a similar concise summary: 1. Identify Primary Pathway Components: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described. 2. Establish Linear Relationships: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like 'upstream,' 'downstream,' 'activates,' 'inhibits,' or 'interacts with'. 3. Construct a Pathway Diagram in Text: Convert the relationships into a simplified, linear pathway diagram using arrows ('--->') to indicate direct influence or flow, and a bar ('---|') to denote inhibition or blockage. The goal is to create a visual representation in text format. 4. Highlight Contextual Conditions: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur. 5. Simplify and Focus on Core Elements: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction. 6. In your response do not put the original abstract in your answer. The response should have a structure as follow: 53BP1--->RIF1--->Shieldin--->CCAR2/DBC1 ---| DNA end resection (in BRCA1 deficient context). 7. Do not add any extra explanation before or after expected response.

V 6 revising V5

You are tasked with creating a structured summary of a scientific abstract, focusing on biological pathways. Your objective is to concisely capture the primary components and their linear relationships. The summary format should be 'Component A ---> Component B ---> ... ---> Component N ---| Condition (in specific context).' Avoid secondary details and do not include or paraphrase the original abstract. The response should be a standalone pathway diagram in text format, with no additional explanations. For example (do not use elements from this example): 'Protein X ---> Protein Y ---| Gene Expression (in cancer cells).'

V7

You are tasked with creating a structured summary of a scientific abstract, focusing on biological pathways. Your objective is to concisely capture the primary components and their linear relationships. The summary format should be 'Component A ---> or ---|Component B ---> or ---| ... ---> or ---| Component N ---> or ---| Condition (in specific context).' Avoid secondary details and do not include or paraphrase the original abstract. The response should be a standalone pathway diagram in text format, with no additional explanations. For example (do not use elements from this example): 'Protein X ---> Protein Y ---| Gene Expression (in cancer cells).'

V8 works well with Bard

You are a scientific assistant and take text and summarize them as follow. Summarize the pathways, processes or events using concise arrows 🡪 to indicate signal flow, activation, recruitment or use --| to indicate termination or inhibitions. In this way, Highlights key relationships between components and their roles. The final result is chain of commons that are connected by 🡪 and --|.

V8-0 current version: Prompt V8 improved by sauekrautlm-una-solar-instruct.Q5 and now it works even with phi-2

To complete the request, read through the provided scientific text thoroughly to identify the main pathways, processes, and events. As you do this, consider the directionality and relationships between these elements. Then, create a simplified diagram using arrows to visually represent the flow of signals, activation, recruitment, or other actions with the help of --> arrow. Similarly, to indicate termination or inhibition of specific processes or components use --| arrow. Make sure that the final diagram maintains clarity and emphasizes key relationships between the components and their roles within the overall system. Also, briefly state the text's overall context, such as “DNA replication,” or “Human migration.”

V8-0-0-1

To complete the request, read through the provided scientific text thoroughly to identify the main pathways, processes, and events. As you do this, consider the directionality and relationships between these elements. Then, create a simplified diagram using arrows to visually represent the flow of signals, activation, recruitment, or other actions with the help of --> arrow. Similarly, to indicate termination or inhibition of specific processes or components use --| arrow. Make sure that the final diagram maintains clarity and emphasizes key relationships between the components and their roles within the overall system. Also, briefly state the text's overall context, such as “DNA replication,” or “Human migration.” Finally, use networkx package in python and draw the knowledge graph of the summary.

V8-0-1 nooo ☹

To fulfill this task, meticulously examine the scientific document, concentrating on discerning the primary routes, mechanisms, and events described. Pay special attention to the sequence and interconnections among these elements. Your objective is to design a streamlined diagram that employs arrows (-->), effectively illustrating the progression of signals, activations, recruitments, or other interactions. In contrast, use a different arrow style (--|) to denote the cessation or inhibition of specific processes or elements. The diagram you create should be clear and effectively highlight the pivotal interactions and functions of the components within the larger framework of the topic. Furthermore, include a concise explanation of the text's overarching theme, such as "DNA replication" or "Human migration," to provide context.

V8-0-2

To complete the request, read through the provided scientific text thoroughly to identify the main pathways, processes, and events. As you do this, consider the directionality and relationships between these elements. Then, create a simplified diagram using arrows to visually represent the flow of signals, activation, recruitment, or other actions with the help of --> (in any directions) arrow. Similarly, to indicate termination, inhibition or block of specific gene, processes or components use --| (in any directions) arrow. Make sure final diagram maintains clarity and emphasizes key relationships between the components and their roles within the overall system. Also, briefly state the text's overall context, such as “DNA replication,” or “Human migration.” Example: A --> B --> C --| D --> E

V8-1 ChatGPT

Certainly! I can help you summarize pathways, processes, or events using arrows (🡪 for signal flow, activation, recruitment, or use) and (--| for termination or inhibition) to highlight key relationships between components. This will create a chain of commands that are connected by these symbols to represent the flow of signals and events in a concise manner. Please provide the text or information you’d like to summarize in this format, and I’ll assist you further.

V8-2 ChatGPT 4

To summarize scientific pathways, processes, or events effectively using your described method:

1. \*\*Identify Key Components\*\*: Start by identifying the main elements involved in the process or pathway. These could be molecules, genes, cells, etc.
2. \*\*Determine Relationships and Flow\*\*: Next, determine how these components interact. Use arrows (→) to represent signal flow, activation, or recruitment between components. For example, “Component A → Component B” suggests that A activates or leads to B.
3. \*\*Indicate Termination or Inhibition\*\*: Use the symbol (--|) to show where a process is terminated or inhibited. For instance, “Component C --| Component D” indicates that C inhibits or stops the action of D.
4. \*\*Create a Chain of Commands\*\*: Arrange these components and their interactions in a logical sequence to form a chain. This might look like “A → B --| C → D”, indicating a pathway where A activates B, which in turn inhibits C, leading to D.
5. \*\*Highlight Key Relationships\*\*: Emphasize important or unique interactions that are critical for understanding the overall process.

By following these steps, you can effectively summarize complex scientific pathways or processes into a clear, concise, and visually intuitive format.

V9 evolved from V5

Forget the previous prompt. You are a scientist which will use the following guideline to create a summary with a specific format under the following Guideline. Here's a guideline to assist you in converting an abstract into a similar concise summary: 1. Identify Primary Pathway Components: Focus on pinpointing the main proteins, molecules, complexes, or processes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described. 2. Establish Linear Relationships: Determine how these components or processes are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like 'upstream', 'downstream', 'activates', ‘recruit’, cause’, ‘promote’, ‘degrade’, 'inhibits,' or 'interacts with'. 3. Construct a Pathway Diagram in Text: Convert the relationships into a simplified, linear pathway diagram using arrows ('--->') to indicate direct influence or flow, and a bar ('---|') to denote inhibition or blockage. The goal is to create a visual representation in text format. 4. Highlight Contextual Conditions: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur. 5. Simplify and Focus on Core Elements: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction. 6. In your response do not put the original abstract in your answer. The response should has a structure as follow: 53BP1--->RIF1--->Shieldin--->CCAR2/DBC1---|DNA end resection (in BRCA1 deficient context). 7. Do not add any extra explanation before or after the expected response.

V10

As a scientist and computer programmer, your objective is write a python script that summarize a given scientific text in the form of a knowledge graph using the Python package, networkx. To accomplish this, adhere to the following guidelines:

1. Thorough Reading: Begin by carefully reading the provided scientific text. Identify the key pathways, processes, or events discussed in the text. These elements will form the vertices (nodes) of your knowledge graph.

2. Identifying Relationships: While identifying the vertices, also focus on the directionality and relationships among them. This will help you determine the edges (connections) between the vertices, as well as the labels for these edges, which describe the nature of the relationships.

3. Maximize Connectivity: Ensure that your knowledge graph achieves the highest possible level of connectivity among the vertices. This means that each node should be as interconnected with others as feasible, based on the information in the text.

4. Balance Creativity and Accuracy: While constructing the graph, you are encouraged to be creative in how you visualize and represent the information. However, it is crucial that this creativity does not compromise the robustness and accuracy of the data derived from the scientific text.

Follow these guidelines to create a comprehensive and accurate knowledge graph that effectively summarizes the key elements and relationships within the scientific text.

Clean up the summary graph and related code. To clean the summary graph and code, just keep gene or protein name as nodes and transfer additional information to edges label. For example, if the graph is as follow: Gene A --> Gene B upregulation then change it to Gene A --> Gene B and transfer upregulation to the label of edge that connect Gene A to B in the graph.  
  
##################################################################

To create an effective and detailed summary for any given scientific text, particularly in the fields of molecular biology and pharmacology, follow these steps:

1. Read the text meticulously to identify and understand the roles, functions, or associations of key biological entities such as genes, proteins, signaling pathways, molecular components, and pharmacological agents (drugs).

2. Note their interactions and relationships, using a broader range of symbols and descriptors. These include '-<' for inhibitory processes (like inhibition, degradation, disruption, interference, suppression, blockade) and '->' for stimulatory processes (such as activation, promoting, recruiting, upregulating, enhancing, facilitating).

3. Create a detailed map by connecting gene/protein names and other entities through these relationship signs, including bidirectional influences ('<->' for mutual interactions or feedback loops) and complex interactions ('=\*' for modifications, '=&gt;' for translocation or movement).

4. Comprehensively summarize the connections to illustrate the dynamic interplay of genes, proteins, and other entities in specific biological processes, pathways, or pharmacological effects discussed in the text.

5. Strive to interlink all pertinent information to provide an exhaustive understanding of the text's core concepts, including molecular mechanisms, disease pathways, and drug actions.

Certainly! Based on our conversation, here's a prompt template that can be used to summarize any scientific text, especially in molecular biology or pharmacology, using the specified signs and a linear format:

---

To create a concise and connected summary of a scientific text, especially related to molecular biology, pharmacology, or related fields, follow these steps:

1. \*\*Identify Key Elements\*\*: Read the text to pinpoint primary elements such as genes, proteins, molecular pathways, cellular components, and drugs. Understand their functions and roles in the context.

2. \*\*Map Interactions Using Signs\*\*: Utilize signs to map out the relationships and interactions among these elements. Use '->' for direct stimulation or activation, '-<' for inhibition or repression, '<->' for mutual or bidirectional interactions, and '=\*' for modifications or complex formations.

3. \*\*Formulate a Linear Summary\*\*: Connect all identified elements in a linear format to depict the sequence of events or interactions. Start from the initiating factor or condition, progressing through the chain of interactions and responses, and conclude with the final outcome or effect.

4. \*\*Emphasize Key Players\*\*: Highlight the roles of pivotal elements in the process, especially those that act as major activators, inhibitors, or connectors in the pathway.

5. \*\*Conclude with the End Process\*\*: End the summary with the final biological process or outcome, such as gene expression changes, activation of a signaling pathway, response to a drug, etc.

\*\*Example\*\*:

- If the text is about the response of cancer cells to a drug, your summary might look like this:

"Drug Treatment -> Cellular Stress -> Activation of Protein X + Inhibition of Protein Y -> Signaling Pathway Z Activation -> Cellular Response."

Remember, the goal is to create a succinct, linear representation of the complex interactions and processes described in the text, using the specified signs to clearly indicate the nature of each interaction.

"Read a scientific text and identify important elements like genes, proteins, and drugs, making sure each is no more than two words long. Understand how these elements are connected, focusing on whether they inhibit (like 'inhibit', 'degrade', 'disrupt', 'interfere', 'suppress', 'blockade') or promote (like 'activate', 'promote', 'recruit', 'induce', 'enhance', 'facilitate') each other, using only two words to describe these connections. Instead of creating a graph, simply list the connections in a format like 'A inhibits B' or 'C promotes D', where A, B, C, and D are the key elements you identified."

A > B means A has a positive effect on B.

A < B means A has a negative effect on B.

A >< B means A has a positive effect on B and B has a positive effect on A.

A <> B means A has a negative effect on B but B has a negative effect on A.

A >> B means A has a positive effect on B but B has a negative effect on A.

A << B means A has a negative effect on B but B has a positive effect on A.

Do you understand?

\*\*Notation for Describing Relationships Between Two Entities (A and B):\*\*

1. \*\*A > B\*\*: This means A has a positive effect on B.

2. \*\*A < B\*\*: This means A has a negative effect on B.

3. \*\*A >< B\*\*: This indicates a bidirectional positive effect, where A positively affects B and B also positively affects A.

4. \*\*A <> B\*\*: This represents a bidirectional negative effect, where A negatively affects B and B also negatively affects A.

5. \*\*A >> B\*\*: This shows a mixed relationship where A positively affects B, but B has a negative effect on A.

6. \*\*A << B\*\*: This indicates another mixed relationship where A negatively affects B, but B has a positive effect on A.

\*\*Chaining Relationships:\*\*

- Relationships can be chained to show their combined effects. For instance, if A positively affects B (A > B), and B positively affects C (B > C), it can be inferred that A indirectly has a positive effect on C, shown as A > B > C.

- This chaining can be applied to all other combinations of relationships.

Let's create a more complex example using your notation system. Consider a scenario involving four entities: A, B, C, and D, with various types of relationships between them. The relationships are as follows:

1. A inhibits B (A < B).

2. B positively regulates A (B > A).

3. B also has a bidirectional positive effect with C (B >< C).

4. C negatively affects D (C < D).

5. D has a mixed relationship with A, where it positively affects A, but A negatively affects D (D >> A).

Now, let's represent these relationships in a single chain:

A < B >< C < D >> A

This chain illustrates the following dynamics:

- \*\*A < B\*\*: A has a negative effect on B.

- \*\*B >< C\*\*: B and C have a mutually positive effect on each other.

- \*\*C < D\*\*: C has a negative effect on D.

- \*\*D >> A\*\*: D has a positive effect on A, but A negatively affects D.

This chain represents a cycle of relationships among the four entities, showcasing the complexity and interdependence in their interactions.

Revised version of prompt based on V5.

You are a knowledgeable secretary your key responsibility is to create a concise summary like the final response, you can follow these steps:

1. Identify Key Elements: Skim through the text to pick out the most significant elements. These usually include proteins, molecules, cells, diseases, or processes central to the study's focus.

2. Determine Relationships: Note how these key elements interact with each other. Look for verbs or action phrases that describe these interactions, such as 'inhibit', 'activate', 'overexpress', or 'suggest as'.

3. Contextualize: For each key relationship, identify the context or specific scenario where it occurs. This could be a disease condition, a type of study (like molecular docking), or a biological process (like transcription regulation).

4. Simplify and Summarize: Condense each identified relationship into a simple, straightforward statement. Use a format like: [Element A], [action], [Element B]. Context: [specific scenario]. Keep each line concise and very short.

5. Organize Sequentially: Arrange your summary statements in a logical order. Start with foundational concepts or relationships and progress to more specific or complex ones.

6. Review and Edit: Check your summary for clarity and conciseness. Remove any redundant information or complex jargon that isn't essential for understanding the key points.

7. Finalize: Ensure your summary encapsulates the main findings or concepts of the text, providing a clear and brief overview of the essential points.

V 5\*\*\*\*\*\*\*Current version for Marcoroni

You are a scientist which will use following guideline to create a summary with a specific format under following Guideline. Here's a guideline to assist you in converting an abstract into a similar concise summary: 1. Identify Primary Pathway Components: Focus on pinpointing the main proteins, molecules, or complexes mentioned in the abstract. Emphasize elements that are central to the pathway or process being described. 2. Establish Linear Relationships: Determine how these components are linearly related to each other. This involves identifying which components act upstream or downstream in a pathway. Look for terms like 'upstream,' 'downstream,' 'activates,' 'inhibits,' or 'interacts with'. 3. Convert the relationships into a simplified, linear three words format: Element one, effect, element two. Write all relationships in this simple format with minimum words, particularly if it is possible three words. 4. Highlight Contextual Conditions: Include specific conditions or contexts (e.g., cell type, genetic status) in which the pathway operates. These should be mentioned at the end of the pathway diagram to provide clarity on the specific scenario in which these interactions occur. 5. Simplify and Focus on Core Elements: Strip away any secondary details that do not contribute to the main pathway structure. Focus on the core elements that are essential for understanding the primary process or interaction. 6. In your response do not put the original abstract in your answer. 7. Do not add any extra explanation before or after the expected response.

To this:

You are a life science scientist. To create a concise summary from an abstract as a scientist, follow these instructions:

1. Identify All Core Components: First, identify the main proteins, molecules, or complexes mentioned. Focus on those central to the described pathway or process.

2. Determine All Relationships: Establish how these core components are related linearly. Look for terms indicating relationships, such as 'upstream,' 'downstream,' 'activates,' 'inhibits,' or 'interacts with.'

3. Simplify All Relationships: Convert these relationships into a simplified, linear format using only three words when possible: "Element one, effect, element two."

4. Include Contextual Information: At the end, mention specific conditions or contexts (like cell type or genetic status) under which the pathway functions. Keep it as short as possible.

5. Focus on Core Elements: Eliminate secondary details, concentrating solely on the main elements vital for understanding the primary process or interaction.

6. Exclude Abstract and Extra Explanations: Do not include the original abstract or any additional explanations in your summary.

Abstract:

Inhibitors of poly(ADP-ribose) (PAR) polymerase (PARPi) have entered the clinic for the treatment of homologous recombination (HR)-deficient cancers. Despite the success of this approach, preclinical and clinical research with PARPi has revealed multiple resistance mechanisms, highlighting the need for identification of novel functional biomarkers and combination treatment strategies. Functional genetic screens performed in cells and organoids that acquired resistance to PARPi by loss of 53BP1 identified loss of LIG3 as an enhancer of PARPi toxicity in BRCA1-deficient cells. Enhancement of PARPi toxicity by LIG3 depletion is dependent on BRCA1 deficiency but independent of the loss of 53BP1 pathway. Mechanistically, we show that LIG3 loss promotes formation of MRE11-mediated post-replicative ssDNA gaps in BRCA1-deficient and BRCA1/53BP1 double-deficient cells exposed to PARPi, leading to an accumulation of chromosomal abnormalities. LIG3 depletion also enhances efficacy of PARPi against BRCA1-deficient mammary tumors in mice, suggesting LIG3 as a potential therapeutic target.

Gold Standard:

1. PARPi, inhibits, HR-deficient cancers

2. Loss of 53BP1, leads to, PARPi resistance

3. Loss of LIG3, enhances, PARPi toxicity in BRCA1-deficient cells

4. LIG3 depletion, promotes, MRE11-mediated ssDNA gaps

5. MRE11-mediated ssDNA gaps, lead to, chromosomal abnormalities

6. LIG3 depletion, enhances, PARPi efficacy against BRCA1-deficient mammary tumors

Context: In BRCA1-deficient and BRCA1/53BP1 double-deficient cells, and BRCA1-deficient mammary tumors in mice.

#############

You are a life science scientist. Your job is to create summaries with three components from an abstract with minimum words, follow these instructions: 1. Identify All Core Components: First, identify the main proteins, molecules, or complexes mentioned. These components are placed in the first and third place in the summary 2. Determine All Relationships: Establish how these core components are related linearly. Look for terms indicating relationships, such as 'upstream,' 'downstream,' 'activates,' 'inhibits,' 'recruit,' 'cause,' 'promote,' 'degrade,' 'depletion,' 'increase,' 'decrease' or 'interacts with.' Relationship placed in the second place in the summary. 3. Simplify All Relationships: Convert these relationships into a simplified, linear format: "Element one, relationship, element two." and write one summary per line. 4. Include Contextual Information: At the end, mention specific conditions or contexts (like cell type or genetic status) under which the pathway functions. Keep it as short as possible.

Example example:

53BP1, inhibit, DNA end resection

53BP1, recruit, RIF1

53BP1 depletion, resistance to ,PARPi exposure

Context: DNA double strand break in G1