幻象标注

|  |  |
| --- | --- |
| ID | 10(0) |
| 领域 | Bio-Medical |
| 用户问题 | Name synonym of Acrokeratosis paraneoplastica. |
| 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 possible synonyms for Acrokeratosis paraneoplastica are: - Bazex syndrome - Bazex-Dupré-Christol syndrome - Acrokeratosis neoplastica - Triad syndrome - Bazex syndrome of multiple basal cell carcinomas - Bazex syndrome of carcinomas of pharynx and esophagus - Fingerprint-acral-keratoderma - Specifically for the clinical presentation of palmoplantar keratoderma with dermatoscopic abnormal hand fingerprint patterns. |
| 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. Bazex syndrome is a synonym for Acrokeratosis paraneoplastica. 2. Bazex-Dupré-Christol syndrome is another name for Acrokeratosis paraneoplastica. 3. Acrokeratosis neoplastica and Triad syndrome are also synonymous with Acrokeratosis paraneoplastica. 4. 'Bazex syndrome of multiple basal cell carcinomas' and 'Bazex syndrome of carcinomas of pharynx and esophagus' are alternative names for Acrokeratosis paraneoplastica. 5. The term 'Fingerprint-acral-keratoderma' is specifically connected to the clinical presentation of palmoplantar keratoderma with dermatoscopic abnormal hand fingerprint patterns as a substitute for Acrokeratosis paraneoplastica. |
| 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 | 1,3,3,7,7 |

|  |  |
| --- | --- |
| ID | 47(1) |
| 领域 | Bio-Medical |
| 用户问题 | Is Weaver syndrome similar to Sotos? |
| 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, Weaver syndrome is similar to Sotos syndrome in some ways. Weaver syndrome is a rare genetic disorder characterized by overgrowth and distinctive facial features. Similarly, Sotos syndrome is also a rare genetic disorder associated with overgrowth and distinctive facial features. Both syndromes share certain common features, such as taller than average height, advanced bone age, large head circumference, and intellectual disability. However, there are also some differences between the two syndromes. Weaver syndrome is typically associated with accelerated bone age, while Sotos syndrome is characterized by delayed bone age. Weaver syndrome is also associated with a specific genetic mutation in the EZH2 gene, while Sotos syndrome is caused by various genetic mutations, including NSD1 gene mutations in around 90% of cases. Overall, while both syndromes have some similarities, they can be distinguished by their specific features, genetic causes, and diagnostic criteria. A thorough clinical evaluation and genetic testing are usually required to accurately diagnose and differentiate between the two syndromes. |
| 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. Weaver syndrome is a rare genetic disorder characterized by overgrowth and distinctive facial features. 2. Sotos syndrome is a rare genetic disorder associated with overgrowth and distinctive facial features. 3. Features common to both Weaver and Sotos syndromes include taller than average height, advanced bone age, large head circumference, and intellectual disability. 4. Weaver syndrome is typically associated with accelerated bone age and a specific genetic mutation in the EZH2 gene. 5. Sotos syndrome is characterized by delayed bone age and is caused by various genetic mutations, including NSD1 gene mutations in around 90% of cases. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1,1,1,1,3 |

|  |  |
| --- | --- |
| ID | 81(2) |
| 领域 | Bio-Medical |
| 用户问题 | List the releases of JASPAR database |
| 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 | Here is a list of the releases of the JASPAR database: 1. JASPAR 1.0: The initial release in 1996 containing a collection of known transcription factor binding sites. 2. JASPAR 2.0: Released in 1998 with an improved and expanded collection of binding sites. 3. JASPAR 2.1: Released in 2002 featuring updates to the database structure, added motifs, and improved search functionality. 4. JASPAR 3.0: Released in 2004 with a major overhaul of the database, introducing new motifs, integrating new tools, and enhancing the user interface. 5. JASPAR 4.0: Released in 2008, this release included a substantial increase in the number of motifs and the addition of phylogenetic footprints. 6. JASPAR 4.2: Released in 2010, focusing on quality control and updates to the database content. 7. JASPAR 2010: Released in 2010 with significant updates to the database content, including new motif collections and refined motif annotations. 8. JASPAR 2014: Released in 2014, this release introduced JASPAR CORE, a collection of high-quality, non-redundant transcription factor binding site motifs. 9. JASPAR 2018: Released in 2018, featuring updated motif collections, improved data integration, and enhanced visualization tools. 10. JASPAR 2022: The most recent release as of the date of this response, it includes a comprehensive collection of accurately annotated transcription factor binding site motifs, incorporating diverse species and highlighting functional elements in the non-coding genome. Please note that there may have been additional minor updates and patches between these major releases. |
| 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. JASPAR 1.0, the initial release of the JASPAR database, was launched in 1996 containing transcription factor binding sites. 2. JASPAR 2.0 was released in 1998 with an expanded collection of binding sites. 3. The release of JASPAR 3.0 occurred in 2004, introducing new motifs, new tools, and an enhanced user interface. 4. In 2018, JASPAR 2018 was released, featuring updated motif collections, improved data integration, and enhanced visualization tools. 5. The most recent release mentioned is JASPAR 2022, which includes a comprehensive collection of annotated transcription factor binding site motifs, diverse species, and functional elements in the non-coding 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 | 1,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 99(3) |
| 领域 | Bio-Medical |
| 用户问题 | What is the function of the viral KP4 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 | The viral KP4 protein is a protein produced by certain types of viruses, such as rice gall dwarf virus and cereal yellow dwarf virus. The specific function of the KP4 protein is to suppress the host plant's defense response and promote virus multiplication within the infected plant cell. The KP4 protein acts as a suppressor of RNA silencing, which is an innate defense mechanism in plants that helps control the spread of viruses. RNA silencing involves the degradation of viral RNA, preventing virus replication and spread. However, the KP4 protein interferes with this process by inhibiting the formation of small interfering RNAs (siRNAs), which are involved in RNA silencing. By inhibiting RNA silencing, the viral KP4 protein promotes virus multiplication and movement within the host plant. It helps the virus to evade the plant's defense mechanisms, allowing it to establish a successful infection and propagate. |
| 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 viral KP4 protein is produced by certain types of viruses, including the rice gall dwarf virus and cereal yellow dwarf virus. 2. The KP4 protein suppresses the host plant's defense response and promotes virus multiplication inside the infected plant cell. 3. The KP4 protein acts as a suppressor of RNA silencing, an innate defense mechanism in plants against viruses. 4. RNA silencing in plants involves the degradation of viral RNA to prevent virus replication and spread. 5. The KP4 protein inhibits the formation of small interfering RNAs (siRNAs) which are involved in RNA silencing. |
| 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 | 3,1,7,1,7 |

|  |  |
| --- | --- |
| ID | 124(4) |
| 领域 | Bio-Medical |
| 用户问题 | Is DITPA a thyroid hormone analog utilized in experimental and clinical studies |
| 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, DITPA is not a thyroid hormone analog utilized in experimental and clinical studies. DITPA, also known as 3,5-diiodothyropropionic acid, is a synthetic derivative of thyroid hormone that has been investigated for its potential therapeutic effects on heart failure. It is a selective thyromimetic compound that activates the cardiac thyroid hormone receptor and has shown promise in preclinical studies. However, its clinical development has been discontinued due to concerns about potential side effects and lack of clear efficacy benefits. |
| 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. DITPA, also known as 3,5-diiodothyropropionic acid, is not a thyroid hormone analog utilized in experimental and clinical studies. 2. DITPA is a synthetic derivative of thyroid hormone. 3. DITPA has been investigated for its potential therapeutic effects on heart failure. 4. DITPA is a selective thyromimetic compound that activates the cardiac thyroid hormone receptor. 5. The clinical development of DITPA has been discontinued due to concerns about potential side effects and lack of clear efficacy benefits. |
| 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 | 1,3,1,1,7 |

|  |  |
| --- | --- |
| ID | 144(5) |
| 领域 | Bio-Medical |
| 用户问题 | What is the COUGER tool? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | The COUGER tool refers to the Data COUGER (Constraint discovery Over Uninterpreted GEnetic Reasoning) tool. It is a software tool used for discovering models and constraints from data in the field of genetic programming. It employs genetic programming techniques to automatically generate models and constraints from input-output data pairs. These models and constraints can be useful in various areas such as system identification, hypothesis testing, and knowledge discovery in various domains including engineering, computer science, and biology. |
| 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 COUGER tool, or Data COUGER, is a software tool used in the field of genetic programming. 2. The COUGER tool aids in the discovery of models and constraints from data. 3. The process of the COUGER tool involves the use of genetic programming techniques. 4. The application of COUGER tool includes areas such as system identification, hypothesis testing, and knowledge discovery. 5. Fields such as engineering, computer science, and biology can benefit from the use of the COUGER 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 | 2,2,3,3,3 |

|  |  |
| --- | --- |
| ID | 145(6) |
| 领域 | Bio-Medical |
| 用户问题 | Are there drugs for Tick-borne Encephalitis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Yes, there are vaccines and antiviral drugs available for the treatment and prevention of Tick-borne Encephalitis (TBE).  Vaccines: Tick-borne Encephalitis vaccines are recommended for individuals living in or traveling to areas where the disease is endemic. There are several effective vaccines available, including inactivated vaccines and live attenuated vaccines. These vaccines provide protection against Tick-borne Encephalitis virus and can significantly reduce the risk of infection. Antiviral Drugs: In cases where an individual has been infected with Tick-borne Encephalitis virus, antiviral drugs can be used to help manage the symptoms and reduce complications. Ribavirin is one antiviral drug that has been used in the treatment of Tick-borne Encephalitis, although its effectiveness and specific use may vary depending on the country and specific situation. It is important to consult with a healthcare professional or travel medicine specialist for specific advice on vaccination and treatment options for Tick-borne Encephalitis, as recommendations may vary based on factors such as location, individual health status, and travel plans. |
| 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 vaccines and antiviral drugs available for the treatment and prevention of Tick-borne Encephalitis (TBE). 2. Tick-borne Encephalitis vaccines are recommended for individuals living in or traveling to areas where the disease is endemic. 3. There are inactivated vaccines and live attenuated vaccines available for TBE. 4. Antiviral drugs can be used to manage symptoms and reduce complications in individuals infected with the Tick-borne Encephalitis virus. 5. Ribavirin is an antiviral drug used in the treatment of Tick-borne Encephalitis. |
| 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 | 151(7) |
| 领域 | Bio-Medical |
| 用户问题 | Which genome browser database for DNA shape annotations is available? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | One of the genome browser databases that includes DNA shape annotations is the ENCODE Project Consortium. They have developed a comprehensive database known as the "Encyclopedia of DNA Elements" (ENCODE) that includes various functional annotations, including DNA shape. The ENCODE browser allows researchers to visualize and analyze DNA shape data alongside other genomic features. |
| 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 ENCODE Project Consortium includes DNA shape annotations in their database. 2. The ENCODE Project Consortium has developed the "Encyclopedia of DNA Elements" database. 3. The "Encyclopedia of DNA Elements" (ENCODE) contains various functional annotations, including DNA shape. 4. The ENCODE browser is a tool that allows researchers to visualize and analyze DNA shape data. 5. DNA shape data can be analyzed alongside other genomic features through the ENCODE browser. |
| 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 | 7,1,7,2,7 |

|  |  |
| --- | --- |
| ID | 174(8) |
| 领域 | Bio-Medical |
| 用户问题 | Which syndromes are associated with mutations in the EZH2 gene? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Mutations in the EZH2 gene are primarily associated with a group of rare developmental disorders collectively known as "EZH2-related overgrowth syndromes." These syndromes are characterized by excessive growth and variable additional features. The two main syndromes caused by EZH2 gene mutations are: 1. Weaver syndrome: This syndrome is characterized by prenatal and postnatal overgrowth, advanced bone age, distinctive facial features, intellectual disability, and poor muscle tone (hypotonia). Affected individuals often have abnormalities of the urinary tract, such as structural malformations or recurrent urinary tract infections. 2. Coffin-Siris syndrome: This syndrome is characterized by intellectual disability, developmental delays, distinctive facial features, and abnormalities of the fifth fingers and/or toes. Some affected individuals also experience feeding difficulties, heart defects, and skeletal abnormalities. It is important to note that EZH2 gene mutations can result in a spectrum of clinical features, and affected individuals may not perfectly fit into a single syndrome category. Genetic testing is crucial for accurate diagnosis. |
| 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. Mutations in the EZH2 gene are associated with "EZH2-related overgrowth syndromes." 2. Weaver syndrome is one of the main syndromes caused by EZH2 gene mutations, characterized by characteristics like prenatal and postnatal overgrowth, advanced bone age, distinctive facial features, and intellectual disability. 3. Weaver syndrome can involve abnormalities of the urinary tract, such as structural malformations or recurrent urinary tract infections. 4. Coffin-Siris syndrome is also caused by EZH2 gene mutations, characterized by intellectual disability, developmental delays, distinctive facial features, and abnormalities of the fifth fingers and/or toes. 5. Individuals with Coffin-Siris syndrome may experience feeding difficulties, heart defects, and skeletal abnormalities. |
| 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 | 1,1,7,2,1 |

|  |  |
| --- | --- |
| ID | 193(9) |
| 领域 | Bio-Medical |
| 用户问题 | List human proteins that are subject to a dimer-to-tetramer transition. |
| 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 human proteins that undergo a dimer-to-tetramer transition. Some examples include: 1. Hemoglobin: Hemoglobin is a protein found in red blood cells that transports oxygen. It exists as a tetramer composed of two alpha chains and two beta chains. 2. Glutathione S-transferase: Glutathione S-transferase is an enzyme involved in the detoxification of various compounds. It can exist as a dimer or a tetramer, depending on the binding of certain cofactors. 3. DNA polymerase: DNA polymerase is an enzyme involved in DNA replication. Certain DNA polymerases, such as DNA polymerase III, exist as a dimer or a tetramer. 4. C-reactive protein: C-reactive protein is an acute-phase protein that is produced in response to inflammation. It can exist as a dimer or a pentamer. 5. Aspartate transcarbamylase: Aspartate transcarbamylase is an enzyme involved in the biosynthesis of pyrimidine nucleotides. It exists as a dimer in its inactive form and undergoes a dimer-to-tetramer transition upon activation. 6. Pyruvate kinase: Pyruvate kinase is an enzyme involved in glycolysis, the metabolic pathway that converts glucose into energy. It can exist as a dimer or a tetramer, with the tetramer form being more active. 7. Carbonic anhydrase: Carbonic anhydrase is an enzyme that catalyzes the reversible conversion of carbon dioxide and water into carbonic acid. It can exist as a dimer or a tetramer. Please note that this is not an exhaustive list, and there may be other human proteins that undergo a dimer-to-tetramer transition. |
| 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. Hemoglobin, a protein in red blood cells, exists as a tetramer composed of two alpha chains and two beta chains. 2. Glutathione S-transferase is an enzyme involved in detoxification and can exist as a dimer or a tetramer. 3. Certain DNA polymerases, such as DNA polymerase III, exist as a dimer or a tetramer. 4. C-reactive protein, an acute-phase protein produced in response to inflammation, can exist as a dimer or a pentamer. 5. Pyruvate kinase, an enzyme involved in converting glucose into energy, can exist as a dimer or a tetramer. |
| 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 | 210(10) |
| 领域 | Bio-Medical |
| 用户问题 | Which protein has been found to interact with phospholamban (PLN) and is also an anti-apoptotic protein? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,5,5 |
| 模型回复 | One protein that has been found to interact with phospholamban (PLN) and is also an anti-apoptotic protein is Bcl-2 (B-cell lymphoma 2). Bcl-2 is known to regulate mitochondrial membrane permeability and prevent apoptosis or programmed cell death. It has been shown to interact with PLN in cardiac muscle cells, contributing to the regulation of calcium homeostasis and apoptotic signaling in these 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. Bcl-2 (B-cell lymphoma 2) protein interacts with phospholamban (PLN). 2. Bcl-2 is an anti-apoptotic protein. 3. Bcl-2 is known to regulate mitochondrial membrane permeability. 4. Bcl-2 prevents apoptosis or programmed cell death. 5. Bcl-2 has been shown to interact with PLN in cardiac muscle 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 | 7,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 218(11) |
| 领域 | Bio-Medical |
| 用户问题 | Has vitamin D has been shown to reduce incidence of falls in older people in clinical trials? |
| 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 | Yes, clinical trials have shown that vitamin D supplementation can help reduce the incidence of falls in older people. Several studies have consistently demonstrated a positive association between vitamin D supplementation and a reduced risk of falls. One notable study is a meta-analysis published in the Journal of the American Medical Association (JAMA) in 2004. The analysis included data from 12 randomized controlled trials involving over 3,000 participants aged 65 or older. It found that vitamin D supplementation reduced the risk of falls by 22%. Similarly, another meta-analysis published in the British Medical Journal (BMJ) in 2010 reviewed 20 randomized controlled trials with over 29,000 participants. The analysis showed that vitamin D supplementation reduced the risk of falls by 19%. These studies and others provide strong evidence that vitamin D supplementation can be effective in reducing the risk of falls among older individuals. However, it is important to note that individual results may vary, and it's always recommended to consult with a healthcare professional before starting any supplementation. |
| 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. Clinical trials have shown that vitamin D supplementation can help reduce the incidence of falls in older people. 2. A meta-analysis published in the Journal of the American Medical Association (JAMA) in 2004 found that vitamin D supplementation reduced the risk of falls by 22%. 3. This analysis included data from 12 randomized controlled trials involving over 3,000 participants aged 65 or older. 4. A meta-analysis published in the British Medical Journal (BMJ) in 2010 reviewed 20 randomized controlled trials with over 29,000 participants and showed that vitamin D supplementation reduced the risk of falls by 19%. 5. It's always recommended to consult with a healthcare professional before starting any supplementation. |
| 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 | 1,1,7,7,8 |

|  |  |
| --- | --- |
| ID | 222(12) |
| 领域 | Bio-Medical |
| 用户问题 | Is there any association between Jarid2 and miR-155 in Th17 cells? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Yes, there is an association between Jarid2 and miR-155 in Th17 cells. Studies have shown that Jarid2, a member of the Polycomb group proteins, is involved in the regulation of miR-155 expression in Th17 cells.  In Th17 cells, which are a specialized subset of T cells involved in autoimmune and inflammatory responses, miR-155 is known to play a crucial role in modulating the Th17 cell differentiation and function. Jarid2 has been identified as a negative regulator of Th17 cell differentiation, and it has been found to directly bind to the promoter region of the miR-155 gene, leading to its repression. By inhibiting the expression of miR-155, Jarid2 exerts a suppressive effect on Th17 cell differentiation and function. This association between Jarid2 and miR-155 highlights the intricate regulatory networks that control immune cell function and can have implications for understanding and potentially modulating Th17 cell-mediated inflammatory responses in diseases such as autoimmune disorders. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Jarid2 and miR-155 are associated in Th17 cells based on scientific studies. 2. Jarid2 is a member of the Polycomb group proteins. 3. In Th17 cells, which are a subset of T cells, miR-155 plays a crucial role in their differentiation and function. 4. Jarid2 directly binds to the promoter region of the miR-155 gene, leading to its repression. 5. The association between Jarid2 and miR-155 controls immune cell function and can have implications for understanding Th17 cell-mediated inflammatory responses in diseases like autoimmune 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 | 1,2,1,7,7 |

|  |  |
| --- | --- |
| ID | 224(13) |
| 领域 | Bio-Medical |
| 用户问题 | How many genes does the human hoxD cluster contain? |
| 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 human HoxD cluster contains a total of nine 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 human HoxD cluster contains a total of nine 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 | 1 |

|  |  |
| --- | --- |
| ID | 268(14) |
| 领域 | Bio-Medical |
| 用户问题 | List phosphorylation consensus motifs for Casein Kinase 1 (CK1)? |
| 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 | Here are some phosphorylation consensus motifs for Casein Kinase 1 (CK1): 1. S/T-X-X-D/E: This motif represents a serine or threonine followed by any two amino acids and then an aspartic acid or glutamic acid residue. This motif is frequently phosphorylated by CK1 isoforms. 2. S/T-X-X-X-D/E: Similar to the above motif, but with an additional amino acid inserted between the second and third position. This motif is also recognized by CK1 isoforms. 3. pS/pT-X-X-D/E: Here, "p" denotes a phosphorylated serine or threonine residue. CK1 can recognize and phosphorylate serine or threonine residues followed by any two amino acids and then an aspartic acid or glutamic acid residue. It is important to note that these motifs are not exclusive to CK1 and can also be recognized by other kinases. Therefore, the context and neighboring amino acids around the consensus motif are also important factors in determining CK1 phosphorylation site specificity. |
| 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. Casein Kinase 1 (CK1) recognizes and phosphorylates the consensus motif S/T-X-X-D/E. 2. CK1 also recognizes and phosphorylates the consensus motif S/T-X-X-X-D/E. 3. The motif pS/pT-X-X-D/E, denoting a phosphorylated serine or threonine residue, can be recognized and phosphorylated by CK1. 4. Phosphorylation consensus motifs for CK1 are not exclusive to this kinase and can be recognized by other kinases. 5. Context and neighboring amino acids around the consensus motif are essential factors in determining CK1 phosphorylation site specificity. |
| 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 | 305(15) |
| 领域 | Bio-Medical |
| 用户问题 | Which are the different proteins/isoforms encoded but the ASPH (aspartate beta-hydroxylase) gene in humans? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 1,1,5 |
| 模型回复 | The ASPH gene in humans encodes for a protein called aspartyl/asparaginyl beta-hydroxylase (ASPH). This protein exists in at least two isoforms: 1. ASRGL1 isoform: This isoform is the full-length protein consisting of 778 amino acids. It contains the complete aspartyl/asparaginyl beta-hydroxylase domain. 2. ASRGL1-short isoform: This isoform is a shorter version of the protein, consisting of 288 amino acids. It lacks the C-terminal region found in the full-length isoform. These isoforms of ASPH are involved in various biological processes such as angiogenesis, cancer progression, and collagen maturation. |
| 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 human ASPH gene encodes for a protein known as aspartyl/asparaginyl beta-hydroxylase (ASPH). 2. There are at least two isoforms of the ASPH protein: ASRGL1 and ASRGL1-short. 3. The ASRGL1 isoform is a full-length protein consisting of 778 amino acids. 4. The ASRGL1-short isoform is shorter and consists of 288 amino acids. 5. The isoforms of ASPH are involved in biological processes such as angiogenesis, cancer progression, and collagen maturation. |
| 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 | 1,7,2,7,1 |

|  |  |
| --- | --- |
| ID | 330(16) |
| 领域 | Bio-Medical |
| 用户问题 | When was empagliflozin FDA approved? |
| 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 | Empagliflozin was FDA approved on August 1, 2014. |
| 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. Empagliflozin was FDA approved on August 1, 2014. |
| 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 | 350(17) |
| 领域 | Bio-Medical |
| 用户问题 | What are the results of loss of the protein Lon1 in the plant Arabidopsis? |
| 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 loss of the protein Lon1 in Arabidopsis can have several consequences. Some of the observed results include: 1. Impaired plant growth: Loss of Lon1 in Arabidopsis leads to stunted growth, reduced root length, and smaller leaves compared to wild-type plants. 2. Delayed flowering: Arabidopsis plants lacking Lon1 show a delay in the process of flowering. The timing of flower production is shifted, resulting in late flowering compared to the wild-type plants. 3. Reduced seed production: In the absence of Lon1, Arabidopsis plants exhibit a decrease in seed production. The number of seeds produced is reduced, resulting in lower overall reproductive success. 4. Altered chloroplast function: Loss of Lon1 affects the regulation and maintenance of chloroplasts in Arabidopsis. This leads to impaired photosynthetic efficiency and reduced chlorophyll content, impacting the plant's ability to generate energy through photosynthesis. 5. Enhanced susceptibility to stress: Arabidopsis plants without Lon1 display increased sensitivity to various stress conditions, such as high temperature and oxidative stress. The plants are more prone to damage and exhibit decreased tolerance to environmental challenges. 6. Altered gene expression: The absence of Lon1 affects the expression of numerous genes involved in various cellular processes. This includes genes associated with energy metabolism, stress response, and hormone signaling pathways. Overall, the loss of the protein Lon1 in Arabidopsis disrupts various physiological processes, leading to impaired growth, reproductive output, and stress tolerance. |
| 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 loss of the protein Lon1 in Arabidopsis leads to impaired plant growth with symptoms like stunted growth, reduced root length, and smaller leaves. 2. Arabidopsis plants without Lon1 have delayed flowering, resulting in late flowering compared to normal plants. 3. In the absence of Lon1, Arabidopsis plants have reduced seed production which affects their overall reproductive success. 4. Loss of Lon1 alters chloroplast function in Arabidopsis plants, leading to impaired photosynthetic efficiency and reduced chlorophyll content. 5. Without Lon1, Arabidopsis plants show increased sensitivity to various stress conditions like high temperature and oxidative 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 | 1,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 409(18) |
| 领域 | Bio-Medical |
| 用户问题 | Does a linker histone exist in the yeast 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 | Yes, linker histones do exist in the yeast 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. Linker histones exist in the yeast 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 | 418(19) |
| 领域 | Bio-Medical |
| 用户问题 | Is there evidence that tomato juice lowers cholesterol levels? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,5,5 |
| 模型回复 | There is some evidence suggesting that tomato juice may have the potential to lower cholesterol levels. Tomatoes are a rich source of lycopene, a potent antioxidant that has been associated with various health benefits. Some studies have found that lycopene consumption can lead to a modest reduction in total and LDL cholesterol levels. One study published in the British Journal of Nutrition involved overweight women who consumed tomato juice daily for eight weeks. The researchers observed a significant decrease in LDL cholesterol levels compared to the control group. Another study published in the Journal of Nutrition and Metabolism found that regular consumption of tomato juice for four weeks resulted in a decrease in total cholesterol and LDL cholesterol levels in overweight adults. While these studies provide some evidence of the potential cholesterol-lowering effects of tomato juice, it is important to note that the observed effects are modest, and individual results may vary. It is recommended to incorporate a balanced diet and lifestyle changes in combination with tomato juice consumption for better cholesterol management. Additionally, more research is needed to establish a clearer understanding of the mechanisms and long-term effects of tomato juice on cholesterol levels. |
| 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. Tomatoes are a rich source of lycopene, an antioxidant associated with various health benefits. 2. Some research findings suggest lycopene consumption can lead to a modest reduction in total and LDL cholesterol levels. 3. A study published in the British Journal of Nutrition showed that overweight women who consumed tomato juice daily for eight weeks had significantly decreased LDL cholesterol levels. 4. The Journal of Nutrition and Metabolism published a study that found regular consumption of tomato juice for four weeks resulted in a decrease in total cholesterol and LDL cholesterol levels in overweight adults. 5. The observed cholesterol-lowering effects of tomato juice are considered modest, and results may vary among individuals. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1,1,1,7,1 |

|  |  |
| --- | --- |
| ID | 472(20) |
| 领域 | Bio-Medical |
| 用户问题 | How do Hsp70 and Hsp110 affect mRNA stability? |
| 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 | Hsp70 and Hsp110 are both heat shock proteins that play important roles in protein folding and quality control in cells.  Although Hsp70 and Hsp110 are not directly involved in mRNA stability, they can indirectly affect mRNA stability through their interactions with other proteins and cellular pathways. Here are a few possible mechanisms through which Hsp70 and Hsp110 can influence mRNA stability: 1. mRNA binding proteins: Hsp70 and Hsp110 can interact with various RNA-binding proteins, such as HuR, to modulate their activities. HuR, for example, is an mRNA stability factor that can protect mRNA from degradation. Similarly, Hsp70 and Hsp110 may interact with other mRNA-binding proteins and affect their stability-regulating functions. 2. mRNA decay pathways: Hsp70 and Hsp110 can interact with components of mRNA decay pathways, such as RNA helicases and exonucleases. These interactions can modulate the efficiency or speed of mRNA decay, thus indirectly impacting mRNA stability. 3. Transcriptional regulation: Hsp70 and Hsp110 can influence the transcriptional activity of specific genes, including those involved in mRNA stability regulation. By modulating the transcription levels of these genes, Hsp70 and Hsp110 can indirectly affect mRNA stability. 4. Protein homeostasis: Hsp70 and Hsp110 are primarily involved in protein folding and quality control. Dysregulation of protein homeostasis can lead to the accumulation of misfolded or unfolded proteins, which can trigger cellular stress responses, including the degradation of unstable mRNAs. In this way, Hsp70 and Hsp110 can indirectly impact mRNA stability through their role in maintaining protein homeostasis. It is important to note that the specific mechanisms through which Hsp70 and Hsp110 affect mRNA stability may vary depending on the cellular context and the specific mRNA targets involved. Further research is needed to fully understand the details of their impact on mRNA stability. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Hsp70 and Hsp110 are heat shock proteins that play roles in protein folding and quality control in cells. 2. Hsp70 and Hsp110 can interact with RNA-binding proteins, such as HuR, to modulate their activities. 3. Hsp70 and Hsp110 can interact with components of mRNA decay pathways, such as RNA helicases and exonucleases. 4. Hsp70 and Hsp110 can influence the transcriptional activity of specific genes, including those involved in mRNA stability regulation. 5. Dysregulation of protein homeostasis can trigger cellular stress responses, which can impact mRNA stability. Hsp70 and Hsp110 indirectly affect mRNA stability through their role in maintaining protein homeostasis. |
| 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 | 481(21) |
| 领域 | Bio-Medical |
| 用户问题 | Which deiodinases are present in skeletal muscle? |
| 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 | Skeletal muscle contains all three types of deiodinases: type 1 (DIO1), type 2 (DIO2), and type 3 (DIO3). However, the relative expression levels of these deiodinases may vary depending on the physiological and pathological conditions of the muscle. |
| 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. Skeletal muscle contains type 1 deiodinase (DIO1). 2. Skeletal muscle contains type 2 deiodinase (DIO2). 3. Skeletal muscle contains type 3 deiodinase (DIO3). 4. The relative expression levels of the deiodinases in skeletal muscle may vary depending on the muscle's physiological and pathological 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 | 1,1,1,1 |

|  |  |
| --- | --- |
| ID | 534(22) |
| 领域 | Bio-Medical |
| 用户问题 | List inflammatory caspase proteins? |
| 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 | Some examples of inflammatory caspase proteins include: 1. Caspase-1 (also known as interleukin-1 beta-converting enzyme, IL-1β-converting enzyme, or ICE) 2. Caspase-4 (also known as caspase-11 in mice) 3. Caspase-5 4. Caspase-12 (predominantly found in humans, absent in mice) 5. Caspase-14 (predominantly expressed in the skin, involved in inflammatory response) 6. Caspase-13 (predominantly expressed in mice, involved in innate immunity) These caspase proteins play critical roles in the initiation and regulation of inflammatory responses in various cellular contexts and 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. Caspase-1 is also known as interleukin-1 beta-converting enzyme, IL-1β-converting enzyme, or ICE. 2. Caspase-4 is also known as caspase-11 in mice. 3. Caspase-12 is predominantly found in humans and absent in mice. 4. Caspase-14 is predominantly expressed in the skin and involved in inflammatory response. 5. Caspase-13 is predominantly expressed in mice and involved in innate immunity. |
| 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 | 579(23) |
| 领域 | Bio-Medical |
| 用户问题 | Is there any link between the aurora B kinase and the polycomb protein ring1B? |
| 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 | Yes, there is a link between Aurora B kinase and the polycomb protein Ring1B. Aurora B kinase and Ring1B have been shown to interact and regulate cellular processes together. One study published in the journal Cell Reports found that Aurora B kinase phosphorylates Ring1B, leading to its stabilization and increased protein levels. This phosphorylation of Ring1B by Aurora B kinase enhances the recruitment of Ring1B to target gene loci, resulting in enhanced gene repression and increased proliferation of cancer cells. Another study published in Nature Communications demonstrated that Aurora B kinase physically interacts with the polycomb repressive complex 1 (PRC1), which contains Ring1B. This interaction between Aurora B kinase and PRC1 promotes proper chromosome segregation and mitotic progression. These studies suggest that Aurora B kinase plays a role in the regulation of PRC1 activity through its interaction with Ring1B, contributing to various cellular processes such as gene repression, proliferation, and 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. Aurora B kinase and Ring1B have been scientifically shown to interact and regulate cellular processes together. 2. Aurora B kinase phosphorylates Ring1B, leading to its stabilization and increased protein levels, according to a study published in the journal Cell Reports. 3. This phosphorylation of Ring1B by Aurora B kinase results in enhanced gene repression and increased proliferation of cancer cells. 4. A research in Nature Communications found that Aurora B kinase physically interacts with the polycomb repressive complex 1 (PRC1), which includes Ring1B. 5. The interaction of Aurora B kinase and PRC1 contributes to proper chromosome segregation and mitotic progression. |
| 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 | 7,7,7,1,1 |

|  |  |
| --- | --- |
| ID | 597(24) |
| 领域 | Bio-Medical |
| 用户问题 | What are the most frequent non-canonical sequence motifs at the donor and acceptor splice sites in vertebrates? |
| 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 frequent non-canonical sequence motifs at the donor and acceptor splice sites in vertebrates tend to be variations of the consensus splice site sequences. Here are some examples: Donor Site: 1. GT-AG: This is the canonical donor splice site sequence in vertebrates, where the intron typically starts with a "GT" dinucleotide. 2. GC-AG: This alternative donor splice site sequence is the second most frequently used in vertebrates. 3. AT-AC: Another alternative donor splice site sequence, which is less common than the canonical and GC-AG sequences. Acceptor Site: 1. AG-G: This is the canonical acceptor splice site sequence in vertebrates, where the intron typically ends with an "AG" dinucleotide. 2. AC-G: This alternative acceptor splice site sequence is used less frequently than the canonical AG-G motif. 3. AT-G: Another alternative acceptor splice site sequence, which is less common than the canonical and AC-G sequences. It is important to note that while these are some of the most frequent non-canonical motifs, there can still be considerable variation and diversity in the sequences recognized by spliceosomes in vertebrates. |
| 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 canonical donor splice site sequence in vertebrates typically starts with a "GT" dinucleotide. 2. The alternative donor splice site sequences in vertebrates include "GC-AG" and "AT-AC". 3. "GC-AG" is the second most frequently used sequence at the donor splice site in vertebrates. 4. The canonical acceptor splice site sequence in vertebrates typically ends with an "AG" dinucleotide. 5. Alternate acceptor splice site sequences in vertebrates include "AC-G" and "AT-G". |
| 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 | 629(25) |
| 领域 | Bio-Medical |
| 用户问题 | Which event results in the acetylation of S6K1? |
| 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 event that results in the acetylation of S6K1 is the activation of the mTOR signaling pathway. mTOR, or mammalian target of rapamycin, is a kinase that regulates various cellular processes including protein synthesis, cell growth, and metabolism. When mTOR is activated, it phosphorylates and activates S6K1, which then recruits acetyltransferases to acetylate and modify S6K1. This acetylation of S6K1 plays a role in its stability, localization, and activity, thereby influencing downstream signaling pathways involved in cell growth and proliferation. |
| 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 acetylation of S6K1 is a result of the activation of the mTOR signaling pathway. 2. mTOR, or mammalian target of rapamycin, is a kinase. 3. This kinase regulates various cellular processes including protein synthesis, cell growth, and metabolism. 4. When mTOR is activated, it phosphorylates and activates S6K1. 5. The acetylation of S6K1 influences downstream signaling pathways involved in cell growth and proliferation. |
| 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 | 2,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 632(26) |
| 领域 | Bio-Medical |
| 用户问题 | What is the cause of episodic ataxia type 6? |
| 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 | Episodic ataxia type 6 (EA6) is a genetic disorder caused by mutations in the CACNA1A gene, which provides instructions for making a protein called the alpha-1A subunit of a calcium channel. These calcium channels are responsible for regulating the flow of calcium ions into cells. Mutations in the CACNA1A gene disrupt the normal function of these channels, leading to episodic ataxia type 6. The specific mechanisms by which these mutations cause symptoms are still being researched, but it is believed that the impaired calcium channel function disrupts the normal communication between nerve cells, resulting in the characteristic episodes of ataxia (lack of muscle coordination) experienced by individuals with EA6. |
| 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. Episodic ataxia type 6 (EA6) is a genetic disorder. 2. EA6 is caused by mutations in the CACNA1A gene. 3. The CACNA1A gene provides instructions for making a protein called the alpha-1A subunit of a calcium channel. 4. These calcium channels regulate the flow of calcium ions into cells. 5. The impairment in calcium channel function due to mutations in the CACNA1A gene is believed to disrupt normal communication between nerve cells, resulting in episodes of ataxia. |
| 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 | 1,2,1,1,7 |

|  |  |
| --- | --- |
| ID | 646(27) |
| 领域 | Bio-Medical |
| 用户问题 | Are chromomethylases present in animal genomes? |
| 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, chromomethylases are present in animal genomes. Chromomethylases are enzymes that play a role in DNA methylation, a process that involves adding a methyl group to DNA molecules, thereby affecting gene expression. While it was previously thought that chromomethylases were exclusive to plants and fungi, recent studies have identified similar proteins in a variety of animal species. These animal chromomethylases show similarities to their plant counterparts in terms of protein structure and catalytic activity, suggesting a conservation of function across different organisms. However, the exact roles and mechanisms of chromomethylases in animal genomes are still 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. Chromomethylases are present in animal genomes. 2. Chromomethylases are enzymes involved in the process of DNA methylation. 3. DNA methylation involves adding a methyl group to DNA molecules which affects gene expression. 4. Previously, chromomethylases were thought to be exclusive to plants and fungi. 5. Recent studies have found similar proteins to chromomethylases in a variety of animal species. |
| 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 | 7,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 650(28) |
| 领域 | Bio-Medical |
| 用户问题 | List packages for transcription factor binding sites' (TFBS) analysis available in R/Bioconductor |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,2,5 |
| 模型回复 | 1. biomaRt 2. motifmatchr 3. MotifDb 4. JASPAR 5. RSAT 6. TFBSTools 7. PWMEnrich 8. ChIPseeker 9. rGADEM 10. TFBSTools 11. DECIPHER 12. MEME 13. rBGL 14. CisGenome Browser 15. rGADEM 16. iRegulon 17. TFMPvalue 18. ClusterProfiler 19. chromVAR 20. CoRSIVdenovo |
| 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. biomaRt is a package available in R/Bioconductor for transcription factor binding sites' (TFBS) analysis. 2. motifmatchr is a package available in R/Bioconductor for transcription factor binding sites' (TFBS) analysis. 3. MotifDb is a package available in R/Bioconductor for transcription factor binding sites' (TFBS) analysis. 4. JASPAR is a package available in R/Bioconductor for transcription factor binding sites' (TFBS) analysis. 5. RSAT is a package available in R/Bioconductor for transcription factor binding sites' (TFBS) 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 | 7,7,1,1,7 |

|  |  |
| --- | --- |
| ID | 721(29) |
| 领域 | Bio-Medical |
| 用户问题 | List clinical trials for prevention of sarcopenia |
| 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 | 1. Title: "Exercise and Nutrition Intervention to Prevent Sarcopenia in Older Adults"  Location: National Institutes of Health Clinical Center, Bethesda, Maryland, United States  Description: This randomized controlled trial aims to evaluate the effectiveness of exercise and nutrition interventions in preventing sarcopenia in older adults. Participants will be assigned to either an exercise group, a nutrition group, or a combination of exercise and nutrition group. Various outcomes will be assessed, including muscle mass, strength, and physical function.   2. Title: "Effect of Protein Supplementation on Sarcopenia Prevention"  Location: University Hospital, Ghent, Belgium  Description: This clinical trial aims to assess the effect of protein supplementation on preventing sarcopenia in older adults. Participants will be randomly assigned to either receive a protein supplement or a placebo. Different muscle-related outcomes, such as muscle mass, strength, and mobility, will be measured throughout the study period.   3. Title: "Resistance Training for the Prevention of Sarcopenia in Postmenopausal Women"  Location: University of Wisconsin-Madison, Madison, Wisconsin, United States  Description: This clinical trial focuses on evaluating the impact of resistance training on preventing sarcopenia in postmenopausal women. Participants will engage in a supervised resistance training program for a specified duration. Muscle strength, lean muscle mass, and physical performance will be assessed pre- and post-intervention.   4. Title: "Effect of Vitamin D Supplementation on Sarcopenia Prevention in Elderly"  Location: Hadassah Hebrew University Medical Center, Jerusalem, Israel  Description: This trial investigates the potential of vitamin D supplementation in preventing sarcopenia in elderly individuals. Participants will be randomly assigned to receive either vitamin D supplements or a placebo. Muscle mass, strength, bone health, and physical performance will be assessed throughout the study.   5. Title: "Exercise Intervention for Sarcopenia Prevention in Chronic Obstructive Pulmonary Disease (COPD) Patients"  Location: Harvard Medical School, Boston, Massachusetts, United States  Description: This clinical trial focuses on evaluating the effectiveness of exercise interventions in preventing sarcopenia among individuals with chronic obstructive pulmonary disease (COPD). Participants will be randomly assigned to either a supervised exercise group or a control group. Muscle mass, strength, lung function, and physical activity level will be assessed throughout the study.   Note: This list is not exhaustive, and it is recommended to consult relevant clinical trial databases or healthcare professionals for the most up-to-date information on clinical trials for preventing sarcopenia. |
| 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 National Institutes of Health Clinical Center in Bethesda, Maryland conducted a clinical trial on the effectiveness of exercise and nutrition interventions in preventing sarcopenia in older adults. 2. University Hospital in Ghent, Belgium held a clinical trial to determine the effect of protein supplementation on sarcopenia prevention in older adults. 3. University of Wisconsin-Madison hosted a clinical trial focusing on the impact of resistance training on sarcopenia prevention in postmenopausal women. 4. Hadassah Hebrew University Medical Center in Jerusalem, Israel, conducted a study on the potential of vitamin D supplementation in preventing sarcopenia in elderly individuals. 5. Harvard Medical School in Boston, Massachusetts carried out a clinical trial evaluating the effectiveness of exercise interventions in preventing sarcopenia in COPD 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 | 7,1,7,7,7 |

|  |  |
| --- | --- |
| ID | 722(30) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the database of molecular recognition features in membrane proteins? |
| 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 database of molecular recognition features in membrane proteins is called Membrane Protein Recognition Database (MPRDB). |
| 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 Membrane Protein Recognition Database (MPRDB) is the database of molecular recognition features in membrane proteins. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 2 |

|  |  |
| --- | --- |
| ID | 745(31) |
| 领域 | Bio-Medical |
| 用户问题 | Is rivaroxaban metabolized in kidneys? |
| 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, rivaroxaban is primarily metabolized in the kidneys. Approximately two-thirds of the drug is eliminated through renal excretion, while the remaining one-third is metabolized in the liver. It is important to note that rivaroxaban is a direct oral anticoagulant (DOAC) and is primarily eliminated unchanged in urine. |
| 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. Rivaroxaban is primarily metabolized in the kidneys. 2. Approximately two-thirds of rivaroxaban is eliminated through renal excretion. 3. One-third of rivaroxaban is metabolized in the liver. 4. Rivaroxaban is a direct oral anticoagulant (DOAC). 5. Rivaroxaban is primarily eliminated unchanged in urine. |
| 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 | 2,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 763(32) |
| 领域 | Bio-Medical |
| 用户问题 | Which genes are regulated by TRalpha2 in the heart? |
| 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 genes regulated by TRalpha2 in the heart can vary depending on the specific context and experimental conditions. However, some genes known to be regulated by TRalpha2 in the heart include: 1. Myosin heavy chain (MYH) genes: TRalpha2 has been shown to regulate the expression of various MYH genes, including MYH6 and MYH7, which are important for heart muscle contraction. 2. Alpha-myosin heavy chain (α-MHC): TRalpha2 can regulate the expression of the α-MHC gene (MYH6), which is highly expressed in adult cardiac muscle and plays a role in cardiac contractility. 3. Beta-myosin heavy chain (β-MHC): TRalpha2 can also regulate the expression of the β-MHC gene (MYH7), which is upregulated during cardiac hypertrophy and heart failure. 4. Sarcoendoplasmic reticulum Ca2+ ATPase (SERCA2): TRalpha2 has been shown to regulate the expression of SERCA2, an important calcium pump protein involved in cardiac muscle relaxation and contraction. 5. Angiotensinogen (AGT): TRalpha2 can regulate the expression of AGT, a precursor protein involved in the renin-angiotensin system, which plays a role in regulating blood pressure and cardiovascular function. It is important to note that this is not an exhaustive list and the specific genes regulated by TRalpha2 in the heart can vary depending on the experimental 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. TRalpha2 has been shown to regulate the expression of various Myosin heavy chain (MYH) genes, including MYH6 and MYH7. 2. MYH genes are important for heart muscle contraction. 3. TRalpha2 can regulate the expression of the α-MHC gene (MYH6), which plays a role in cardiac contractility. 4. TRalpha2 can also regulate the expression of the β-MHC gene (MYH7), which is upregulated during cardiac hypertrophy and heart failure. 5. TRalpha2 has been shown to regulate the expression of Sarcoendoplasmic reticulum Ca2+ ATPase (SERCA2) and Angiotensinogen (AGT), proteins involved in cardiac muscle relaxation and contraction, and blood pressure regulation, respectively. |
| 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 | 786(33) |
| 领域 | Bio-Medical |
| 用户问题 | List available biomedical question answering systems. |
| 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. BioASK: A biomedical question answering system developed by the National Center for Biotechnology Information (NCBI). It provides answers to user queries through its Question Answering Pipeline (QAP). 2. AskHERMES: An automated biomedical question answering system developed by the University of Colorado School of Medicine. It utilizes deep learning techniques and biomedically-focused natural language processing to provide answers to user queries. 3. AskGene: A biomedical question answering system developed by the University of California, Los Angeles. It focuses on answering queries related to gene and protein functions, interactions, and diseases. 4. AskCI: A biomedical question answering system developed by the Bio-NLP Research Group at University Hospital Goettingen. It specializes in answering questions related to clinical informatics, medical treatments, and patient information. 5. Watson for Drug Discovery: IBM's Watson-based question answering system that specifically focuses on answering queries related to bioinformatics, drug discovery, and medical literature. 6. PubQA: A biomedical question answering system developed by the National Institute for Research in Computer Science and Automation (INRIA). It provides answers to questions related to scientific publications and medical literature. 7. BioBOOST: A biomedical question answering system developed by the University of Alicante, Spain. It specializes in answering questions related to gene/protein annotation, biology, and genetics. 8. ASKMED: A biomedical question answering system developed by the Instituto Politecnico Nacional, Mexico. It is designed to assist physicians and medical professionals by providing answers to clinical questions. 9. SABIO-RK: A biomedical question answering system developed by the Centre for Biological Sequence Analysis, Technical University of Denmark. It focuses on answering queries related to biochemical reactions and pathways. 10. ALICE: An AI-powered biomedical question answering system developed by Q2 Scientific. It assists researchers in accessing and interpreting biological and biomedical data by providing answers to their queries. |
| 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. BioASK is a biomedical question answering system developed by the National Center for Biotechnology Information (NCBI). 2. AskHERMES is an automated biomedical question answering system developed by the University of Colorado School of Medicine. 3. AskGene is a biomedical question answering system developed by the University of California, Los Angeles. 4. AskCI was developed by the Bio-NLP Research Group at University Hospital Goettingen and it deals with questions related to clinical informatics, medical treatments, and patient information. 5. Watson for Drug Discovery is IBM's Watson-based question answering system that focuses on bioinformatics, drug discovery, and medical literature. |
| 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 | 7,1,7,1,1 |

|  |  |
| --- | --- |
| ID | 794(34) |
| 领域 | Bio-Medical |
| 用户问题 | Which trancription factor activates the betalain 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 transcription factor known as AmMYB308 is responsible for activating the betalain pathway. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. AmMYB308 is a transcription factor. 2. AmMYB308 activates the betalain 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 | 1,7 |

|  |  |
| --- | --- |
| ID | 883(35) |
| 领域 | Bio-Medical |
| 用户问题 | Global quantitative phosphoproteomic analyses are emerging. List the preferred technologies for the enrichment for phosphorylated peptides? |
| 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 preferred technologies for the enrichment of phosphorylated peptides in global quantitative phosphoproteomic analyses include: 1. Immobilized Metal Affinity Chromatography (IMAC): This technique uses metal ions such as Fe3+ or Ga3+ immobilized on a solid support to selectively bind to phosphorylated peptides. 2. Titanium Dioxide (TiO2) Chromatography: TiO2 beads have high affinity for phosphorylated peptides and allow for specific enrichment of phosphorylated species. 3. Metal Oxide Affinity Chromatography (MOAC): MOAC involves the use of metal oxide-based materials like Al(OH)3 or ZrO2 to selectively capture and enrich phosphorylated peptides. 4. Anti-Phospho Antibody-Based Immunoaffinity: Antibodies that specifically recognize phosphorylated residues can be used to enrich phosphorylated peptides from complex protein mixtures. 5. Strong Cation Exchange (SCX) Chromatography: SCX chromatography separates peptides based on their charge properties, which can be utilized for selective enrichment of phosphorylated peptides. 6. Multidimensional Protein Identification Technology (MudPIT): MudPIT combines the use of strong cation exchange chromatography with reverse-phase liquid chromatography to selectively enrich and identify phosphorylated peptides. 7. Metal-Chelate Affinity Chromatography (MCAC): MCAC uses immobilized transition metal ions and metal chelating moieties coupled to solid supports for phosphopeptide enrichment. It's important to note that different enrichment techniques may have different selectivity and efficiency, and they may be used alone or in combination to achieve comprehensive phosphoproteome analysis. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Immobilized Metal Affinity Chromatography (IMAC) is a technology used in global quantitative phosphoproteomic analyses for the enrichment of phosphorylated peptides. 2. Titanium Dioxide (TiO2) Chromatography is utilized for specific enrichment of phosphorylated peptides. 3. Metal Oxide Affinity Chromatography (MOAC) is used to selectively capture and enrich phosphorylated peptides. 4. Anti-Phospho Antibody-Based Immunoaffinity is used to enrich phosphorylated peptides from complex protein mixtures. 5. Multidimensional Protein Identification Technology (MudPIT) is used in phosphoproteomic analyses to enrich and identify phosphorylated peptides. |
| 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 | 901(36) |
| 领域 | Bio-Medical |
| 用户问题 | Which disorder is rated by Palmini 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 Palmini classification system rates brain tumors. It is commonly used to classify and grade different types of brain tumors, including gliomas, meningiomas, and other central nervous system tumors. It helps in determining the prognosis and appropriate treatment for individuals with brain tumors. |
| 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 Palmini classification system is used to rate brain tumors. 2. The Palmini classification system helps to classify and grade various types of brain tumors including gliomas and meningiomas. 3. The Palmini classification system is utilized to determine the prognosis and appropriate treatment for individuals with brain tumors. 4. Gliomas and meningiomas are types of brain tumors. 5. Central nervous system tumors can be classified and graded by the Palmini classification. |
| 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 | 7,1,7,1,7 |

|  |  |
| --- | --- |
| ID | 905(37) |
| 领域 | Bio-Medical |
| 用户问题 | Are viruses involved in the etiology of human subacute thyroiditis? |
| 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, viruses are not believed to be directly involved in the etiology of human subacute thyroiditis. Subacute thyroiditis is typically caused by inflammation of the thyroid gland, and the specific cause is not fully understood. It is thought to be an autoimmune condition, where the body's immune system mistakenly attacks the thyroid gland. Although viral infections can sometimes trigger or contribute to the development of subacute thyroiditis, the viruses themselves are not considered to be the primary cause of 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. Viruses are not believed to be directly involved in the etiology of human subacute thyroiditis. 2. Subacute thyroiditis is typically caused by inflammation of the thyroid gland. 3. The specific cause of subacute thyroiditis is not fully understood. 4. Subacute thyroiditis is thought to be an autoimmune condition where the body's immune system mistakenly attacks the thyroid gland. 5. Viral infections can sometimes trigger or contribute to the development of subacute thyroiditis. |
| 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 | 3,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 963(38) |
| 领域 | Bio-Medical |
| 用户问题 | Is STAT3 involved in EIF2AK2-dependent suppression of autophagy? |
| 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 is limited evidence regarding the direct involvement of STAT3 in EIF2AK2-dependent suppression of autophagy. EIF2AK2, also known as PKR (Protein kinase R), has been shown to suppress autophagy through various mechanisms, such as inhibiting the phosphorylation of ULK1 (unc-51 like autophagy activating kinase 1).  On the other hand, STAT3 (Signal Transducer and Activator of Transcription 3) has been primarily studied in the context of its role in inflammation and cancer. It is known to have a complex role in the regulation of autophagy, with evidence suggesting both pro-autophagic and anti-autophagic functions depending on the cellular context. While there are reports indicating that STAT3 can influence autophagy indirectly through interactions with upstream regulators or downstream effectors of autophagy pathways, there isn't strong evidence linking STAT3 to EIF2AK2-dependent suppression of autophagy specifically. Further investigation is required to elucidate the potential crosstalk or regulatory interactions between these two proteins in the context of autophagy 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. EIF2AK2, also known as Protein kinase R (PKR), is known to suppress autophagy. 2. The suppression of autophagy by EIF2AK2 is achieved through various mechanisms such as inhibiting the phosphorylation of ULK1. 3. STAT3, or Signal Transducer and Activator of Transcription 3, is primarily studied in the context of inflammation and cancer. 4. STAT3 has a complex role in the regulation of autophagy with indications of both pro-autophagic and anti-autophagic functions. 5. There are reports suggesting that STAT3 can influence autophagy indirectly through interactions with upstream regulators or downstream effectors of autophagy pathways. |
| 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 | 973(39) |
| 领域 | Bio-Medical |
| 用户问题 | Describe what is the usage of the Theatre software tool for genomic analysis. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,5,3 |
| 模型回复 | The Theatre software tool for genomic analysis is used in various aspects of genomics research and analysis. Some important usages of this tool include: 1. Genome assembly: Theatre software helps in the process of assembling and aligning genomic reads to construct a complete genome sequence. It can handle large datasets and efficiently align and merge overlapping reads to generate accurate genome assemblies. 2. Variant calling: This tool enables the identification of genetic variations such as single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels) within a genome. It applies sophisticated algorithms to detect variants based on alignment and coverage data, allowing researchers to understand genetic diversity and identify potential disease-causing mutations. 3. Gene expression analysis: Theatre software facilitates the analysis of gene expression levels and differential expression between different samples. By utilizing RNA-Seq data, it quantifies transcript abundance and identifies genes that are upregulated or downregulated in specific conditions or disease states. 4. Comparative genomics: The tool enables the comparison of genomic sequences across different species or individuals to identify conserved regions, genetic variations, and evolutionary relationships. It aids in understanding genetic differences and similarities between organisms, facilitating studies on evolution, phylogenetics, and genome evolution. 5. Functional annotation: Theatre software helps in annotating genomic sequences by assigning biological functions to genes and non-coding regions. It integrates various databases and algorithms to predict gene functions, identify protein domains, annotate regulatory elements, and provide insights into the biological relevance and potential functions of identified genes. 6. Pathway analysis: By utilizing data from multiple sources and databases, the tool allows users to analyze and interpret pathways and biological processes affected by genetic variations or gene expression changes. It helps in understanding the functional implications of genomic alterations and their role in disease development. 7. Visualization: The tool provides interactive visualizations, allowing researchers to explore genomic data using graphical interfaces. It enables the visualization of genomic features, gene expression patterns, variant distribution, and other genomic elements, aiding in the interpretation and communication of complex genomic data. Overall, the Theatre software tool is a versatile platform that facilitates a wide range of genomic analysis tasks, empowering researchers to gain insights into complex biological processes, genetic variations, and their role in health and 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. Theatre software tool for genomic analysis is used in various aspects of genomics research and analysis. 2. The Theatre software tool helps in the process of assembling and aligning genomic reads to construct a complete genome sequence. 3. This tool enables the identification of genetic variations such as single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels) within a genome. 4. The Theatre software facilitates the analysis of gene expression levels and differential expression between different samples. 5. Theatre software helps in annotating genomic sequences by assigning biological functions to genes and non-coding regions. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1,7,1,7,1 |

|  |  |
| --- | --- |
| ID | 997(40) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the execution time (complexity) of the Smith-Waterman algorithm for the alignment of two sequences |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 3,5,5 |
| 模型回复 | The execution time (complexity) of the Smith-Waterman algorithm for the alignment of two sequences is generally considered to be O(n^2\*m), where n and m are the lengths of the two sequences being aligned. This is because the algorithm compares every possible pair of elements in the two sequences, which results in a nested loop structure with a time complexity of O(n\*m). The algorithm's performance can be further improved with various optimizations and heuristics, but the worst-case time complexity remains O(n^2\*m). |
| 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 Smith-Waterman algorithm is used for the alignment of two sequences. 2. The general execution time (complexity) of the Smith-Waterman algorithm is O(n^2\*m). 3. In the Smith-Waterman algorithm, n and m represent the lengths of the two sequences being aligned. 4. The Smith-Waterman algorithm compares every possible pair of elements in the two sequences. 5. Various optimizations and heuristics can be applied to improve the performance of the Smith-Waterman algorithm, but the worst-case time complexity remains O(n^2\*m). |
| 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 | 1004(41) |
| 领域 | Bio-Medical |
| 用户问题 | Which SLC family is FLVCR1 a member of? |
| 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 | FLVCR1 is a member of the SLC50 family. |
| 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. FLVCR1 is a member of the SLC50 family. |
| 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 | 1047(42) |
| 领域 | Bio-Medical |
| 用户问题 | List GATA-1 interacting partners as discovered with the help of the biotinylation tagging approach. |
| 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 | There are several proteins that have been identified as interacting partners of GATA-1 using the biotinylation tagging approach. Some of these include: 1. FOG-1 (Friend of GATA-1): FOG-1 is a transcriptional cofactor that interacts with GATA-1 to regulate erythroid and megakaryocytic differentiation. 2. TAL1/SCL (T-cell Acute Lymphoblastic Leukemia 1/ Stem Cell Leukemia): TAL1 is a transcription factor that forms a complex with GATA-1 to regulate erythroid gene expression. 3. FOG-2: FOG-2 is another member of the FOG protein family that interacts with GATA-1 to regulate erythroid differentiation. 4. LIM domain only protein 2 (LMO2): LMO2 forms a complex with GATA-1 and TAL1 to regulate erythroid gene expression. 5. GFI-1 (Growth Factor Independence 1): GFI-1 is a transcriptional repressor that interacts with GATA-1 to regulate erythroid and megakaryocytic differentiation. 6. TIF1β (Transcriptional Intermediary Factor 1β): TIF1β interacts with GATA-1 to regulate erythroid gene expression. These are just a few examples of the proteins that have been identified as interacting partners of GATA-1 using the biotinylation tagging approach. There may be additional proteins that have not been mentioned here. |
| 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. Proteins have been identified as interacting partners of GATA-1 using the biotinylation tagging approach. 2. FOG-1 is a protein that interacts with GATA-1 to regulate erythroid and megakaryocytic differentiation. 3. TAL1 is a protein that forms a complex with GATA-1 to regulate erythroid gene expression. 4. FOG-2 is a protein that interacts with GATA-1 to regulate erythroid differentiation. 5. LMO2 forms a complex with GATA-1 and TAL1 to regulate erythroid 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 | 1,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 1072(43) |
| 领域 | Bio-Medical |
| 用户问题 | What is the outcome of TAF10 interacting with the GATA1 transcription factor? |
| 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 specific outcome of TAF10 interacting with the GATA1 transcription factor will depend on the cellular context and the specific regulatory elements involved. However, in general, TAF10 is a subunit of the TFIID complex, which is involved in the initiation of transcription at promoters of protein-coding genes. GATA1 is a transcription factor that regulates the expression of genes involved in hematopoiesis and erythropoiesis. When TAF10 interacts with GATA1, it can potentially modulate the transcriptional activity of GATA1 on its target genes. TAF10 may help recruit the TFIID complex to GATA1-regulated promoters, facilitating the assembly of the transcription initiation machinery and increasing the expression of GATA1 target genes. Conversely, TAF10 may also compete with other transcription factors or co-regulators for binding to GATA1, potentially inhibiting its activity. The exact outcome of TAF10-GATA1 interaction could also be influenced by additional co-regulators, chromatin remodeling factors, and other transcriptional regulators present at the target gene promoters. Thus, the specific molecular and functional consequences of TAF10-GATA1 interaction will need further investigation in specific experimental settings and gene contexts. |
| 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. TAF10 is a subunit of the TFIID complex, which is involved in the initiation of transcription at promoters of protein-coding genes. 2. GATA1 is a transcription factor that regulates the expression of genes involved in hematopoiesis and erythropoiesis. 3. TAF10 can potentially modulate the transcriptional activity of GATA1 on its target genes. 4. TAF10 may help recruit the TFIID complex to GATA1-regulated promoters, potentially increasing the expression of GATA1 target genes. 5. TAF10 can compete with other transcription factors or co-regulators for binding to GATA1, potentially inhibiting GATA1's 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 | 1,1,1,1,7 |

|  |  |
| --- | --- |
| ID | 1082(44) |
| 领域 | Bio-Medical |
| 用户问题 | Are there any Decision support systems for chronic pain management ? |
| 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, there are decision support systems (DSS) available for chronic pain management. These systems aim to assist healthcare professionals in making informed decisions about the treatment and management of chronic pain conditions.  DSS for chronic pain management often incorporate various tools and features, such as: 1. Clinical guidelines: DSS can provide healthcare professionals with access to current clinical guidelines for chronic pain management. These guidelines offer evidence-based recommendations for diagnosis, treatment, and monitoring. 2. Decision algorithms: DSS may include decision algorithms that help healthcare professionals systematically assess and analyze patient's symptoms, medical history, and other relevant factors to determine the most appropriate treatment plan. 3. Risk assessment: DSS can assist in evaluating the potential risks associated with specific pain management interventions, such as opioid prescriptions. It helps healthcare professionals weigh the benefits against the risks to make more informed decisions. 4. Treatment recommendations: These DSS offer recommendations for different treatment options based on the patient's specific characteristics, preferences, and previous responses to therapies. The recommendations are often personalized to the individual patient's needs. 5. Monitoring and tracking: DSS may include features for monitoring and tracking patients' progress, response to treatment, and side effects. This allows healthcare professionals to modify treatment plans as necessary. 6. Education and resources: Some DSS provide educational materials and resources for patients, including self-help strategies, lifestyle modifications, and information about support groups.  It is important to note that DSS should always be used in conjunction with the expertise of healthcare professionals and should not substitute for individualized medical advice. |
| 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. Decision support systems (DSS) are available for chronic pain management. 2. DSS for chronic pain management can provide healthcare professionals with access to current clinical guidelines. 3. DSS may include decision algorithms to help assess and analyze a patient's symptoms, history, and other factors for treatment planning. 4. DSS can assist in evaluating potential risks associated with specific pain management interventions. 5. DSS may include features for monitoring and tracking patients' progress, response to treatment, and side effects. |
| 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 | 1149(45) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the subcellular localization of the protein angiogenin? |
| 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 subcellular localization of the protein angiogenin is primarily in the nucleus. It has been found to be present in both the nuclear and cytoplasmic compartments, but its predominant location is within the nucleus. |
| 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 angiogenin is primarily located in the nucleus of a cell. 2. Angiogenin can be found in both the nuclear and cytoplasmic compartments of a cell. |
| 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 |

|  |  |
| --- | --- |
| ID | 1161(46) |
| 领域 | Bio-Medical |
| 用户问题 | How does ranolazine affect kinase signaling activation in the heart? |
| 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 | Ranolazine is a medication commonly used in the treatment of chronic angina. It works by affecting the sodium channels in the heart, but its precise mechanism of action is not fully understood. However, ranolazine has been shown to affect kinase signaling activation in the heart by inhibiting a key enzyme known as protein kinase C (PKC). PKC is a family of kinases that play a crucial role in multiple signaling pathways, including those involved in cardiac ischemia and heart failure. PKC activation in the heart can lead to increased calcium and sodium influx, which can disrupt cellular homeostasis and contribute to various heart conditions. Ranolazine has been found to inhibit PKC in cardiac muscle cells, thus reducing its activation in response to various stimuli. By doing so, it helps to improve metabolic efficiency and decrease oxygen consumption in the heart muscle, thereby relieving ischemic symptoms associated with angina. Moreover, ranolazine has also been shown to modulate the activity of other kinases in the heart. For example, it can inhibit the activation of extracellular signal-regulated kinase (ERK), a kinase involved in cell proliferation and survival pathways. By modulating the activity of these kinases, ranolazine exerts its therapeutic effects in the heart. Overall, ranolazine's inhibition of PKC and modulation of other kinases ultimately helps to stabilize cardiac electrical activity, improve myocardial oxygen supply and demand balance, and reduce symptoms associated with chronic angina. |
| 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. Ranolazine is a medication used in the treatment of chronic angina. 2. Ranolazine affects kinase signaling activation in the heart by inhibiting a key enzyme known as protein kinase C (PKC). 3. PKC is a family of kinases that play a role in multiple signaling pathways, including those involved in cardiac ischemia and heart failure. 4. Ranolazine inhibits the activation of extracellular signal-regulated kinase (ERK), a kinase involved in cell proliferation and survival pathways. 5. Ranolazine helps to stabilize cardiac electrical activity, improve myocardial oxygen supply and demand balance, and reduce symptoms associated with chronic angina. |
| 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 | 1,7,1,7,1 |

|  |  |
| --- | --- |
| ID | 1225(47) |
| 领域 | Bio-Medical |
| 用户问题 | Is the regulation of Vsr endonuclease independent of the growth phase of bacteria? |
| 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 regulation of Vsr endonuclease is dependent on the growth phase of bacteria.  Vsr endonuclease is an enzyme involved in DNA repair and has been found to play a role in regulating the mutation frequency in certain bacteria. The expression and activity of Vsr endonuclease are controlled by various factors, including the growth phase of the bacteria. During the exponential growth phase, when bacteria are actively dividing and replicating their DNA, the expression of Vsr endonuclease is typically upregulated. This is because DNA replication errors and mismatched bases can occur more frequently during this phase, and Vsr endonuclease helps in repairing these mistakes. In contrast, during the stationary phase, when the bacterial population becomes static and growth slows down, the expression of Vsr endonuclease is often downregulated. This is because the rate of DNA replication errors and mismatches decreases in stationary-phase bacteria, making the activity of Vsr endonuclease less necessary. Overall, the regulation of Vsr endonuclease is influenced by the growth phase of bacteria, with higher expression and activity during the exponential phase and lower expression during the stationary phase. |
| 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 regulation of Vsr endonuclease is dependent on the growth phase of bacteria. 2. Vsr endonuclease is an enzyme involved in DNA repair. 3. The expression of Vsr endonuclease is typically upregulated during the exponential growth phase of bacteria. 4. During the stationary phase, the expression of Vsr endonuclease in bacteria is often downregulated. 5. Vsr endonuclease plays a role in regulating the mutation frequency in certain 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 | 7,1,7,7,1 |

|  |  |
| --- | --- |
| ID | 1233(48) |
| 领域 | Bio-Medical |
| 用户问题 | What are the computational tools for the prediction of beta-barrel transmembrane proteins? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | There are several computational tools available for the prediction of beta-barrel transmembrane proteins. Some of the commonly used tools include: 1. PredictProtein: Includes several methods such as PRED-TMBB, PRED-TMBB-NN, and TMSEG for predicting transmembrane beta-barrel proteins. 2. TMBETA-NET: A web server that predicts transmembrane beta-strands, which are building blocks of beta-barrel transmembrane proteins. 3. TMBHMM: A Hidden Markov Model-based method for predicting transmembrane beta-barrel proteins. 4. BOCTOPUS: A method that combines multiple sequence alignment, Hidden Markov Models, and artificial neural networks for the prediction of beta-barrel transmembrane proteins. 5. BOMP: Beta-Barrel Outer Membrane Protein Predictor, which uses machine learning algorithms to predict beta-barrel proteins in Gram-negative bacteria. 6. PRED-GPCR: A tool specifically designed for the prediction of G-protein coupled receptors (GPCRs) which are a subclass of beta-barrel transmembrane proteins. These tools use a variety of approaches including machine learning, sequence-based analysis, and structure-based analysis to predict beta-barrel transmembrane proteins. It is worth noting that the accuracy of these tools may vary depending on the specific protein and the quality of input data. Therefore, it is often recommended to use multiple tools and compare the results for more reliable predictions. |
| 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. PredictProtein is a computational tool for predicting beta-barrel transmembrane proteins. 2. TMBETA-NET is a web server that predicts transmembrane beta-strands, the building blocks of beta-barrel transmembrane proteins. 3. TMBHMM is a Hidden Markov Model-based method for predicting transmembrane beta-barrel proteins. 4. BOCTOPUS combines multiple sequence alignment, Hidden Markov Models, and artificial neural networks for the prediction of beta-barrel transmembrane proteins. 5. BOMP is a beta-barrel outer membrane protein predictor, which uses machine learning algorithms to predict beta-barrel proteins in Gram-negative 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 | 1251(49) |
| 领域 | Bio-Medical |
| 用户问题 | Galassi classification is used for which disorder? |
| 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 Galassi classification is primarily used for the classification and grading of Colorectal Cancer. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Galassi classification is used for the classification and grading of Colorectal 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 |