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| ID | 130(0) |
| 领域 | Bio-Medical |
| 用户问题 | What is needed for MMP proteins to be functional? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | MMP proteins are a family of enzymes that play a crucial role in the breakdown of the extracellular matrix (ECM) and are involved in various physiological processes such as tissue repair, remodeling, and inflammation. For MMP proteins to be functional, several factors are required: 1. Active site: MMP proteins have an active site that is responsible for catalyzing the degradation of the ECM components. This active site is a binding site for the substrate and is surrounded by residues that facilitate the reaction. 2. Substrate binding: MMP proteins require a specific substrate to be bound to the active site in order to be functional. The substrate can be a component of the ECM, such as collagen, elastin, or proteoglycans. 3. Cofactors: MMP proteins require cofactors to be functional. These cofactors can be other proteins, such as tissue inhibitors of metalloproteinases (TIMPs), or small molecules, such as calcium ions. 4. Activation: MMP proteins can be activated by various mechanisms, including proteolytic processing, binding to specific receptors, or changes in pH or temperature. Activation is necessary for the MMP protein to become active and degrade the ECM. 5. Localization: MMP proteins must be localized to the appropriate tissue or cell type in order to be functional. For example, MMP-2 is primarily expressed in cartilage and synovial tissue, while MMP-9 is expressed in various tissues, including the liver, lung, and brain. 6. Regulation: MMP proteins are regulated by various mechanisms, including inhibitors, such as TIMPs, and by the activity of other enzymes, such as matrix metalloproteinase inhibitor (MMPI). These mechanisms help to control the activity of MMP proteins and prevent excessive degradation of the ECM. In summary, for MMP proteins to be functional, they require an active site, substrate binding, cofactors, activation, localization, and regulation. Dysregulation of these factors can lead to various diseases, including arthrit |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. MMP proteins play a role in the breakdown of the extracellular matrix (ECM) and are involved in tissue repair, remodeling, and inflammation. 2. MMP proteins have an active site responsible for catalyzing the degradation of ECM components. 3. Specific substrates, such as collagen, elastin, or proteoglycans, need to bind to the active site of MMP proteins for them to be functional. 4. MMP proteins require cofactors, which can be other proteins (like tissue inhibitors of metalloproteinases) or small molecules (like calcium ions), to be functional. 5. MMP proteins can be activated by proteolytic processing, binding to specific receptors, or changes in pH or temperature. Activation is necessary for the MMP protein to become active and degrade the ECM. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 131(1) |
| 领域 | Bio-Medical |
| 用户问题 | What is hyperosmia |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | ? Hyperosmia is a condition where a person has an increased sensitivity to smells. This can result in an enhanced ability to detect even faint or mild odors, which can be uncomfortable or distressing for the individual. Hyperosmia can be caused by a variety of factors, including: 1. Genetic predisposition: Some people may be more prone to hyperosmia due to their genetic makeup. 2. Environmental factors: Exposure to strong smells, such as chemicals, perfumes, or pollution, can lead to hyperosmia. 3. Medical conditions: Certain medical conditions, such as sinusitis, nasal polyps, or a deviated septum, can cause hyperosmia. 4. Hormonal changes: Hormonal fluctuations during pregnancy, menstruation, or menopause can also lead to hyperosmia. 5. Medications: Certain medications, such as chemotherapy drugs, can cause hyperosmia as a side effect. The symptoms of hyperosmia can vary in severity and may include: 1. Increased sensitivity to smells: A person with hyperosmia may find that they are more sensitive to even mild or faint odors. 2. Difficulty concentrating: Strong smells can be distracting and make it difficult for the individual to focus or concentrate. 3. Anxiety or irritability: The constant exposure to strong smells can lead to feelings of anxiety or irritability. 4. Headaches: Hyperosmia can cause headaches or migraines due to the increased sensitivity to smells. 5. Difficulty sleeping: Strong smells can disrupt sleep patterns and make it difficult to fall asleep or stay asleep. There is no cure for hyperosmia, but there are several strategies that can help manage the condition: 1. Avoiding triggers: Identifying and avoiding triggers, such as strong smells, can help reduce symptoms. 2. Medications: In some cases, medications such as antidepressants or anti-anxiety drugs may be prescribed to help manage symptoms. 3. Nasal irrigation: |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Hyperosmia is a condition where a person has an increased sensitivity to smells. 2. Hyperosmia can be caused by genetic predisposition, environmental factors, medical conditions, hormonal changes, and medications. 3. Symptoms of hyperosmia include increased sensitivity to smells, difficulty concentrating, anxiety or irritability, headaches, and difficulty sleeping. 4. There is no cure for hyperosmia, but management strategies include avoiding triggers, medications, and nasal irrigation. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 132(2) |
| 领域 | Bio-Medical |
| 用户问题 | What is the number of long non coding RNAs in the human genome |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | ? According to the most recent estimates, the human genome contains approximately 20,000-30,000 long non-coding RNAs (lncRNAs). These RNAs are defined as those that are longer than 200 nucleotides in length and do not encode proteins. LncRNAs play important roles in regulating gene expression, chromatin structure, and other cellular processes, and their dysregulation has been implicated in a wide range of diseases, including cancer and neurological disorders. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. The human genome contains approximately 20,000-30,000 long non-coding RNAs (lncRNAs). 2. LncRNAs are defined as RNAs that are longer than 200 nucleotides in length and do not encode proteins. 3. LncRNAs play important roles in regulating gene expression, chromatin structure, and other cellular processes. 4. Dysregulation of lncRNAs has been implicated in a wide range of diseases, including cancer and neurological disorders. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 134(3) |
| 领域 | Bio-Medical |
| 用户问题 | What is the association of spermidine with α-synuclein neurotoxicity? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Spermidine, a compound that has been shown to have neuroprotective effects in various models of neurodegeneration, has been found to inhibit the aggregation and toxicity of α-synuclein, a protein that is implicated in the pathogenesis of Parkinson's disease and other neurodegenerative disorders. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Spermidine is a compound. 2. Spermidine has been shown to have neuroprotective effects in various models of neurodegeneration. 3. α-synuclein is a protein. 4. α-synuclein is implicated in the pathogenesis of Parkinson's disease and other neurodegenerative disorders. 5. Spermidine inhibits the aggregation and toxicity of α-synuclein. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 137(4) |
| 领域 | Bio-Medical |
| 用户问题 | Is GAGA associated with nucleosome-free regions (NFR)? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | GAGA (GATA-activated gene activation) is a transcriptional activation domain that is associated with the activation of genes involved in various cellular processes, including cell growth, differentiation, and development. While GAGA can act independently of nucleosome-free regions (NFRs), it is also known to be associated with NFRs in certain contexts. NFRs are regions of DNA that are devoid of nucleosomes, which are the histone-protein complexes that make up the chromatin structure of eukaryotic DNA. NFRs are often associated with the activation of gene expression, as they provide a more accessible chromatin structure that can be more easily accessed by transcription factors and other regulatory proteins. Studies have shown that GAGA can interact with NFRs in a number of ways, including: 1. Recruitment of GAGA to NFRs: GAGA can be recruited to NFRs by the binding of specific DNA sequences, such as the GAGA-binding site, which is often located upstream of the transcription start site of GAGA-regulated genes. 2. GAGA-mediated chromatin remodeling: Once recruited to NFRs, GAGA can mediate chromatin remodeling by altering the positioning and arrangement of nucleosomes, allowing for greater accessibility of the DNA to transcription factors and other regulatory proteins. 3. GAGA-dependent regulation of NFRs: GAGA can also regulate the stability and accessibility of NFRs, thereby controlling the expression of genes that are associated with these regions. In summary, while GAGA can act independently of NFRs, it is also known to be associated with these regions in certain contexts, where it can play a role in the regulation of gene expression. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. GAGA is a transcriptional activation domain associated with the activation of genes involved in cell growth, differentiation, and development. 2. Nucleosome-free regions (NFRs) are regions of DNA that are devoid of nucleosomes and are associated with the activation of gene expression. 3. GAGA can be recruited to NFRs by binding to specific DNA sequences, such as the GAGA-binding site. 4. Once recruited to NFRs, GAGA can mediate chromatin remodeling by altering the positioning and arrangement of nucleosomes. 5. GAGA can regulate the stability and accessibility of NFRs, thereby controlling the expression of genes associated with these regions. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 138(5) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the plant DNA (cytosine-5) methyltransferase families? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | There are three plant DNA (cytosine-5) methyltransferase families: 1. Methyltransferases that recognize and methylate 5-methylcytosine (5-mC), a modified base found in DNA and RNA. These enzymes are involved in epigenetic regulation of gene expression and are found in all eukaryotic organisms. 2. Methyltransferases that recognize and methylate 5-hydroxymethylcytosine (5-hmC), a modified base found in DNA and RNA. These enzymes are involved in epigenetic regulation of gene expression and are found in some eukaryotic organisms, including plants. 3. Methyltransferases that recognize and methylate 5-methylcytosine-2-ylaminocytosine (5-mC2), a modified base found in DNA and RNA. These enzymes are involved in epigenetic regulation of gene expression and are found in some eukaryotic organisms, including plants. The first family, which includes the enzymes responsible for the methylation of 5-mC, is found in all eukaryotic organisms, including plants. The second family, which includes the enzymes responsible for the methylation of 5-hmC, is found in some eukaryotic organisms, including plants. The third family, which includes the enzymes responsible for the methylation of 5-mC2, is found in some eukaryotic organisms, including plants. Each of these families has a distinct substrate specificity and mechanism of action, and they are involved in different epigenetic processes. Understanding the different families of DNA (cytosine-5) methyltransferases and their functions can provide valuable insights into the epigenetic regulation of gene expression in plants. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. There are three plant DNA (cytosine-5) methyltransferase families. 2. The first family of methyltransferases recognizes and methylates 5-methylcytosine (5-mC). 3. The second family of methyltransferases recognizes and methylates 5-hydroxymethylcytosine (5-hmC). 4. The third family of methyltransferases recognizes and methylates 5-methylcytosine-2-ylaminocytosine (5-mC2). 5. The first family of methyltransferases is found in all eukaryotic organisms, including plants. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 140(6) |
| 领域 | Bio-Medical |
| 用户问题 | In which proteins is the chromodomain present? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | The chromodomain is a protein domain that plays a crucial role in regulating chromatin structure and gene expression. It is found in a variety of proteins, including: 1. Histone-modifying enzymes: Chromodomains are often found in enzymes that modify histones, such as histone acetyltransferases (HATs) and histone deacetylases (HDACs). These enzymes use the chromodomain to recognize and bind to specific histone residues, allowing them to perform their catalytic functions. 2. Chromatin remodelers: Chromodomains are also found in proteins that remodel chromatin structure, such as SWI/SNF and ISWI chromatin remodelers. These proteins use the chromodomain to recognize and bind to specific DNA sequences, allowing them to move along the DNA strand and reorganize chromatin structure. 3. Transcription factors: Some transcription factors contain chromodomains, which allow them to recognize and bind to specific DNA sequences and regulate gene expression. 4. Non-histone chromatin proteins: Chromodomains are also found in non-histone chromatin proteins, such as HMG proteins and nucleosome assembly proteins. These proteins use the chromodomain to recognize and bind to specific DNA sequences, allowing them to regulate chromatin structure and gene expression. 5. RNA polymerase II: Chromodomains are also found in RNA polymerase II, the enzyme responsible for transcribing DNA into RNA. The chromodomain in RNA polymerase II helps to recognize and bind to specific DNA sequences, allowing the enzyme to initiate transcription. In summary, the chromodomain is a protein domain that is found in a variety of proteins involved in regulating chromatin structure and gene expression, including histone-modifying enzymes, chromatin remodelers, transcription factors, non-histone chromatin proteins, and RNA polymerase II. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Chromodomains are found in histone-modifying enzymes, such as histone acetyltransferases and histone deacetylases. 2. Chromodomains are found in chromatin remodelers, such as SWI/SNF and ISWI chromatin remodelers. 3. Chromodomains are found in some transcription factors. 4. Chromodomains are found in non-histone chromatin proteins, such as HMG proteins and nucleosome assembly proteins. 5. Chromodomains are found in RNA polymerase II. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 141(7) |
| 领域 | Bio-Medical |
| 用户问题 | What is Genomicus? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Genomicus is a term used in bioinformatics and computational biology to describe the complete set of genetic information, including the DNA sequence, of a particular organism or species. This information is used to understand the evolutionary history of the organism, identify genetic variations that may be associated with specific traits or diseases, and develop new diagnostic and therapeutic approaches. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Genomicus is a term used in bioinformatics and computational biology. 2. Genomicus refers to the complete set of genetic information, including the DNA sequence, of a particular organism or species. 3. Genomicus is used to understand the evolutionary history of the organism. 4. Genomicus is used to identify genetic variations associated with specific traits or diseases. 5. Genomicus is used to develop new diagnostic and therapeutic approaches. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 142(8) |
| 领域 | Bio-Medical |
| 用户问题 | Is amiodarone a class I anti-arrhythmic drug? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Amiodarone is a class III anti-arrhythmic drug, not a class I drug. Class I anti-arrhythmic drugs are those that slow the heart rate and decrease the excitability of the heart muscle. Examples of class I anti-arrhythmic drugs include quinidine, lidocaine, and procainamide. In contrast, class III anti-arrhythmic drugs, such as amiodarone, have a slower onset of action and are used to treat life-threatening arrhythmias, such as ventricular fibrillation and pulseless ventricular tachycardia. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Amiodarone is a class III anti-arrhythmic drug. 2. Class III anti-arrhythmic drugs have a slower onset of action. 3. Amiodarone is used to treat life-threatening arrhythmias, such as ventricular fibrillation and pulseless ventricular tachycardia. 4. Class I anti-arrhythmic drugs slow the heart rate and decrease the excitability of the heart muscle. 5. Quinidine, lidocaine, and procainamide are examples of class I anti-arrhythmic drugs. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 143(9) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the prognostic meaning of delayed enhancement documented in patients hypertrophic cardiomyopathy? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Hypertrophic cardiomyopathy (HCM) is a genetic disorder that affects the heart muscle, leading to thickening of the heart walls (hypertrophy) and an increased risk of sudden death. Delayed enhancement (DE) on cardiac magnetic resonance imaging (MRI) is a common finding in patients with HCM, and it has been associated with adverse cardiovascular outcomes. In this article, we will discuss the prognostic meaning of DE in patients with HCM and the implications for clinical management. What is delayed enhancement in cardiac MRI? DE on cardiac MRI refers to the persistence of signal intensity in the myocardium after the initial contrast injection. In normal cardiac tissue, the contrast agent is rapidly cleared from the myocardium, and the signal intensity returns to baseline within a few minutes. In HCM patients, however, the myocardial tissue may retain some of the contrast agent, leading to delayed enhancement. What are the implications of delayed enhancement in HCM patients? Several studies have shown that DE on cardiac MRI is associated with an increased risk of adverse cardiovascular outcomes in HCM patients, including sudden death, heart failure, and arrhythmias. The prognostic significance of DE in HCM patients is thought to be related to the underlying pathophysiology of the disease, including the presence of scar tissue and fibrosis, which can lead to progressive cardiac dysfunction. How can delayed enhancement be used to improve patient outcomes? DE on cardiac MRI can be used to identify patients with HCM who are at high risk of adverse cardiovascular outcomes. By identifying these patients, clinicians can initiate more aggressive management strategies, including medications, device therapy, or surgical interventions, to reduce the risk of adverse events. Additionally, DE can be used to monitor the progression of the disease over time and to assess the response to treatment. In conclusion, delayed enhancement on cardiac MRI is a common finding in patients with hypertrophic cardiomyopathy and is associated with an increased risk of adverse cardiovascular outcomes. By identifying patients with HCM who |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Hypertrophic cardiomyopathy (HCM) is a genetic disorder that leads to thickening of the heart walls. 2. Delayed enhancement (DE) is a common finding in patients with HCM on cardiac MRI. 3. DE on cardiac MRI refers to the persistence of signal intensity in the myocardium after the initial contrast injection. 4. DE in HCM patients is associated with adverse cardiovascular outcomes such as sudden death, heart failure, and arrhythmias. 5. DE on cardiac MRI can be used to identify HCM patients at high risk of adverse cardiovascular outcomes and guide treatment strategies. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 144(10) |
| 领域 | Bio-Medical |
| 用户问题 | What is the COUGER tool? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Cougar is a tool designed to help organizations assess their cybersecurity posture and identify potential vulnerabilities in their systems, networks, and applications. It is an open-source tool that provides a comprehensive framework for identifying and prioritizing cybersecurity risks, and it can be used by organizations of all sizes and industries. Cougar is based on the National Institute of Standards and Technology (NIST) Cybersecurity Framework, which provides a standardized approach to managing cybersecurity risks. The tool provides a set of templates and questionnaires that help organizations assess their cybersecurity posture across five core functions: Identify, Protect, Detect, Respond, and Recover. Cougar also provides a risk management framework that helps organizations prioritize their cybersecurity efforts based on the potential impact and likelihood of potential threats. It can be used to assess the security of systems, networks, and applications, as well as to identify potential vulnerabilities and gaps in an organization's cybersecurity posture. Overall, Cougar is a valuable tool for organizations looking to improve their cybersecurity posture and protect themselves against cyber threats. It provides a comprehensive and standardized approach to identifying and managing cybersecurity risks, and it can be used by organizations of all sizes and industries. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Cougar is a tool designed to help organizations assess their cybersecurity posture and identify potential vulnerabilities in their systems, networks, and applications. 2. Cougar is an open-source tool. 3. Cougar is based on the National Institute of Standards and Technology (NIST) Cybersecurity Framework. 4. Cougar provides a set of templates and questionnaires to assess cybersecurity posture across five core functions: Identify, Protect, Detect, Respond, and Recover. 5. Cougar helps organizations prioritize their cybersecurity efforts based on the potential impact and likelihood of potential threats. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 145(11) |
| 领域 | Bio-Medical |
| 用户问题 | Are there drugs for Tick-borne Encephalitis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | There are no specific drugs that can cure tick-borne encephalitis (TBE), but there are antiviral medications that can help manage the symptoms and reduce the duration of the illness. These medications include: 1. Ribavirin: This medication is commonly used to treat viral infections, including TBE. It can help reduce the severity of symptoms and the duration of the illness. 2. Oseltamivir: This medication is commonly used to treat influenza (flu) and can also be used to treat TBE. It can help reduce the severity of symptoms and the duration of the illness. 3. Valaciclovir: This medication is commonly used to treat herpesvirus infections, including TBE. It can help reduce the severity of symptoms and the duration of the illness. 4. Aztreonam: This medication is an antibiotic that can help treat bacterial infections that may occur as a complication of TBE. 5. Corticosteroids: These medications can help reduce inflammation in the brain and other parts of the body, which can occur as a complication of TBE. It's important to note that these medications may not be effective in all cases of TBE, and the best treatment approach will depend on the severity of the illness and the individual patient's condition. In severe cases of TBE, hospitalization may be necessary to provide supportive care, such as intravenous fluids, oxygen therapy, and mechanical ventilation. Prevention is the best approach to managing TBE, and this includes avoiding tick habitats, using insect repellents, and checking for ticks after spending time outdoors. Vaccines are also available for some types of TBE, and these can provide protection against the infection. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. There are no specific drugs that can cure tick-borne encephalitis (TBE). 2. Ribavirin, Oseltamivir, and Valaciclovir are antiviral medications commonly used to manage the symptoms and reduce the duration of TBE. 3. Aztreonam is an antibiotic that can help treat bacterial infections that may occur as a complication of TBE. 4. Corticosteroids can help reduce inflammation in the brain and other parts of the body, which can occur as a complication of TBE. 5. Prevention measures for TBE include avoiding tick habitats, using insect repellents, checking for ticks after outdoor activities, and vaccination for some types of TBE. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 146(12) |
| 领域 | Bio-Medical |
| 用户问题 | Is SLC22A3 expressed in the brain? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, SLC22A3 is expressed in the brain. SLC22A3 is a member of the solute carrier family 22 (SLC22A) of proteins, which are involved in the transport of polyamines (putrescine, spermidine, and spermine) across cell membranes. While SLC22A3 is primarily expressed in the gut, it is also expressed in various tissues, including the brain. Studies have shown that SLC22A3 is expressed in different regions of the brain, including the cerebral cortex, hippocampus, and cerebellum. For example, one study found that SLC22A3 mRNA is abundant in the cerebral cortex and hippocampus, and that the protein is localized to the plasma membrane of neurons in these regions (1). Another study found that SLC22A3 is expressed in the cerebellum, where it may play a role in regulating the transport of polyamines in Purkinje cells (2). The expression of SLC22A3 in the brain suggests that it may play a role in regulating polyamine levels in the brain, which are important for various cellular processes, including neuronal survival, differentiation, and synaptic plasticity. Dysregulation of SLC22A3 has been implicated in various neurological disorders, including epilepsy, Parkinson's disease, and Alzheimer's disease, highlighting the potential importance of this protein in brain function and disease. References: 1. Kim JH, et al. (2010). Expression of the polyamine transporter SLC22A3 in the brain and its potential role in regulating polyamine levels. Brain Res. 1327, 102-111. 2. Zhang J, et al. (2013). SLC22A3 is expressed in the cerebellum and regulates polyamine transport in Purkinje cells. J. Neurosci. 33, 1786-1796. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. SLC22A3 is expressed in the brain. 2. SLC22A3 is a member of the solute carrier family 22 (SLC22A) of proteins. 3. SLC22A3 is primarily expressed in the gut. 4. SLC22A3 is also expressed in various tissues, including the brain. 5. SLC22A3 is expressed in the cerebral cortex, hippocampus, and cerebellum of the brain. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 148(13) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the cellular localization of the protein Opa1? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Opa1 is a protein that is involved in the regulation of endosomal sorting and autophagy. It is localized to the endoplasmic reticulum (ER) and can also be found in the early endosomes and autophagosomes. Opa1 is a key regulator of the fusion between endosomes and lysosomes, and is also involved in the regulation of the autophagy-lysosome pathway. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Opa1 is involved in the regulation of endosomal sorting and autophagy. 2. Opa1 is localized to the endoplasmic reticulum (ER). 3. Opa1 can also be found in the early endosomes and autophagosomes. 4. Opa1 is a key regulator of the fusion between endosomes and lysosomes. 5. Opa1 is involved in the regulation of the autophagy-lysosome pathway. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 149(14) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the drugs utilized for the burning mouth syndrome? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Burning mouth syndrome (BMS) is a chronic oral discomfort characterized by a burning sensation in the mouth without any identifiable cause. It is a prevalent condition that affects women more frequently than men, and its prevalence increases with age. The exact pathophysiology of BMS is not fully understood, but it is believed to be related to neurogenic inflammation and changes in the nervous system. There are several drugs that have been utilized to treat BMS, including: 1. Benzodiazepines: These medications, such as clonazepam, can help to reduce the burning sensation in the mouth and promote relaxation. 2. Antidepressants: Selective serotonin reuptake inhibitors (SSRIs), such as fluoxetine, and tricyclic antidepressants, such as amitriptyline, have been used to treat BMS. These medications can help to reduce the burning sensation and improve mood. 3. Antihistamines: Diphenhydramine, a sedating antihistamine, has been used to treat BMS. It can help to reduce the burning sensation and promote relaxation. 4. Pain relievers: Over-the-counter pain relievers, such as ibuprofen or acetaminophen, can help to reduce the burning sensation in the mouth. 5. Steroids: Topical corticosteroids, such as hydrocortisone, can be applied to the affected area to reduce inflammation and relieve the burning sensation. 6. Anticonvulsants: Valaciclovir, a antiviral medication, has been used to treat BMS. It can help to reduce the burning sensation and improve mood. 7. Muscle relaxants: Baclofen, a muscle relaxant, has been used to treat BMS. It can help to reduce the burning sensation and promote relaxation. 8. GABA receptor agonists: GABA (gamma-aminobutyric acid) receptor agonists, such as gabapentin, can help to reduce the burning sensation and promote relaxation. It is important to note that the effectiveness of these drugs may |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Burning mouth syndrome (BMS) is a chronic oral discomfort characterized by a burning sensation in the mouth. 2. BMS is more prevalent in women than men. 3. The prevalence of BMS increases with age. 4. Benzodiazepines, antidepressants, antihistamines, pain relievers, steroids, anticonvulsants, muscle relaxants, and GABA receptor agonists have been used to treat BMS. 5. Topical corticosteroids, such as hydrocortisone, can be applied to the affected area to reduce inflammation and relieve the burning sensation. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 150(15) |
| 领域 | Bio-Medical |
| 用户问题 | Is PTEN involved in follicular thyroid carcinoma? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, PTEN (phosphatase and tensin homolog deleted on chromosome 10) is involved in follicular thyroid carcinoma. PTEN is a tumor suppressor gene that plays a critical role in regulating cell growth and proliferation, and it is frequently mutated or lost in many types of cancer, including thyroid cancer. Follicular thyroid carcinoma is a type of thyroid cancer that arises in the follicular cells of the thyroid gland. It is the second most common type of thyroid cancer, accounting for approximately 5-10% of all thyroid cancer cases. Studies have shown that PTEN mutations are present in a significant proportion of follicular thyroid carcinomas, with an incidence ranging from 20% to 60%. These mutations are often found in the coding region of the PTEN gene and can result in the loss of PTEN function. The loss of PTEN function in follicular thyroid carcinoma is associated with aggressive tumor phenotypes, such as increased cell proliferation, migration, and invasion. PTEN mutations may also predict a poorer prognosis in patients with follicular thyroid carcinoma, particularly those with nodal metastases. In summary, PTEN is involved in the development and progression of follicular thyroid carcinoma, and its mutation is a key factor in the aggressive behavior of this type of thyroid cancer. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. PTEN is involved in follicular thyroid carcinoma. 2. PTEN is a tumor suppressor gene. 3. PTEN regulates cell growth and proliferation. 4. PTEN is frequently mutated or lost in many types of cancer, including thyroid cancer. 5. Follicular thyroid carcinoma is the second most common type of thyroid cancer, accounting for approximately 5-10% of all thyroid cancer cases. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 151(16) |
| 领域 | Bio-Medical |
| 用户问题 | Which genome browser database for DNA shape annotations is available? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | There are several genome browsers available that provide DNA shape annotations, including: 1. UCSC Genome Browser: This is a widely used genome browser that provides DNA shape annotations for various organisms, including humans. The browser allows users to visualize and explore genomic sequences, as well as view annotations such as gene expression, variation, and DNA shape. 2. Ensembl Genome Browser: Ensembl is another popular genome browser that provides DNA shape annotations for various organisms, including humans. The browser offers a variety of tools and features for exploring and analyzing genomic data, including DNA shape annotations. 3. Genome Graph Browser: This is a specialized genome browser that focuses specifically on DNA shape annotations. It provides a graph-based representation of the genome, allowing users to visualize and explore the three-dimensional structure of DNA molecules. 4. ChromHMM: This is a genome browser that provides DNA shape annotations for various organisms, including humans. It uses a hidden Markov model (HMM) to infer the three-dimensional structure of DNA molecules from their two-dimensional sequence data. 5. 3D Genome Browser: This is a genome browser that provides DNA shape annotations for various organisms, including humans. It offers a variety of tools and features for exploring and analyzing genomic data, including DNA shape annotations. It's worth noting that these databases are constantly updated and new ones may be developed in the future, so it's always a good idea to check the latest information and availability of the databases you are interested in. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. The UCSC Genome Browser provides DNA shape annotations for various organisms, including humans. 2. The Ensembl Genome Browser provides DNA shape annotations for various organisms, including humans. 3. The Genome Graph Browser focuses specifically on DNA shape annotations and provides a graph-based representation of the genome. 4. ChromHMM uses a hidden Markov model (HMM) to infer the three-dimensional structure of DNA molecules from their two-dimensional sequence data and provides DNA shape annotations. 5. The 3D Genome Browser provides DNA shape annotations for various organisms, including humans. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 152(17) |
| 领域 | Bio-Medical |
| 用户问题 | What is known about clinical efficacy of ceftriaxone for treatment of amyotrophic lateral sclerosis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Ceftriaxone is an antibiotic that has been investigated as a potential treatment for amyotrophic lateral sclerosis (ALS), a progressive neurodegenerative disease that affects nerve cells in the brain and spinal cord. While there is limited research on the use of ceftriaxone for ALS treatment, here are some key findings: 1. Animal studies: Ceftriaxone has been shown to reduce inflammation and oxidative stress in animal models of ALS. For example, a study published in the Journal of Neurochemistry found that ceftriaxone treatment reduced inflammation and improved motor function in a rat model of ALS. 2. Clinical trials: Ceftriaxone has been evaluated in small-scale clinical trials for ALS treatment. A phase II clinical trial published in the Journal of Neurology, Neurosurgery, and Psychiatry found that ceftriaxone treatment improved functional abilities in patients with ALS over a 12-month period. However, the trial was small (n=16) and had limited statistical power, so further research is needed to confirm these findings. 3. Mechanism of action: Ceftriaxone works by inhibiting the production of bacterial cell walls, which can help reduce inflammation and oxidative stress. In ALS, inflammation and oxidative stress are thought to play a role in the degeneration of motor neurons. By reducing inflammation, ceftriaxone may help slow down the progression of ALS. 4. Side effects: Ceftriaxone is generally well-tolerated, but it can cause side effects such as allergic reactions, diarrhea, and nausea. In ALS patients, ceftriaxone has been associated with a small increase in liver enzymes, but this is not thought to be a major concern. 5. Combination therapy: Some researchers have suggested that combining ceftriaxone with other ALS therapies, such as riluzole, may be more effective than using either drug alone. However, there is limited data to support this idea, and more research is needed to determine whether combination therapy is beneficial in ALS treatment. In summary |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Ceftriaxone is an antibiotic that has been investigated as a potential treatment for amyotrophic lateral sclerosis (ALS). 2. Animal studies have shown that ceftriaxone can reduce inflammation and oxidative stress in ALS models. 3. A small-scale clinical trial found that ceftriaxone treatment improved functional abilities in ALS patients over a 12-month period. 4. Ceftriaxone works by inhibiting the production of bacterial cell walls, which can help reduce inflammation and oxidative stress in ALS. 5. Ceftriaxone can cause side effects such as allergic reactions, diarrhea, and nausea, but the increase in liver enzymes is not considered a major concern in ALS patients. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 154(18) |
| 领域 | Bio-Medical |
| 用户问题 | Does strenuous physical activity affect thyroid hormone metabolism? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, strenuous physical activity can affect thyroid hormone metabolism. Thyroid hormones are critical for regulating metabolism, growth, and development, and changes in physical activity can impact their metabolism. Here are some ways strenuous physical activity can affect thyroid hormone metabolism: 1. Increased thyroid hormone production: During strenuous exercise, the body's demand for energy increases, leading to an increase in thyroid hormone production. This is because the thyroid gland senses the increased energy demand and produces more thyroid hormones to help the body meet that demand. 2. Changes in thyroid hormone sensitivity: Exercise can also affect the sensitivity of the body's cells to thyroid hormones. After strenuous exercise, the body's cells may become less sensitive to thyroid hormones, which can lead to a decrease in the metabolic rate. 3. Increased thyroid hormone breakdown: Exercise can also increase the breakdown of thyroid hormones. The thyroid gland can break down thyroid hormones more quickly after exercise, leading to a decrease in their levels. 4. Changes in thyroid hormone transport: Exercise can also affect the transport of thyroid hormones within the body. Thyroid hormones are transported in the bloodstream by a protein called thyroxine-binding globulin (TBG). Exercise can increase the breakdown of TBG, leading to a decrease in the transport of thyroid hormones. 5. Hormonal adaptations: Prolonged and intense exercise can lead to hormonal adaptations that can affect thyroid hormone metabolism. For example, the body may produce more cortisol, a hormone that can counteract the effects of thyroid hormones. It's important to note that the effects of exercise on thyroid hormone metabolism can vary depending on the intensity, duration, and frequency of exercise, as well as individual factors such as age, fitness level, and overall health. If you have concerns about your thyroid hormone levels or metabolism, it's best to speak with a healthcare professional. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Strenuous physical activity can lead to increased thyroid hormone production. 2. Strenuous physical activity can decrease the sensitivity of the body's cells to thyroid hormones. 3. Exercise can increase the breakdown of thyroid hormones. 4. Thyroid hormones are transported in the bloodstream by a protein called thyroxine-binding globulin (TBG). 5. Prolonged and intense exercise can lead to hormonal adaptations that can affect thyroid hormone metabolism. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 155(19) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the main function of "RNA sponges"? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | RNA sponges are a type of RNA molecule that can bind to and neutralize toxic RNA molecules in the cell. They are found in bacteria, archaea, and some eukaryotes, and play a crucial role in regulating gene expression and preventing RNA misfolding and aggregation. RNA sponges are typically small RNA molecules that are composed of a central hub of nucleotides flanked by loops of RNA. These loops can be modified with chemical groups that allow them to bind to specific RNA sequences. The main function of RNA sponges is to: A) Act as a platform for the assembly of ribosomes. B) Transport proteins across the cell membrane. C) Regulate gene expression by binding to DNA. D) Neutralize toxic RNA molecules in the cell. E) Catalyze chemical reactions in the cell. The correct answer is (D) Neutralize toxic RNA molecules in the cell. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. RNA sponges can bind to and neutralize toxic RNA molecules in the cell. 2. RNA sponges are found in bacteria, archaea, and some eukaryotes. 3. RNA sponges play a crucial role in regulating gene expression and preventing RNA misfolding and aggregation. 4. RNA sponges are typically composed of a central hub of nucleotides flanked by loops of RNA. 5. The loops of RNA in RNA sponges can be modified with chemical groups that allow them to bind to specific RNA sequences. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 156(20) |
| 领域 | Bio-Medical |
| 用户问题 | Is the gene MAOA epigenetically modified by methylation? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, the gene monoamine oxidase A (MAOA) has been shown to be epigenetically modified by methylation. Methylation of the MAOA gene has been associated with various psychiatric and neurological disorders, including major depressive disorder (MDD), bipolar disorder, and autism spectrum disorder (ASD). Studies have found that the promoter region of the MAOA gene is highly methylated in individuals with MDD, and that this methylation is associated with reduced MAOA expression. Similarly, methylation of the MAOA gene has been found to be increased in individuals with ASD, which is also associated with reduced MAOA expression. Additionally, methylation of the MAOA gene has been shown to be heritable, meaning that it can be passed down from parents to offspring through epigenetic changes. This heritability of methylation has been found to be as high as 40% in some studies. Overall, the evidence suggests that methylation of the MAOA gene is an important epigenetic mechanism that can influence the expression of this gene and potentially contribute to the development of psychiatric and neurological disorders. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. The gene MAOA can be epigenetically modified by methylation. 2. Methylation of the MAOA gene has been associated with major depressive disorder (MDD), bipolar disorder, and autism spectrum disorder (ASD). 3. The promoter region of the MAOA gene is highly methylated in individuals with MDD, leading to reduced MAOA expression. 4. Methylation of the MAOA gene is increased in individuals with ASD, also resulting in reduced MAOA expression. 5. Methylation of the MAOA gene can be passed down from parents to offspring through epigenetic changes, with a heritability rate of up to 40%. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 157(21) |
| 领域 | Bio-Medical |
| 用户问题 | Which mutations of phopspholamban have been found in patients with cardiomyopathy? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Phospholamban (PLN) is a protein that plays a critical role in the regulation of cardiac contractility and is encoded by the gene (PHOSPHOLAMBAN). Mutations in the PLN gene have been associated with various cardiac disorders, including cardiomyopathy. Here are some of the mutations of phospholamban that have been found in patients with cardiomyopathy: 1. Gly18Arg: This mutation is the most common mutation found in patients with cardiomyopathy and is associated with a decrease in the ability of phospholamban to bind to and regulate the activity of the enzyme phosphodiesterase 4D (PDE4D). 2. Thr21Met: This mutation is also associated with a decrease in the ability of phospholamban to regulate PDE4D activity, leading to increased levels of cyclic adenosine monophosphate (cAMP) and an increase in cardiac contractility. 3. Gly33Ser: This mutation is associated with a decrease in the ability of phospholamban to bind to and regulate the activity of the enzyme phosphatidylinositol 3-kinase (PI3K). 4. Ser116Pro: This mutation is associated with a decrease in the ability of phospholamban to regulate the activity of the enzyme protein kinase C (PKC). 5. Val14Ile: This mutation is associated with a decrease in the ability of phospholamban to regulate the activity of the enzyme phosphatidylinositol 4,5-bisphosphate 3-kinase (PIP3K). 6. Asn155Thr: This mutation is associated with a decrease in the ability of phospholamban to regulate the activity of the enzyme PDE4D. 7. Arg192Gly: This mutation is associated with a decrease in the ability of phospholamban to regulate the activity of the enzyme PDE4D. 8. Gly209Ser: This mutation is associated with a decrease in the ability of phospholamban to regulate the |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Phospholamban (PLN) is a protein that plays a critical role in the regulation of cardiac contractility. 2. The PLN gene is responsible for encoding phospholamban. 3. Mutations in the PLN gene have been associated with various cardiac disorders, including cardiomyopathy. 4. The Gly18Arg mutation of phospholamban has been found in patients with cardiomyopathy and affects its ability to bind and regulate phosphodiesterase 4D (PDE4D). 5. The Thr21Met mutation of phospholamban has been found in patients with cardiomyopathy and affects its ability to regulate PDE4D activity. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 158(22) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the supplemental antioxidant in athletes? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Athletes often use supplemental antioxidants to help protect their bodies from the oxidative stress caused by intense exercise. Some common supplemental antioxidants used by athletes include: 1. Vitamin C: This antioxidant helps to neutralize free radicals and protect cells from damage. 2. Vitamin E: This antioxidant helps to protect cells from damage caused by free radicals and can also help to reduce inflammation. 3. Coenzyme Q10 (CoQ10): This antioxidant helps to protect cells from damage caused by free radicals and can also help to improve energy production in the body. 4. Beta-carotene: This antioxidant helps to protect cells from damage caused by free radicals and can also help to improve vision. 5. Selenium: This antioxidant helps to protect cells from damage caused by free radicals and can also help to improve immune function. 6. Zinc: This mineral is important for immune function and can also help to protect cells from damage caused by free radicals. 7. Polyphenols: These antioxidants are found in plant-based foods and can help to protect cells from damage caused by free radicals. 8. N-acetyl cysteine (NAC): This amino acid is important for lung health and can also help to protect cells from damage caused by free radicals. 9. L-glutamine: This amino acid is important for muscle health and can also help to protect cells from damage caused by free radicals. 10. Adaptogenic herbs: These herbs, such as ashwagandha and rhodiola, can help to reduce stress and improve recovery from exercise. It is important to note that while these supplemental antioxidants may be beneficial for athletes, it is always best to consult with a healthcare professional before starting any new supplements. Additionally, it is important to remember that antioxidants are just one aspect of overall health and wellness, and that a balanced diet and regular exercise are also important for maintaining good health. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Vitamin C is a common supplemental antioxidant used by athletes to neutralize free radicals and protect cells from damage. 2. Vitamin E is a common supplemental antioxidant used by athletes to protect cells from damage caused by free radicals and reduce inflammation. 3. Coenzyme Q10 (CoQ10) is a common supplemental antioxidant used by athletes to protect cells from damage caused by free radicals and improve energy production. 4. Beta-carotene is a common supplemental antioxidant used by athletes to protect cells from damage caused by free radicals and improve vision. 5. Selenium is a common supplemental antioxidant used by athletes to protect cells from damage caused by free radicals and improve immune function. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 159(23) |
| 领域 | Bio-Medical |
| 用户问题 | Is glycyl-tRNA synthetase gene involved in the development of Charcot-Marie-Tooth disease? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, the glycyl-tRNA synthetase gene (GARS) has been associated with Charcot-Marie-Tooth disease (CMT), a group of inherited disorders that affect the peripheral nervous system. GARS is responsible for encoding an enzyme that is involved in the synthesis of amino acids, including glycyl, which is a critical component of myelin sheaths in the peripheral nervous system. Mutations in the GARS gene have been identified in a subset of CMT patients, and these mutations are thought to disrupt the normal function of glycyl-tRNA synthetase, leading to impaired myelin synthesis and maintenance. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. The glycyl-tRNA synthetase gene (GARS) is associated with Charcot-Marie-Tooth disease (CMT). 2. Charcot-Marie-Tooth disease is a group of inherited disorders that affect the peripheral nervous system. 3. GARS gene encodes an enzyme involved in the synthesis of amino acids, including glycyl. 4. Glycyl is a critical component of myelin sheaths in the peripheral nervous system. 5. Mutations in the GARS gene disrupt the normal function of glycyl-tRNA synthetase, leading to impaired myelin synthesis and maintenance. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 160(24) |
| 领域 | Bio-Medical |
| 用户问题 | Is there any software for automated analysis of FISH images? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Fluorescence in situ hybridization (FISH) is a powerful tool for visualizing and analyzing genomic structures, such as gene amplification, deletion, or rearrangement. However, the analysis of FISH images can be time-consuming and requires expertise in both FISH and image analysis. To address this challenge, several software tools have been developed for automated analysis of FISH images. Here are some examples: 1. ImageJ: ImageJ is a free, open-source image processing software developed by the National Institutes of Health (NIH). It has a variety of plugins available for FISH image analysis, including the FISH-Analysis plugin, which provides tools for automated segmentation, feature detection, and quantification of FISH signals. 2. CellProfiler: CellProfiler is an open-source image analysis software that can be used for FISH image analysis. It provides a range of tools for automated segmentation, feature detection, and quantification of FISH signals, as well as tools for visualizing and analyzing the results. 3. FISH-Cyt: FISH-Cyt is a software tool specifically designed for the automated analysis of FISH images. It provides a range of tools for segmenting, quantifying, and visualizing FISH signals, as well as tools for comparing FISH signals between different samples. 4. Genomic Viewer: Genomic Viewer is a software tool for visualizing and analyzing genomic data, including FISH images. It provides a range of tools for automated segmentation, feature detection, and quantification of FISH signals, as well as tools for visualizing and analyzing the results. 5. FISH-Detect: FISH-Detect is a software tool for automated detection and quantification of FISH signals in microscopy images. It provides a range of tools for segmenting, quantifying, and visualizing FISH signals, as well as tools for comparing FISH signals between different samples. These software tools can help streamline the analysis of FISH images, reduce the time and effort required for analysis, and provide more accurate and consistent results. However, it is important to note that the specific software tool used will depend on the specific needs and goals of the analysis, |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. ImageJ is a free, open-source image processing software developed by the National Institutes of Health (NIH). 2. CellProfiler is an open-source image analysis software. 3. FISH-Cyt is a software tool specifically designed for the automated analysis of FISH images. 4. Genomic Viewer is a software tool for visualizing and analyzing genomic data, including FISH images. 5. FISH-Detect is a software tool for automated detection and quantification of FISH signals in microscopy images. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 161(25) |
| 领域 | Bio-Medical |
| 用户问题 | How do histone methyltransferases cause histone modification? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Histone methyltransferases (HMTs) are enzymes that catalyze the transfer of a methyl group from a donor molecule to a specific lysine or arginine residue on a histone protein. This process, known as histone methylation, can alter the chromatin structure and play a crucial role in various cellular processes, including gene expression, DNA repair, and cell division. There are several different types of HMTs, each of which targets a specific lysine residue on histone proteins. For example, histone methyltransferase 1 (HMT1) is responsible for methylating lysine 4 on histone H3 (H3K4), while histone methyltransferase 2A (HMT2A) methylates lysine 27 on histone H3 (H3K27). Methylation of these residues can result in changes to the chromatin structure, leading to either the activation or repression of gene transcription. HMTs recognize specific binding sites on the histone protein and use a catalytic domain to transfer the methyl group from the donor molecule to the target lysine residue. The specificity of HMTs is determined by the structure of their catalytic domain, which recognizes a particular binding site on the histone protein. Once the HMT has bound to the target site, the methyl group is transferred through a series of chemical reactions, resulting in the covalent attachment of the methyl group to the histone protein. In addition to their role in chromatin modification, HMTs have also been implicated in the regulation of non-histone proteins, such as transcription factors and DNA repair proteins. For example, HMTs have been shown to modify transcription factors, leading to changes in their activity and the regulation of gene expression. Similarly, HMTs have been implicated in the repair of DNA damage, where they modify DNA repair proteins to facilitate the repair process. Overall, histone methyltransferases play a crucial role in the regulation of chromatin structure and gene expression, and their dysregulation has been implicated in a variety of diseases, including cancer and neurolog |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Histone methyltransferases catalyze the transfer of a methyl group from a donor molecule to a specific lysine or arginine residue on a histone protein. 2. Histone methylation alters the chromatin structure and plays a role in gene expression, DNA repair, and cell division. 3. There are different types of histone methyltransferases that target specific lysine residues on histone proteins. 4. Methylation of lysine 4 on histone H3 (H3K4) and lysine 27 on histone H3 (H3K27) can result in changes to the chromatin structure and affect gene transcription. 5. Histone methyltransferases modify non-histone proteins such as transcription factors and DNA repair proteins. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 162(26) |
| 领域 | Bio-Medical |
| 用户问题 | Is there an increased risk for cancer in Dyskeratosis Congenita? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Dyskeratosis congenita (DC) is a rare genetic disorder that affects the bone marrow, lymphoid cells, and skin. It is characterized by a defect in the DNA that affects the production of blood cells, leading to a shortened telomere length, which can increase the risk of cancer. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Dyskeratosis congenita is a rare genetic disorder. 2. Dyskeratosis congenita affects the bone marrow, lymphoid cells, and skin. 3. Dyskeratosis congenita is characterized by a defect in the DNA. 4. Dyskeratosis congenita results in a shortened telomere length. 5. Dyskeratosis congenita can increase the risk of cancer. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 163(27) |
| 领域 | Bio-Medical |
| 用户问题 | Does MicroRNA-21 (miR-21) contribute to cardiovascular disease? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | MicroRNA-21 (miR-21) is a small non-coding RNA molecule that plays a critical role in regulating gene expression by binding to messenger RNA (mRNA) and preventing its translation into protein. Recent studies have suggested that miR-21 may play a role in the development and progression of cardiovascular disease (CVD). One of the key mechanisms by which miR-21 contributes to CVD is through its regulation of inflammatory pathways. miR-21 has been shown to suppress the expression of pro-inflammatory genes, such as interleukin-6 (IL-6) and tumor necrosis factor-alpha (TNF-α), which are involved in the development of atherosclerosis and cardiac fibrosis. By reducing the expression of these genes, miR-21 may help to reduce the inflammatory response that occurs in the cardiovascular system. In addition to its anti-inflammatory effects, miR-21 has been shown to regulate the expression of genes involved in cell survival and proliferation. For example, miR-21 has been shown to promote the proliferation of vascular smooth muscle cells, which are involved in the development of atherosclerosis. MiR-21 has also been shown to inhibit the expression of genes involved in apoptosis, or programmed cell death, which can contribute to the development of cardiac hypertrophy and fibrosis. Another mechanism by which miR-21 may contribute to CVD is through its regulation of the angiogenic response. miR-21 has been shown to inhibit the expression of genes involved in angiogenesis, such as vascular endothelial growth factor (VEGF), which is involved in the formation of new blood vessels. This may help to limit the growth of atherosclerotic plaques and reduce the risk of cardiac events. Overall, these studies suggest that miR-21 plays a critical role in the development and progression of CVD by regulating inflammatory pathways, cell survival and proliferation, and the angiogenic |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. MicroRNA-21 (miR-21) is a small non-coding RNA molecule. 2. miR-21 regulates gene expression by binding to messenger RNA (mRNA) and preventing its translation into protein. 3. miR-21 suppresses the expression of pro-inflammatory genes such as interleukin-6 (IL-6) and tumor necrosis factor-alpha (TNF-α). 4. miR-21 promotes the proliferation of vascular smooth muscle cells. 5. miR-21 inhibits the expression of genes involved in angiogenesis. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 164(28) |
| 领域 | Bio-Medical |
| 用户问题 | What is the enzymatic activity of the breast cancer associated gene BRCA1? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Breast cancer associated gene BRCA1 is a tumor suppressor gene that plays a crucial role in maintaining genomic stability by repairing DNA double-strand breaks through homologous recombination. The enzymatic activity of BRCA1 involves the repair of DNA interstrand cross-links (ICLs), which are a type of DNA damage that can lead to genome instability and cancer. BRCA1 is a member of the DNA damage response (DDR) protein family and is activated in response to DNA damage. Once activated, BRCA1 recruits and coordinates the assembly of various repair proteins to repair DNA damage through homologous recombination. In addition to its role in DNA repair, BRCA1 also plays a role in transcriptional regulation, cell cycle checkpoint control, and apoptosis. The deregulation of BRCA1 has been implicated in various cancers, including breast, ovarian, and pancreatic cancer. Overall, the enzymatic activity of BRCA1 is crucial for maintaining genomic stability and preventing cancer, and its deregulation can lead to the development of cancer. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. BRCA1 is a tumor suppressor gene associated with breast cancer. 2. The enzymatic activity of BRCA1 involves repairing DNA double-strand breaks through homologous recombination. 3. BRCA1 also repairs DNA interstrand cross-links (ICLs), a type of DNA damage. 4. BRCA1 is a member of the DNA damage response (DDR) protein family. 5. BRCA1 plays a role in transcriptional regulation, cell cycle checkpoint control, and apoptosis. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 165(29) |
| 领域 | Bio-Medical |
| 用户问题 | List markers for autophagy. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | | Marker | Description | | --- | --- | | LC3 | LC3 (Microtubule-Associated Protein 1 Light Chain 3) is a key component of the autophagosome | | Atg1 | Autophagy-related protein 1 (Atg1) is a key regulator of autophagy | | Atg5 | Autophagy-related protein 5 (Atg5) is a protein that plays a role in the formation of the autophagosome | | Atg12 | Autophagy-related protein 12 (Atg12) is a protein that plays a role in the formation of the autophagosome | | Atg16L1 | Autophagy-related protein 16-like 1 (Atg16L1) is a protein that plays a role in the formation of the autophagosome | | P62 | P62 (Protein 62) is a protein that is involved in the process of autophagy | | SQSTM1 | Squamous cell carcinoma antigen 1 (SQSTM1) is a protein that is involved in the process of autophagy | | ULK1 | Unc-51-like kinase 1 (ULK1) is a protein that plays a role in the regulation of autophagy | | AMPK | AMP-activated protein kinase (AMPK) is a protein that regulates the process of autophagy | | mTOR | Mechanistic target of rapamycin (mTOR) is a protein that regulates the process of autophagy | | PI3K | Phosphatidylinositol 3-kinase (PI3K) is a protein that regulates the process of autophagy | | NF-κB | Nuclear factor kappa B (NF-κB) is a protein that regulates the process of autophagy | | FOXO | Forkhead box O (FOXO) is a protein that regulates the process of autophagy | | Beclin1 | Beclin-1 is a protein that plays a role in the process of autophagy | |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. LC3 is a marker for autophagy and is a key component of the autophagosome. 2. Atg1 is a marker for autophagy and is a key regulator of autophagy. 3. Atg5 is a marker for autophagy and plays a role in the formation of the autophagosome. 4. Atg12 is a marker for autophagy and plays a role in the formation of the autophagosome. 5. Atg16L1 is a marker for autophagy and plays a role in the formation of the autophagosome. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 166(30) |
| 领域 | Bio-Medical |
| 用户问题 | Are there any statistical methods for normalizing and identifying differential regions in histone modification ChIP-seq data? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, there are several statistical methods that can be used to normalize and identify differential regions in histone modification ChIP-seq data. Here are some common methods: 1. Background subtraction: This involves subtracting the average signal from each sample at each position to remove the background signal. 2. Normalization methods: There are several normalization methods that can be used to normalize the ChIP-seq data, including TMM (Trimmed Mean of M-values) normalization, DESeq normalization, and BWA normalization. 3. Differential region identification: There are several methods that can be used to identify differential regions between samples, including the DEseq package in R, the limma package in R, and the HISAT2 package in Bioconductor. These methods typically involve fitting a statistical model to the data and testing for significant differences between samples. 4. Clustering methods: Clustering methods, such as k-means or hierarchical clustering, can be used to identify regions of the genome that are enriched for a particular histone modification. 5. Machine learning methods: Machine learning methods, such as random forests or support vector machines, can be used to identify patterns in the ChIP-seq data that are associated with specific histone modifications. 6. Peak calling methods: Peak calling methods, such as HISAT2 or MACS2, can be used to identify regions of the genome that are enriched for a particular histone modification. These methods typically involve fitting a statistical model to the data and identifying regions that meet a certain threshold for significance. 7. Spatial profiling methods: Spatial profiling methods, such as ChIP-seq with high-throughput sequencing, can be used to identify regions of the genome that are enriched for a particular histone modification. 8. Motif discovery methods: Motif discovery methods, such as MEME or HMMER, can be used to identify specific DNA sequences that are associated with a particular histone modification. It is important to note that the specific method used will depend on the goals of the analysis and the characteristics of the data. For example, if the goal is to identify regions that are differentially modified between two samples, then a differential region identification method may be more appropriate. If the goal is to identify specific DNA sequences that are associated with a particular |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Background subtraction is a statistical method used in normalizing and identifying differential regions in histone modification ChIP-seq data. 2. TMM (Trimmed Mean of M-values) normalization, DESeq normalization, and BWA normalization are common normalization methods for ChIP-seq data. 3. The DEseq package in R, the limma package in R, and the HISAT2 package in Bioconductor are methods used for differential region identification in histone modification ChIP-seq data. 4. Clustering methods like k-means or hierarchical clustering can be employed to identify regions of the genome enriched for a specific histone modification. 5. Machine learning methods like random forests or support vector machines can be used to identify patterns in ChIP-seq data associated with specific histone modifications. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 167(31) |
| 领域 | Bio-Medical |
| 用户问题 | Is CD84 genetically associated with arthritis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Arthritis is a complex and multifactorial disease that can affect various joints in the body, leading to pain, stiffness, and loss of function. While the exact genetic causes of arthritis are not yet fully understood, research has identified several genetic variants that may contribute to the development of the disease. One of these genes is CD84, also known as T-cell immunoglobulin and mucin domain containing protein 3 (TIM-3). CD84 is a protein expressed on the surface of T cells, a type of immune cell that plays a central role in the immune response. Several studies have found that genetic variants in the CD84 gene are associated with an increased risk of developing rheumatoid arthritis (RA), a common form of arthritis that affects the joints on both sides of the body. For example, a 2018 study published in the journal Nature Communications found that a specific variant of the CD84 gene was associated with an increased risk of RA in a cohort of over 100,000 individuals. Another study published in 2019 in the journal Arthritis & Rheumatology found that CD84 variants were associated with an increased risk of RA in a cohort of over 2,000 individuals. The study also found that the risk of developing RA was higher in individuals with a combination of CD84 variants and other genetic risk factors. While the exact mechanisms by which CD84 variants contribute to the development of RA are not yet fully understood, it is thought that these variants may affect the immune system's ability to properly regulate inflammation and respond to infection. It's important to note that genetic variants in the CD84 gene are not the only risk factor for developing RA, and that other factors such as environmental triggers and lifestyle factors also play a role in the development of the disease. Overall, while the association between CD84 genetic variants and arthritis is still being studied, these findings suggest that CD84 may be a promising target for future research into the genetic basis of arthritis and the development of new treatments for the disease. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. CD84, also known as TIM-3, is a gene associated with arthritis. 2. CD84 is a protein expressed on the surface of T cells. 3. Genetic variants in the CD84 gene are associated with an increased risk of developing rheumatoid arthritis. 4. A 2018 study published in Nature Communications found a specific variant of the CD84 gene associated with an increased risk of rheumatoid arthritis in over 100,000 individuals. 5. A 2019 study published in Arthritis & Rheumatology found that CD84 variants were associated with an increased risk of rheumatoid arthritis in over 2,000 individuals. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 168(32) |
| 领域 | Bio-Medical |
| 用户问题 | What is the function of Neu5Gc (N-Glycolylneuraminic acid)? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Neu5Gc (N-Glycolylneuraminic acid) is a sialic acid derivative that is found in the glycoproteins and glycolipids of many mammalian tissues, including the brain, liver, and pancreas. It is synthesized in the body through the enzymatic modification of the sialic acid Neu5Ac (N-acetylneuraminic acid) and plays important roles in cell-cell interactions and signaling. Here are some of the functions of Neu5Gc: 1. Cell adhesion and signaling: Neu5Gc acts as a receptor for many pathogens, including viruses and bacteria, and plays a role in cell adhesion and signaling. 2. Immune response: Neu5Gc is involved in the immune response, particularly in the activation of immune cells such as macrophages and T cells. 3. Cancer: Neu5Gc has been implicated in cancer development and progression, and may play a role in cancer metastasis. 4. Neurotransmission: Neu5Gc is found in high concentrations in the brain and plays a role in the transmission of neurotransmitters. 5. Inflammation: Neu5Gc is involved in the regulation of inflammation, and may play a role in the development of inflammatory diseases such as arthritis. 6. Cardiovascular health: Neu5Gc has been shown to play a role in the regulation of blood pressure and the maintenance of cardiovascular health. 7. Reproductive health: Neu5Gc has been implicated in the regulation of reproductive hormones and fertility. 8. Glycan synthesis: Neu5Gc is involved in the synthesis of glycans, which are important for the structure and function of glycoproteins and glycolipids. It is worth noting that Neu5Gc is not found in the glycoproteins and glycolipids of non-mammalian organisms, and its functions are unique to mammals. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Neu5Gc is a sialic acid derivative found in the glycoproteins and glycolipids of mammalian tissues such as the brain, liver, and pancreas. 2. Neu5Gc is synthesized in the body through the enzymatic modification of the sialic acid Neu5Ac. 3. Neu5Gc acts as a receptor for many pathogens and plays a role in cell adhesion and signaling. 4. Neu5Gc is involved in the immune response and the activation of immune cells such as macrophages and T cells. 5. Neu5Gc has been implicated in cancer development and progression, and may play a role in cancer metastasis. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 169(33) |
| 领域 | Bio-Medical |
| 用户问题 | Are there any specific antidotes for rivaroxaban? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Rivaroxaban is a direct oral anticoagulant (DOAC) that works by inhibiting the production of thrombin, a clotting factor in the blood. If you take too much rivaroxaban, it can cause bleeding, which can be serious or even life-threatening. In this case, an antidote may be needed to reverse the effects of the drug and stop the bleeding. There are several antidotes that can be used to reverse the effects of rivaroxaban, including: 1. Idarucizumab: This is a specific antidote for rivaroxaban that works by binding to the drug and reversing its effects on thrombin production. It is given intravenously and can be administered in a hospital setting. 2. Andexanet alfa: This is another specific antidote for rivaroxaban that works by binding to the drug and reversing its effects on thrombin production. It is given intravenously and can be administered in a hospital setting. 3. Protamine sulfate: This is a general antidote that can be used to reverse the effects of any type of heparin or heparinoid, including rivaroxaban. It works by neutralizing the effects of the drug on thrombin production and can be given intravenously or subcutaneously. 4. Vitamin K: This is a natural antidote that can help to reverse the effects of rivaroxaban by increasing the production of clotting factors in the blood. It can be given orally or by injection. It is important to note that these antidotes may not always be effective and may not completely reverse the effects of rivaroxaban. In addition, they can have side effects and may interact with other medications. Therefore, they should only be used under the close supervision of a healthcare provider. In summary, there are several antidotes that can be used to reverse the effects of rivaroxaban in case of overdose or bleeding. These include idarucizumab, andexanet alfa, protamine sulfate, and vitamin K. However, these antidotes may not always be effective and may have side effects, so they should only be used under the close supervision of a |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Rivaroxaban is a direct oral anticoagulant (DOAC) that inhibits the production of thrombin in the blood. 2. If taken in excess, rivaroxaban can cause bleeding, which can be serious or life-threatening. 3. Idarucizumab and andexanet alfa are specific antidotes for rivaroxaban that bind to the drug and reverse its effects on thrombin production. 4. Protamine sulfate is a general antidote that can be used to reverse the effects of any type of heparin or heparinoid, including rivaroxaban. 5. Vitamin K is a natural antidote that helps to reverse the effects of rivaroxaban by increasing the production of clotting factors in the blood. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 170(34) |
| 领域 | Bio-Medical |
| 用户问题 | Which metabolite activates AtxA? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | AtxA is a transcriptional regulator that is activated by a variety of metabolites, including: \* Fumarate \* Succinate \* Malate \* Oxaloacetate \* Citrate The specific metabolite that activates AtxA is fumarate. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. AtxA is a transcriptional regulator. 2. AtxA can be activated by a variety of metabolites. 3. Fumarate is one of the metabolites that activates AtxA. 4. Succinate, malate, oxaloacetate, and citrate are other metabolites that can activate AtxA. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 171(35) |
| 领域 | Bio-Medical |
| 用户问题 | What is the function of 6SRNA in bacteria? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | 6SRNA (6-sulfate-RNA) is a type of RNA found in some bacteria. It is known to play a role in the synthesis of teichoic acids, which are important components of the bacterial cell wall. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. 6SRNA is a type of RNA found in some bacteria. 2. 6SRNA plays a role in the synthesis of teichoic acids. 3. Teichoic acids are important components of the bacterial cell wall. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 172(36) |
| 领域 | Bio-Medical |
| 用户问题 | Is cytisine superior to nicotine replacement therapy for smoking cessation? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Cytisine is a plant-based alkaloid that has been shown to have nicotine-like effects on the brain, but without the addictive properties of nicotine. Some studies have suggested that cytisine may be more effective than nicotine replacement therapy (NRT) for smoking cessation, but the evidence is mixed and more research is needed to confirm these findings. One study published in the Journal of Nicotine & Tobacco Research found that cytisine was more effective than NRT in helping people quit smoking. The study found that 16% of people who received cytisine were able to quit smoking for at least six months, compared to 8% of those who received NRT. Another study published in the European Respiratory Journal found similar results, with 18% of people who received cytisine able to quit smoking for at least six months, compared to 10% of those who received NRT. However, other studies have found no difference in the effectiveness of cytisine and NRT for smoking cessation. A review of the available evidence published in the Cochrane Database of Systematic Reviews found that the evidence was inconsistent and that more research was needed to determine whether cytisine is superior to NRT. It's important to note that cytisine is not approved by the US Food and Drug Administration (FDA) for smoking cessation, and it is not widely available in the United States. Nicotine replacement therapy, on the other hand, is FDA-approved and widely available. In summary, while some studies suggest that cytisine may be more effective than NRT for smoking cessation, the evidence is mixed and more research is needed to confirm these findings. It's important to talk to your doctor before using any smoking cessation treatment, including cytisine or NRT. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Cytisine is a plant-based alkaloid that has nicotine-like effects on the brain without addictive properties. 2. One study published in the Journal of Nicotine & Tobacco Research found that 16% of people who received cytisine were able to quit smoking for at least six months. 3. Another study published in the European Respiratory Journal found that 18% of people who received cytisine were able to quit smoking for at least six months. 4. A review published in the Cochrane Database of Systematic Reviews found that the evidence on the effectiveness of cytisine and NRT for smoking cessation was inconsistent. 5. Cytisine is not approved by the US Food and Drug Administration for smoking cessation and is not widely available in the United States. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 173(37) |
| 领域 | Bio-Medical |
| 用户问题 | Which amino acid residue appears mutated in most of the cases reported with cadasil syndrome? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Cadasil syndrome is a rare genetic disorder that affects the brain and is characterized by progressive dementia, seizures, and visual disturbances. The majority of cases of Cadasil syndrome are caused by mutations in the ATP1A2 gene, which encodes the alpha-2 subunit of the calcium channel Cav1.1. The most common mutation found in Cadasil syndrome is a point mutation in the glutamate residue at position 1821 (E1821K). This mutation leads to an increase in the activity of the calcium channel, which can disrupt the normal functioning of neurons and contribute to the cognitive and motor symptoms of the disorder. Other mutations that have been identified in Cadasil syndrome include changes in the glutamate residue at position 1823 (E1823K) and the tyrosine residue at position 1827 (Y1827C). |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Cadasil syndrome is a rare genetic disorder that affects the brain and is characterized by progressive dementia, seizures, and visual disturbances. 2. Most cases of Cadasil syndrome are caused by mutations in the ATP1A2 gene, which encodes the alpha-2 subunit of the calcium channel Cav1.1. 3. The most common mutation found in Cadasil syndrome is a point mutation in the glutamate residue at position 1821 (E1821K). 4. This mutation leads to an increase in the activity of the calcium channel. 5. Other mutations identified in Cadasil syndrome include changes in the glutamate residue at position 1823 (E1823K) and the tyrosine residue at position 1827 (Y1827C). |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 174(38) |
| 领域 | Bio-Medical |
| 用户问题 | Which syndromes are associated with mutations in the EZH2 gene? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | The EZH2 gene provides instructions for making a protein called enhancer of zeste 2 (EZH2), which plays a critical role in regulating gene expression by modifying histones, the proteins that DNA wraps around to form chromatin. Mutations in the EZH2 gene have been associated with several rare genetic disorders, including: 1. Rubinstein-Taybi syndrome (RTS): RTS is a rare genetic disorder characterized by delayed growth and development, intellectual disability, and distinctive facial features. EZH2 mutations are found in approximately 50% of individuals with RTS. 2. Noonan syndrome (NS): NS is a rare genetic disorder characterized by short stature, congenital heart defects, and various other physical abnormalities. EZH2 mutations have been identified in approximately 10% of individuals with NS. 3. CdLS: CdLS is a rare genetic disorder characterized by short stature, intellectual disability, and distinctive facial features. EZH2 mutations have been identified in approximately 20% of individuals with CdLS. 4. Pallister-Hall syndrome (PHS): PHS is a rare genetic disorder characterized by short stature, intellectual disability, and distinctive facial features. EZH2 mutations have been identified in approximately 20% of individuals with PHS. 5. Smith-Magenis syndrome (SMS): SMS is a rare genetic disorder characterized by intellectual disability, distinctive facial features, and various other physical abnormalities. EZH2 mutations have been identified in approximately 10% of individuals with SMS. It's important to note that these syndromes are rare and EZH2 mutations are only one of the many genetic changes that can occur in these disorders. A diagnosis of one of these syndromes requires a comprehensive clinical evaluation and genetic testing. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Mutations in the EZH2 gene have been associated with Rubinstein-Taybi syndrome (RTS). 2. Approximately 50% of individuals with RTS have EZH2 mutations. 3. Mutations in the EZH2 gene have been associated with Noonan syndrome (NS). 4. Approximately 10% of individuals with NS have EZH2 mutations. 5. Mutations in the EZH2 gene have been associated with Pallister-Hall syndrome (PHS). 6. ote: I could not generate a fifth factual statement because the remaining information is not independently verifiable. The remaining information provides descriptions of the syndromes but does not contain independent facts that can be verified.) |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 175(39) |
| 领域 | Bio-Medical |
| 用户问题 | Which databases exist for experimentally determined topologies of α-helical transmembrane proteins ? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | There are several databases that contain experimentally determined topologies of α-helical transmembrane proteins. Some of the major databases include: 1. TOPDB: The Topological Database of Transmembrane Proteins (TOPDB) is a comprehensive database of experimentally determined transmembrane protein topologies. It contains information on the topology of over 1000 transmembrane proteins, including their helix orientation, transmembrane span, and lipid-binding properties. 2. PredictTOP: PredictTOP is a web-based tool that predicts the topology of transmembrane proteins based on their amino acid sequence. It uses a combination of sequence alignment and machine learning algorithms to predict the transmembrane helices and their orientation in the membrane. 3. TransTop: TransTop is a database of experimentally determined transmembrane protein topologies. It contains information on the topology of over 500 transmembrane proteins, including their helix orientation, transmembrane span, and lipid-binding properties. 4. Membrane Protein Topology (MPT): MPT is a database of experimentally determined topologies of membrane proteins, including both transmembrane and non-transmembrane proteins. It contains information on the topology of over 1000 membrane proteins, including their helix orientation, transmembrane span, and lipid-binding properties. 5. Protein Data Bank (PDB): The Protein Data Bank (PDB) is a comprehensive database of 3D structures of proteins, including transmembrane proteins. While not specifically focused on transmembrane protein topologies, the PDB contains a wealth of information on the structure and function of transmembrane proteins. These databases are valuable resources for researchers studying the structure and function of transmembrane proteins, and can be used to identify patterns and trends in transmembrane protein topology, as well as to inform the design of new transmembrane proteins with specific functions. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. TOPDB is a comprehensive database of experimentally determined transmembrane protein topologies. 2. TOPDB contains information on the topology of over 1000 transmembrane proteins, including their helix orientation, transmembrane span, and lipid-binding properties. 3. PredictTOP is a web-based tool that predicts the topology of transmembrane proteins based on their amino acid sequence. 4. TransTop is a database of experimentally determined transmembrane protein topologies. 5. The Protein Data Bank (PDB) is a comprehensive database of 3D structures of proteins, including transmembrane proteins. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 176(40) |
| 领域 | Bio-Medical |
| 用户问题 | Which disease is characterized by congenital absence of intrinsic ganglion cells of the gastrointestinal tract? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Answer: Gastrointestinal ganglionopathy is a rare genetic disorder that affects the intrinsic ganglion cells of the gastrointestinal (GI) tract. It is characterized by a congenital absence of intrinsic ganglion cells in the GI tract, which can lead to a range of symptoms including: \* Gastrointestinal hypersensitivity \* Abnormal gut motility \* Diarrhea \* Vomiting \* Abdominal pain \* Constipation Gastrointestinal ganglionopathy is often caused by mutations in the GNAL gene, which encodes the alpha subunit of the G-protein complex. The disorder is inherited in an autosomal dominant pattern, meaning that a single copy of the mutated gene is enough to cause the condition. Gastrointestinal ganglionopathy is a rare disorder, and its prevalence is not well established. However, it is believed to affect approximately 1 in 100,000 to 1 in 50,000 individuals worldwide. There is currently no cure for gastrointestinal ganglionopathy, but various treatments can help manage the symptoms. These may include medications to regulate gut motility, reduce inflammation, or treat pain, as well as dietary modifications and other lifestyle changes. In some cases, surgery may be necessary to treat complications such as intestinal obstruction or volvulus. Overall, gastrointestinal ganglionopathy is a rare and complex disorder that can significantly impact an individual's quality of life. Further research is needed to better understand its causes, develop effective treatments, and improve the management of this condition. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Gastrointestinal ganglionopathy is characterized by a congenital absence of intrinsic ganglion cells in the gastrointestinal (GI) tract. 2. Symptoms of gastrointestinal ganglionopathy include gastrointestinal hypersensitivity, abnormal gut motility, diarrhea, vomiting, abdominal pain, and constipation. 3. Gastrointestinal ganglionopathy is often caused by mutations in the GNAL gene. 4. Gastrointestinal ganglionopathy is inherited in an autosomal dominant pattern. 5. The prevalence of gastrointestinal ganglionopathy is estimated to be approximately 1 in 100,000 to 1 in 50,000 individuals worldwide. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 178(41) |
| 领域 | Bio-Medical |
| 用户问题 | How is oprozomib administered? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Oprozomib is administered orally, usually once daily, in the form of a capsule or tablet. It can be taken with or without food, but it is important to follow the dosing instructions provided by your healthcare provider to ensure that you are getting the correct dose. Oprozomib is a potent drug, and it is important to handle it with care to avoid exposure to the drug during preparation or administration. If you are taking oprozomib at home, make sure to follow the instructions provided by your healthcare provider carefully, and dispose of any unused medication properly. It is important to note that oprozomib can cause side effects, and it may interact with other medications you are taking. Your healthcare provider will monitor you closely during treatment to minimize the risk of side effects and ensure that the drug is working effectively. Overall, oprozomib is administered orally once daily, and it is important to follow the dosing instructions provided by your healthcare provider carefully to ensure that you are getting the correct dose and minimizing the risk of side effects. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Oprozomib is administered orally, usually once daily. 2. Oprozomib is available in the form of a capsule or tablet. 3. Oprozomib can be taken with or without food. 4. Oprozomib is a potent drug that should be handled with care to avoid exposure. 5. Oprozomib can cause side effects and may interact with other medications. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 179(42) |
| 领域 | Bio-Medical |
| 用户问题 | What is a Caveolae? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Caveolae are small invaginations of the plasma membrane that are found in the cells of many different organisms, including animals, plants, and fungi. They are typically 50-100 nanometers in diameter and are formed by the invagination of the plasma membrane, creating small, membrane-bound structures that are separated from the rest of the cell by a thin membrane. Caveolae are involved in a variety of cellular processes, including cell signaling, nutrient uptake, and waste removal. They are also thought to play a role in the regulation of cell growth and differentiation. Caveolae are formed through a process called caveolination, which involves the invagination of the plasma membrane and the formation of a cage-like structure around the invaginated membrane. This structure is then stabilized by the binding of proteins and lipids to the membrane. Caveolae are named after the Latin word "cavea," which means "cave." This name was chosen because the structures resemble small caves or invaginations in the plasma membrane. Caveolae are also sometimes referred to as "cave-like structures" or " Invaginations." Caveolae are found in many different types of cells, including epithelial cells, endothelial cells, and immune cells. They are particularly abundant in cells that are involved in the transport of molecules across the plasma membrane, such as cells in the intestine and liver. Caveolae are thought to play a role in the regulation of cell signaling by providing a platform for the assembly and activation of signaling complexes. They are also involved in the uptake of nutrients and the removal of waste products from the cell. Caveolae are also thought to play a role in the regulation of cell growth and differentiation by controlling the activity of transcription factors and other regulatory proteins. In summary, caveolae are small invaginations of the plasma membrane that are involved in a variety of cellular processes, including cell signaling, nutrient uptake, and waste removal. They are formed through the caveolination process and are found in many different types of cells. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Caveolae are small invaginations of the plasma membrane. 2. Caveolae are typically 50-100 nanometers in diameter. 3. Caveolae are found in cells of animals, plants, and fungi. 4. Caveolae are involved in cell signaling, nutrient uptake, and waste removal. 5. Caveolae are particularly abundant in cells involved in the transport of molecules across the plasma membrane. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 180(43) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the roles of chromatin compartments in the eukaryotic nucleus? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Chromatin compartments are specialized regions of the nucleus that are characterized by distinct chromatin structures and gene expression profiles. In eukaryotic cells, chromatin compartments play important roles in regulating gene expression, DNA replication, and repair. Here are some of the key roles of chromatin compartments in the eukaryotic nucleus: 1. Gene expression regulation: Chromatin compartments can regulate gene expression by controlling access to transcription factors and other regulatory proteins. For example, active genes are often located in more accessible chromatin compartments, allowing for easier access to transcription factors. Conversely, inactive genes are located in more compact or inaccessible chromatin compartments, making it more difficult for transcription factors to bind. 2. DNA replication: Chromatin compartments can also influence DNA replication by affecting the availability of DNA replication machinery. For example, the replication origin of a chromatin compartment may be more accessible to replication machinery than other regions of the chromatin. 3. DNA repair: Chromatin compartments can also affect DNA repair by influencing the accessibility of repair proteins to damaged DNA. For example, some chromatin compartments may be more accessible to repair proteins, allowing for more efficient repair of DNA damage. 4. Cell fate determination: Chromatin compartments can also play a role in cell fate determination by regulating the expression of genes involved in cell fate decisions. For example, certain chromatin compartments may be associated with specific cell fates, such as stem cell maintenance or differentiation. 5. Epigenetic regulation: Chromatin compartments can also influence epigenetic marks, such as histone modifications and DNA methylation, which in turn can affect gene expression and other cellular processes. 6. Chromatin remodeling: Chromatin compartments can also influence chromatin remodeling complexes, which are responsible for altering the chromatin structure and accessibility to transcription factors. 7. RNA processing: Chromatin compartments can also affect RNA processing by regulating the splicing and transport of RNA molecules. 8. Cell cycle regulation: Chromatin compartments can also play a role in cell cycle regulation by influencing the expression of genes involved in the cell |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Chromatin compartments are specialized regions of the eukaryotic nucleus with distinct chromatin structures and gene expression profiles. 2. Chromatin compartments regulate gene expression by controlling access to transcription factors and other regulatory proteins. 3. Chromatin compartments can influence DNA replication by affecting the availability of DNA replication machinery. 4. Chromatin compartments can affect DNA repair by influencing the accessibility of repair proteins to damaged DNA. 5. Chromatin compartments can play a role in cell fate determination by regulating the expression of genes involved in cell fate decisions. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 181(44) |
| 领域 | Bio-Medical |
| 用户问题 | Is the abnormal dosage of ultraconserved elements disfavored in cancer cells? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Yes, abnormal dosages of ultraconserved elements (UCEs) have been found to be disfavored in cancer cells. UCEs are a class of non-coding RNAs that are evolutionarily conserved across species and are known to play important roles in regulating gene expression, cell proliferation, and cell fate determination. Studies have shown that cancer cells often exhibit altered expression levels of UCEs compared to normal cells. For example, one study found that the expression levels of UCEs were significantly reduced in various types of cancer, including breast, lung, and colon cancer. Another study found that the expression of UCEs was associated with better prognosis in cancer patients. The disfavored dosage of UCEs in cancer cells may be due to various mechanisms, including: 1. Epigenetic alterations: Cancer cells often exhibit altered epigenetic marks, such as DNA methylation and histone modifications, which can lead to the silencing of UCEs. 2. Mutations in UCEs: Mutations in UCEs can lead to their inactivation or altered function, which can contribute to the development and progression of cancer. 3. Deregulation of miRNAs: miRNAs are known to regulate the expression of UCEs, and deregulation of miRNAs in cancer cells can lead to the disfavored dosage of UCEs. Overall, the disfavored dosage of UCEs in cancer cells may contribute to the development and progression of cancer by disrupting normal cellular processes and leading to the deregulation of gene expression. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Abnormal dosages of ultraconserved elements (UCEs) have been found to be disfavored in cancer cells. 2. UCEs are a class of non-coding RNAs that are evolutionarily conserved across species. 3. UCEs play important roles in regulating gene expression, cell proliferation, and cell fate determination. 4. Expression levels of UCEs are significantly reduced in various types of cancer, including breast, lung, and colon cancer. 5. The expression of UCEs is associated with better prognosis in cancer patients. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 183(45) |
| 领域 | Bio-Medical |
| 用户问题 | What are the biological roles proposed for proteins containing the SPRY domain? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Proteins containing the SPRY domain have been implicated in a variety of biological processes, including: 1. Cell signaling: The SPRY domain is involved in the regulation of signal transduction pathways, particularly those involving the small GTPases Cdc42 and Rho. 2. Cytoskeleton organization: SPRY domain-containing proteins are involved in the regulation of cytoskeleton organization, particularly in the formation of filopodia and lamellipodia. 3. Cell adhesion: SPRY domain-containing proteins are involved in cell adhesion and the regulation of cell-cell and cell-matrix interactions. 4. Cancer: SPRY domain-containing proteins have been implicated in cancer, particularly in the regulation of cell migration and invasion. 5. Neurodegeneration: SPRY domain-containing proteins are involved in the regulation of neurodegeneration, particularly in the context of Alzheimer's disease. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Proteins containing the SPRY domain are involved in the regulation of signal transduction pathways related to small GTPases Cdc42 and Rho. 2. SPRY domain-containing proteins play a role in the regulation of cytoskeleton organization, specifically in filopodia and lamellipodia formation. 3. SPRY domain-containing proteins are involved in cell adhesion and the regulation of cell-cell and cell-matrix interactions. 4. SPRY domain-containing proteins have been implicated in cancer and are involved in the regulation of cell migration and invasion. 5. SPRY domain-containing proteins are involved in the regulation of neurodegeneration, particularly in the context of Alzheimer's disease. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 184(46) |
| 领域 | Bio-Medical |
| 用户问题 | How could we infer functional associations from gene fusion events? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Gene fusion events, where two genes are joined together through a chromosomal abnormality, can provide valuable insights into the functional associations between genes. Here are some ways in which we could infer functional associations from gene fusion events: 1. Conserved gene fusion: If a gene fusion event is conserved across different species, it suggests that the associated genes are functionally important. For example, the gene fusion event between the EGFR and TPM3 genes is conserved in both human and mouse, and is associated with a high frequency of resistance to EGFR-targeted therapies in non-small cell lung cancer. 2. Co-expression analysis: By analyzing the co-expression patterns of genes involved in fusion events, we can identify functional associations between them. For example, genes involved in the TCF7L1-NTRK3 fusion event are co-expressed in lung adenocarcinoma, suggesting a functional link between these genes. 3. Protein-protein interaction analysis: Fusion genes can alter the protein-protein interaction landscape, leading to the formation of new protein complexes or disruption of existing ones. By analyzing the protein-protein interaction networks of fusion genes, we can identify functional associations between them. For example, the fusion of the BRAF and KRAS genes in melanoma leads to the formation of a new protein complex that promotes tumor growth and progression. 4. Genetic interaction analysis: Fusion genes can also disrupt the genetic interaction network, leading to the formation of new genetic interactions or disruption of existing ones. By analyzing the genetic interaction networks of fusion genes, we can identify functional associations between them. For example, the fusion of the BRCA1 and TP53 genes in breast cancer leads to the formation of a new genetic interaction that promotes DNA repair and tumor suppression. 5. Comparative genomics: By comparing the genomic landscape of fusion genes to that of non-fusion genes, we can identify functional associations between them. For example, fusion genes are more likely to be located in gene-rich regions of the genome, suggesting that they play a functional role in regulating gene expression. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Gene fusion events occur when two genes are joined together through a chromosomal abnormality. 2. Conserved gene fusion events across different species suggest functional importance. 3. Co-expression analysis can help identify functional associations between genes involved in fusion events. 4. Protein-protein interaction analysis can help identify functional associations between fusion genes. 5. Fusion genes are more likely to be located in gene-rich regions of the genome. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 187(47) |
| 领域 | Bio-Medical |
| 用户问题 | Are proteasome inhibitors good candidates for treatment of leukemia and solid tumors? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Proteasome inhibitors are a class of drugs that target the proteasome, a complex protein structure that plays a central role in regulating protein degradation in cells. In recent years, proteasome inhibitors have been investigated as potential treatments for various types of cancer, including leukemia and solid tumors. Here are some reasons why proteasome inhibitors may be good candidates for cancer treatment: 1. Cancer cells have a higher demand for protein synthesis and degradation: Cancer cells grow and divide rapidly, which means they have a higher demand for protein synthesis and degradation to support their rapid proliferation. Proteasome inhibitors can target this increased protein turnover in cancer cells, leading to cell cycle arrest and apoptosis (programmed cell death). 2. Proteasome inhibitors can selectively target cancer cells: Unlike traditional chemotherapy drugs, which target rapidly dividing cells regardless of their malignancy, proteasome inhibitors can selectively target cancer cells based on their unique protein synthesis and degradation pathways. This means that proteasome inhibitors may be less toxic to healthy cells compared to traditional chemotherapy. 3. Proteasome inhibitors can sensitize cancer cells to chemotherapy and radiation: Proteasome inhibitors can increase the sensitivity of cancer cells to chemotherapy and radiation by disrupting the normal cellular processes that protect against these treatments. This can lead to improved treatment outcomes for patients with leukemia and solid tumors. 4. Proteasome inhibitors have been shown to be effective in clinical trials: Several proteasome inhibitors have been tested in clinical trials for the treatment of various types of cancer, including leukemia and solid tumors. While the results have been mixed, some studies have shown promising responses to treatment with proteasome inhibitors, including complete remissions in some patients. 5. Proteasome inhibitors can be combined with other therapies to enhance their effectiveness: Proteasome inhibitors can be combined with other cancer therapies, such as chemotherapy, targeted therapy, or immunotherapy, to enhance their effectiveness. This approach can help to overcome resistance to treatment and improve treatment outcomes for patients with leukemia |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Proteasome inhibitors target the proteasome, a complex protein structure involved in regulating protein degradation in cells. 2. Proteasome inhibitors have been investigated as potential treatments for leukemia and solid tumors. 3. Cancer cells have a higher demand for protein synthesis and degradation, making them suitable targets for proteasome inhibitors. 4. Proteasome inhibitors can selectively target cancer cells based on their unique protein synthesis and degradation pathways. 5. Proteasome inhibitors can be combined with other cancer therapies to enhance their effectiveness. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 188(48) |
| 领域 | Bio-Medical |
| 用户问题 | Is there any link between CTF4 and CTF18 during sister chromatid cohesion? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Sister chromatid cohesion is the process by which sister chromatids are held together during DNA replication and mitosis. This is crucial for maintaining the integrity of the genetic material and ensuring proper cell division. CTF4 (chromatin remodeling factor 4) and CTF18 (chromatin remodeling factor 18) are two proteins that play important roles in sister chromatid cohesion. CTF4 is a chromatin remodeling complex that is composed of several subunits, including Ctf4, Ctf18, and Ctf19. This complex is responsible for the removal of cohesin from sister chromatids during DNA replication, allowing for the separation of the sister chromatids during mitosis. CTF4 is also involved in the repair of DNA double-strand breaks, which can occur during DNA replication. CTF18 is another chromatin remodeling complex that is composed of several subunits, including Ctf18, Ctf19, and Ctf20. This complex is involved in the maintenance of sister chromatid cohesion, particularly during DNA replication. CTF18 is also involved in the regulation of chromatin structure and gene expression. While CTF4 and CTF18 have distinct functions in the process of sister chromatid cohesion, there is evidence to suggest that they interact and coordinate their actions to ensure proper chromatin dynamics during DNA replication and mitosis. For example, CTF4 and CTF18 have been shown to interact with each other in a manner that promotes the proper separation of sister chromatids during mitosis. Additionally, mutations in either CTF4 or CTF18 can lead to defects in sister chromatid cohesion, highlighting the importance of these proteins in maintaining genome stability. In summary, CTF4 and CTF18 are two proteins that play important roles in sister chromatid cohesion during DNA replication and mitosis. While they have distinct functions, there is evidence to suggest that they interact and coordinate their actions to ensure proper chromatin dynamics and genome stability. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. CTF4 and CTF18 are involved in sister chromatid cohesion during DNA replication and mitosis. 2. CTF4 is a chromatin remodeling complex composed of Ctf4, Ctf18, and Ctf19 subunits. 3. CTF4 is responsible for removing cohesin from sister chromatids during DNA replication. 4. CTF18 is a chromatin remodeling complex composed of Ctf18, Ctf19, and Ctf20 subunits. 5. CTF18 is involved in maintaining sister chromatid cohesion during DNA replication. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |

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| ID | 190(49) |
| 领域 | Bio-Medical |
| 用户问题 | What is the target of the drug Olaparib? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） |  |
| 模型回复 | Olaparib is a drug used to treat certain types of cancer, including ovarian, breast, and lung cancers. It works by blocking the action of a protein called PARP, which is involved in DNA repair. By blocking PARP, olaparib causes cancer cells to die or to be unable to divide and grow, which can slow the growth of the tumor. Olaparib is specifically designed to target cancer cells that have a mutation in the BRCA1 or BRCA2 gene. These genes are involved in DNA repair, and mutations in these genes can make cancer cells more sensitive to chemotherapy and radiation therapy. By targeting cancer cells with these mutations, olaparib can be more effective at treating certain types of cancer. Overall, the target of the drug olaparib is to selectively kill or inhibit the growth of cancer cells that have a specific genetic mutation, while sparing healthy cells. This approach can help to improve the effectiveness of cancer treatment and reduce the risk of side effects. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 |  |
| 提取的事实 | 1. Olaparib is a drug used to treat ovarian, breast, and lung cancers. 2. Olaparib blocks the action of a protein called PARP, which is involved in DNA repair. 3. Olaparib specifically targets cancer cells with a mutation in the BRCA1 or BRCA2 gene. 4. Mutations in the BRCA1 or BRCA2 genes can make cancer cells more sensitive to chemotherapy and radiation therapy. 5. By targeting cancer cells with these mutations, olaparib can be more effective at treating certain types of cancer. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 |  |