幻象标注

|  |  |
| --- | --- |
| ID | 3410(0) |
| 领域 | Bio-Medical |
| 用户问题 | In which chromosome are transgenes inserted in the case of the LiPS-A3S line? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | In the case of the LiPS-A3S line, transgenes are inserted into chromosome 19. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. In the case of the LiPS-A3S line, transgenes are inserted into chromosome 19. |
| 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 | 2 |

|  |  |
| --- | --- |
| ID | 3430(1) |
| 领域 | Bio-Medical |
| 用户问题 | Which tool exist for predicting drug synergy with deep learning? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | There are several tools available for predicting drug synergy using deep learning techniques. Some of them include: 1. DeepSynergy: It is a deep learning-based tool that predicts drug synergy by using convolutional neural networks (CNNs) and recurrent neural networks (RNNs). It uses molecular descriptors and drug-target interactions as input to predict drug synergy. 2. DeepSynergyNet: This tool utilizes deep neural networks and graph convolutional networks (GCNs) to predict drug-drug synergy. It considers both chemical structures and gene expression data to make predictions. 3. DeepSynth: DeepSynth is a deep learning-based method that uses graph convolutional neural networks (GCNs) to predict drug synergy based on chemical structures. It takes molecular fingerprints as input and predicts the probability of drug synergy. 4. GIN-NNT: GIN-NNT (Graph Isomorphism Network-based Neural Network Toolkit) is a deep learning framework specifically designed for predicting drug synergy. It employs graph neural networks (GNNs) to learn from the molecular graph representation of drugs and predict synergy. 5. DeeSyGNA: This tool uses deep learning to predict drug synergy in the context of gene expression data. It employs deep neural networks to integrate multiple data sources, including gene expression profiles and drug molecular structures, for accurate synergy prediction. It is important to note that these tools may have different capabilities, input requirements, and performance levels. Researchers should carefully evaluate and choose the tool that best suits their specific needs and data types. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. DeepSynergy is a tool that predicts drug synergy using convolutional neural networks (CNNs) and recurrent neural networks (RNNs). 2. DeepSynergyNet uses deep neural networks and graph convolutional networks (GCNs) in predicting drug-drug synergy. 3. DeepSynth is a deep learning-based tool that employs graph convolutional neural networks (GCNs) for drug synergy prediction based on chemical structures. 4. GIN-NNT is a deep learning framework specifically designed for predicting drug synergy using graph neural networks (GNNs). 5. DeeSyGNA uses deep learning for drug synergy prediction in the context of gene expression data by integrating multiple data sources including gene expression profiles and drug molecular structures. |
| 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 | 1,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 3433(2) |
| 领域 | Bio-Medical |
| 用户问题 | Which cloud-based platform has been developed for comparing GWAS? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | The cloud-based platform developed for comparing GWAS is called "Comparison of GWAS" (Com-GWAS). |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. "Comparison of GWAS" (Com-GWAS) is a cloud-based platform developed for comparing GWAS. |
| 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 | 7 |

|  |  |
| --- | --- |
| ID | 3434(3) |
| 领域 | Bio-Medical |
| 用户问题 | Can CMB305 be used against sarcomas? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Yes, CMB305 is a potential treatment option for sarcomas. CMB305 is an immunotherapy that combines a modified virus called C134 with the NY-ESO-1 protein, which is commonly expressed in several types of cancer including sarcomas. The modified virus C134 helps deliver the NY-ESO-1 protein to tumor cells, which then stimulates an immune response against the cancer cells expressing NY-ESO-1. This immune response can potentially lead to the destruction of tumor cells and a reduction in tumor size. CMB305 has shown promising results in early clinical trials for sarcomas, particularly in combination with other immunotherapies or chemotherapy drugs. However, further research and clinical trials are needed to determine its long-term efficacy and safety for sarcoma treatment. It is always important to consult with a healthcare professional for specific treatment options and recommendations. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. CMB305 is an immunotherapy that is potentially used for the treatment of sarcomas. 2. CMB305 combines a modified virus called C134 with the NY-ESO-1 protein. 3. The NY-ESO-1 protein is commonly expressed in several types of cancer including sarcomas. 4. The modified virus C134 in CMB305 helps deliver the NY-ESO-1 protein to tumor cells, stimulating an immune response against the cancer cells expressing NY-ESO-1. 5. CMB305 has shown promising results in early clinical trials for sarcomas. |
| 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 | 1,2,1,1,1 |

|  |  |
| --- | --- |
| ID | 3461(4) |
| 领域 | Bio-Medical |
| 用户问题 | What are manifestations of the Saint's Triad? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The Saint's Triad is a concept derived from Christian theology that refers to the threefold expressions of holiness or sanctity. These manifestations or aspects of the Saint's Triad are: 1. Purity: This aspect of the Saint's Triad relates to the idea of moral and spiritual purity. It implies living a life that is free from sin and corruption, striving to be pure in thoughts, actions, and intentions. Purity is often associated with traits like honesty, integrity, chastity, and innocence. 2. Humility: Humility is another manifestation of the Saint's Triad and refers to a modest and unassuming approach to life. It involves recognizing one's limitations, weaknesses, and faults, and not seeking personal glory or recognition. Humility emphasizes selflessness, service to others, and a willingness to learn and grow. 3. Charity: Charity, also known as love in Christian theology, is the third aspect of the Saint's Triad. It encompasses not only acts of kindness and generosity but also an unconditional love for all beings. Charity involves self-sacrifice, compassion, forgiveness, and a desire to help others in need. It is considered the supreme virtue and the fulfillment of all other commandments in Christianity. These manifestations of the Saint's Triad are interconnected and often seen as interdependent, with each aspect supporting and enhancing the others. Together, they represent a comprehensive model of holiness and are considered essential qualities for individuals striving for spiritual growth and moral integrity in their Christian faith. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Saint's Triad is a concept from Christian theology representing threefold expressions of holiness or sanctity. 2. Purity is one aspect of the Saint's Triad and signifies moral and spiritual purity, often associated with honesty, integrity, chastity, and innocence. 3. Humility is another manifestation of the Saint's Triad, highlighting a modest approach to life, selflessness, and a willingness to learn and grow. 4. Charity, also recognized as love in Christian theology, is the third aspect of the Saint's Triad, involving kindness, generosity, compassion, forgiveness, and a desire to help others. 5. These three manifestations of the Saint's Triad are seen as interconnected and interdependent within the framework of the Christian faith. |
| 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 | 2,2,2,2,7 |

|  |  |
| --- | --- |
| ID | 3470(5) |
| 领域 | Bio-Medical |
| 用户问题 | Is overexpression of LY6K associated with better prognosis for non-small cell lung cancer patients? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,3,5 |
| 模型回复 | There is not enough research available to make a definite conclusion about the association between overexpression of LY6K and prognosis for non-small cell lung cancer (NSCLC) patients. LY6K, also known as lymphocyte antigen 6 complex, locus K, is a gene that has been found to be overexpressed in certain cancers, including NSCLC. However, the exact role of LY6K in cancer progression and prognosis is still not well-understood. Some studies have suggested that high expression of LY6K may be associated with poor prognosis and more aggressive tumor characteristics in NSCLC patients. For example, a study published in the International Journal of Oncology in 2017 found that higher levels of LY6K expression were associated with advanced tumor stage and lymph node metastasis in NSCLC patients. Another study published in Oncology Reports in 2019 reported similar findings, with higher LY6K expression being correlated with larger tumor size, lymph node metastasis, and advanced tumor stage. However, more research is needed to confirm these findings and fully understand the impact of LY6K overexpression on NSCLC prognosis. Additionally, there may be other factors and genetic alterations that interact with LY6K expression and influence patient outcomes. Therefore, it is important to consult with medical professionals and rely on the latest scientific literature for accurate and up-to-date information regarding LY6K and NSCLC prognosis. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. LY6K, also known as lymphocyte antigen 6 complex, locus K, is a gene overexpressed in certain cancers, including non-small cell lung cancer. 2. The exact role of LY6K in cancer progression and prognosis is not fully understood. 3. Some studies suggest that high expression of LY6K is associated with poor prognosis and aggressive tumor characteristics in NSCLC patients. 4. A study published in the International Journal of Oncology in 2017 associated higher levels of LY6K expression with advanced tumor stage and lymph node metastasis in NSCLC patients. 5. A study published in Oncology Reports in 2019 reported similar findings, associating higher LY6K expression with larger tumor size, lymph node metastasis, and advanced tumor stage. |
| 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 | 1,1,1,7,7 |

|  |  |
| --- | --- |
| ID | 3473(6) |
| 领域 | Bio-Medical |
| 用户问题 | List Cdk targets that are dephosphorylated during cytokinesis |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,3,5 |
| 模型回复 | 1. CDK1/Cyclin B complex: CDK1 is a key regulator of cell division and is activated by phosphorylation. However, during cytokinesis, CDK1 needs to be dephosphorylated to control the exit from mitosis. This dephosphorylation is mediated by phosphatase enzymes such as CDC25. 2. Myosin: Myosin is a motor protein that plays a crucial role in cytokinesis by generating contractile forces to drive cell furrowing. Phosphorylation of myosin by CDK1 inhibits its activity. Therefore, during cytokinesis, myosin needs to be dephosphorylated to become activated and promote contractile ring contraction. Phosphatases such as PP1 and PP2A mediate the dephosphorylation of myosin. 3. Ect2: Ect2 is a Rho family guanine nucleotide exchange factor (GEF) that activates the small GTPase RhoA during cytokinesis. Phosphorylation of Ect2 by CDK1 inhibits its activity. To enable RhoA activation and subsequent contractile ring assembly, Ect2 needs to be dephosphorylated. The phosphatase PP1 has been implicated in the dephosphorylation of Ect2. 4. Anillin: Anillin is a cytoskeletal protein that binds to the actin cytoskeleton and plays a role in cytokinesis. Phosphorylation of anillin by CDK1 regulates its localization and interaction with other cytokinesis proteins. During cytokinesis, anillin needs to be dephosphorylated to promote furrow ingression. Phosphatases such as PP1 and PP2A are involved in the dephosphorylation of anillin. 5. Cofilin: Cofilin is an actin-binding protein that regulates actin dynamics during cytokinesis. Phosphorylation of cofilin by CDK1 inhibits its actin-depolymerizing activity. Dephosphorylation of cofilin by phosphatases such as chronophin and slingshot is required for actin remodeling and furrow ingression during cytokinesis. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. CDK1 is a key regulator of cell division and is dephosphorylated during cytokinesis. 2. Myosin, a motor protein that plays a critical part in cytokinesis, needs to be dephosphorylated during this process. 3. Ect2, a Rho family guanine nucleotide exchange factor (GEF), is dephosphorylated during cytokinesis. 4. Anillin, a cytoskeletal protein that has a role in cytokinesis, is dephosphorylated during cytokinesis. 5. Cofilin, an actin-binding protein, is dephosphorylated during cytokinesis. |
| 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 | 1,3,3,1,3 |

|  |  |
| --- | --- |
| ID | 3508(7) |
| 领域 | Bio-Medical |
| 用户问题 | What is Xanamem? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Xanamem is an experimental drug developed by Cortexyme Inc., an American biotechnology company. It is being investigated as a potential treatment for Alzheimer's disease. Xanamem works by targeting a specific bacterial enzyme called gingipains that are believed to play a role in the development and progression of Alzheimer's disease. By inhibiting gingipains, Xanamem aims to reduce inflammation and neurodegeneration in the brain, potentially slowing down the cognitive decline associated with Alzheimer's disease. However, it is important to note that Xanamem is still undergoing clinical trials, and its safety and efficacy are yet to be fully established. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Xanamem is an experimental drug developed by Cortexyme Inc. 2. Cortexyme Inc. is an American biotechnology company. 3. Xanamem targets a specific bacterial enzyme called gingipains. 4. Gingipains is believed to be involved in the development and progression of Alzheimer's disease. 5. Xanamem is still undergoing clinical trials for treatment 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 | 2,1,7,1,1 |

|  |  |
| --- | --- |
| ID | 3520(8) |
| 领域 | Bio-Medical |
| 用户问题 | What is the role of the Hof1-Cyk3 interaction in yeast? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | The Hof1-Cyk3 interaction plays a crucial role in cytokinesis, the process of cell division, in yeast.  Hof1 (Homologue of Fifteen) and Cyk3 (Cytokinesis protein 3) are two proteins that interact with each other during the final stages of cytokinesis. This interaction is necessary for proper actomyosin ring contraction and septum formation, which are essential steps in completing cell division. During cytokinesis, the actomyosin ring, composed of actin and myosin filaments, constricts and forms a contractile ring at the division site. The Hof1-Cyk3 complex interacts with the actomyosin ring, recruiting additional proteins involved in septum formation and cell wall synthesis. Specifically, the Hof1-Cyk3 complex helps to stabilize and maintain the actomyosin ring and promotes constriction by regulating the activity of myosin. It also recruits enzymes required for septum formation, such as chitin synthase, to the division site. The septum is a structure that forms between the two daughter cells during cytokinesis and eventually becomes the cell wall. Overall, the interaction between Hof1 and Cyk3 is necessary for proper actomyosin ring contraction, septum formation, and completion of cytokinesis in yeast. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Hof1-Cyk3 interaction plays a crucial role in cytokinesis, the process of cell division, in yeast. 2. Hof1 and Cyk3 are two proteins that interact with each other during the final stages of cytokinesis in yeast. 3. This interaction is necessary for proper actomyosin ring contraction and septum formation. 4. The Hof1-Cyk3 complex interacts with the actomyosin ring and recruits additional proteins involved in septum formation and cell wall synthesis. 5. The Hof1-Cyk3 complex helps to stabilize and maintain the actomyosin ring and promotes constriction by regulating the activity of myosin. It also recruits enzymes required for septum formation, such as chitin synthase, to the division site. |
| 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 | 1,1,2,3,3 |

|  |  |
| --- | --- |
| ID | 3598(9) |
| 领域 | Bio-Medical |
| 用户问题 | Which T-UCRs have been implicated in gastric cancer? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Several T-UCRs (tumor-associated ultraconserved regions) have been implicated in gastric cancer. Some of them are: 1. T-UCR uc.339: This T-UCR has been found to be downregulated in gastric cancer tissues compared to normal gastric tissues. Its decreased expression has been associated with poor prognosis and metastasis in gastric cancer patients. 2. T-UCR uc.158: The expression of this T-UCR has been reported to be reduced in gastric cancer tissues. It has been suggested to act as a tumor suppressor by inhibiting cancer cell growth and invasion. 3. T-UCR uc.338: Increased expression of this T-UCR has been observed in gastric cancer tissues. Higher levels of uc.338 have been associated with advanced tumor stage and lymph node metastasis, indicating its potential role in the progression of gastric cancer. 4. T-UCRs uc.73 and uc.174: These T-UCRs have been identified as potential diagnostic and prognostic biomarkers for gastric cancer. Increased expression of uc.73 and uc.174 has been observed in gastric cancer tissues, and their levels have been correlated with tumor stage and patient survival. It is important to note that the field of T-UCRs and their involvement in cancer is still relatively new, and further research is required to fully understand their roles in gastric cancer development and progression. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. T-UCR uc.339 is downregulated in gastric cancer tissues compared to normal gastric tissues. 2. Decreased expression of T-UCR uc.339 has been associated with poor prognosis and metastasis in gastric cancer patients. 3. T-UCR uc.158's downregulation is found in gastric cancer tissues and it seemingly acts as a tumor suppressor. 4. Increased expression of T-UCR uc.338 has been observed in gastric cancer tissues. 5. T-UCRs uc.73 and uc.174 have been identified as potential diagnostic and prognostic biomarkers for gastric 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 | 7,7,1,7,7 |

|  |  |
| --- | --- |
| ID | 3607(10) |
| 领域 | Bio-Medical |
| 用户问题 | What is the Lupus Severity Index (LSI)? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,4 |
| 模型回复 | The Lupus Severity Index (LSI) is a tool used to measure the severity of systemic lupus erythematosus (SLE), a chronic autoimmune disease. It assesses disease activity and organ damage to determine the overall severity of the disease. The LSI takes into account various clinical and laboratory parameters such as skin rashes, joint inflammation, kidney function, blood cell counts, and antibodies. It provides a numerical score that helps healthcare professionals monitor disease progression and response to treatment. The higher the LSI score, the more severe the lupus is considered to be. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Lupus Severity Index (LSI) is utilized to measure the severity of systemic lupus erythematosus (SLE). 2. The Lupus Severity Index assesses disease activity and organ damage. 3. The LSI takes into account various clinical and laboratory parameters such as skin rashes, joint inflammation, kidney function, blood cell counts, and antibodies. 4. The Lupus Severity Index provides a numerical score that assists healthcare professionals in monitoring disease progression and response to treatment. 5. The higher the LSI score, the more severe the lupus is considered to be. |
| 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 | 1,4,1,1,1 |

|  |  |
| --- | --- |
| ID | 3615(11) |
| 领域 | Bio-Medical |
| 用户问题 | Which disorders are caused by de novo mutations in ZSWIM6? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | At present, there are no known disorders that are specifically caused by de novo mutations in the ZSWIM6 gene. ZSWIM6 is a protein-coding gene that is involved in various biological processes. While de novo mutations in the ZSWIM6 gene may exist, there is limited information available regarding their specific phenotypic effects. Further research is needed to understand the potential association between de novo mutations in ZSWIM6 and specific disorders or clinical conditions. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. There are currently no known disorders that are specifically caused by de novo mutations in the ZSWIM6 gene. 2. ZSWIM6 is a protein-coding gene. 3. ZSWIM6 gene is involved in various biological processes. 4. There might be de novo mutations in the ZSWIM6 gene, but their specific phenotypic effects are unclear. 5. Further research is needed to understand the potential association between de novo mutations in ZSWIM6 and specific disorders or clinical conditions. |
| 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 | 5,1,1,5,1 |

|  |  |
| --- | --- |
| ID | 3626(12) |
| 领域 | Bio-Medical |
| 用户问题 | Which disease can be classified using the Koos Classification? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The Koos Classification is a system used to classify osteoarthritis (OA) of the knee. OA is a degenerative joint disease characterized by the breakdown of cartilage in the joint, leading to pain and stiffness. The Koos Classification helps to categorize the severity and impact of OA on an individual's daily activities and quality of life. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Koos Classification is a system used to classify osteoarthritis of the knee. 2. Osteoarthritis is a degenerative joint disease. 3. Osteoarthritis is characterized by the breakdown of cartilage in the joint. 4. Osteoarthritis leads to pain and stiffness. 5. The Koos Classification categorizes the severity and impact of osteoarthritis on an individual's daily activities and quality of life. |
| 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 | 1,1,4,1,4 |

|  |  |
| --- | --- |
| ID | 3628(13) |
| 领域 | Bio-Medical |
| 用户问题 | What are the in vivo effects of AZD8601? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,1,5 |
| 模型回复 | AZD8601 is a regenerative medicine product that falls under the category of cardiac progenitor cell therapy. It is designed to stimulate the repair and regeneration of damaged heart tissue. In vivo studies of AZD8601 have shown several effects: 1. Improved Cardiac Function: AZD8601 has demonstrated the ability to improve cardiac function in preclinical animal models of heart failure. It promotes the growth and differentiation of cardiac progenitor cells, which can contribute to the repair of damaged tissue and enhance heart function. 2. Reduced Scar Formation: In vivo studies have shown that AZD8601 treatment can reduce the formation of scar tissue after a heart attack or other cardiac injury. Scar tissue can impair heart function, so limiting its formation is beneficial for recovery. 3. Increased Blood Vessel Formation: AZD8601 has been shown to promote angiogenesis, the formation of new blood vessels, in the heart tissue. This effect can improve blood supply to the damaged area and support tissue healing and regeneration. 4. Anti-inflammatory Properties: AZD8601 has demonstrated anti-inflammatory effects in vivo. Inflammation is a key component of cardiac injury and can exacerbate tissue damage. By reducing inflammation, AZD8601 may help create a more favorable environment for tissue repair. 5. Enhanced Cell Survival: AZD8601 has been found to promote the survival of cardiac progenitor cells within the damaged heart tissue. This allows the cells to exert their regenerative potential for a more extended period, aiding in tissue repair. These in vivo effects suggest that AZD8601 holds promise as a potential therapy for heart failure and cardiac tissue repair. Further clinical trials are ongoing to evaluate its safety and efficacy in humans. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. AZD8601 is a regenerative medicine product that falls under the category of cardiac progenitor cell therapy. 2. AZD8601 has shown to improve cardiac function in preclinical animal models by promoting the growth and differentiation of cardiac progenitor cells. 3. Studies have shown that AZD8601 can reduce the formation of scar tissue after a cardiac injury. 4. AZD8601 has been found to promote the formation of new blood vessels in heart tissue. 5. In vivo studies demonstrated that AZD8601 can reduce inflammation and promote the survival of cardiac progenitor cells within damaged heart tissue. |
| 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 | 1,1,7,7,1 |

|  |  |
| --- | --- |
| ID | 3640(14) |
| 领域 | Bio-Medical |
| 用户问题 | How are SAHFS created? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,3 |
| 模型回复 | SAHFs (Sequential Attestation Hints Files) are created during the boot process of the operating system on an Intel-based computer system with a Trusted Platform Module (TPM) installed. Here is a general overview of how SAHFs are created: 1. Boot Process: The process begins when the computer is powered on or restarted. During the boot process, the system firmware (e.g., BIOS, UEFI) initializes the hardware components. 2. TPM Initialization: If a TPM is present, the system firmware initializes and configures the TPM. The TPM is a dedicated chip on the motherboard that stores cryptographic keys, securely measures the components of the system, and performs cryptographic operations. 3. Measurement: As the boot process continues, the system firmware measures the integrity of various components of the system, such as the firmware code, bootloader, kernel, and other critical components. The measurements are usually performed using cryptographic hash functions. 4. Attestation: Once the measurements are collected, the system firmware generates an attestation for this bundle of measurements using the private key of the TPM. The attestation is a cryptographic proof that the measurements were taken and signed by a valid TPM. 5. SAHF Creation: The attestation generated in the previous step forms the basis for creating the SAHF. The SAHF is a digitally signed file that contains the measurements and the attestation information. It is usually created by the firmware or an operating system component. 6. Persistence: The SAHF is securely stored in a specific location on the system, typically within the TPM. This ensures that the SAHF remains protected and tamper-resistant. SAHFs are primarily used in the context of trusted boot mechanisms to verify the integrity of the system's boot chain, making them an essential component of securing the system's boot process. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Sequential Attestation Hints Files (SAHFs) are created during the boot process of the operating system on an Intel-based computer system with a Trusted Platform Module (TPM) installed. 2. A TPM is a dedicated chip on the motherboard that stores cryptographic keys, securely measures the components of the system, and performs cryptographic operations. 3. During the boot process, the system firmware measures the integrity of various components of the system, such as the firmware code, bootloader, kernel. 4. A SAHF is a digitally signed file that contains the measurements and attestation information. 5. SAHFs are primarily used in the context of trusted boot mechanisms to verify the integrity of the system's boot chain. |
| 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 | 7,1,1,7,7 |

|  |  |
| --- | --- |
| ID | 3672(15) |
| 领域 | Bio-Medical |
| 用户问题 | What is the function of the PDZ domain in SATB1? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | The PDZ (PSD-95, Dlg1, ZO-1) domain in SATB1 is responsible for protein-protein interactions. PDZ domains are common protein interaction modules found in many proteins and are involved in organizing protein complexes and signaling pathways. In SATB1, the PDZ domain allows for binding to specific target proteins, facilitating the formation of protein complexes. This domain is important for SATB1's role as a genome organizer and transcription factor. SATB1 uses its PDZ domain to interact with various proteins involved in chromatin remodeling, transcriptional regulation, and epigenetic modifications. Through these interactions, SATB1 helps orchestrate the 3D organization of the genome and regulate gene expression. Overall, the PDZ domain in SATB1 plays a crucial role in mediating protein-protein interactions that are essential for its function as a genome organizer and transcription factor. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The PDZ domain in SATB1 is responsible for protein-protein interactions. 2. PDZ domains are common protein interaction modules found in many proteins. 3. PDZ domains are involved in organizing protein complexes and signaling pathways. 4. The PDZ domain enables SATB1 to interact with proteins involved in chromatin remodeling, transcriptional regulation, and epigenetic modifications. 5. SATB1 uses its PDZ domain to regulate gene expression and orchestrate the 3D organization 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 | 3,1,1,2,2 |

|  |  |
| --- | --- |
| ID | 3678(16) |
| 领域 | Bio-Medical |
| 用户问题 | What is the basis of the BLISS technique? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | The BLISS technique is based on the principles of positive psychology and cognitive-behavioral therapy. It incorporates various elements such as mindfulness, gratitude, savoring positive experiences, positive self-affirmation, and setting intentions to enhance overall well-being and happiness. The technique aims to rewire the brain's neural pathways and focus on positive emotions and thoughts to improve overall mental health and life satisfaction. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The BLISS technique is based on positive psychology and cognitive-behavioral therapy principles. 2. As part of the BLISS technique, mindfulness and gratitude are incorporated. 3. Positive self-affirmation and setting intentions are elements of the BLISS technique. 4. The aim of the BLISS technique is to improve overall mental health and life satisfaction. 5. The BLISS technique intends to rewire the brain's neural pathways to focus on positive emotions and thoughts. |
| 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 | 7,7,7,1,7 |

|  |  |
| --- | --- |
| ID | 3679(17) |
| 领域 | Bio-Medical |
| 用户问题 | List 3 NK3R antagonists. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | 1. Aprepitant: It is a selective NK3R antagonist commonly used in chemotherapy-induced nausea and vomiting. It works by blocking the action of substance P at the NK3 receptor. 2. Vestipitant: This is another NK3 receptor antagonist that is being investigated for its potential use in various conditions including anxiety disorders, substance use disorders, and schizophrenia. It works by inhibiting the binding of substance P to the NK3 receptor. 3. Talnetant: It is a potent and selective NK3 receptor antagonist that has been studied for its potential use in various psychiatric disorders, including depression and anxiety. Talnetant blocks the neurotransmitter substance P from binding to the NK3 receptor, thereby modulating mood and behavior. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Aprepitant is a selective NK3R antagonist used in chemotherapy-induced nausea and vomiting. 2. Vestipitant is an NK3 receptor antagonist which is investigated for potential use in conditions including anxiety disorders, substance use disorders, and schizophrenia. 3. Talnetant is a potent and selective NK3 receptor antagonist which has been studied for its potential use in psychiatric disorders, including depression and anxiety. 4. The action of substance P at the NK3 receptor can be blocked by certain drugs such as Aprepitant. 5. NK3R antagonists work by inhibiting the binding of substance P to the NK3 receptor, thereby modulating mood and behavior. |
| 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 | 7,1,1,7,1 |

|  |  |
| --- | --- |
| ID | 3691(18) |
| 领域 | Bio-Medical |
| 用户问题 | Which drug is the first oral ghrelin receptor inverse agonist to be profiled in healthy subjects? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The first oral ghrelin receptor inverse agonist to be profiled in healthy subjects is called TTP-970. TTP-970 is a drug developed by Takeda Pharmaceutical Company Limited. It is being studied for its potential in treating metabolic disorders and obesity. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. TTP-970 is the first oral ghrelin receptor inverse agonist to be profiled in healthy subjects. 2. TTP-970 is a drug developed by Takeda Pharmaceutical Company Limited. 3. The drug TTP-970 is being studied for its potential use in treating metabolic disorders. 4. TTP-970 is also being studied for its potential use in treating obesity. |
| 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 | 7,7,7,7 |

|  |  |
| --- | --- |
| ID | 3693(19) |
| 领域 | Bio-Medical |
| 用户问题 | What is the protective efficacy of vaxchora against moderate to severe cholera? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The protective efficacy of Vaxchora against moderate to severe cholera has been reported to be approximately 90%. Studies have shown that the vaccine provides significant protection against Vibrio cholerae, the bacterium that causes cholera. However, it is important to note that while Vaxchora can provide a high level of protection, it does not provide complete immunity, and it is still possible for individuals to contract milder forms of cholera or become carriers of the bacteria. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The protective efficacy of Vaxchora against moderate to severe cholera is approximately 90%. 2. Vaxchora provides significant protection against Vibrio cholerae, which is the bacterium that causes cholera. 3. Vaxchora does not provide complete immunity against cholera. 4. It is possible for individuals vaccinated with Vaxchora to contract milder forms of cholera. 5. It's possible for individuals vaccinated with Vaxchora to become carriers of the cholera bacteria. |
| 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 | 1,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 3716(20) |
| 领域 | Bio-Medical |
| 用户问题 | Which was the first cholera vaccine approved in the US? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The first cholera vaccine approved in the United States was Dukoral, which received approval from the U.S. Food and Drug Administration (FDA) in 2016. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Dukoral was the first cholera vaccine approved in the United States. 2. Dukoral received approval from the U.S. Food and Drug Administration in 2016. |
| 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 | 2,2 |

|  |  |
| --- | --- |
| ID | 3737(21) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the most common monogenic cause of common variable immunodeficiency (CVID) in Europeans? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The most common monogenic cause of Common Variable Immunodeficiency (CVID) in Europeans is mutations in the TNFRSF13B gene, which encodes the TACI protein. These mutations are responsible for approximately 10-15% of CVID cases in Europeans. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Common Variable Immunodeficiency (CVID) in Europeans is most commonly caused by mutations in the TNFRSF13B gene. 2. The TNFRSF13B gene encodes the TACI protein. 3. The mutations in the TNFRSF13B gene are responsible for approximately 10-15% of CVID cases in Europeans. |
| 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 | 2,1,1 |

|  |  |
| --- | --- |
| ID | 3743(22) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the role of the IFIT1 gene in Systemic Lupus Erythematosus (SLE)? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The IFIT1 gene, also known as interferon-induced protein with tetratricopeptide repeats 1, plays a role in the pathogenesis of Systemic Lupus Erythematosus (SLE).  SLE is an autoimmune disease characterized by the production of autoantibodies against self-components, leading to chronic inflammation and tissue damage. Interferons, particularly type I interferons, have been implicated in the pathogenesis of SLE. The IFIT1 gene is an interferon-stimulated gene (ISG) that is upregulated in response to viral infection or exposure to interferons. Studies have shown that IFIT1 expression is elevated in the peripheral blood cells and skin of individuals with SLE. It is believed that the increased expression of IFIT1 in SLE is a result of the overactive type I interferon response observed in the disease. The exact role of IFIT1 in SLE is not fully understood, but it is thought to contribute to the disease by promoting abnormal immune responses. IFIT1 may enhance the production of autoantibodies by B cells, as well as the production of inflammatory cytokines by immune cells. Additionally, IFIT1 may play a role in the dysregulation of immune cell signaling pathways that contribute to the chronic inflammation seen in SLE. Overall, the overexpression of IFIT1 in SLE suggests that it may contribute to the pathogenesis of the disease by promoting abnormal immune responses and chronic inflammation. Further research is needed to fully elucidate the precise mechanisms by which IFIT1 influences SLE. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The IFIT1 gene, also known as interferon-induced protein with tetratricopeptide repeats 1, plays a role in the pathogenesis of Systemic Lupus Erythematosus (SLE). 2. Systemic Lupus Erythematosus is an autoimmune disease characterized by the production of autoantibodies against self-components, leading to chronic inflammation and tissue damage. 3. IFIT1 gene is an interferon-stimulated gene that is upregulated in response to viral infection or exposure to interferons. 4. IFIT1 expression is elevated in the peripheral blood cells and skin of individuals with SLE. 5. IFIT1 may enhance the production of autoantibodies by B cells, as well as the production of inflammatory cytokines by immune cells. |
| 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 | 1,1,1,7,7 |

|  |  |
| --- | --- |
| ID | 3752(23) |
| 领域 | Bio-Medical |
| 用户问题 | What is the use of the Liverpool Elbow Score? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The Liverpool Elbow Score is a clinical tool used in orthopedics to assess the severity and outcomes of elbow conditions such as injuries, fractures, and arthritis. It is particularly helpful in evaluating patients with rheumatoid arthritis.  The score includes various parameters such as pain, range of motion, stability, radiographic evidence, and functional ability. Each parameter is assigned a value, and the total score provides an objective measurement of the severity of elbow dysfunction. The use of the Liverpool Elbow Score allows clinicians to standardize the evaluation process and track the progress of patients over time. It helps in determining the most appropriate treatment approach, assessing the success of interventions, and providing an indication of prognosis or potential disability. Overall, the Liverpool Elbow Score improves communication between healthcare professionals, facilitates research and clinical trials, and aids in enhancing patient care and outcomes. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Liverpool Elbow Score is a clinical tool used in orthopedics to assess elbow conditions such as injuries, fractures, and arthritis. 2. The score is particularly helpful in evaluating patients with rheumatoid arthritis. 3. The Liverpool Elbow Score includes parameters such as pain, range of motion, stability, radiographic evidence, and functional ability. 4. The use of the Liverpool Elbow Score helps in standardizing the evaluation process and tracking the progress of patients over time. 5. The Liverpool Elbow Score is used to determine the most appropriate treatment approach, assess the success of interventions, and provide an indication of prognosis or potential disability. |
| 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 | 1,7,1,1,6 |

|  |  |
| --- | --- |
| ID | 3763(24) |
| 领域 | Bio-Medical |
| 用户问题 | Describe efforts on Sarcoma from the 100,000 Genomes Project |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The 100,000 Genomes Project was a pioneering initiative launched by the UK government in 2012 with the aim of sequencing and analyzing 100,000 whole genomes from patients with rare diseases, cancer, and infectious diseases. The project aimed to improve the understanding of genetic factors influencing diseases, develop personalized treatments, and ultimately improve patient outcomes. With regards to sarcomas, a few efforts were made as part of the project: 1. Establishing a comprehensive sarcoma dataset: The project aimed to collect genomic data from sarcoma patients to create a comprehensive dataset. This involved sequencing the whole genomes of sarcoma patients and analyzing the genetic variations specific to the disease. This dataset provided insights into the genetic alterations that drive sarcoma development and progression. 2. Identifying potential treatment targets: By analyzing the genomic data from sarcoma patients, researchers were able to identify specific genetic mutations and alterations that might be driving the cancer. This information helped in identifying potential treatment targets for developing new therapies or repurposing existing drugs for sarcoma patients. 3. Understanding sarcoma subtypes: Sarcoma is a diverse group of cancers with numerous subtypes, each having distinct genetic characteristics. The 100,000 Genomes Project aimed to identify and classify different subtypes of sarcoma based on genetic profiling. This information helped clinicians and researchers better understand the molecular basis of each subtype, which in turn could lead to more effective diagnosis, prognosis, and treatment strategies. 4. Enabling clinical trials and research: The availability of genomic data from sarcoma patients through the 100,000 Genomes Project facilitated the development of clinical trials and research studies focused on sarcoma. Researchers could use this data to design targeted therapies or investigate the efficacy of existing treatments for specific sarcoma subtypes. Overall, the efforts on sarcoma within the 100,000 Genomes Project aimed to improve our understanding of the genetics underlying sarcoma, identify potential treatment targets, and enable personalized medicine approaches for better patient outcomes. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The 100,000 Genomes Project was launched by the UK government in 2012. 2. This project aimed to sequence and analyze 100,000 whole genomes from patients with rare diseases, cancer, and infectious diseases. 3. As part of the project, genomic data from sarcoma patients was collected to create a comprehensive dataset. 4. The 100,000 Genomes Project sought to identify and classify different subtypes of sarcoma based on genetic profiling. 5. The availability of genomic data from sarcoma patients through the 100,000 Genomes Project facilitated the development of clinical trials and research studies focused on sarcoma. |
| 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 | 1,2,1,7,1 |

|  |  |
| --- | --- |
| ID | 3777(25) |
| 领域 | Bio-Medical |
| 用户问题 | Does protein ALEX1 contain armadillo repeats? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | No, protein ALEX1 does not contain armadillo repeats. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Protein ALEX1 does not contain armadillo repeats. |
| 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 | 3 |

|  |  |
| --- | --- |
| ID | 3789(26) |
| 领域 | Bio-Medical |
| 用户问题 | List enzymes that removes histone modifications. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | 1. Histone demethylases: These enzymes remove methyl groups from histone proteins. Examples include LSD1/KDM1A, UTX/KDM6A, and JMJD3/KDM6B. 2. Histone deacetylases (HDACs): These enzymes remove acetyl groups from lysine residues on histone proteins. Examples include HDAC1, HDAC2, and HDAC3. 3. Histone ubiquitin ligases: These enzymes remove ubiquitin moieties from histone proteins. Examples include USP16 and USP22. 4. Protein arginine deiminases (PADs): These enzymes remove methyl groups from arginine residues on histone proteins through a process called citrullination. 5. Histone methyltransferase (HMT) inhibitors: Although not enzymes that directly remove histone modifications, HMT inhibitors indirectly lead to the removal of methyl groups from histones by preventing their addition. 6. Histone acetyltransferase (HAT) inhibitors: Similar to HMT inhibitors, HAT inhibitors indirectly remove acetyl groups from histones by inhibiting their addition. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Histone demethylases are enzymes that remove methyl groups from histone proteins. 2. Histone deacetylases, such as HDAC1, HDAC2, and HDAC3, remove acetyl groups from lysine residues on histone proteins. 3. Histone ubiquitin ligases, such as USP16 and USP22, remove ubiquitin moieties from histone proteins. 4. Protein arginine deiminases remove methyl groups from arginine residues on histone proteins through a process called citrullination. 5. Histone methyltransferase inhibitors and histone acetyltransferase inhibitors lead to the removal of methyl and acetyl groups from histones respectively by preventing their addition. |
| 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 | 1,1,3,2,1 |

|  |  |
| --- | --- |
| ID | 3806(27) |
| 领域 | Bio-Medical |
| 用户问题 | Does head ct increase brain tumor risk? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | No, a head CT scan does not increase the risk of developing a brain tumor. CT scans use a form of X-ray technology to create detailed images of the brain and other parts of the body. The radiation exposure from a single head CT is typically minimal, and the associated risk of developing a tumor from the radiation exposure is extremely low. However, repeated or excessive exposure to radiation over time may slightly increase the risk of developing a tumor. It is always important to weigh the potential benefits of a CT scan against any potential risks, and healthcare providers take precautions to minimize radiation exposure as much as possible. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. A head CT scan does not increase the risk of developing a brain tumor. 2. CT scans use a form of X-ray technology to create detailed images of the brain and other parts of the body. 3. The radiation exposure from a single head CT is typically minimal. 4. Repeated or excessive exposure to radiation over time may slightly increase the risk of developing a tumor. 5. Healthcare providers take precautions to minimize radiation exposure as much as possible. |
| 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 | 3,1,3,1,1 |

|  |  |
| --- | --- |
| ID | 3809(28) |
| 领域 | Bio-Medical |
| 用户问题 | Which type of pluripotency is Otx2 associated with? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Otx2 is associated with the pluripotency of epiblast 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 | 1 |
| 提取的事实 | 1. Otx2 is associated with the pluripotency of epiblast cells. |
| 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 | 4 |

|  |  |
| --- | --- |
| ID | 3815(29) |
| 领域 | Bio-Medical |
| 用户问题 | How many DNaseI hypersensitive sites (DHS) mark the murine beta globin locus region? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | There are several DNaseI hypersensitive sites (DHS) that mark the murine beta globin locus region. Specifically, there are five known DHS sites in this region, which are referred to as HS1, HS2, HS3, HS4, and HS5. These sites are important for the regulation of gene expression by allowing transcription factors and other regulatory proteins to access the DNA and control gene activity. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. There are several DNaseI hypersensitive sites (DHS) that mark the murine beta globin locus region. 2. There are five known DHS sites in the murine beta globin locus region. 3. The five known DHS sites are referred to as HS1, HS2, HS3, HS4, and HS5. 4. DHS sites are important for the regulation of gene expression. 5. DHS sites allow transcription factors and other regulatory proteins to access the DNA and control gene 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 | 1,7,2,1,1 |

|  |  |
| --- | --- |
| ID | 3822(30) |
| 领域 | Bio-Medical |
| 用户问题 | List as many European influenza vaccines as possible. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | 1. Fluarix Quad (GSK) 2. Vaxigrip Tetra (Sanofi Pasteur) 3. Influvac (Mylan) 4. Fluad (Seqirus) 5. Fluenz Tetra (AstraZeneca) 6. Begrivac (Novartis) 7. Pandemrix (GSK) 8. Optaflu (Novartis) 9. Celtura (Valneva) 10. Suvendy Flu (Sinovac) 11. Agrippal (Seqirus) 12. Intanza (Sanofi Pasteur) 13. Anflu (LG Life Sciences) 14. Tetraxim (Sanofi Pasteur) 15. Inflexal V (Crucell) |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Fluarix Quad is a European influenza vaccine produced by GSK. 2. Vaxigrip Tetra is a European influenza vaccine produced by Sanofi Pasteur. 3. Influvac is a European influenza vaccine produced by Mylan. 4. Fluad is a European influenza vaccine produced by Seqirus. 5. Fluenz Tetra is a European influenza vaccine produced by AstraZeneca. |
| 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 | 1,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 3832(31) |
| 领域 | Bio-Medical |
| 用户问题 | Is the Paramyxovirus geneome segmented, negative-sense RNA? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Yes, the Paramyxovirus genome is segmented and consists of negative-sense RNA. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The Paramyxovirus genome is segmented. 2. The Paramyxovirus genome consists of negative-sense RNA. |
| 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 | 3,1 |

|  |  |
| --- | --- |
| ID | 3869(32) |
| 领域 | Bio-Medical |
| 用户问题 | Roflumilast Cream is effective for which disease? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Roflumilast cream is not approved or proven to be effective for any specific disease. Roflumilast is primarily used as an oral medication for the treatment of chronic obstructive pulmonary disease (COPD) in tablet form. The use of Roflumilast cream for any other condition would be off-label and not supported by sufficient evidence or approval from regulatory agencies. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Roflumilast cream is not approved for any specific disease. 2. Roflumilast is primarily used as an oral medication. 3. Roflumilast is used in tablet form for the treatment of chronic obstructive pulmonary disease (COPD). 4. The use of Roflumilast cream for conditions other than COPD is termed as off-label usage. 5. The off-label usage is not supported by sufficient evidence or approval from regulatory agencies. |
| 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 | 6,1,1,6,7 |

|  |  |
| --- | --- |
| ID | 3885(33) |
| 领域 | Bio-Medical |
| 用户问题 | Which tools have been developed for identifying and visualising ncRNA promoters? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Several tools have been developed for identifying and visualizing ncRNA (non-coding RNA) promoters. Here are a few examples: 1. PromoterInspector: PromoterInspector is a web-based tool that can identify and visualize promoters of different types of genes, including ncRNAs. It integrates various promoter prediction algorithms and offers an interactive visualization of predicted promoter regions. 2. Cister: Cister is a computational tool specifically designed for identifying promoters of long non-coding RNAs (lncRNAs). It uses machine learning algorithms and sequence-specific features to predict lncRNA promoters. Cister provides a user-friendly web interface for visualization of predicted promoter regions. 3. PlantProm DB: PlantProm DB is a comprehensive database that contains experimentally validated promoters of several plant species, including ncRNAs. It offers a search interface with various filters for querying and visualizing promoter sequences and associated annotations. 4. Genomica: Genomica is a versatile genome browser that allows visualization of various genomic features, including ncRNA promoters. It integrates with several databases and annotation sources to provide a comprehensive view of genome-wide promoter landscapes. 5. JASPAR: JASPAR is a widely used open-access database of transcription factor binding profiles. While it primarily focuses on cis-regulatory elements, it also includes regulatory elements associated with ncRNA promoters. JASPAR provides visualization tools for exploring and comparing predicted promoter regions. These tools are just a few examples, and new tools are continuously being developed to address the challenges of identifying and visualizing ncRNA promoters. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. PromoterInspector is a web-based tool that can identify and visualize promoters of various types of genes, including ncRNAs. 2. Cister is a computational tool specifically designed for identifying promoters of long non-coding RNAs (lncRNAs). 3. PlantProm DB is a database that contains experimentally validated promoters of several plant species, including ncRNAs. 4. Genomica is a genome browser that allows visualization of various genomic features, including ncRNA promoters. 5. JASPAR is an open-access database of transcription factor binding profiles that includes regulatory elements associated with ncRNA promoters. |
| 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 | 1,3,1,3,1 |

|  |  |
| --- | --- |
| ID | 3918(34) |
| 领域 | Bio-Medical |
| 用户问题 | List example genes that SWIM tool has identified and which are down-regulated in glioblastoma |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,3,5 |
| 模型回复 | The SWIM tool has identified several genes that are down-regulated in glioblastoma. Some examples of these genes include: 1. TP53: This gene encodes the tumor protein p53, which acts as a tumor suppressor. Down-regulation of TP53 is frequently observed in glioblastoma, allowing for uncontrolled cell growth and proliferation. 2. PTEN: The PTEN gene encodes the phosphatase and tensin homolog protein, which is also a tumor suppressor. Down-regulation or loss of PTEN function is associated with increased cell survival and proliferation in glioblastoma. 3. RB1: The RB1 gene encodes the retinoblastoma protein, which plays a crucial role in regulating the cell cycle. Down-regulation of RB1 results in the loss of cell cycle control and increased cell proliferation in glioblastoma. 4. EGFR: The epidermal growth factor receptor gene encodes a receptor protein that promotes cell growth and survival. However, overexpression and subsequent down-regulation of EGFR are commonly observed in glioblastoma, leading to uncontrolled cell growth. 5. PDGFRA: The platelet-derived growth factor receptor A gene encodes a receptor protein involved in cell proliferation and differentiation. Down-regulation of PDGFRA has been reported in glioblastoma, contributing to increased cell proliferation and tumor progression. It is important to note that the down-regulation of these genes is not exclusive to glioblastoma and can occur in other types of cancers as well. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The SWIM tool has identified the TP53 gene as one that is down-regulated in glioblastoma. 2. TP53 gene encodes the tumor protein p53, acting as a tumor suppressor. 3. The PTEN gene, which encodes for the phosphatase and tensin homolog protein, is also identified by the SWIM tool as being down-regulated in glioblastoma. 4. The SWIM tool has identified RB1, a gene that encodes the retinoblastoma protein, as being down-regulated in glioblastoma. 5. The platelet-derived growth factor receptor A gene, PDGFRA, has been reported to be down-regulated in glioblastoma as identified by the SWIM tool. |
| 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 | 3,1,1,3,3 |

|  |  |
| --- | --- |
| ID | 3926(35) |
| 领域 | Bio-Medical |
| 用户问题 | Which R packages have been developed for studying TADs? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | There are several R packages that have been developed for studying Topologically Associating Domains (TADs). Some popular ones include: 1. TADkit: A package for visualizing and analyzing chromatin interaction data, including identifying TAD boundaries and interactions. It provides interactive visualization features and various analysis tools.   2. HiCseg: This package offers statistical methods to detect TAD boundaries from Hi-C data. It uses a hidden Potts model segmentation approach to identify domains based on chromatin interaction patterns. 3. TADpole: TADpole is a package that provides tools for analyzing TAD boundary strength and insulation score. It can be used to detect and assess the significance of TAD boundaries based on Hi-C data. 4. HiTC: HiTC is a comprehensive package that supports various aspects of Hi-C data analysis, including TAD detection. It offers multiple methods to identify TAD boundaries and visualize chromatin interactions. 5. TADbit: TADbit is a versatile package for the analysis, visualization, and modeling of chromatin interactions. It provides tools for detecting TADs, studying TAD dynamics, and integrating multiple datasets. 6. chromoR: This package focuses on TAD calling and annotation using Hi-C data. It offers multiple methods to detect TAD boundaries and provides functionalities to analyze and visualize TADs. These are just a few examples of R packages that have been developed for studying TADs. There may be other packages available as well, depending on specific research requirements and preferences. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. TADkit is an R package designed for visualizing and analyzing chromatin interaction data tied to Topologically Associating Domains (TADs). 2. HiCseg is an R package designed for detecting TAD boundaries from Hi-C data. 3. TADpole is an R package offering tools for analyzing TAD boundary strength and insulation score. 4. HiTC is an R package that supports various aspects of Hi-C data analysis, including TAD detection. 5. The TADbit R package allows for analysis, visualization, and modelling of chromatin interactions. |
| 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 | 7,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 3927(36) |
| 领域 | Bio-Medical |
| 用户问题 | Which bioconductor tool has been developed for accessing bacterial regulatory networks? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | One bioconductor tool developed for accessing bacterial regulatory networks is the `RegNetwork` package. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The `RegNetwork` package is a bioconductor tool developed for accessing bacterial regulatory networks. |
| 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 | 2 |

|  |  |
| --- | --- |
| ID | 3933(37) |
| 领域 | Bio-Medical |
| 用户问题 | What are the end products of the shikimate pathway? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The end products of the shikimate pathway include: 1. Aromatic amino acids: The shikimate pathway is responsible for the synthesis of three essential aromatic amino acids: phenylalanine, tyrosine, and tryptophan. 2. Other secondary metabolites: The shikimate pathway is also involved in the synthesis of a variety of important secondary metabolites, including alkaloids, flavonoids, lignin, tannins, and vitamin K. 3. Coenzyme Q10: The shikimate pathway is involved in the synthesis of coenzyme Q10, a key component of the electron transport chain and an important cellular antioxidant. 4. Ubiquinone: The shikimate pathway is also involved in the synthesis of ubiquinone, a molecule that plays a critical role in electron transport and oxidative phosphorylation. 5. Folate: The shikimate pathway is responsible for the synthesis of folate, an essential vitamin involved in DNA synthesis and repair. 6. Gibberellins: The shikimate pathway is also involved in the synthesis of gibberellins, a class of plant hormones that regulate various aspects of plant growth and development. It is important to note that the final products of the shikimate pathway can vary depending on the organism and cell type. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The shikimate pathway produces three essential aromatic amino acids: phenylalanine, tyrosine, and tryptophan. 2. The shikimate pathway is involved in the synthesis of secondary metabolites such as alkaloids, flavonoids, lignin, tannins, and vitamin K. 3. Coenzyme Q10, a key component of the electron transport chain and cellular antioxidant, is synthesized through the shikimate pathway. 4. The shikimate pathway synthesizes ubiquinone, a molecule that plays a role in electron transport and oxidative phosphorylation. 5. Folate, a vitamin essential for DNA synthesis and repair, is produced by the shikimate 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 | 1,1,2,1,2 |

|  |  |
| --- | --- |
| ID | 3936(38) |
| 领域 | Bio-Medical |
| 用户问题 | Is cabergoline used for treatment of the Nelson's syndrome ? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Yes, cabergoline is commonly used for the treatment of Nelson's syndrome. Nelson's syndrome is a condition that typically occurs in individuals who have undergone bilateral adrenalectomy (surgical removal of both adrenal glands) to treat Cushing's disease. It is characterized by the enlargement of a pituitary adenoma (tumor) and excessive production of adrenocorticotropic hormone (ACTH). Cabergoline, a dopamine agonist medication, is often prescribed to suppress the growth and secretion of the pituitary adenoma, thereby reducing the symptoms associated with Nelson's syndrome. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Cabergoline is used for the treatment of Nelson's syndrome. 2. Nelson's syndrome typically occurs in individuals who have undergone surgical removal of both adrenal glands, known as bilateral adrenalectomy. 3. Nelson's syndrome is characterized by enlargement of a pituitary adenoma and excessive production of adrenocorticotropic hormone. 4. Cabergoline is a dopamine agonist medication. 5. Cabergoline is used to suppress the growth and secretion of the pituitary adenoma in Nelson's syndrome 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 | 1,1,4,1,4 |

|  |  |
| --- | --- |
| ID | 3939(39) |
| 领域 | Bio-Medical |
| 用户问题 | What is the main manifestation of Liebenberg syndrome? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Liebenberg syndrome, also known as Liebenberg's syndrome or Facio-Auriculo-Vertebral Sequence (FAVS), is a rare congenital disorder characterized by a range of structural abnormalities affecting the face, ears, and spine. The main manifestation and defining features of Liebenberg syndrome include: 1. Facial abnormalities: Individuals with Liebenberg syndrome may have facial asymmetry, underdeveloped cheekbones, and malformation of the upper lip, particularly a cleft lip or palate. The ears may be abnormally shaped and positioned (auricular deformities), often appearing low-set or rotated backward. 2. Auricular (ear) abnormalities: Liebenberg syndrome typically involves various ear anomalies, such as abnormally shaped ears, poorly developed earlobes, and hearing impairments (e.g., conductive or sensorineural hearing loss). 3. Vertebral defects: Liebenberg syndrome is associated with vertebral anomalies, such as fused or missing vertebrae, abnormal curvature of the spine (scoliosis or kyphosis), and limited mobility of the neck. These are the main manifestations of Liebenberg syndrome, although individuals may also present with additional anomalies affecting other body systems. It is important to note that the severity and specific features of Liebenberg syndrome can vary among affected individuals. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Liebenberg syndrome is a rare congenital disorder characterized by a range of structural abnormalities affecting the face, ears, and spine. 2. Facial abnormalities in individuals with Liebenberg syndrome can include facial asymmetry, underdeveloped cheekbones, and malformation of the upper lip, often appearing as a cleft lip or palate. 3. Abnormalities in ear shape and position (auricular deformities) are common in Liebenberg syndrome, often resulting in low-set or backward-rotated ears. 4. Liebenberg syndrome can involve various ear anomalies, such as abnormally shaped ears, poorly developed earlobes, and hearing impairments including conductive or sensorineural hearing loss. 5. Vertebral anomalies like fused or missing vertebrae, abnormal curvature of the spine (scoliosis or kyphosis), and limited mobility of the neck are associated with Liebenberg syndrome. |
| 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 | 1,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 3977(40) |
| 领域 | Bio-Medical |
| 用户问题 | List orally bioavailable MPS1 kinase inhibitors |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | 1. NMS-P937: This is a potent and selective orally bioavailable MPS1 kinase inhibitor that has shown promise in preclinical studies for the treatment of various types of cancer. 2. BOS-172722: Another orally available MPS1 kinase inhibitor that has demonstrated good pharmacokinetic properties and potent anti-proliferative activity in cancer cell lines. 3. AZD7648: An orally bioavailable, potent, and selective MPS1 kinase inhibitor that is being evaluated in clinical trials for the treatment of advanced solid tumors. 4. NVP-BEZ235: Although not specifically designed as an MPS1 kinase inhibitor, it has been shown to have activity against MPS1 kinase and is orally bioavailable. 5. Mps-BAY2a: A novel orally bioavailable MPS1 kinase inhibitor with potent anti-tumor activity in preclinical models. It is important to note that the development of orally bioavailable MPS1 kinase inhibitors is an active area of research, and there may be other compounds in various stages of development with oral bioavailability as well. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. NMS-P937 is an orally bioavailable MPS1 kinase inhibitor that has been used in preclinical studies for treating different cancer types. 2. BOS-172722 is a orally available MPS1 kinase inhibitor with good pharmacokinetic properties and has shown anti-proliferative activity in cancer cell lines. 3. AZD7648 is an orally bioavailable MPS1 kinase inhibitor and is currently being tested in clinical trials for the treatment of advanced solid tumors. 4. NVP-BEZ235 is not specifically designed as an MPS1 kinase inhibitor, but it is orally bioavailable and has shown activity against MPS1 kinase. 5. Mps-BAY2a is an orally bioavailable MPS1 kinase inhibitor with potent anti-tumor activity in preclinical models. |
| 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 | 1,1,1,2,3 |

|  |  |
| --- | --- |
| ID | 4031(41) |
| 领域 | Bio-Medical |
| 用户问题 | Was golimumab tested for diabetes? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Yes, golimumab has been studied for its potential use in diabetes. While its primary indication is the treatment of autoimmune diseases such as rheumatoid arthritis, psoriatic arthritis, and ankylosing spondylitis, golimumab has also been investigated in clinical trials for its potential role in managing type 1 diabetes. These trials aim to evaluate the effectiveness and safety of golimumab in improving glycemic control and reducing the progression of autoimmune destruction of pancreatic beta cells in type 1 diabetes patients. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Golimumab is primarily indicated for the treatment of autoimmune diseases like rheumatoid arthritis, psoriatic arthritis, and ankylosing spondylitis. 2. Golimumab has been studied for its potential use in diabetes. 3. Clinical trials have been conducted to investigate the potential role of golimumab in managing type 1 diabetes. 4. The trials on golimumab aim to evaluate its effectiveness and safety in improving glycemic control in patients with type 1 diabetes. 5. These trials also aim to investigate golimumab's role in reducing the progression of autoimmune destruction of pancreatic beta cells in type 1 diabetes 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 | 1,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 4055(42) |
| 领域 | Bio-Medical |
| 用户问题 | Is progeria caused by an autosomal recessive gene? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5, |
| 模型回复 | Yes, progeria is caused by an autosomal recessive gene mutation. Most cases of progeria result from a mutation in the LMNA gene, which is inherited in an autosomal recessive pattern. This means that an individual must inherit two copies of the mutated gene (one from each parent) in order to develop the 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 | 1 |
| 提取的事实 | 1. Progeria is caused by an autosomal recessive gene mutation. 2. Most cases of progeria result from a mutation in the LMNA gene. 3. The mutation of the LMNA gene is inherited in an autosomal recessive pattern. 4. An individual must inherit two copies of the mutated gene from each parent to develop progeria. |
| 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 | 3,1,3,7 |

|  |  |
| --- | --- |
| ID | 4082(43) |
| 领域 | Bio-Medical |
| 用户问题 | What are common variants at 12q14 and 12q24 associated with? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,3 |
| 模型回复 | There are several common variants located at 12q14 and 12q24 that have been associated with various diseases and traits. Here are a few notable associations: 1. BMI (Body Mass Index): Multiple studies have found associations between common variants at 12q14 and 12q24 regions and body mass index, a measure of body fat. These variants have been linked to obesity and higher BMI. 2. Diabetes: Variants at 12q14 have been found to be associated with the risk of type 2 diabetes, a chronic metabolic disease characterized by high blood sugar levels. 3. Blood Pressure: Certain variants at 12q14 have been associated with higher blood pressure levels, increasing the risk of hypertension. 4. Multiple Sclerosis: Some studies have identified associations between common variants at 12q14 and increased risk of multiple sclerosis, a neurodegenerative autoimmune disease affecting the central nervous system. 5. Height: Variants in the 12q24 region have been linked to height differences in populations, with some variants associated with taller or shorter stature. It is important to note that these are just a few examples, and further research is necessary to fully understand the specific genetic variants and their associations with various diseases and traits. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Common variants located at 12q14 and 12q24 have been linked to various diseases and traits. 2. Multiple studies have found a relation between common variants at 12q14 and 12q24 and body mass index (BMI). 3. Variants at 12q14 have been associated with the risk of type 2 diabetes. 4. Certain variants at 12q14 are associated with higher blood pressure levels. 5. Associations between common variants at 12q14 and increased risk of multiple sclerosis have been found. 6. Variants in the 12q24 region are linked to height differences. |
| 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 | 1,7,7,7,7,1 |

|  |  |
| --- | --- |
| ID | 4096(44) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the ligands of the Roundabout (Robo) receptors? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The ligands of the Roundabout (Robo) receptors are netrins. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The ligands of the Roundabout (Robo) receptors are netrins. |
| 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 | 2 |

|  |  |
| --- | --- |
| ID | 4112(45) |
| 领域 | Bio-Medical |
| 用户问题 | Is there a role for TFII-I in megakaryopoiesis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,3 |
| 模型回复 | Yes, there is a role for TFII-I (transcription factor II-I) in megakaryopoiesis, which is the process of platelet production in the bone marrow. TFII-I is a transcription factor that plays a crucial role in regulating gene expression.  Several studies have suggested that TFII-I is involved in the development and differentiation of megakaryocytes, which are the precursor cells for platelets. TFII-I has been shown to regulate the expression of various genes involved in megakaryocyte maturation and platelet formation. One study found that TFII-I is required for proper megakaryopoiesis, as mice lacking TFII-I showed impaired megakaryocyte development and reduced platelet production. Another study showed that TFII-I regulates the expression of genes involved in cytoskeletal rearrangements, which are crucial for platelet formation and release. Furthermore, TFII-I has been implicated in regulating thrombopoietin (TPO) signaling, which is a key pathway involved in megakaryopoiesis. TFII-I interacts with the TPO receptor, c-Mpl, and is involved in downstream signaling events that promote megakaryocyte differentiation and platelet production. Overall, these studies suggest that TFII-I plays an important role in megakaryopoiesis by regulating gene expression, cytoskeletal rearrangements, and TPO signaling. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. TFII-I (Transcription Factor II-I) plays a role in megakaryopoiesis, the process of platelet production in the bone marrow. 2. TFII-I is a transcription factor that regulates gene expression. 3. Megakaryocytes, which are precursor cells for platelets, have their development and differentiation affected by TFII-I. 4. TFII-I has been linked to the regulation of thrombopoietin (TPO) signaling, a key pathway involved in megakaryopoiesis. 5. TFII-I interacts with the TPO receptor c-Mpl and is involved in signaling events that promote megakaryocyte differentiation and platelet production. |
| 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 | 1,1,1,3,1 |

|  |  |
| --- | --- |
| ID | 4145(46) |
| 领域 | Bio-Medical |
| 用户问题 | Is atenolol metabolized by CYP2D6? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Yes, atenolol is primarily metabolized by the enzyme CYP2D6. This enzyme is responsible for the conversion of atenolol into its active metabolite, metoprolol. However, not all individuals have the same activity level of CYP2D6, which can impact the rate of atenolol metabolism and potentially alter its effectiveness. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Atenolol is metabolized by the enzyme CYP2D6. 2. The enzyme CYP2D6 is responsible for the conversion of atenolol into metoprolol. 3. Different individuals can have different activity levels of the CYP2D6 enzyme. 4. The activity level of the CYP2D6 enzyme can impact the rate of atenolol metabolism. 5. The variations in atenolol's metabolism rate can potentially alter its 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 | 3,3,1,3,3 |

|  |  |
| --- | --- |
| ID | 4158(47) |
| 领域 | Bio-Medical |
| 用户问题 | List versions of ExpansionHunter |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,3,4 |
| 模型回复 | As an AI language model, I can provide information about ExpansionHunter, which is a software tool for detecting and analyzing repeat expansions in DNA sequence data. However, I cannot provide a comprehensive list of all versions of ExpansionHunter, as the tool is constantly being updated and improved. Instead, I can provide you with some of the major versions that have been released: 1. ExpansionHunter (v1.0): This was the initial release of the software, which provided a fast and accurate method for detecting repeat expansions from high-throughput DNA sequencing data. 2. ExpansionHunter (v2.0): This version introduced significant improvements in terms of sensitivity, specificity, and runtime performance. It also included additional features and tools for downstream analysis of repeat expansion data. 3. ExpansionHunter (v3.0): This version integrated machine learning algorithms to further enhance the accuracy of repeat expansion detection. It also introduced new visualization and reporting tools for easier interpretation of the results. 4. ExpansionHunter (v4.0): This version focused on optimizing the software for the detection of specific repeat expansion disorders, such as Huntington's disease. It included disease-specific models and features tailored to improve detection sensitivity and specificity for these disorders. 5. ExpansionHunter (v5.0): The latest major version release at the time of this response, v5.0, featured various improvements and bug fixes. It aimed at enhancing the user experience, refining the accuracy of repeat expansion detection, and expanding the range of supported repeat motifs and disorders. Please note that version numbers and specific features may vary, as software tools may undergo minor version updates, patches, or bug fixes between major releases. It is always recommended to check the official ExpansionHunter documentation or website for the most up-to-date information about the versions available. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. ExpansionHunter is a software tool for detecting and analyzing repeat expansions in DNA sequence data. 2. The initial release of ExpansionHunter (v1.0) provided a fast and accurate method for detecting repeat expansions from high-throughput DNA sequencing data. 3. ExpansionHunter (v2.0) introduced significant improvements in sensitivity, specificity, and runtime performance. 4. ExpansionHunter (v3.0) utilized machine learning algorithms to improve the accuracy of repeat expansion detection. 5. ExpansionHunter (v4.0) focused on optimizing the software for the detection of specific repeat expansion disorders, such as Huntington'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 | 1,1,1,7,8 |

|  |  |
| --- | --- |
| ID | 4164(48) |
| 领域 | Bio-Medical |
| 用户问题 | What is the role of Adamts18 in hormone receptor signaling? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,4 |
| 模型回复 | Currently, there is limited research available on the specific role of Adamts18 in hormone receptor signaling. Adamts18 is a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) family of proteases. These proteases are involved in various physiological processes, including extracellular matrix remodeling, tissue development, and inflammatory response.  While there is no direct evidence suggesting a role for Adamts18 in hormone receptor signaling, it is worth noting that members of the ADAMTS family have been implicated in different aspects of hormone signaling. For example, ADAMTS1 and ADAMTS8 have been shown to modulate the activity of the estrogen receptor, a hormone receptor involved in cellular responses to estrogen. Additionally, ADAMTS1 has been reported to impact the function of the androgen receptor, which mediates the effects of androgens like testosterone. Further research is needed to determine if Adamts18 plays a role in hormone receptor signaling or if it has any involvement in other aspects of hormone-related processes. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Adamts18 is a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) family of proteases. 2. ADAMTS proteins are involved in various physiological processes, including extracellular matrix remodeling, tissue development, and inflammatory response. 3. Members of the ADAMTS family have been implicated in different aspects of hormone signaling. 4. ADAMTS1 and ADAMTS8 have been shown to modulate the activity of the estrogen receptor. 5. ADAMTS1 has been reported to impact the function of the androgen receptor. |
| 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 | 1,1,1,2,7 |

|  |  |
| --- | --- |
| ID | 4208(49) |
| 领域 | Bio-Medical |
| 用户问题 | What is the mode of action of Thiazovivin? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,3 |
| 模型回复 | Thiazovivin is a small molecule inhibitor that acts as a specific activator of Rho-associated coiled-coil kinase (ROCK). It enhances ROCK activity by stabilizing its active conformation, leading to increased phosphorylation of its downstream targets. ROCK is a serine/threonine-protein kinase involved in regulating various cellular processes, including actin cytoskeleton organization, cell adhesion, cell motility, and cell contractility. By modulating ROCK activity, Thiazovivin can impact cellular functions related to these processes. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Thiazovivin is a small molecule inhibitor. 2. Thiazovivin acts as a specific activator of Rho-associated coiled-coil kinase (ROCK). 3. Thiazovivin enhances ROCK activity by stabilizing its active conformation. 4. ROCK is a serine/threonine-protein kinase involved in regulating various cellular processes. 5. By modulating ROCK activity, Thiazovivin can impact cellular functions related to certain processes, including actin cytoskeleton organization, cell adhesion, cell motility, and cell contractility. |
| 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 | 1,1,7,1,1 |