幻象标注

|  |  |
| --- | --- |
| ID | 1304(0) |
| 领域 | Bio-Medical |
| 用户问题 | List common features of Shapiro 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 | Shapiro syndrome, also known as familial dysautonomia type II, is a rare genetic disorder that primarily affects the autonomic nervous system. Common features of Shapiro syndrome include: 1. Labile blood pressure: Individuals with Shapiro syndrome often experience fluctuations in blood pressure, ranging from low to high. This can lead to symptoms such as dizziness, lightheadedness, and fainting. 2. Orthostatic hypotension: Orthostatic hypotension is a drop in blood pressure upon standing up. Persons with Shapiro syndrome may experience this, which can cause symptoms such as dizziness and blurred vision. 3. Sweating abnormalities: Shapiro syndrome can result in abnormal sweating patterns, including absent sweating (anhidrosis) or excessively sweating (hyperhidrosis). This abnormality typically affects the feet and legs symmetrically. 4. Gastrointestinal issues: Individuals with Shapiro syndrome may experience gastrointestinal problems such as constipation, delayed gastric emptying, and difficulty swallowing. 5. Lack of tears: Affected individuals may have reduced or absent ability to produce tears, leading to dry eyes. 6. Difficulty regulating body temperature: Shapiro syndrome can disrupt the body's ability to regulate temperature, resulting in sensitivity to heat or cold. 7. Speech and swallowing difficulties: Some individuals may have speech and swallowing difficulties due to reduced coordination of the muscles involved in these actions. 8. Sensory disturbances: Sensation abnormalities can occur in Shapiro syndrome, including numbness, tingling, and decreased ability to perceive pain or temperature changes. 9. Reduced sensitivity to pain: People with Shapiro syndrome may exhibit diminished pain perception, which can lead to injuries that go unnoticed. 10. Episodes of unresponsiveness: Occasionally, individuals with Shapiro syndrome may experience episodes of unresponsiveness or decreased arousal, resembling fainting or loss of consciousness. It is important to note that the severity and combination of symptoms can vary among individuals with Shapiro syndrome. Common characteristics, such as those mentioned above, may be present in varying degrees for each affected person. |
| 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. Shapiro syndrome is also known as familial dysautonomia type II. 2. Shapiro syndrome is a genetic disorder that primarily affects the autonomic nervous system. 3. Common features of Shapiro syndrome include fluctuations in blood pressure, orthostatic hypotension, sweating abnormalities, and gastrointestinal issues. 4. People with Shapiro syndrome may have a reduced or absent ability to produce tears, leading to dry eyes. 5. Individuals with Shapiro syndrome may experience episodes of unresponsiveness or decreased arousal, resembling fainting or loss of consciousness. |
| 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 | 3,1,1,3,1 |

|  |  |
| --- | --- |
| ID | 1320(1) |
| 领域 | Bio-Medical |
| 用户问题 | Which disease is linked to mutations within BRAG1? |
| 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 disease has been directly linked to mutations within BRAG1 (also known as CBFA2T3). However, BRAG1 mutations have been associated with a chromosomal translocation involving the RUNX1 gene, which is the most common genetic alteration seen in acute myeloid leukemia (AML). |
| 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. BRAG1 is also known as CBFA2T3. 2. No disease has been directly linked to mutations within BRAG1. 3. BRAG1 mutations have been associated with a chromosomal translocation involving the RUNX1 gene. 4. The RUNX1 gene chromosomal translocation is the most common genetic alteration seen in acute myeloid leukemia (AML). |
| 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 | 3,6,7,1 |

|  |  |
| --- | --- |
| ID | 1362(2) |
| 领域 | Bio-Medical |
| 用户问题 | Which protein is the main inhibitor of protein phosphatase 1 (PP1)? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | The main inhibitor of protein phosphatase 1 (PP1) is a protein called protein inhibitor 1 (I-1). |
| 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 inhibitor 1 (I-1) is the main inhibitor of protein phosphatase 1 (PP1). |
| 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 |

|  |  |
| --- | --- |
| ID | 1374(3) |
| 领域 | Bio-Medical |
| 用户问题 | Which mechanisms underlie adaptive mutagenesis (stationary-phase mutagenesis) in Bacillus subtilis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,4,5 |
| 模型回复 | Adaptive mutagenesis, also known as stationary-phase mutagenesis, is a mechanism by which bacteria like Bacillus subtilis can generate genetic diversity and increase the chances of survival in stressful conditions such as nutrient limitation or high-density populations. Several mechanisms have been proposed to underlie adaptive mutagenesis in Bacillus subtilis: 1. Error-prone DNA polymerases: Under stress conditions, the accuracy of DNA replication can be reduced due to the action of error-prone DNA polymerases, such as DNA polymerase IV (Pol IV) or DNA polymerase V (Pol V). These polymerases have a lower fidelity than the replicative DNA polymerase III (Pol III) and can introduce more errors during DNA synthesis, leading to an increased mutation rate. 2. Activation of stress response systems: During stationary phase, several stress response pathways are activated in Bacillus subtilis. These pathways, such as the SOS response or the RpoS (sigma factor subunit) regulon, can induce the expression of error-prone DNA polymerases and other mutagenic enzymes, enhancing the mutagenesis rate. 3. Recombination and repair processes: The DNA repair and recombination systems of Bacillus subtilis, such as homologous recombination, can be stimulated during stationary phase. Recombination events can lead to the acquisition of genetic variations from the environment or from other cells within the population. 4. Unstable repetitive DNA sequences: Bacillus subtilis contains unstable repetitive DNA sequences, such as dinucleotide repeats or simple sequence repeats (SSRs). These repetitive sequences can undergo replication slippage or strand slippage during DNA replication, resulting in the generation of insertions or deletions (indels) in the genome. 5. Regulatory network alterations: Stationary-phase mutagenesis can involve alterations in the regulatory networks that control DNA repair and mutagenesis. For example, changes in the expression or activity of transcription factors or other regulatory proteins can lead to increased mutagenesis. It is important to note that the precise mechanisms of adaptive mutagenesis in Bacillus subtilis are still under investigation, and further research is needed to fully understand this 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. Adaptive mutagenesis is a mechanism by which bacteria like Bacillus subtilis can generate genetic diversity and increase the chances of survival in stressful conditions. 2. Error-prone DNA polymerases such as DNA polymerase IV and V can reduce the accuracy of DNA replication, increasing the mutation rate in Bacillus subtilis under stress conditions. 3. During stationary phase, stress response pathways like the SOS response or the RpoS regulon can be activated in Bacillus subtilis and promote mutagenesis. 4. Bacillus subtilis uses DNA repair and recombination systems, such as homologous recombination, to acquire genetic variations from the environment or from other cells during stationary phase. 5. Bacillus subtilis contains unstable repetitive DNA sequences that can undergo replication or strand slippage, leading to insertions or deletions in 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 | 1,1,7,1,7 |

|  |  |
| --- | --- |
| ID | 1399(4) |
| 领域 | Bio-Medical |
| 用户问题 | What causes erucism? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,3,4 |
| 模型回复 | Erucism is caused by the ingestion or inhalation of mustard plants, mainly from the Brassicaceae family. This family includes plants such as mustard greens, mustard seeds, broccoli, cauliflower, cabbage, and radishes. Erucism occurs due to the presence of glucosinolates in these plants. When the plants are chewed, crushed, or otherwise processed, an enzyme called myrosinase is released, which converts glucosinolates into isothiocyanates. These isothiocyanates are responsible for the pungent, spicy taste and aroma of mustard plants. For some individuals, consumption or exposure to mustard plants can result in the development of symptoms known as erucism. These symptoms include skin rashes, blisters, and itching, as well as respiratory symptoms like nasal congestion, coughing, and shortness of breath. The severity of erucism can vary depending on the individual's sensitivity and the amount of exposure. It is worth noting that not everyone will experience erucism, and the condition is generally not life-threatening. However, individuals with known allergies to mustard or Brassicaceae family plants should avoid consumption or contact with these plants to prevent the development of erucism. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 2 |
| 提取的事实 | 1. Erucism is caused by the ingestion or inhalation of mustard plants, mainly from the Brassicaceae family. 2. Mustard plants, broccoli, cauliflower, cabbage, and radishes are part of the Brassicaceae family. 3. When consumed or chewed, an enzyme in these plants known as myrosinase converts glucosinolates into isothiocyanates, which can lead to erucism. 4. Symptoms of erucism include skin rashes, blisters, itching, nasal congestion, coughing, and shortness of breath. 5. People with allergies to mustard or Brassicaceae family plants should avoid contact with them to prevent erucism. |
| 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 |  |

|  |  |
| --- | --- |
| ID | 1413(5) |
| 领域 | Bio-Medical |
| 用户问题 | What are the indications for hydrochlorothiazide? |
| 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 | Hydrochlorothiazide is a medication used to treat various conditions such as: 1. Hypertension: It is commonly prescribed to manage high blood pressure. Hydrochlorothiazide can lower blood pressure by reducing the volume of fluid in the blood vessels and relaxing the blood vessel walls. 2. Edema: It can be used to treat fluid retention caused by conditions such as congestive heart failure, liver cirrhosis, or kidney disorders. Hydrochlorothiazide helps the body eliminate excess water and salt through increased urine production. 3. Nephrolithiasis: In some cases, hydrochlorothiazide may be recommended to prevent the formation of certain types of kidney stones by reducing the concentration of calcium in the urine. 4. Diabetes insipidus: This medication can be used to treat diabetes insipidus, a condition characterized by excessive thirst and excretion of large volumes of dilute urine. Hydrochlorothiazide helps to decrease urine production and improve fluid balance. 5. Osteoporosis: Hydrochlorothiazide may be prescribed off-label to help prevent bone loss in postmenopausal women or individuals at risk of osteoporosis. It is important to note that the specific use of hydrochlorothiazide can vary depending on the individual's medical condition and the judgment of their healthcare provider. Always consult a healthcare professional for personalized 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. Hydrochlorothiazide is used to treat hypertension by reducing the volume of fluid in the blood vessels and relaxing the blood vessel walls. 2. This medication can be used to treat edema related to conditions like congestive heart failure, liver cirrhosis, or kidney disorders. 3. Hydrochlorothiazide may be recommended for the prevention of certain types of kidney stones by reducing the concentration of calcium in the urine. 4. The medication can be used to treat diabetes insipidus which is characterized by excessive thirst and excretion of large volumes of dilute urine. 5. Hydrochlorothiazide can be used off-label to prevent bone loss in postmenopausal women or individuals at risk of osteoporosis. |
| 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 | 1447(6) |
| 领域 | Bio-Medical |
| 用户问题 | Has silicon been used in treatment of incontinence ? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,4 |
| 模型回复 | Yes, silicon has been used in the treatment of urinary incontinence. One common procedure involves the implantation of a silicone sling or tape underneath the urethra to provide support and improve bladder control. This procedure is known as a midurethral sling or transvaginal tape procedure and is commonly used to treat stress urinary incontinence in women. The silicone sling helps to provide support to the urethra and prevent urine leakage during physical activity or stress. |
| 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. Silicon has been used in the treatment of urinary incontinence. 2. Silicone sling or tape implantation is a common procedure for treating urinary incontinence. 3. The procedure involving the silicon tape or sling is known as a midurethral sling or transvaginal tape procedure. 4. The midurethral sling or transvaginal tape procedure is commonly used to treat stress urinary incontinence in women. 5. The silicone sling helps to provide support to the urethra and prevent urine leakage during physical activity or stress. |
| 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 | 2,1,2,1,1 |

|  |  |
| --- | --- |
| ID | 1454(7) |
| 领域 | Bio-Medical |
| 用户问题 | What is the association between moon cycle and rupture risk of intracranial aneurysms? |
| 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 is limited research on the association between the moon cycle and rupture risk of intracranial aneurysms. Some studies have suggested a potential link between lunar phases and increased ruptures of aneurysms, but these findings are not widely accepted or supported. One study published in the journal "Neurosurgery" in 2001 analyzed the relationship between lunar phases and aneurysmal rupture. The study reported a slightly higher rate of aneurysmal ruptures during the waxing gibbous phase of the lunar cycle (the period between the first quarter and full moon) compared to other phases. However, the findings were not statistically significant, and the study had several limitations, including a small sample size and potential confounding factors. Another study published in the "Journal of Neurology, Neurosurgery, and Psychiatry" in 2006 examined the association between lunar phases and aneurysmal rupture using a larger sample size. The study found no significant relationship between lunar phases and aneurysmal rupture risk. Overall, the existing evidence on the association between moon cycles and rupture risk of intracranial aneurysms is inconclusive. Further research with larger sample sizes and better study designs would be needed to draw more definitive conclusions on this topic. |
| 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. Some studies have suggested a potential link between lunar phases and increased ruptures of aneurysms. 2. A study published in the "Neurosurgery" journal in 2001 analyzed the relationship between lunar phases and aneurysmal rupture. 3. The "Neurosurgery" study reported a slightly higher rate of aneurysmal ruptures during the waxing gibbous phase of the lunar cycle. 4. A study published in the "Journal of Neurology, Neurosurgery, and Psychiatry" in 2006 found no significant relationship between lunar phases and aneurysmal rupture risk. 5. The existing evidence on the association between moon cycles and rupture risk of intracranial aneurysms is inconclusive. |
| 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 | 2,2,7,7,1 |

|  |  |
| --- | --- |
| ID | 1477(8) |
| 领域 | Bio-Medical |
| 用户问题 | Does HuR protein regulate the splicing process? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | Yes, HuR protein, also known as Hu antigen R or ELAVL1, is involved in the regulation of splicing process. HuR is an RNA-binding protein that is primarily located in the nucleus and binds to target RNA molecules. It has been shown to interact with various spliceosomal components and modulate alternative splicing of specific pre-mRNA transcripts. HuR can influence splicing by binding to specific intronic or exonic RNA sequences, thus promoting or inhibiting the recognition of splice sites during splicing. It can either enhance or repress the inclusion or exclusion of specific exons, leading to alternative splicing events. HuR has been particularly implicated in the regulation of alternative splicing in cancer, where it can modulate the expression of oncogenic isoforms or splicing events related to cell proliferation, apoptosis, and other cancer-related processes. Overall, HuR protein plays a crucial role in post-transcriptional gene regulation, including the regulation of splicing process, by binding to RNA transcripts and influencing their splicing 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. HuR protein, also known as Hu antigen R or ELAVL1, is involved in the regulation of the splicing process. 2. HuR is an RNA-binding protein that primarily locates in the nucleus and binds to target RNA molecules. 3. HuR protein has been shown to interact with various spliceosomal components and modulate alternative splicing of specific pre-mRNA transcripts. 4. HuR can influence splicing by binding to specific intronic or exonic RNA sequences, promoting or inhibiting the recognition of splice sites during splicing. 5. HuR has been particularly implicated in the regulation of alternative splicing in 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 | 2,4,7,3,7 |

|  |  |
| --- | --- |
| ID | 1492(9) |
| 领域 | Bio-Medical |
| 用户问题 | Describe the known functions for the prothymosin alpha c-terminal peptide? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | The prothymosin alpha C-terminal peptide, also known as PTMA-CTP, is a bioactive peptide derived from prothymosin alpha (ProTα). Although the functions of PTMA-CTP are still being investigated, several known functions have been identified: 1. Immune modulation: PTMA-CTP has been found to have immunomodulatory properties. It can activate certain immune cells, such as macrophages and natural killer cells, enhancing their functions including phagocytosis and cytokine production. This immune modulation helps in the defense against pathogens and tumor cells. 2. Anti-inflammatory effects: PTMA-CTP has been shown to possess anti-inflammatory properties. It can reduce the production of pro-inflammatory cytokines, such as tumor necrosis factor-alpha (TNF-α) and interleukin-6 (IL-6), and inhibit the activation of inflammatory signaling pathways. This anti-inflammatory activity suggests potential therapeutic applications in inflammatory diseases. 3. Wound healing: Studies have demonstrated that PTMA-CTP promotes wound healing by accelerating reepithelialization, collagen deposition, and angiogenesis. It also modulates the immune response during wound repair, facilitating a more efficient healing process. 4. Neuroprotection: Recent research indicates potential neuroprotective effects of PTMA-CTP. It has been shown to protect neurons from oxidative stress-induced cell death and inhibit neuroinflammation, suggesting a possible role in the prevention and treatment of neurological disorders such as Alzheimer's disease. 5. Antitumor activity: PTMA-CTP has shown promising antitumor effects in various cancer models. It can induce apoptosis (programmed cell death) in cancer cells, inhibit tumor growth, reduce angiogenesis, and enhance the effectiveness of chemotherapy drugs. These findings suggest a potential role in cancer therapy. It is worth noting that research on PTMA-CTP is ongoing, and further studies are needed to fully understand its mechanisms of action and explore its potential therapeutic applications. |
| 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 prothymosin alpha C-terminal peptide, also known as PTMA-CTP, is derived from prothymosin alpha (ProTα). 2. PTMA-CTP has been found to possess immunomodulatory properties, capable of activating immune cells like macrophages and natural killer cells. 3. Research has shown PTMA-CTP to have anti-inflammatory properties, reducing the production of certain pro-inflammatory cytokines and inhibiting inflammatory signaling pathways. 4. Studies have suggested that PTMA-CTP can act in wound healing by accelerating reepithelialization, collagen deposition and angiogenesis. 5. PTMA-CTP has been concluded from research to demonstrate potential antitumor effects in various cancer models, suggesting a potential role in cancer therapy. |
| 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 | 2,7,3,7,7 |

|  |  |
| --- | --- |
| ID | 1516(10) |
| 领域 | Bio-Medical |
| 用户问题 | Which peptide plays a pivotal role in human cystatin C fibrillization? |
| 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 peptide that plays a pivotal role in human cystatin C fibrillization is the L68 peptide. |
| 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 L68 peptide plays a pivotal role in human cystatin C fibrillization. |
| 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 | 1574(11) |
| 领域 | Bio-Medical |
| 用户问题 | Does the concentration of protein HIF-1α increase after the administration of the cytoprotective prodrug"amifostine" (ethyol) ? |
| 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 | There is limited research available on the specific effect of the cytoprotective prodrug amifostine (Ethyol) on the concentration of protein HIF-1α. However, some studies have investigated the potential modulation of HIF-1α by amifostine. One study published in the Journal of Biochemical and Molecular Toxicology in 2013 investigated the effect of amifostine on HIF-1α expression in human colorectal cancer cells. The researchers found that amifostine treatment decreased the protein levels of HIF-1α in these cells. Another study published in the journal Molecular Medicine Reports in 2015 examined the effects of amifostine on HIF-1α in a rat model of myocardial ischemia-reperfusion injury. The researchers observed that amifostine treatment reduced the expression of HIF-1α in the heart tissue of rats subjected to ischemia-reperfusion injury. Based on these limited studies, it appears that amifostine may have a suppressive effect on the concentration of HIF-1α in certain circumstances. However, more research is needed to fully understand the relationship between amifostine administration and HIF-1α concentration. |
| 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. Amifostine is a cytoprotective prodrug. 2. Studies have been conducted to investigate the influence of amifostine on the concentration of protein HIF-1α. 3. A 2013 study published in the Journal of Biochemical and Molecular Toxicology found that amifostine treatment decreased the protein levels of HIF-1α in human colorectal cancer cells. 4. A 2015 study published in Molecular Medicine Reports researched the effects of amifostine on HIF-1α in a rat model of myocardial ischemia-reperfusion injury. 5. The 2015 study observed a reduction of HIF-1α expression in the heart tissue of rats treated with amifostine and subjected to ischemia-reperfusion injury. |
| 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 | 1588(12) |
| 领域 | Bio-Medical |
| 用户问题 | Which histone marks are deposited by Set7? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | Set7, also known as SETD7, is a histone methyltransferase enzyme that specifically adds a methyl group to the lysine residue at position 4 (K4) of histone H3. This histone modification is known as H3K4 methylation and is associated with transcriptional activation and gene expression regulation. |
| 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. Set7 is also known as SETD7. 2. Set7 is a histone methyltransferase enzyme. 3. Set7 adds a methyl group to the lysine residue at position 4 of histone H3. 4. The modification made by Set7 to histone H3 is known as H3K4 methylation. 5. H3K4 methylation is associated with transcriptional activation and gene expression regulation. |
| 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 | 1,1,3,1,1 |

|  |  |
| --- | --- |
| ID | 1620(13) |
| 领域 | Bio-Medical |
| 用户问题 | How many disulfide bridges has the protein hepcidin got? |
| 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 protein hepcidin typically contains four disulfide bridges. These bridges are formed by the oxidation of cysteine residues, and they play an important role in stabilizing the protein's structure and maintaining its function. |
| 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 protein hepcidin typically contains four disulfide bridges. 2. Disulfide bridges are formed by the oxidation of cysteine residues. 3. Disulfide bridges play a role in stabilizing the protein's structure. 4. The function of a protein is maintained via disulfide bridges. |
| 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 | 1,1,1,6 |

|  |  |
| --- | --- |
| ID | 1643(14) |
| 领域 | Bio-Medical |
| 用户问题 | What is the localization of the protein encoded by the gene DNAJC11? |
| 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 protein encoded by the gene DNAJC11 is localized in the endoplasmic reticulum (ER). |
| 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 protein encoded by the gene DNAJC11 is localized in the endoplasmic reticulum (ER). |
| 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 |

|  |  |
| --- | --- |
| ID | 1655(15) |
| 领域 | Bio-Medical |
| 用户问题 | Are ultraconserved elements depleted among copy number variants (CNVs)? |
| 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 | Ultraconserved elements (UCEs) are genomic regions that are highly conserved across species and are thought to have essential biological functions. Copy number variants (CNVs) are structural genomic variations that involve changes in the number of copies of a particular genomic region. While there is limited research specifically focusing on the depletion of ultraconserved elements among CNVs, some studies have indirectly addressed this question. One study by Sudmant et al. (2015) investigated the impact of CNVs on UCEs and found that, on average, UCEs were underrepresented in CNVs compared to non-ultraconserved regions. The study showed that while CNVs significantly overlapped with non-ultraconserved regions, they were less likely to involve UCEs. Additionally, another study by Cardoso-Moreira et al. (2016) examined the impact of CNVs on gene expression and found that CNVs were significantly less likely to encompass UCEs compared to non-ultraconserved regions. This suggests that UCEs may be more resistant to structural genomic variations, such as CNVs. Overall, the currently available studies suggest that ultraconserved elements are less depleted among copy number variants compared to non-ultraconserved regions. However, more research is needed to fully understand the relationship between UCEs and CNVs. |
| 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. Ultraconserved elements (UCEs) are genomic regions that are highly conserved across species and are thought to have essential biological functions. 2. Copy number variants (CNVs) are structural genomic variations that involve changes in the number of copies of a particular genomic region. 3. A study by Sudmant et al. (2015) found that UCEs were, on average, underrepresented in CNVs compared to non-ultraconserved regions. 4. A study by Cardoso-Moreira et al. (2016) found that CNVs were significantly less likely to encompass UCEs compared to non-ultraconserved regions. 5. UCEs might be more resistant to structural genomic variations, such as CNVs. |
| 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 | 1665(16) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the substrate of the haspin kinase during mitosis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | The substrate of the haspin kinase during mitosis is the histone H3 protein. Haspin kinase phosphorylates serine 10 of histone H3 to facilitate proper chromosome condensation and segregation during mitosis. |
| 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 substrate of the haspin kinase during mitosis is the histone H3 protein. 2. Haspin kinase can phosphorylate serine 10 of histone H3. 3. Phosphorylation of histone H3 by haspin kinase facilitates proper chromosome condensation. 4. Haspin kinase also aids in chromosome segregation during mitosis. |
| 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 |

|  |  |
| --- | --- |
| ID | 1696(17) |
| 领域 | Bio-Medical |
| 用户问题 | What is the mechanism of viroid replication? |
| 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 | Viroids are small, single-stranded, circular RNA molecules that replicate within the host plant cells. The mechanism of viroid replication involves various steps: 1. Entry: Viroids enter the host plant cells through natural plant wounds or by transmission through vectors like insects, nematodes, or pollen. 2. Uncoating: Once inside the host cell, viroids are uncoated by the host enzymes, resulting in the release of the RNA molecule. 3. Replication Initiation: Viroids replicate their RNA using the host's cellular machinery. The first step in replication is the binding of a viroid-specific RNA polymerase (an enzyme) to a sequence in the viroid RNA known as the central conserved region (CCR). 4. RNA Polymerization: The RNA polymerase initiates the synthesis of a complementary RNA strand, using the viroid RNA as a template. This results in the synthesis of a new RNA strand known as the antigenome. 5. Template Switching: During RNA polymerization, the RNA polymerase can switch templates from the original viroid RNA to the newly synthesized antigenome. This switch occurs at specific sites, known as replication intermediates (RIs) or hairpin structures within the viroid RNA, where the polymerase dissociates from the template and rebinds to the antigenome. 6. Rolling Circle Replication: The template switching process results in the production of multiple antigenome copies. These antigenomes can then serve as templates for the synthesis of more viroid RNA molecules. This process is known as rolling circle replication, as the RNA polymerase continuously moves along the antigenomes, generating long, concatemeric RNA strands. 7. Cleavage and Ligation: The long concatemeric RNA strands are then cleaved into individual viroid RNA molecules by host ribonucleases. These individual viroid RNAs are then ligated, resulting in the formation of mature viroid RNA molecules ready for further replication or encapsidation. Overall, the replication of viroids is a complex process involving interactions between viroid RNA, host enzymes, and viroid-specific RNA polymerase, which allows viroids to replicate within the host cells and spread throughout the plant. |
| 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. Viroids are small, single-stranded, circular RNA molecules that replicate within the host plant cells. 2. Viroids enter the host plant cells through natural plant wounds or transmission through vectors like insects, nematodes, or pollen. 3. The replication of viroids involves the binding of a viroid-specific RNA polymerase to a sequence in the viroid RNA known as the central conserved region (CCR). 4. During viroid replication, the RNA polymerase can switch templates from the original viroid RNA to the newly synthesized antigenome at specific sites known as replication intermediates or hairpin structures. 5. The long concatemeric RNA strands produced during replication are cleaved into individual viroid RNA molecules by host ribonucleases, then ligated, forming mature viroid RNA molecules. |
| 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 | 1,1,3,1,1 |

|  |  |
| --- | --- |
| ID | 1723(18) |
| 领域 | Bio-Medical |
| 用户问题 | Does fibronectin constitute a serum biomarker for Duchenne muscular dystrophy? |
| 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, fibronectin has been studied as a potential serum biomarker for Duchenne muscular dystrophy (DMD). Fibronectin is a glycoprotein that plays a role in cell adhesion and tissue repair. In DMD, the loss of dystrophin protein leads to muscle degeneration and fibrosis, which may result in elevated levels of fibronectin in the serum. Several studies have investigated the association between fibronectin levels and DMD. One study published in the Journal of Clinical Medicine found that serum fibronectin levels were significantly elevated in DMD patients compared to healthy controls. Another study in the Journal of Neuromuscular Diseases reported similar findings, suggesting that serum fibronectin could serve as a potential biomarker for DMD. However, it is important to note that while elevated fibronectin levels have been observed in DMD, it is not specific to this condition. Fibronectin is a general marker of tissue damage and repair, and its levels can be influenced by various factors. Therefore, further research is needed to validate fibronectin as a reliable and specific biomarker for DMD. |
| 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. Fibronectin is a glycoprotein that plays a role in cell adhesion and tissue repair. 2. Duchenne muscular dystrophy is characterized by the loss of dystrophin protein leading to muscle degeneration and fibrosis. 3. Elevated levels of fibronectin in the serum have been observed in Duchenne muscular dystrophy patients. 4. One study published in the Journal of Clinical Medicine reported significantly elevated serum fibronectin levels in Duchenne muscular dystrophy patients when compared to healthy controls. 5. Fibronectin is a nonspecific marker of tissue damage and repair, and its levels can be influenced by various factors. |
| 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 | 1,1,7,3,1 |

|  |  |
| --- | --- |
| ID | 1763(19) |
| 领域 | Bio-Medical |
| 用户问题 | Data from which major epigenome projects are contained in the DeepBlue epigenomic data server? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,4,5 |
| 模型回复 | The DeepBlue epigenomic data server contains data from various major epigenome projects, including: 1. ENCODE (Encyclopedia of DNA Elements): A project that aims to identify functional elements in the human genome, including protein-coding genes, non-coding genes, and regulatory elements. 2. Roadmap Epigenomics: A project that focuses on characterizing epigenomic landscapes of various human tissues and cell types. It provides a comprehensive map of DNA methylation, histone modifications, and chromatin accessibility across the human genome. 3. BLUEPRINT: A project that focuses on understanding the epigenomic regulation of blood cells and immune responses. It aims to create a reference map of epigenetic changes in normal and diseased human blood cell types. 4. Cistrome: A project that aims to provide comprehensive cataloging of transcription factor binding sites and epigenetic modifications in various cell types. It includes data from ChIP-seq experiments and DNase-seq assays. 5. Epigenomics Roadmap for Psychiatric Disease: A project that focuses on examining epigenomic changes in psychiatric disorders. It provides data on DNA methylation, histone modifications, and chromatin accessibility in brain tissues. These are just a few examples of the major epigenome projects whose data is contained in the DeepBlue epigenomic data server. There may be other projects and datasets available 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 DeepBlue epigenomic data server contains data from the ENCODE project, which aims to identify functional elements in the human genome. 2. The Roadmap Epigenomics project, which focuses on characterizing epigenomic landscapes of various human tissues and cell types, has data stored in the DeepBlue epigenomic data server. 3. The DeepBlue server contains data from the BLUEPRINT, a project that focuses on the epigenomic regulation of blood cells and immune responses. 4. Data from the Cistrome project, which provides comprehensive cataloging of transcription factor binding sites and epigenetic modifications in various cell types, can be found on DeepBlue. 5. The Epigenomics Roadmap for Psychiatric Disease, a project focused on epigenomic changes in psychiatric disorders, has its data stored in the DeepBlue epigenomic data server. |
| 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 | 1792(20) |
| 领域 | Bio-Medical |
| 用户问题 | Which tool employs self organizing maps for analyzing synonymous codon usage? |
| 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 tool that employs self-organizing maps (SOMs) for analyzing synonymous codon usage is the Codon Usage Analyzer (CUA). CUA is a web-based tool developed by the Bioinformatics and Structural Biochemistry Laboratory at the University of Brasília, Brazil. It uses SOMs to group synonymous codons based on their usage patterns in a given set of sequences, helping to identify synonymous codon bias and optimize 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 | 1 |
| 提取的事实 | 1. The Codon Usage Analyzer (CUA) is a tool that employs self-organizing maps for analyzing synonymous codon usage. 2. CUA is a web-based tool. 3. The Codon Usage Analyzer was developed by the Bioinformatics and Structural Biochemistry Laboratory. 4. This tool was developed at the University of Brasília, Brazil. 5. The CUA uses self-organizing maps to identify synonymous codon bias and optimize gene expression. |
| 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 | 1,7,2,7,3 |

|  |  |
| --- | --- |
| ID | 1793(21) |
| 领域 | Bio-Medical |
| 用户问题 | What is MINDY-1? |
| 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 | MINDY-1 refers to an artificial intelligence model developed by the OpenAI research organization. It is a language model similar to GPT-3, trained on a large dataset of text from the internet. MINDY-1 is designed to understand and generate human-like text responses to various queries or prompts. It possesses the ability to engage in conversation, answer questions, generate creative content, and perform various other natural language processing tasks. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 2 |
| 提取的事实 | 1. MINDY-1 is an artificial intelligence model developed by the OpenAI research organization. 2. MINDY-1 is a language model similar to GPT-3. 3. MINDY-1 was trained on a large dataset of text from the internet. 4. The model can understand and generate human-like text responses to various queries or prompts. 5. MINDY-1 can engage in conversation, answer questions, generate creative content, and perform other natural language processing tasks. |
| 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 |  |

|  |  |
| --- | --- |
| ID | 1810(22) |
| 领域 | Bio-Medical |
| 用户问题 | Which software package is available for the analysis of conserved genomic loci? |
| 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 software package available for the analysis of conserved genomic loci is the Comparative Genomic Locus (CGL) Analysis tool. It is an open-source software package specifically designed for the identification and analysis of conserved genomic loci across multiple species or strains. CGL Analysis provides functionality for comparing gene sequences, generating phylogenetic trees, and visualizing conserved genomic regions. It is commonly used in comparative genomics and evolutionary studies. |
| 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 Comparative Genomic Locus (CGL) Analysis tool is a software package used for the analysis of conserved genomic loci. 2. The Comparative Genomic Locus (CGL) Analysis tool is an open-source software. 3. The software's functions include identification and analysis of conserved genomic loci across multiple species or strains. 4. CGL Analysis is capable of comparing gene sequences, generating phylogenetic trees, and visualizing conserved genomic regions. 5. The Comparative Genomic Locus (CGL) Analysis tool is commonly used in comparative genomics and evolutionary studies. |
| 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 | 2,7,3,7,7 |

|  |  |
| --- | --- |
| ID | 1860(23) |
| 领域 | Bio-Medical |
| 用户问题 | Please list 3 diseases associated with the PIEZO2 gene. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | 1. Distal Arthrogryposis Type 5: Also known as Gordon Syndrome, this disorder is caused by mutations in the PIEZO2 gene. It is characterized by joint contractures (arthrogryposis), especially in the hands and feet, as well as distinctive facial features, scoliosis, and clubfoot. 2. MoyaMoya Disease: Some studies have suggested the involvement of PIEZO2 gene mutations in the development of MoyaMoya disease, a rare cerebrovascular disorder. This condition causes the narrowing or closing of certain arteries in the brain, leading to an increased risk of stroke and other neurological symptoms. 3. Distal Hereditary Motor Neuropathy (dHMN) type V: dHMN type V is a rare genetic disorder characterized by progressive muscle weakness and atrophy, particularly in the hands and feet. Mutations in the PIEZO2 gene have been identified as a causative factor, leading to the motor neuron dysfunction associated with 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 | 1 |
| 提取的事实 | 1. Distal Arthrogryposis Type 5, also known as Gordon Syndrome, is caused by mutations in the PIEZO2 gene. 2. Some studies have suggested the involvement of PIEZO2 gene mutations in the development of MoyaMoya disease. 3. MoyaMoya disease is a rare cerebrovascular disorder that causes the narrowing or closing of certain arteries in the brain. 4. Distal Hereditary Motor Neuropathy (dHMN) type V is a rare genetic disorder characterized by progressive muscle weakness and atrophy, particularly in the hands and feet. 5. Mutations in the PIEZO2 gene have been identified as a causative factor in Distal Hereditary Motor Neuropathy (dHMN) type V. |
| 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 | 1,7,1,1,7 |

|  |  |
| --- | --- |
| ID | 1867(24) |
| 领域 | Bio-Medical |
| 用户问题 | What is promoted by ERAP1-ERAP2 dimerization? |
| 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 | ERAP1-ERAP2 dimerization promotes the trimming of peptide antigens for presentation on major histocompatibility complex class I (MHC-I) molecules. ERAP1 and ERAP2 are two closely related enzymes involved in antigen processing, specifically in the final steps of trimming peptide antigens in the endoplasmic reticulum (ER) before they are loaded onto MHC-I molecules. Dimerization of ERAP1 and ERAP2 enhances their enzymatic activity and substrate specificity. It allows the two enzymes to work cooperatively and efficiently process longer peptides into shorter, optimal epitopes for binding to MHC-I molecules. This dimerization also facilitates the translocation of peptide substrates between the active sites of ERAP1 and ERAP2, ensuring efficient trimming and generation of antigenic peptides. Overall, ERAP1-ERAP2 dimerization plays a crucial role in antigen processing and immune recognition by ensuring the proper generation of MHC-I-presented peptide antigens. |
| 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. ERAP1-ERAP2 dimerization promotes the trimming of peptide antigens for presentation on MHC-I molecules. 2. ERAP1 and ERAP2 are enzymes involved in antigen processing. 3. These enzymes are involved in the final steps of trimming peptide antigens in the endoplasmic reticulum before they are loaded onto MHC-I molecules. 4. Dimerization of ERAP1 and ERAP2 enhances their enzymatic activity and substrate specificity. 5. ERAP1-ERAP2 dimerization plays a crucial role in antigen processing and immune recognition. |
| 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 | 7,1,1,3,7 |

|  |  |
| --- | --- |
| ID | 1890(25) |
| 领域 | Bio-Medical |
| 用户问题 | What is the function of R-spondin 1 and noggin in non-damaged gallbladders? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | In non-damaged gallbladders, R-spondin 1 and noggin play important roles in maintaining the normal structure and function of the gallbladder. R-spondin 1 is a protein that acts as a potent activator of the Wnt signaling pathway. This pathway is involved in various cellular processes, including cell proliferation, differentiation, and tissue regeneration. In the gallbladder, R-spondin 1 helps to maintain the proliferation and renewal of the epithelial cells lining the gallbladder. It promotes the growth and survival of these cells, ensuring the integrity of the gallbladder lining. Noggin, on the other hand, is a protein that functions as an antagonist of bone morphogenetic proteins (BMPs). BMPs are a group of growth factors that regulate cell differentiation and tissue development. In the gallbladder, noggin acts to inhibit the action of BMPs, which could otherwise lead to inappropriate cell differentiation or tissue formation. By blocking BMP signaling, noggin helps maintain the proper balance of cell types within the gallbladder epithelium. Overall, R-spondin 1 and noggin work together to ensure the normal growth, renewal, and differentiation of cells in the non-damaged gallbladder, contributing to its regular physiological 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 | 1 |
| 提取的事实 | 1. R-spondin 1 is a protein that activates the Wnt signaling pathway. 2. The Wnt signaling pathway is involved in cell proliferation, differentiation, and tissue regeneration. 3. In the gallbladder, R-spondin 1 contributes to the proliferation and renewal of the epithelial cells. 4. Noggin is a protein that functions as an antagonist of bone morphogenetic proteins (BMPs). 5. In the gallbladder, noggin inhibits the action of BMPs to maintain the balance of cell types within the gallbladder epithelium. |
| 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 | 1,1,6,1,7 |

|  |  |
| --- | --- |
| ID | 1937(26) |
| 领域 | Bio-Medical |
| 用户问题 | Does NADPH oxidase 5 require any subunit for function? |
| 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, NADPH oxidase 5 (NOX5) requires several subunits for its function. NOX5 is a member of the NADPH oxidase enzyme family, which generates reactive oxygen species (ROS) by transferring electrons from NADPH to molecular oxygen. However, NOX5 differs from other NADPH oxidases as it is calcium-dependent and lacks the typical membrane-associated subunits found in other NOX isoforms. The subunits required for NOX5 function include: 1. NOX5 itself: NOX5 is the catalytic subunit responsible for generating ROS. 2. Calcium-binding domain: NOX5 contains calcium-binding EF hands that are required for its activation. NOX5 activation is dependent on the binding of intracellular calcium ions. 3. Poldip2: Polymerase delta-interacting protein 2 (Poldip2) is a regulatory subunit that interacts with NOX5 and is necessary for NOX5 activation. Poldip2 has been shown to stabilize NOX5 protein levels and enhance its ROS production. 4. Duox maturation factor (DUOXA): While DUOXA subunits are typically required for the maturation and cell surface expression of dual oxidase (DUOX) enzymes, recent studies have suggested that DUOXA1 and DUOXA2 may also interact with NOX5 and affect its expression in certain cell types. However, it should be noted that the exact subunit requirements for NOX5 function are still an active area of research, and further studies are needed to fully understand the regulatory mechanisms of NOX5. |
| 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. NADPH oxidase 5 (NOX5) is a member of the NADPH oxidase enzyme family, which generates reactive oxygen species. 2. The functioning of NOX5 differs from other NADPH oxidases as it is calcium-dependent and lacks the typical membrane-associated subunits. 3. NOX5 contains calcium-binding EF hands required for its activation, which depends on the binding of intracellular calcium ions. 4. Polymerase delta-interacting protein 2 (Poldip2) is a regulatory subunit necessary for NOX5 activation. 5. DUOXA1 and DUOXA2, typically required for dual oxidase (DUOX) enzymes, may also interact with NOX5 and affect its expression. |
| 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 | 1944(27) |
| 领域 | Bio-Medical |
| 用户问题 | What is the connection between furin and hepcidin? |
| 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 | Furin and hepcidin are both proteins that play important roles in the regulation of iron metabolism. Furin is a proprotein convertase enzyme that is involved in the processing and activation of various proteins. It cleaves specific peptide bonds within precursor proteins, leading to their functional activation. Furin has been shown to cleave and activate prohepcidin, a precursor form of hepcidin. Hepcidin is a small peptide hormone primarily produced by the liver. It is a key regulator of iron homeostasis in the body. Hepcidin regulates iron levels by binding to and inhibiting the action of ferroportin, a transmembrane protein that exports iron from cells. When hepcidin binds to ferroportin, it leads to degradation of ferroportin, preventing iron from being released into the blood. The connection between furin and hepcidin lies in the processing and activation of prohepcidin. Prohepcidin is initially synthesized as an inactive precursor molecule and needs to be processed to its active form, hepcidin. Furin plays a critical role in this process by cleaving prohepcidin and converting it into active hepcidin. Overall, furin is involved in the activation of hepcidin, which in turn regulates iron levels in the body. This connection highlights the intricate molecular mechanisms involved in iron homeostasis and the role of different proteins in this 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. Furin is a proprotein convertase enzyme involved in the processing and activation of various proteins. 2. Furin cleaves and activates prohepcidin, a precursor form of hepcidin. 3. Hepcidin is a small peptide hormone primarily produced by the liver, regulating iron homeostasis. 4. Hepcidin regulates iron levels by binding to and inhibiting the action of ferroportin. 5. Furin is involved in the conversion of prohepcidin into active hepcidin, which regulates iron levels in the body. |
| 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 | 1,1,1,1,2 |

|  |  |
| --- | --- |
| ID | 1956(28) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the largest metabolic gene cluster 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） | 5,5,5 |
| 模型回复 | The largest metabolic gene cluster in yeast is the galactose gene cluster. It contains 14 genes involved in the metabolism of galactose. |
| 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 largest metabolic gene cluster in yeast is the galactose gene cluster. 2. The galactose gene cluster contains 14 genes. 3. These 14 genes contained in the galactose gene cluster are involved in the metabolism of galactose. |
| 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 | 2,7,1 |

|  |  |
| --- | --- |
| ID | 1967(29) |
| 领域 | Bio-Medical |
| 用户问题 | What is the role of LIMT lncRNA? |
| 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 | LIMT lncRNA, also known as LncRNA in Macrophages Induced by TLR4, is a long non-coding RNA molecule that plays a role in immune response and inflammation. It was discovered as a downstream target of Toll-like receptor 4 (TLR4) signaling, which is involved in the recognition of pathogens and activation of immune responses. LIMT lncRNA is mainly expressed in macrophages, a type of immune cells that play a crucial role in innate immune response. Upon activation of TLR4 signaling by bacterial lipopolysaccharides (LPS) or other microbial components, LIMT lncRNA is upregulated in macrophages. LIMT lncRNA has been found to regulate the inflammatory response by modulating the expression of pro-inflammatory genes. It interacts with transcription factors and chromatin remodeling complexes to control the expression of genes involved in the production of pro-inflammatory cytokines like interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF-α), and interleukin-1 beta (IL-1β). Furthermore, LIMT lncRNA has been shown to regulate the polarization of macrophages into the M1 pro-inflammatory phenotype. It promotes the expression of M1-specific genes and inhibits the expression of M2 anti-inflammatory genes, contributing to an amplified pro-inflammatory response. Overall, LIMT lncRNA has emerged as a key player in the regulation of immune response and inflammation, particularly in macrophages. Its dysregulation can potentially contribute to inflammatory disorders and uncovering its mechanisms may provide insights into the development of new therapies for inflammatory diseases. |
| 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. LIMT lncRNA interacts with transcription factors and chromatin remodeling complexes to control the expression of genes involved in the production of pro-inflammatory cytokines. 2. LIMT lncRNA regulates the polarization of macrophages into the M1 pro-inflammatory phenotype. 3. LIMT lncRNA promotes the expression of M1-specific genes and inhibits the expression of M2 anti-inflammatory genes. 4. LIMT lncRNA, is a long non-coding RNA molecule involved in immune response and inflammation. 5. LIMT lncRNA's dysregulation can potentially contribute to inflammatory 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 | 2,3,2,4,7 |

|  |  |
| --- | --- |
| ID | 1984(30) |
| 领域 | Bio-Medical |
| 用户问题 | Which R / bioconductor package is used for performing SNP enrichment analysis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | One package commonly used for performing SNP enrichment analysis in R / Bioconductor is g:Profiler. |
| 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 g:Profiler package in R / Bioconductor is commonly used for performing SNP enrichment analysis. |
| 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 |

|  |  |
| --- | --- |
| ID | 2015(31) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the key players on radial glial specification to ependymal cells? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | There are several key players involved in the specification of radial glial cells to ependymal cells. These include: 1. Transcription factors: Transcription factors play a crucial role in specifying the differentiation of radial glial cells into ependymal cells. For example, FoxJ1 and Gli3 are transcription factors that promote the differentiation of ependymal cells. 2. Notch signaling pathway: Notch signaling is involved in the specification of radial glial cells into ependymal cells. Activation of the Notch pathway leads to the expression of transcription factors such as FoxJ1, which in turn promotes ependymal cell differentiation. 3. Ciliary neurotrophic factor (CNTF): CNTF is a neurotrophic factor that plays a role in the specification of ependymal cells. It has been shown to promote the differentiation of radial glial cells into ependymal cells. 4. Sonic Hedgehog (Shh) signaling pathway: Shh signaling is crucial for the specification of radial glial cells into ependymal cells. Shh, a morphogen, activates the Gli transcription factors, which in turn regulate the expression of genes involved in ependymal cell specification. 5. Extracellular matrix components: The extracellular matrix, including components such as laminin, also plays a role in the specification of radial glial cells to ependymal cells. These components provide a structural framework and signaling cues for cell differentiation. It is important to note that the specific mechanisms and players involved in radial glial specification to ependymal cells may vary depending on the specific context and species being studied. |
| 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. Transcription factors like FoxJ1 and Gli3 promote the differentiation of radial glial cells into ependymal cells. 2. The Notch signaling pathway is involved in the specification of radial glial cells into ependymal cells. 3. The ciliary neurotrophic factor (CNTF) promotes the differentiation of radial glial cells into ependymal cells. 4. Sonic Hedgehog (Shh) signaling pathway is crucial for the specification of radial glial cells into ependymal cells. 5. Extracellular matrix components, including laminin, play a role in the specification of radial glial cells to ependymal 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 | 1,2,3,6,1 |

|  |  |
| --- | --- |
| ID | 2065(32) |
| 领域 | Bio-Medical |
| 用户问题 | How are triple negative gliomas characterized? |
| 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 | Triple negative gliomas are characterized by the absence of three specific cell surface markers: estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). These markers are typically found on the surface of normal cells and are indicators for targeted therapies in certain cancers. However, in triple negative gliomas, these markers are not present, making it more challenging to target and treat the tumor using traditional therapeutic approaches. Triple negative gliomas are often characterized by their aggressive growth, poorer prognosis, and resistance to conventional treatment methods. |
| 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. Triple negative gliomas are characterized by the absence of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). 2. ER, PR, and HER2 are typically found on the surface of normal cells and are indicators for targeted therapies in certain cancers. 3. The absence of ER, PR, and HER2 makes triple negative gliomas more challenging to target and treat using traditional therapeutic approaches. 4. Triple negative gliomas are often characterized by aggressive growth. 5. Triple negative gliomas are generally resistant to conventional treatment methods and have a poorer prognosis. |
| 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 | 2,1,3,2,3 |

|  |  |
| --- | --- |
| ID | 2069(33) |
| 领域 | Bio-Medical |
| 用户问题 | What is TOPAZ1? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | TOPAZ1 (The Ohio State University Pointing and Zipping Robot #1) is a robotic system developed at The Ohio State University in the field of robotics and automation. It is a robotic arm mounted on a mobile platform that can perform various tasks such as grasping objects, pointing at targets, and zipping up a jacket. TOPAZ1 is designed to assist people with physical disabilities in performing activities of daily living, specifically those with limited hand dexterity. The system incorporates advanced sensing, perception, and control algorithms to enable the robot to interact with the environment and objects effectively. TOPAZ1 serves as a research platform for exploring technologies that can enhance the autonomy and capabilities of assistive robots. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 2 |
| 提取的事实 | 1. TOPAZ1 is a robotic system developed at The Ohio State University. 2. The Ohio State University designed TOPAZ1 for the field of robotics and automation. 3. TOPAZ1 is a robotic arm mounted on a mobile platform capable of performing tasks like grasping objects, pointing at targets, and zipping up a jacket. 4. The primary purpose of TOPAZ1 is to assist individuals with physical disabilities, particularly those with limited hand dexterity. 5. TOPAZ1 uses advanced sensing, perception, and control algorithms to interact with the environment and objects. |
| 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 |  |

|  |  |
| --- | --- |
| ID | 2075(34) |
| 领域 | Bio-Medical |
| 用户问题 | Which gene controls the expression of GATA-1 isoforms? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | The GATA1 gene itself controls the expression of GATA-1 isoforms. GATA1 is a transcription factor that binds to its own promoter region and regulates the transcription and alternative splicing of the GATA1 gene. This process results in the production of various isoforms of the GATA-1 protein. |
| 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 GATA1 gene controls the expression of GATA-1 isoforms. 2. GATA1 is a transcription factor. 3. GATA1 gene binds to its own promoter region. 4. GATA1 gene regulates the transcription and alternative splicing of itself. 5. The process controlled by the GATA1 gene results in the production of various isoforms of the GATA-1 protein. |
| 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 | 1,1,3,3,1 |

|  |  |
| --- | --- |
| ID | 2076(35) |
| 领域 | Bio-Medical |
| 用户问题 | What is MIRA-seq? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,4 |
| 模型回复 | MIRA-seq, also known as MicroRNA Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) Analysis, is a technique used to measure the expression levels of microRNAs (small non-coding RNA molecules) in biological samples. It is a type of quantitative PCR method specifically designed for studying the expression of microRNAs, which are involved in the regulation of gene expression. MIRA-seq involves reverse transcription of microRNA molecules into complementary DNA (cDNA) using specific primers. This cDNA is then amplified using quantitative polymerase chain reaction (qPCR) techniques. Through the use of fluorescent probes or intercalating dyes, the amplification of the specific microRNAs can be monitored in real-time. The resulting data provides information about the relative expression levels of different microRNAs in a sample, allowing for the comparison of expression patterns between different biological conditions or samples. MIRA-seq is a valuable tool in microRNA research as it enables the quantification of microRNA expression levels with high specificity and sensitivity. It can be used to investigate the roles of microRNAs in various biological processes, such as development, disease progression, and response to treatment. |
| 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. MIRA-seq, or MicroRNA Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) Analysis, measures the expression levels of microRNAs in biological samples. 2. MicroRNAs are involved in the regulation of gene expression. 3. MIRA-seq involves reverse transcription of microRNA molecules into complementary DNA (cDNA) using specific primers. 4. The technique of MIRA-seq uses fluorescent probes or intercalating dyes to monitor the amplification of specific microRNAs in real-time. 5. MIRA-seq can be used to investigate the roles of microRNAs in various biological processes, such as development, disease progression, and response to treatment. |
| 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 | 1,7,2,4,2 |

|  |  |
| --- | --- |
| ID | 2108(36) |
| 领域 | Bio-Medical |
| 用户问题 | What is the indication of ARCALYST? |
| 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 | ARCALYST (rilonacept) is indicated for the treatment of Cryopyrin-Associated Periodic Syndromes (CAPS), including Familial Cold Autoinflammatory Syndrome (FCAS) and Muckle-Wells Syndrome (MWS) in adults and children 12 years and older. It is also indicated for the treatment of Neonatal-Onset Multisystem Inflammatory Disease (NOMID)/Chronic Infantile Neurologic, Cutaneous, Articular (CINCA) Syndrome in infants and children 4 months and older. |
| 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. ARCALYST (rilonacept) is used for the treatment of Cryopyrin-Associated Periodic Syndromes (CAPS). 2. ARCALYST is indicated for treating Familial Cold Autoinflammatory Syndrome (FCAS) and Muckle-Wells Syndrome (MWS). 3. ARCALYST is used for treating patients of FCAS and MWS who are 12 years old and above. 4. ARCALYST is indicated for treating Neonatal-Onset Multisystem Inflammatory Disease (NOMID)/Chronic Infantile Neurologic, Cutaneous, Articular (CINCA) Syndrome. 5. The treatment of NOMID/CINCA with ARCALYST is indicated for infants and children who are 4 months old and above. |
| 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 | 1,1,1,4,2 |

|  |  |
| --- | --- |
| ID | 2170(37) |
| 领域 | Bio-Medical |
| 用户问题 | List the human acrocentric chromosomes that are involved in Robertsonian translocation. |
| 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 human acrocentric chromosomes that are involved in Robertsonian translocation are: 1. Chromosome 13 (13q14) 2. Chromosome 14 (14q11) 3. Chromosome 15 (15q13) 21q21 22q12 |
| 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. Chromosome 13 (13q14) is a human acrocentric chromosome involved in Robertsonian translocation. 2. Chromosome 14 (14q11) is a human acrocentric chromosome involved in Robertsonian translocation. 3. Chromosome 15 (15q13) is a human acrocentric chromosome involved in Robertsonian translocation. 4. Chromosome 21 (21q21) is a human acrocentric chromosome involved in Robertsonian translocation. 5. Chromosome 22 (22q12) is a human acrocentric chromosome involved in Robertsonian translocation. |
| 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 | 1,1,1,3,3 |

|  |  |
| --- | --- |
| ID | 2237(38) |
| 领域 | Bio-Medical |
| 用户问题 | Which R package could be used for the identification of pediatric brain tumors? |
| 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 'medulloblastoma' package in R could be used for the identification of pediatric brain tumors, specifically focusing on medulloblastoma, which is one type of pediatric brain tumor. This package provides various functions and tools for analysis and visualization of medulloblastoma data, including gene expression and copy number variation data. |
| 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 'medulloblastoma' package is an R package. 2. The 'medulloblastoma' in R could be used for the identification of pediatric brain tumors. 3. Medulloblastoma is a type of pediatric brain tumor. 4. The 'medulloblastoma' package provides various functions and tools for the analysis and visualization of medulloblastoma data. 5. The 'medulloblastoma' package can handle gene expression and copy number variation data. |
| 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 | 3,3,1,2,2 |

|  |  |
| --- | --- |
| ID | 2246(39) |
| 领域 | Bio-Medical |
| 用户问题 | Is NEMO a zinc finger protein? |
| 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, NEMO (NF-κB essential modulator) is not a zinc finger protein. NEMO is an important regulatory protein involved in the NF-κB (nuclear factor kappa-light-chain-enhancer of activated B cells) signaling pathway. It contains several functional domains, including a leucine zipper domain and a coiled-coil domain, but it does not contain any zinc finger motifs. |
| 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. NEMO stands for NF-κB essential modulator. 2. NEMO is a regulatory protein. 3. NEMO is involved in the NF-κB signaling pathway. 4. NEMO contains a leucine zipper domain and a coiled-coil domain. 5. NEMO does not contain any zinc finger motifs. |
| 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 | 1,1,1,1,6 |

|  |  |
| --- | --- |
| ID | 2247(40) |
| 领域 | Bio-Medical |
| 用户问题 | Does TFIIS affect nucleosome positioning? |
| 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, Transcription Elongation Factor TFIIS has been shown to affect nucleosome positioning. TFIIS promotes transcription elongation by stimulating RNA polymerase II backtracking and cleavage of stalled transcripts. This allows the RNA polymerase II to continue transcribing through nucleosomes, which are condensed structures of DNA and histone proteins.  By promoting transcription through nucleosomes, TFIIS can influence nucleosome positioning. It has been shown that TFIIS can displace histone proteins from the DNA template, leading to changes in nucleosome positioning and overall chromatin structure. This remodeling of nucleosomes can have significant effects on gene expression, as the accessibility of DNA to transcription factors and other regulatory proteins is dependent on nucleosome positioning. |
| 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. Transcription Elongation Factor TFIIS, also known as TFIIS, can affect nucleosome positioning. 2. TFIIS promotes transcription elongation by stimulating RNA polymerase II backtracking and cleavage of stalled transcripts. 3. Nucleosomes are condensed structures of DNA and histone proteins. 4. TFIIS can displace histone proteins from DNA, leading to changes in nucleosome positioning and chromatin structure. 5. The accessibility of DNA to transcription factors and other regulatory proteins is dependent on nucleosome positioning. |
| 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 | 3,1,1,3,1 |

|  |  |
| --- | --- |
| ID | 2262(41) |
| 领域 | Bio-Medical |
| 用户问题 | Do origins of replication close to yeast centromeres fire early or late? |
| 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 origins of replication close to yeast centromeres generally fire late during the replication process. This is due to a phenomenon known as centromere-proximal pausing, where replication forks stall in the vicinity of centromeres before they resume replication. This pausing allows replication at regions farther away from the centromeres to progress first, ensuring that the centromere is fully replicated before the replication forks approach it. |
| 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 origins of replication close to yeast centromeres generally fire late during the replication process. 2. This late firing is due to a phenomenon known as centromere-proximal pausing. 3. During centromere-proximal pausing, replication forks stall in the vicinity of centromeres before resuming replication. 4. Centromere-proximal pausing allows replication at regions farther away from the centromeres to progress first. 5. Centromere-proximal pausing ensures that the centromere is fully replicated before the replication forks approach it. |
| 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 | 3,4,1,2,2 |

|  |  |
| --- | --- |
| ID | 2268(42) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the properties of mammalian GA-sequences? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | 1) Conservation: GA-sequences are highly conserved across mammalian species, meaning they remain relatively unchanged across different species over evolutionary time. 2) Abundance: GA-sequences are present in large numbers throughout the mammalian genome, making them a common feature. 3) Repetitive: GA-sequences are repetitive sequences, meaning they occur in multiple copies within the genome. 4) Function: Although the exact function of GA-sequences is not entirely understood, they have been implicated in various biological processes, such as DNA replication, gene regulation, and chromosome stability. 5) Chromosomal location: GA-sequences are distributed across various regions of the genome, including both coding and non-coding regions. 6) Binding sites: GA-sequences can serve as binding sites for specific proteins, such as transcription factors, which can regulate gene expression. 7) Variability: Although highly conserved across species, there can be some variability in the specific sequence or length of GA-sequences within the genome of individual organisms. It is important to note that our understanding of GA-sequences is still evolving, and further research is needed to fully uncover their properties and functions in mammalian genomes. |
| 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. GA-sequences are highly conserved across mammalian species. 2. GA-sequences are present in large numbers throughout the mammalian genome. 3. GA-sequences are repetitive sequences in the genome. 4. GA-sequences have been implicated in various biological processes, like DNA replication, gene regulation, and chromosome stability. 5. GA-sequences can serve as binding sites for specific proteins, such as transcription factors. |
| 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 | 3,2,6,2,2 |

|  |  |
| --- | --- |
| ID | 2291(43) |
| 领域 | Bio-Medical |
| 用户问题 | How many Groucho-related genes (GRG) are contained in the mouse genome? |
| 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 is currently no known gene specifically referred to as Groucho-related gene (GRG) in the mouse genome. |
| 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 is no known gene specifically referred to as Groucho-related gene (GRG) in the mouse 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 | 1 |

|  |  |
| --- | --- |
| ID | 2304(44) |
| 领域 | Bio-Medical |
| 用户问题 | Which RNA polymerase II subunit carries RNA cleavage activity? |
| 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 RNA polymerase II subunit that carries the RNA cleavage activity is called Rpb11. |
| 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 RNA polymerase II subunit called Rpb11 carries the RNA cleavage 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 |

|  |  |
| --- | --- |
| ID | 2321(45) |
| 领域 | Bio-Medical |
| 用户问题 | What is the genetic basis of Ohdo 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 | Ohdo syndrome is a rare genetic disorder that is primarily caused by mutations or changes in the KDM5C gene. The KDM5C gene provides instructions for producing a protein that plays a crucial role in regulating gene expression. This protein is involved in the process of removing certain chemical tags, known as methyl groups, from specific regions of DNA. Methylation is an important mechanism in controlling gene activity. Mutations in the KDM5C gene disrupt the function of the protein it produces, resulting in abnormal gene regulation. This can lead to a wide range of physical and developmental features associated with Ohdo syndrome, including intellectual disability, distinctive facial features, cardiac anomalies, hearing loss, and delayed growth and development. In some cases, Ohdo syndrome can also be caused by changes in the chromodomain helicase DNA-binding protein 7 (CHD7) gene. Mutations in this gene are more commonly associated with another genetic disorder called CHARGE syndrome. However, CHD7 mutations have been identified in a small number of individuals with Ohdo syndrome as well. Overall, the genetic basis of Ohdo syndrome primarily involves mutations in the KDM5C or CHD7 genes, which disrupt the regulation of gene expression and contribute to the characteristic features of the 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. Ohdo syndrome is a genetic disorder primarily caused by mutations in the KDM5C gene. 2. The KDM5C gene provides instructions for producing a protein that plays a crucial role in regulating gene expression by removing methyl groups from specific regions of DNA. 3. Mutations in the KDM5C gene result in abnormal gene regulation and can lead to a wide range of physical and developmental features associated with Ohdo syndrome. 4. In some cases, Ohdo syndrome can be caused by changes in the chromodomain helicase DNA-binding protein 7 (CHD7) gene. 5. Mutations in the CHD7 gene are more commonly associated with another genetic disorder called CHARGE 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 | 2,3,3,1,1 |

|  |  |
| --- | --- |
| ID | 2331(46) |
| 领域 | Bio-Medical |
| 用户问题 | Which R/Bioconductor package has been developed for the analysis of psychiatric disease genes? |
| 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 R/Bioconductor package that has been developed for the analysis of psychiatric disease genes is the "PAGWAS" package. PAGWAS stands for "Pathway Analysis of Genome-Wide Association Studies" and is designed specifically for the analysis of psychiatric and neurodevelopmental disorders. This package provides tools for pathway enrichment analysis, network analysis, and visualization of psychiatric disease-associated genes. |
| 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 "PAGWAS" package is an R/Bioconductor package developed for analyzing psychiatric disease genes. 2. The acronym PAGWAS stands for "Pathway Analysis of Genome-Wide Association Studies". 3. PAGWAS is specifically designed to analyze psychiatric and neurodevelopmental disorders. 4. The PAGWAS package provides tools for pathway enrichment analysis. 5. The PAGWAS package also provides tools for network analysis and visualization of disease-associated genes. |
| 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 | 2,1,2,2,2 |

|  |  |
| --- | --- |
| ID | 2360(47) |
| 领域 | Bio-Medical |
| 用户问题 | Describe swirl sign in intracerebral hemorrhage. |
| 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 swirl sign in intracerebral hemorrhage is a radiological finding that describes a characteristic appearance of the hematoma on contrast-enhanced computed tomography (CT) or magnetic resonance imaging (MRI). It appears as a central non-enhancing region surrounded by a peripheral ring of enhancement, resembling a "swirl" or "target sign." The central non-enhancing region represents the acutely extravasated blood within the brain tissue. This region usually corresponds to the oldest and most coagulated blood within the hematoma. It has higher hematocrit levels and lower protein content, leading to reduced contrast enhancement. On the other hand, the peripheral ring of enhancement represents the active bleeding and inflammation occurring at the periphery of the hematoma. The contrast agent in this region is actively taken up by the surrounding vessels and inflammatory cells, resulting in increased contrast enhancement. The swirl sign is typically seen in the subacute or chronic phase of intracerebral hemorrhage when the hematoma is well-developed and organized. It is often associated with traumatic brain injury, arteriovenous malformations, or anticoagulant-related hemorrhages. The presence of a swirl sign can provide important diagnostic information and guide appropriate management strategies for the patient. |
| 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 swirl sign in intracerebral hemorrhage is a radiological finding that can be seen on contrast-enhanced computed tomography (CT) or magnetic resonance imaging (MRI). 2. The central non-enhancing region of the swirl sign represents the acutely extravasated blood within the brain tissue. 3. This region usually corresponds to the oldest and most coagulated blood within the hematoma, with higher hematocrit levels and lower protein content. 4. The peripheral ring of enhancement in the swirl sign represents the active bleeding and inflammation at the periphery of the hematoma. 5. The swirl sign is often associated with traumatic brain injury, arteriovenous malformations, or anticoagulant-related hemorrhages. |
| 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 | 6,1,3,1,1 |

|  |  |
| --- | --- |
| ID | 2392(48) |
| 领域 | Bio-Medical |
| 用户问题 | What induces Arabidopsis ROF1 expression? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | Arabidopsis ROF1 (Responsive to Dehydration 21) is a stress-responsive gene that is induced under various environmental stresses, particularly drought stress. Several factors and signaling pathways contribute to the induction of ROF1 expression: 1. Drought stress: Water deficit conditions are the main inducer of ROF1 expression. When Arabidopsis plants experience water scarcity, the dehydration stress activates various signaling pathways that lead to the upregulation of ROF1 gene expression. 2. ABA (Abscisic Acid): ABA is a crucial hormone that mediates plant responses to water stress. It plays a significant role in activating the expression of stress-responsive genes, including ROF1. ABA levels increase in response to drought stress, leading to the activation of ABA signaling cascades that induce ROF1 expression. 3. Osmotic stress: ROF1 expression can be induced by osmotic stress, which occurs when plants are exposed to high solute concentrations. Osmotic stress can be mimicked in laboratory conditions by treating plants with osmolytes such as mannitol or polyethylene glycol (PEG). These treatments can induce ROF1 expression. 4. Reactive Oxygen Species (ROS): ROS, including hydrogen peroxide (H2O2), function as secondary messengers in stress signaling pathways. Increased ROS levels are associated with various environmental stresses, including drought stress. ROS accumulation induces the expression of ROF1 and other stress-responsive genes. 5. Other stress-related signaling molecules: Other signaling molecules, including calcium ions (Ca2+), mitogen-activated protein kinases (MAPKs), and nitric oxide (NO), also contribute to ROF1 expression. These signaling molecules are involved in stress perception and signal transduction pathways, ultimately leading to the induction of ROF1 expression. Overall, environmental stresses, particularly drought stress, lead to the induction of ROF1 expression in Arabidopsis through the activation of various signaling pathways and the involvement of stress-related hormones, ROS, and other signaling molecules. |
| 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. Arabidopsis ROF1 is a stress-responsive gene. 2. Drought stress is a major inducer of Arabidopsis ROF1 expression. 3. The hormone Abscisic Acid, or ABA, mediates plant responses to water stress and plays a role in activating ROF1 expression. 4. Osmotic stress, which can occur when plants are exposed to high solute concentrations, can induce ROF1 expression. 5. Increased levels of reactive oxygen species (ROS), including hydrogen peroxide, are associated with the induction of ROF1 expression. |
| 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 | 2,3,3,2,3 |

|  |  |
| --- | --- |
| ID | 2398(49) |
| 领域 | Bio-Medical |
| 用户问题 | What protein is the most common cause of hereditary renal amyloidosis? |
| 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 protein associated with hereditary renal amyloidosis is transthyretin. |
| 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. Transthyretin is the most common protein associated with hereditary renal amyloidosis. |
| 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 |