幻象标注

|  |  |
| --- | --- |
| ID | 2407(0) |
| 领域 | Bio-Medical |
| 用户问题 | Has the proteome of mice hippocampus been analysed? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | Yes, the proteome of mice hippocampus has been extensively studied and analyzed. Several research studies have used mass spectrometry-based proteomic techniques to characterize the protein composition and dynamics in the hippocampus of mice. These studies have identified and quantified thousands of proteins and investigated their functions and roles in various biological processes, including learning, memory, and neurodegenerative 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. The proteome of mice hippocampus has been analyzed. 2. Mass spectrometry-based proteomic techniques are used to study the mice hippocampus proteome. 3. Thousands of proteins have been identified and quantified in the mice hippocampus. 4. Studies have investigated the roles of these proteins in various biological processes. 5. These biological processes include learning, memory, and neurodegenerative diseases. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 7,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 2409(1) |
| 领域 | Bio-Medical |
| 用户问题 | Are mouse chromosomes acrocentric? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,4 |
| 模型回复 | No, mouse chromosomes are not acrocentric. Acrocentric chromosomes have a centromere located near one end, resulting in a very short "p arm" (the shorter arm of the chromosome). Mouse chromosomes, like most mammalian chromosomes, are metacentric or submetacentric, which means that the centromere is located towards the center of the chromosome, resulting in the two arms being relatively similar in length. |
| 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. Acrocentric chromosomes have a centromere located near one end, resulting in a very short "p arm". 2. Mouse chromosomes are not acrocentric. 3. Most mammalian chromosomes, including those of mice, are either metacentric or submetacentric. 4. Metacentric or submetacentric chromosomes have the centromere located towards the center which results in two arms of similar length. |
| 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 | 1,6,4,2 |

|  |  |
| --- | --- |
| ID | 2417(2) |
| 领域 | Bio-Medical |
| 用户问题 | Which siRNA based drug is in clinical trials for the treatment of pancreatic cancer? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | One siRNA based drug currently in clinical trials for the treatment of pancreatic cancer is "AZD 9150". |
| 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 drug "AZD 9150" is currently in clinical trials for the treatment of pancreatic 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 | 5 |

|  |  |
| --- | --- |
| ID | 2419(3) |
| 领域 | Bio-Medical |
| 用户问题 | What is the HPG pore? |
| 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 | The HPG pore refers to the High-Pressure Gas (HPG) Pore. It is a device used in scientific research to study the behavior of fluids and gases within porous materials under high-pressure conditions. The HPG pore can simulate and replicate the physical and chemical processes occurring in subsurface reservoirs, such as oil and gas formations, to better understand fluid flow, transport, and storage capacity within these porous materials. It helps scientists and engineers study various phenomena related to fluid behavior, including capillary pressure, relative permeability, and fluid-rock interactions. Ultimately, the HPG pore aids in the development and optimization of technologies and strategies for enhanced oil recovery, carbon sequestration, and other applications involving subsurface reservoirs. |
| 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. The HPG pore, or High-Pressure Gas pore, is a device used in scientific research. 2. The HPG pore is used to study the behavior of fluids and gases within porous materials under high-pressure conditions. 3. It can simulate and replicate the physical and chemical processes in subsurface reservoirs such as oil and gas formations. 4. It can be used in the study of various phenomena related to fluid behavior, including capillary pressure, relative permeability, and fluid-rock interactions. 5. The HPG pore aids in the development of technologies and strategies for enhanced oil recovery, carbon sequestration, and other applications involving subsurface reservoirs. |
| 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 | 2472(4) |
| 领域 | Bio-Medical |
| 用户问题 | What is the 959 Nematode Genomes initiative? |
| 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 959 Nematode Genomes initiative is a collaborative scientific project aimed at sequencing and analyzing the genomes of 959 different species of nematodes (roundworms). Nematodes are a large and diverse group of organisms that play important roles in various ecosystems, including agriculture, medicine, and ecology. By studying the genomes of these nematode species, researchers hope to gain insights into their biology, evolution, host-parasite interactions, and potential applications in areas such as agriculture, drug discovery, and understanding human diseases. The project involves a global network of scientists working together to generate, analyze, and share genomic data on these nematode species. |
| 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 959 Nematode Genomes initiative is a scientific project that aims to sequence and analyze the genomes of 959 different species of nematodes. 2. Nematodes, also known as roundworms, are a large and diverse group of organisms. 3. These nematodes play important roles in various ecosystems, including agriculture, medicine, and ecology. 4. The project aims to study the biology, evolution and host-parasite interactions of these nematode species. 5. The initiative involves a global network of scientists working together to generate, analyze, and share genomic data on these nematode 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 | 4,1,1,3,1 |

|  |  |
| --- | --- |
| ID | 2557(5) |
| 领域 | Bio-Medical |
| 用户问题 | Which R package has been developed for analyzing Non-invasive prenatal testing (NIPT) data? |
| 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 popular R package for analyzing Non-invasive prenatal testing (NIPT) data is called "nonnest2". It is a versatile software package that offers various statistical methods for analyzing NIPT data, including estimating fetal fraction, detecting aneuploidies (such as Down syndrome), and identifying copy number variations. The nonnest2 package provides users with visualization tools and statistical tests to assess the performance of NIPT assays, as well as tools for data preprocessing and quality control. |
| 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 "nonnest2" is a popular R package used for analyzing Non-invasive prenatal testing (NIPT) data. 2. The "nonnest2" R package offers statistical methods for analyzing NIPT data. 3. With "nonnest2", you can estimate fetal fraction, detect aneuploidies such as Down syndrome, and identify copy number variations. 4. The "nonnest2" R package provides visualization tools and statistical tests to assess the performance of NIPT assays. 5. The "nonnest2" R package also offers tools for data preprocessing and quality control. |
| 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 | 3,7,7,7,1 |

|  |  |
| --- | --- |
| ID | 2560(6) |
| 领域 | Bio-Medical |
| 用户问题 | Describe Achenbach’s syndrome. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | Achenbach syndrome, also known as arterial calcification of infancy or infantile calcification, is a rare genetic disorder characterized by the calcification of arterial walls in infants. This condition primarily affects medium to large-sized arteries in the body. The exact cause of Achenbach syndrome is not fully understood but it is believed to be a result of a defect in the metabolism of calcium and phosphate, leading to abnormal deposition of calcium in the arterial walls. This can cause the arteries to become rigid and narrowed, leading to decreased blood flow to certain organs. Symptoms of Achenbach syndrome typically appear shortly after birth or during early infancy. The most common symptom is ischemic necrosis, which occurs when an organ or tissue does not receive enough oxygen and nutrients due to decreased blood flow. This can lead to tissue damage and the formation of ulcers or necrotic lesions on the skin, especially on the fingers, toes, or other extremities. Other symptoms may include pain, swelling, and limited movement in the affected areas. Diagnosis of Achenbach syndrome involves a combination of clinical examination, imaging tests, and genetic testing. X-rays, ultrasound, or computed tomography (CT) scans can help identify calcifications in the arterial walls. Genetic testing can help confirm the presence of specific gene mutations associated with Achenbach syndrome. There is currently no cure for Achenbach syndrome, and treatment mainly focuses on managing the symptoms and preventing complications. This may include the use of medications to improve blood flow, surgical interventions to remove calcifications or restore blood flow, and wound care to manage ulcers or necrotic lesions. Physical therapy may also be recommended to improve mobility and prevent further complications. Achenbach syndrome has a variable prognosis, as it can range from mild cases with minimal symptoms to severe cases with significant complications. The long-term outlook depends on the extent and location of calcifications, as well as individual factors. Early diagnosis and appropriate treatment can help improve outcomes and quality of life for individuals with Achenbach 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. Achenbach syndrome is a rare genetic disorder characterized by calcification of arterial walls in infants. 2. The disease is believed to be caused by defects in the metabolism of calcium and phosphate. 3. Symptoms of Achenbach syndrome typically appear shortly after birth or during early infancy and include ischemic necrosis, pain, swelling, and limited movement. 4. Diagnosis of Achenbach syndrome involves clinical examination, imaging tests, and genetic testing. 5. Achenbach syndrome has a variable prognosis ranging from mild to severe 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 | 1,2,2,1,1 |

|  |  |
| --- | --- |
| ID | 2581(7) |
| 领域 | Bio-Medical |
| 用户问题 | Which algorithm is used for detection of long repeat expansions? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,4 |
| 模型回复 | One algorithm commonly used for the detection of long repeat expansions is Repeat Finder. Repeat Finder is an algorithm specifically designed to identify long repeat expansions in genomic sequences. It utilizes a combination of suffix tree and pattern matching algorithms to efficiently detect and classify repeat expansions. Another popular algorithm used for this purpose is Tandem Repeats Finder (TRF), which employs a statistical method to detect tandem repeats in DNA sequences. Both algorithms have been extensively used in genomics research to identify and analyze repeat expansions associated with genetic 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. Repeat Finder is an algorithm used for the detection of long repeat expansions in genomic sequences. 2. Repeat Finder combines suffix tree and pattern matching algorithms for detecting and classifying repeat expansions. 3. Tandem Repeats Finder (TRF) is another algorithm used to detect repeats in DNA sequences. 4. The Tandem Repeats Finder uses a statistical method for identifying tandem repeats. 5. Both Repeat Finder and Tandem Repeats Finder are widely used in genomics research for identifying and analyzing repeat expansions associated with genetic 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 | 7,3,1,1,1 |

|  |  |
| --- | --- |
| ID | 2582(8) |
| 领域 | Bio-Medical |
| 用户问题 | Which brain tumors does neuroligin-3 promote? |
| 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 | Neuroligin-3 is a protein that plays a role in synaptic function and has been found to be overexpressed in several types of brain tumors. These include glioblastoma multiforme (GBM), the most common and aggressive form of brain cancer, as well as medulloblastoma and high-grade gliomas. Neuroligin-3 promotes tumor growth and invasion in these brain tumors and is associated with poorer prognosis. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Neuroligin-3 is a protein that plays a role in synaptic function. 2. Neuroligin-3 is overexpressed in several types of brain tumors. 3. Glioblastoma multiforme, medulloblastoma and high-grade gliomas are types of brain tumors where Neuroligin-3 is overexpressed. 4. Neuroligin-3 promotes tumor growth and invasion in glioblastoma multiforme, medulloblastoma and high-grade gliomas. 5. Neuroligin-3 is associated with poorer prognosis in brain tumor 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 | 1,2,2,7,3 |

|  |  |
| --- | --- |
| ID | 2586(9) |
| 领域 | Bio-Medical |
| 用户问题 | What is the approximate size of gas vesicles? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,4 |
| 模型回复 | Gas vesicles typically have a size range between 45 to 200 nanometers (nm) in diameter and can reach lengths of several micrometers (μm). |
| 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. Gas vesicles typically have a diameter that is between 45 to 200 nanometers. 2. Gas vesicles can reach lengths of several micrometers. |
| 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 |

|  |  |
| --- | --- |
| ID | 2589(10) |
| 领域 | Bio-Medical |
| 用户问题 | List BET proteins. |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,4 |
| 模型回复 | 1. BRD2 (Bromodomain containing 2) 2. BRD3 (Bromodomain containing 3) 3. BRD4 (Bromodomain containing 4) 4. BRDT (Bromodomain testis-specific protein) 5. BRPF1 (Bromodomain and PHD finger-containing protein 1) 6. BRPF3 (Bromodomain and PHD finger-containing protein 3) 7. ZMYND8 (Zinc finger, MYND domain containing 8) 8. BRD7 (Bromodomain containing 7) 9. BRD9 (Bromodomain containing 9) 10. BRDT (Bromodomain testis-specific protein) 11. BRPF1 (Bromodomain and PHD finger-containing protein 1) 12. BRPF3 (Bromodomain and PHD finger-containing protein 3) 13. BRD8 (Bromodomain containing 8) 14. BRD1 (Bromodomain-containing protein 1) 15. BRWD1 (Bromodomain and WD repeat-containing protein 1) 16. BRWD3 (Bromodomain and WD repeat-containing protein 3) 17. BRWD2 (Bromodomain and WD repeat-containing protein 2) 18. BAZ2A (Bromodomain adjacent to zinc finger domain protein 2A) 19. BAZ2B (Bromodomain adjacent to zinc finger domain protein 2B) 20. BAZ1A (Bromodomain adjacent to zinc finger domain protein 1A) |
| 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. BRD2 is a type of Bromodomain containing protein, which is also a BET protein. 2. BRD4 and BRD7 are also Bromodomain containing proteins classified as BET proteins. 3. BRPF1 and BRPF3 are categorized as Bromodomain and PHD finger-containing proteins and they belong to the BET proteins. 4. ZMYND8, also known as Zinc finger, MYND domain containing 8, is a BET protein. 5. BAZ2A and BAZ1A are examples of Bromodomain adjacent to zinc finger domain proteins that are classified as BET 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 | 1,3,3,3,3 |

|  |  |
| --- | --- |
| ID | 2610(11) |
| 领域 | Bio-Medical |
| 用户问题 | Which algorithm has been developed for prediction of protein subcellular localization using deep learning? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,5,5 |
| 模型回复 | There are several algorithms that have been developed for the prediction of protein subcellular localization using deep learning. Some of them include: 1. DeepLoc: This algorithm uses a deep recurrent neural network to predict protein subcellular localization from sequence information alone. 2. DeepMIML-SSC: It is a multi-instance multi-label learning algorithm that uses deep learning to predict protein subcellular localization based on multiple sequence segments. 3. DeepLoc-ES: This algorithm predicts protein subcellular localization using a deep learning-based ensemble system. 4. DeepLoc-GO: It combines deep learning and Gene Ontology (GO) information to predict protein subcellular localization. 5. DeepFusionGO: It is a deep fusion-based model that integrates both sequence information and GO annotations to predict protein subcellular localization. These are just a few examples, and there may be other algorithms developed using deep learning for protein subcellular localization prediction 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. DeepLoc algorithm uses a deep recurrent neural network to predict protein subcellular localization from sequence information. 2. DeepMIML-SSC is a multi-instance multi-label learning algorithm that uses deep learning to predict protein subcellular localization based on multiple sequence segments. 3. DeepLoc-ES is an algorithm that predicts protein subcellular localization using a deep learning-based ensemble system. 4. DeepLoc-GO algorithm combines deep learning and Gene Ontology information to predict protein subcellular localization. 5. DeepFusionGO is a model that integrates both sequence information and GO annotations to predict protein subcellular localization. |
| 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 | 2634(12) |
| 领域 | Bio-Medical |
| 用户问题 | What is MULTOVL? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,2 |
| 模型回复 | MULTOVL is an acronym that stands for Multipath Overlapping Virtual Link. It is a term commonly used in networking to describe a technique that allows multiple virtual links or paths to share the same physical link or network connection. This technique is often employed in network redundancy and load balancing strategies to enhance network performance and reliability. By utilizing multiple virtual links, MULTOVL can help distribute network traffic across different paths, increasing bandwidth utilization and providing fault tolerance in case of link failures. |
| 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. MULTOVL stands for Multipath Overlapping Virtual Link. 2. MULTOVL is a technique used in networking. 3. MULTOVL allows multiple virtual links or paths to share the same physical link. 4. The technique of MULTOVL is often employed in network redundancy and load balancing strategies. 5. MULTOVL can help distribute network traffic across different paths. |
| 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 | 2660(13) |
| 领域 | Bio-Medical |
| 用户问题 | Can GDF15 be a biomarker for metformin treatment? |
| 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, GDF15 (Growth Differentiation Factor 15) has been suggested as a potential biomarker for metformin treatment. Metformin is a commonly prescribed medication for type 2 diabetes and has been shown to increase GDF15 levels in the blood. Research studies have found that GDF15 levels are elevated in patients taking metformin, and these levels correlate with metabolic improvements such as reduced glucose levels and improved insulin sensitivity. Additionally, GDF15 levels have been associated with metformin's effects on weight loss and appetite regulation. However, it should be noted that while GDF15 shows promise as a biomarker for metformin treatment, further research is needed to establish its clinical utility as a reliable marker for monitoring the response to metformin therapy. |
| 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. GDF15 (Growth Differentiation Factor 15) is suggested as a potential biomarker for metformin treatment. 2. Metformin is a medication commonly prescribed for type 2 diabetes. 3. GDF15 levels have been found to increase in the blood in patients taking metformin. 4. GDF15 levels are correlated with metabolic improvements such as lower glucose levels and improved insulin sensitivity. 5. GDF15 levels have been associated with metformin's effects on weight loss and appetite 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 | 2,1,3,7,7 |

|  |  |
| --- | --- |
| ID | 2664(14) |
| 领域 | Bio-Medical |
| 用户问题 | Is recursive splicing more common in short introns? |
| 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, recursive splicing is more common in short introns. Recursive splicing is a phenomenon where an intron is spliced into multiple smaller pieces before being completely removed from the pre-mRNA. This process involves the iterative cleavage and ligation of the intron, resulting in multiple rounds of splicing. Short introns provide a greater opportunity for recursive splicing because they can be more easily divided into smaller pieces. In contrast, longer introns may be too large to be efficiently processed through recursive splicing. |
| 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. Recursive splicing refers to the process where an intron is spliced into multiple smaller pieces before being completely removed from the pre-mRNA. 2. Recursive splicing involves the iterative cleavage and ligation of the intron, resulting in multiple rounds of splicing. 3. The process of recursive splicing is more common in short introns. 4. Short introns can be more easily divided into smaller pieces for recursive splicing. 5. Longer introns may be too large to be efficiently processed through recursive splicing. |
| 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 | 1,1,3,3,3 |

|  |  |
| --- | --- |
| ID | 2679(15) |
| 领域 | Bio-Medical |
| 用户问题 | What is the TALE-iD method used for? |
| 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 | The TALE-iD method is used for talent identification in sports. It is a systematic process that assists in identifying individuals who have the potential to excel in a specific sport or athletic activity. The method combines various assessments and evaluations, including physical, technical, tactical, and psychological factors, to determine an individual's talent and potential for future success in their chosen sport. |
| 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. The TALE-iD method is used for talent identification in sports. 2. It is a systematic process that assists in identifying individuals' potential in a specific sport. 3. The TALE-iD method uses various assessments and evaluations to determine individuals' talent and potential. 4. The assessments and evaluations used by the TALE-iD method include physical, technical, tactical, and psychological factors. 5. The TALE-iD method aids in determining individuals' potential for future success in their chosen sports. |
| 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 | 2747(16) |
| 领域 | Bio-Medical |
| 用户问题 | Which Lisp framework has been developed for image processing? |
| 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 Lisp framework that has been developed for image processing is the Common Lisp-based framework called "CL-IMAGE". CL-IMAGE provides functionalities for basic image manipulation such as loading, saving, resizing, cropping, and transforming images. It also supports various image file formats including BMP, PNG, JPEG, and TIFF. |
| 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. CL-IMAGE is a Common Lisp-based framework. 2. CL-IMAGE has been developed for image processing. 3. This framework provides functionalities for basic image manipulation. 4. CL-IMAGE supports loading, saving, resizing, cropping, and transforming images. 5. The supported image file formats of CL-IMAGE include BMP, PNG, JPEG, and TIFF. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 7,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 2759(17) |
| 领域 | Bio-Medical |
| 用户问题 | How many genes in S. cerevisiae are the result of an ancient whole genome duplication? |
| 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 the species Saccharomyces cerevisiae (S. cerevisiae), also known as baker's yeast, an ancient whole genome duplication (WGD) event is widely accepted to have occurred. This event is estimated to have happened approximately 100 million years ago.  As a result of this ancient WGD, the genome of S. cerevisiae contains numerous duplicated genes. Genome sequencing and analysis have revealed that approximately 90% of the genes in S. cerevisiae are the result of this WGD. This translates to around 5,800 genes out of the approximately 6,500 genes of S. cerevisiae being duplicated during this event. |
| 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. An ancient whole genome duplication event occurred in the species Saccharomyces cerevisiae, also known as baker's yeast. 2. This whole genome duplication event in S. cerevisiae is reckoned to have happened approximately 100 million years ago. 3. The genome of S. cerevisiae contains numerous duplicated genes as a result of this ancient whole genome duplication. 4. Genome sequencing and analysis indicated that about 90% of the genes in S. cerevisiae resulted from this whole genome duplication event. 5. Around 5,800 genes out of 6,500 in S. cerevisiae are the result of duplication during this event. |
| 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 | 2763(18) |
| 领域 | Bio-Medical |
| 用户问题 | Which complex is bound by estrogen-related receptor β (Esrrb)? |
| 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 complex that is bound by estrogen-related receptor β (Esrrb) is referred to as the Esrrb complex. |
| 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 complex that is bound by estrogen-related receptor β (Esrrb) is referred to as the Esrrb complex. |
| 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 | 8 |

|  |  |
| --- | --- |
| ID | 2842(19) |
| 领域 | Bio-Medical |
| 用户问题 | What is the role of ZCCHC17? |
| 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 | ZCCHC17, also known as zinc finger CCHC-type containing 17, is an enzyme that plays a role in RNA processing and regulation. Specifically, it functions as a poly(A) RNA polymerase, which adds the poly(A) tail to the 3' end of RNA molecules. The addition of the poly(A) tail is an important step in the maturation and stability of RNA molecules, including mRNA. The poly(A) tail helps protect the RNA from degradation and also plays a role in the process of mRNA export from the nucleus to the cytoplasm. In addition to its poly(A) polymerase activity, ZCCHC17 has been found to have other functions as well. It has been associated with regulating the stability and levels of specific RNA molecules, suggesting its involvement in gene expression control. Studies have also suggested its involvement in the regulation of cellular processes like cell proliferation and cell cycle progression. Overall, ZCCHC17 is an important enzyme involved in RNA metabolism and gene expression regulation, contributing to the proper maturation and function of RNA 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. ZCCHC17, also known as zinc finger CCHC-type containing 17, is an enzyme involved in RNA processing and regulation. 2. ZCCHC17 functions as a poly(A) RNA polymerase, which adds the poly(A) tail to the 3' end of RNA molecules. 3. The addition of the poly(A) tail to RNA molecules aids in their maturation and stability. 4. The poly(A) tail on RNA molecules assists in the protection of the RNA from degradation and plays a role in mRNA export from the nucleus to the cytoplasm. 5. ZCCHC17 has been associated with regulating the stability and levels of specific RNA molecules, suggesting its involvement in gene expression control. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 4,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 2861(20) |
| 领域 | Bio-Medical |
| 用户问题 | Which proteins form the nuclear pore basket in human cells? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The nuclear pore basket in human cells is mainly formed by a protein complex called Nup358/RanBP2. |
| 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 nuclear pore basket in human cells is mainly formed by a protein complex called Nup358/RanBP2. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 4 |

|  |  |
| --- | --- |
| ID | 2919(21) |
| 领域 | Bio-Medical |
| 用户问题 | What type of topoisomerase inhibitor is gepotidacin? |
| 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 | Gepotidacin is a bacterial topoisomerase inhibitor. Specifically, it is an inhibitor of topoisomerase II. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Gepotidacin is a bacterial topoisomerase inhibitor. 2. Gepotidacin is an inhibitor of topoisomerase II. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1, 2 |

|  |  |
| --- | --- |
| ID | 2943(22) |
| 领域 | Bio-Medical |
| 用户问题 | Describe Canvas SPW |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,2,3 |
| 模型回复 | Canvas SPW refers to the Canvas Software Process Workbench, which is a platform that supports the development and execution of software processes. It provides a comprehensive set of tools and features to manage the entire software development lifecycle. Canvas SPW is designed to facilitate collaboration among team members, automate process execution, and provide real-time visibility into the progress of software projects. It allows users to define and customize their software processes using a graphical interface, making it easy to tailor the workflow to specific project requirements. With Canvas SPW, users can create and manage artifacts such as requirements, specifications, designs, and test cases. It also offers features for version control, issue tracking, and release management. These functionalities help to ensure that the development process is well-structured, organized, and efficiently executed. One of the key advantages of Canvas SPW is its ability to support agile methodologies such as Scrum and Kanban. It allows teams to easily create backlog items, plan sprints, and track progress using visual boards and charts. This enables teams to quickly adapt to changing requirements and deliver high-quality software in shorter iterations. Furthermore, Canvas SPW provides comprehensive reporting and analytics capabilities, allowing teams to monitor performance, identify bottlenecks, and make data-driven decisions. It offers customizable dashboards, metrics, and reports to provide stakeholders with insights into project status and progress. Overall, Canvas SPW is a powerful tool for managing software development processes. It streamlines the process, improves collaboration, and enhances visibility, ultimately leading to better software quality and delivery. |
| 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. Canvas SPW is a platform that supports the development and execution of software processes. 2. The platform allows users to customize their software processes using a graphical interface. 3. Canvas SPW offers features for version control, issue tracking, and release management in software development. 4. Canvas SPW supports agile methodologies such as Scrum and Kanban, and allows teams to create backlog items, plan sprints and track progress using visual boards and charts. 5. Canvas SPW provides comprehensive reporting and analytics capabilities, including customizable dashboards, metrics, and reports. |
| 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 | 2960(23) |
| 领域 | Bio-Medical |
| 用户问题 | List STING agonists. |
| 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 | 1. LPS (lipopolysaccharide) 2. Poly(I:C) (polyinosinic:polycytidylic acid) 3. Imiquimod 4. CpG (CpG oligodeoxynucleotides) 5. Resiquimod 6. R848 7. Flagellin 8. Muramyl dipeptide 9. Pam3CSK4 10. Zymosan |
| 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. LPS (lipopolysaccharide) is a STING agonist. 2. Poly(I:C) (polyinosinic:polycytidylic acid) is a STING agonist. 3. Imiquimod is a STING agonist. 4. CpG (CpG oligodeoxynucleotides) is a STING agonist. 5. Resiquimod is a STING agonist. |
| 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 | 2964(24) |
| 领域 | Bio-Medical |
| 用户问题 | Describe SLIC-CAGE |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,2,2 |
| 模型回复 | SLIC-CAGE is a unique segmentation algorithm used in computer vision and image processing. SLIC stands for Simple Linear Iterative Clustering, which is a powerful clustering technique, and CAGE stands for Compact Attribute Grid Extraction, which is a compact representation of image segments. The SLIC-CAGE algorithm combines the SLIC clustering technique with the CAGE representation to achieve efficient and accurate image segmentation. It starts by initializing a grid of evenly spaced superpixels in the image. These superpixels act as initial clusters. Then, the algorithm iteratively assigns pixels to their nearest superpixel based on color similarity and spatial proximity. In each iteration, the algorithm updates the position and color of each superpixel centroid by calculating the mean color and position of the assigned pixels. It continues the assignment and update process until convergence is reached, usually a predefined number of iterations. Once the clustering process is complete, the SLIC-CAGE algorithm constructs the Compact Attribute Grid (CAGE) representation. This representation encodes the attributes of each superpixel, including its centroid position and color. CAGE is a compact data structure that allows for efficient storage and processing of image segments. SLIC-CAGE offers several advantages over traditional segmentation algorithms. It is efficient, as it reduces the computational complexity by clustering only a subset of pixel pairs. It also provides high-quality segmentation results by considering both color similarity and spatial proximity. Overall, SLIC-CAGE is a robust and efficient algorithm that combines the power of SLIC clustering with the compactness of CAGE representation, making it a valuable tool for various applications in computer vision and image processing. |
| 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. SLIC-CAGE is a segmentation algorithm used in computer vision and image processing. 2. SLIC in SLIC-CAGE stands for Simple Linear Iterative Clustering, a clustering technique. 3. CAGE in SLIC-CAGE stands for Compact Attribute Grid Extraction, a compact representation of image segments. 4. The SLIC-CAGE algorithm combines SLIC clustering with CAGE representation in order to segment an image. 5. The Compact Attribute Grid (CAGE) in SLIC-CAGE encodes the attributes of each superpixel, which includes its centroid position and color. |
| 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 | 2978(25) |
| 领域 | Bio-Medical |
| 用户问题 | What are the roles of LEM-3? |
| 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 | LEM-3, also known as Lucid Electro-Magnetic, is a protein involved in synaptic plasticity, a key process that underlies learning and memory formation in the brain. Here are some of the roles of LEM-3: 1. Regulation of synaptic strength: LEM-3 plays a role in modulating the strength of synaptic connections between neurons. It has been shown to regulate the number and function of AMPA-type glutamate receptors, which are crucial for synaptic transmission and synaptic plasticity. 2. Memory consolidation: LEM-3 is involved in the consolidation of memories, which is the process of stabilizing and integrating newly formed memories into long-term storage. It is specifically implicated in the strengthening or weakening of synapses in response to learning experiences. 3. Long-term potentiation (LTP): LEM-3 is part of the molecular machinery that contributes to the induction and maintenance of long-term potentiation, a cellular mechanism underlying the strengthening of synaptic connections. LTP is considered one of the cellular bases for learning and memory. 4. Dendritic spine structure: LEM-3 is involved in the regulation of dendritic spine morphology and density. Dendritic spines are small protrusions on the surface of dendrites that receive synaptic inputs. These structures are highly dynamic and are known to be important for synaptic plasticity and memory formation. 5. Neuronal development: LEM-3 also plays a role in the development and maturation of neurons. It contributes to the formation and refinement of synaptic connections during early brain development. Overall, LEM-3 is a critical player in synaptic plasticity and memory processes, influencing synaptic strength, memory consolidation, dendritic spine structure, and neuronal development. |
| 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. LEM-3 is a protein involved in synaptic plasticity which underlies learning and memory formation in the brain. 2. LEM-3 helps in modulating the strength of synaptic connections between neurons. 3. LEM-3 is involved in the consolidation of memories, a process of stabilizing and integrating new memories into long-term storage. 4. LEM-3 contributes to the induction and maintenance of long-term potentiation - a cellular mechanism underlying the strengthening of synaptic connections. 5. LEM-3 is involved in the regulation of dendritic spine morphology and density, as well as the development and maturation of neurons. |
| 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 | 2,3,3,3,3 |

|  |  |
| --- | --- |
| ID | 2992(26) |
| 领域 | Bio-Medical |
| 用户问题 | List the releases of tmVar |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,2,3 |
| 模型回复 | Here are the releases of tmVar: 1. Release 1.0: This was the initial release of tmVar and was made available on December 4, 2012. It provided the basic functionality of extracting genetic variant-disease relationships from the biomedical literature. 2. Release 2.0: The second release of tmVar came on August 3, 2013. It included improvements in data extraction and entity recognition, making it more accurate and efficient in identifying genetic variant mentions and their associated diseases. 3. Release 3.0: Released on July 14, 2014, tmVar 3.0 introduced new features such as the ability to recognize protein variant mentions and provide links to related databases, enhancing the usability and comprehensiveness of the tool. 4. Release 4.0: On November 30, 2015, tmVar 4.0 was released with significant improvements in performance and coverage. It incorporated the latest version of the annotation pipeline and provided access to a larger collection of genetic variant-disease relationships. 5. Release 5.0: The fifth major release of tmVar was made available on July 3, 2017. It introduced an updated algorithm for variant-disease relationship extraction, resulting in improved accuracy and a higher recall rate. 6. Release 6.0: Released on April 30, 2019, tmVar 6.0 incorporated advancements in machine learning and natural language processing techniques. It provided enhanced recognition and normalization of genetic variant mentions and their associated diseases. 7. Release 7.0: The most recent release, tmVar 7.0, was made available on October 19, 2020. It introduced several new features, including the recognition of copy number variants, improved entity recognition algorithms, and updated databases for variant-disease association information. Please note that the information provided above is based on the available data at the time of generating the response, and there might have been subsequent releases after tmVar 7.0. |
| 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 initial release of tmVar, Release 1.0, was made available on December 4, 2012, with the basic functionality of extracting genetic variant-disease relationships from literature. 2. Release 2.0 of tmVar was released on August 3, 2013, featuring improvements in data extraction and entity recognition. 3. tmVar 3.0 was released on July 14, 2014, introducing features such as recognizing protein variant mentions and providing links to related databases. 4. On November 30, 2015, tmVar 4.0 was released incorporating the latest version of the annotation pipeline and greater access to genetic variant-disease relationships. 5. tmVar 5.0, released on July 3, 2017, introduced an updated algorithm for variant-disease relationship extraction, improving accuracy and recall rate. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 2,2,2,7,7 |

|  |  |
| --- | --- |
| ID | 3018(27) |
| 领域 | Bio-Medical |
| 用户问题 | Which is the database of somatic mutations in normal cells? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | The database of somatic mutations in normal cells is known as The Cancer Genome Atlas (TCGA). It is a comprehensive database that catalogues genomic alterations, including somatic mutations, in various cancer types. TCGA provides valuable information about the genetic changes occurring in both tumor and normal cells, facilitating the understanding of cancer biology and the development of targeted therapies. |
| 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 Cancer Genome Atlas (TCGA) is the database of somatic mutations in normal cells. 2. TCGA catalogues genomic alterations, including somatic mutations, in various cancer types. 3. The Cancer Genome Atlas provides information about the genetic changes occurring in tumor and normal cells. 4. TCGA is used in facilitating the understanding of cancer biology. 5. The development of targeted therapies is one of the applications of The Cancer Genome Atlas. |
| 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 | 3037(28) |
| 领域 | Bio-Medical |
| 用户问题 | Are there graph kernel libraries available implemented in JAVA? |
| 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 several graph kernel libraries implemented in Java. Some of the popular ones are: 1. Kernels4J: This is an open-source library that provides various graph kernel algorithms and implementations, including the classic random walk kernel and subtree kernel. It offers an easy-to-use API for computing and comparing graph kernels in Java. 2. GraphKernels: This library provides a set of graph kernel algorithms and implements them using efficient data structures and algorithms for graph processing. It supports various types of kernels, including graphlet kernels, shortest-path kernels, and Weisfeiler-Lehman kernels. 3. GEDLIB: GEDLIB is a Java library specifically designed for graph edit distance calculation. It provides graph similarity measures based on graph edit distance algorithms and offers graph kernel-based similarity measures as well. 4. MLlib: Apache Spark's MLlib library includes several graph algorithms and utilities that can be used for analyzing large-scale graphs. Although it is primarily focused on distributed computing, it provides various graph processing and mining functionalities, including graph kernel computation. These libraries offer different types of graph kernels and functionalities, so you can choose the one that best suits your requirements. |
| 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. Kernels4J is an open-source library that provides various graph kernel algorithms and implementations in Java. 2. GraphKernels is a Java library that provides a set of graph kernel algorithms and implements them efficiently for graph processing. 3. GEDLIB, a Java library, is specifically designed for graph edit distance calculation. 4. Apache Spark's MLlib library includes several graph algorithms and utilities that can be used for analyzing large-scale graphs. 5. These libraries offer a variety of graph kernels and functionalities allowing options for different requirements. |
| 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 | 1,2,2,1,1 |

|  |  |
| --- | --- |
| ID | 3045(29) |
| 领域 | Bio-Medical |
| 用户问题 | List the four advances integrated into the SHERLOCKv2 platform. |
| 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 | The four advances integrated into the SHERLOCKv2 platform are: 1. SHERLOCKv2 incorporates a Cas13d protein, which is a more compact version of Cas13a. This allows for improved delivery and scalability of the platform. 2. The SHERLOCKv2 platform includes a pre-amplification step, in which a DNA template is first amplified prior to detection. This increases the sensitivity of the assay and enables detection of even low levels of target nucleic acids. 3. SHERLOCKv2 incorporates non-target CRISPR RNA molecules, called excess triggers, which enhance the specificity and reliability of the platform. These excess triggers competitively bind to the target RNA, reducing the chance of false positives. 4. The SHERLOCKv2 platform includes SHERLOCKv2.0 software, which facilitates automated analysis and interpretation of the results. This software allows for high-throughput analysis of multiple samples simultaneously and provides a user-friendly interface for easy data interpretation. |
| 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 SHERLOCKv2 platform incorporates a Cas13d protein, which is a more compact version of Cas13a. 2. The SHERLOCKv2 platform includes a pre-amplification step in which a DNA template is first amplified prior to detection. 3. SHERLOCKv2 uses non-target CRISPR RNA molecules also known as excess triggers. 4. The SHERLOCKv2 platform includes SHERLOCKv2.0 software which facilitates automated analysis and interpretation of the results. 5. The excess triggers in SHERLOCKv2 competitively bind to the target RNA. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1,1,2,2,1 |

|  |  |
| --- | --- |
| ID | 3078(30) |
| 领域 | Bio-Medical |
| 用户问题 | Describe the bartender algorithm |
| 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 | The bartender algorithm is a hypothetical algorithm that is often used as an example in computer science and artificial intelligence to demonstrate complex decision-making processes. It is an algorithm that simulates the behavior of a bartender taking drink orders from customers. The goal of the bartender algorithm is to efficiently and accurately take customer orders, prioritize them, and prepare the drinks in the most optimal manner. The algorithm considers various factors while making decisions, such as the type and complexity of the drink, the order in which the orders were received, and the available resources and time constraints. Here is a high-level description of the bartender algorithm: 1. Receive drink orders: The bartender algorithm starts by receiving drink orders from customers. It may receive multiple orders simultaneously or one at a time. 2. Analyze order complexity: The algorithm analyzes the complexity of each drink order, considering the number of ingredients and the required preparation steps. More complex orders may take longer to prepare. 3. Prioritize orders: The algorithm determines the priority of each order based on factors like waiting time, order complexity, and any special requests. It aims to optimize efficiency and customer satisfaction. 4. Prepare the drinks: The algorithm starts preparing the drinks in the order of priority. It manages available resources, such as ingredients, bartending tools, and equipment to efficiently make the drinks in the shortest possible time. 5. Handle interruptions and emergencies: If any unexpected events occur, such as an equipment failure or running out of certain ingredients, the algorithm adjusts its decision-making process to handle such interruptions and make alternative arrangements. 6. Serve the drinks: Once the drinks are prepared, the algorithm ensures that they are served to the correct customers. It may consider factors like matching order numbers or customer identifiers to avoid any mix-ups. 7. Update status and feedback: The algorithm updates the status of each order, marking it as complete or in-progress. It may also collect feedback or ratings from customers to improve future decision-making. The bartender algorithm is a simple representation of a decision-making process that considers multiple factors and aims to optimize efficiency and customer satisfaction. It can be further enhanced with machine learning techniques, such as learning from previous orders and refining the decision-making process over time. |
| 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 bartender algorithm is a hypothetical algorithm used in computer science and artificial intelligence. 2. The goal of the bartender algorithm is to efficiently and accurately take and prioritize customer orders, prepare the drinks optimally. 3. The bartender algorithm considers factors, order of receipt, type and complexity of drink, and available resources and time constraints. 4. The bartender algorithm adjusts its decision-making process when unexpected events occur to handle such interruptions and make alternate arrangements. 5. The bartender algorithm updates the status of each order and may collect feedback or ratings from customers to improve future decision-making. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 7,7,7,7,2 |

|  |  |
| --- | --- |
| ID | 3100(31) |
| 领域 | Bio-Medical |
| 用户问题 | Which web-based pedigree editors are 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 | There are several web-based pedigree editors available, including: 1. Progeny: Progeny is a comprehensive pedigree editor that allows users to create, edit, and analyze pedigrees. It offers various features such as customizable pedigree symbols, color-coding, and the ability to add medical information to individuals. Progeny also offers integrated genetic and statistical analysis capabilities. 2. Pedigree Editor: Pedigree Editor is a user-friendly web-based tool that enables users to create and edit pedigrees for genetic research or clinical purposes. It offers a simple interface with drag-and-drop functionality and allows users to add different types of information to individuals, such as phenotype, genotype, and medical history. 3. Breeders Assistant: Breeders Assistant is a web-based pedigree editor specifically designed for animal breeders. It offers a range of features tailored to the needs of breeders, including the ability to track and manage breeding lines, view genetic data, and generate reports and pedigrees. 4. PedigreeXP: PedigreeXP is a web-based pedigree editor that offers advanced features for genetics research and breeding programs. It allows users to create pedigrees with complex relationships, incorporate genetic markers, and perform advanced analysis such as inbreeding coefficients and kinship calculations. 5. PedEasy: PedEasy is a free, web-based pedigree editor developed by the National Human Genome Research Institute. It is designed for creating and editing pedigrees for genetic studies and offers features such as standard pedigree symbols, color-coding, and the ability to add detailed medical information. These are just a few examples of the web-based pedigree editors available, and there may be others depending on specific research or breeding needs. |
| 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. Progeny is a web-based pedigree editor that has customizable pedigree symbols, color-coding, and has integrated genetic and statistical analysis capabilities. 2. Pedigree Editor is a web-based tool used for creating and editing pedigrees for genetic research or clinical purposes. 3. Breeders Assistant is a web-based pedigree editor designed specifically for animal breeders, allowing them to track and manage breeding lines, view genetic data, and generate reports. 4. PedigreeXP is a web-based pedigree editor that provides advanced features for genetics research and breeding programs. 5. PedEasy, a free web-based pedigree editor, was developed by the National Human Genome Research Institute for creating and editing pedigrees for genetic 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 | 2,1,4,7,7 |

|  |  |
| --- | --- |
| ID | 3107(32) |
| 领域 | Bio-Medical |
| 用户问题 | Which curated databases exist for spider-venom toxins? |
| 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 curated databases available for spider-venom toxins. Some of the widely used ones include: 1. ArachnoServer: ArachnoServer is a comprehensive database that provides detailed information about spider toxins. It includes data on toxin sequences, structures, biological activities, and target information. It also provides tools for toxin annotation and prediction. 2. SpiderPharm: SpiderPharm is a database specifically focused on spider venom peptides. It contains information on peptide sequences, structures, and activities. It also provides tools for sequence alignment and similarity searches. 3. SpiderToxin: SpiderToxin is a manually curated database that collects information on spider toxins. It contains data on toxin sequences, structures, functional annotations, and other related information. It also provides tools for data querying and visualization. 4. AVITdb: AVITdb (Arthropod Venom and Insecticidal Toxin database) is a comprehensive database that includes information on venomous arthropods, including spiders. It provides data on venom protein sequences, structures, and activities. It also offers tools for data analysis and visualization. These databases are valuable resources for researchers, biochemists, and drug developers interested in spider venom toxins and their potential applications in various fields, such as pharmacology and bioengineering. |
| 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. ArachnoServer is a comprehensive database that provides detailed information about spider toxins. 2. SpiderPharm is a database focused on spider venom peptides, including information on peptide sequences, structures, and activities. 3. SpiderToxin is a manually curated database that collects information on spider toxins. 4. AVITdb (Arthropod Venom and Insecticidal Toxin database) contains information on venomous arthropods, including spiders. 5. These databases are resources for researchers, biochemists, and drug developers interested in spider venom toxins and their potential applications. |
| 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 | 1,7,7,2,1 |

|  |  |
| --- | --- |
| ID | 3111(33) |
| 领域 | Bio-Medical |
| 用户问题 | Does Axitinib prolong survival of Pancreatic Cancer patients? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,4,5 |
| 模型回复 | There is limited evidence regarding the use of Axitinib in the treatment of pancreatic cancer. Axitinib is a tyrosine kinase inhibitor primarily used in the treatment of renal cell carcinoma (a type of kidney cancer). It works by inhibiting the growth of new blood vessels that supply tumors. While some studies have explored the potential use of Axitinib in pancreatic cancer, the results have been mixed. Some preclinical studies have shown promising results, indicating that Axitinib may inhibit pancreatic cancer cell growth and enhance the effectiveness of other treatment modalities. However, clinical trials have not shown significant improvements in overall survival or progression-free survival when Axitinib is used as a monotherapy for pancreatic cancer. Combination therapy studies with Axitinib and other targeted therapies or chemotherapy have shown some potential. Ultimately, more research is needed to determine the efficacy and safety of Axitinib in the treatment of pancreatic cancer. It is always recommended to consult with a healthcare professional for the most up-to-date and individualized treatment options. |
| 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. Axitinib is a tyrosine kinase inhibitor primarily used in the treatment of renal cell carcinoma. 2. Axitinib works by inhibiting the growth of new blood vessels that supply tumors. 3. Some preclinical studies have shown that Axitinib may inhibit pancreatic cancer cell growth. 4. Clinical trials have not shown significant improvements in overall survival or progression-free survival when Axitinib is used as a monotherapy for pancreatic cancer. 5. Combination therapy studies with Axitinib and other targeted therapies or chemotherapy have shown some potential. |
| 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 | 1,1,1,2,2 |

|  |  |
| --- | --- |
| ID | 3113(34) |
| 领域 | Bio-Medical |
| 用户问题 | Through which protein interaction does MLP regulate F-actin dynamics? |
| 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 | Myosin-like protein (MLP) primarily regulates F-actin dynamics through its interaction with actin-binding proteins such as tropomyosin (Tpm) and caldesmon (CaD). These interactions help modulate the assembly and disassembly of F-actin filaments, thereby regulating various cellular processes such as cell migration, cytokinesis, and muscle contraction. MLP's interaction with Tpm stabilizes actin bundles, while its interaction with CaD promotes actin depolymerization, leading to the regulation of F-actin dynamics. |
| 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. Myosin-like protein (MLP) regulates F-actin dynamics through its interaction with actin-binding proteins. 2. The actin-binding proteins that MLP interacts with include tropomyosin (Tpm) and caldesmon (CaD). 3. The interactions between MLP and these proteins modulate the assembly and disassembly of F-actin filaments. 4. MLP's interaction with Tpm stabilizes actin bundles. 5. MLP's interaction with CaD promotes actin depolymerization. |
| 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 | 6,2,2,3,1 |

|  |  |
| --- | --- |
| ID | 3125(35) |
| 领域 | Bio-Medical |
| 用户问题 | How many pseudokinases are there in the human kinome? |
| 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 48 pseudokinases in the human kinome. |
| 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 48 pseudokinases in the human kinome. |
| 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 | 3139(36) |
| 领域 | Bio-Medical |
| 用户问题 | List 3 apoE mimetics. |
| 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 | 1. Eprotirome - It is a synthetic thyroid hormone analog that mimics the action of apoE in regulating lipid metabolism. 2. Sorafenib - Originally developed as a cancer drug, it has been found to have apoE-like properties in reducing plasma lipid levels and promoting lipid clearance. 3. COG133 - This is a peptide mimetic of apoE that has shown potential therapeutic effects in animal models of Alzheimer's disease, by reducing amyloid-beta deposition and inflammation. |
| 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. Eprotirome is a synthetic thyroid hormone analog that mimics the action of apoE in regulating lipid metabolism. 2. Sorafenib, a cancer drug, possesses apoE-like properties that reduce plasma lipid levels and promote lipid clearance. 3. COG133 is a peptide mimetic of apoE with potential therapeutic effects in animal models of Alzheimer's disease, where it reduces amyloid-beta deposition and inflammation. |
| 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 | 2,2,1 |

|  |  |
| --- | --- |
| ID | 3140(37) |
| 领域 | Bio-Medical |
| 用户问题 | What are there sex differences in SAMHD1 activity? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,4 |
| 模型回复 | SAMHD1 is a protein that plays a critical role in the regulation of deoxynucleotide metabolism and restriction of viral infections. While there is limited research on sex differences specifically in SAMHD1 activity, some studies suggest potential differences. One study found that SAMHD1 expression is regulated by estrogen in human breast cancer cells, indicating a potential influence of sex hormones on SAMHD1 activity. Furthermore, this study demonstrated that estrogen treatment leads to a decrease in SAMHD1 expression, suggesting lower SAMHD1 activity in the presence of estrogen. Another study examining SAMHD1 expression in response to HIV-1 infection in peripheral blood mononuclear cells (PBMCs) observed a sex difference in SAMHD1 levels. They found that SAMHD1 levels were higher in PBMCs from females compared to males, potentially suggesting differences in SAMHD1 activity between sexes in the context of viral infections. However, more research is needed to fully understand the extent and implications of sex differences in SAMHD1 activity. It is important to note that biological sex is just one factor among many that can influence protein activity and function, and individual variation within each sex is also significant. |
| 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. SAMHD1 is a protein that plays a critical role in the regulation of deoxynucleotide metabolism and restriction of viral infections. 2. One study found that SAMHD1 expression is regulated by estrogen in human breast cancer cells. 3. The same study demonstrated that estrogen treatment leads to a decrease in SAMHD1 expression. 4. Another study observed a sex difference in SAMHD1 levels in response to HIV-1 infection in peripheral blood mononuclear cells (PBMCs). 5. This study found that SAMHD1 levels were higher in PBMCs from females compared to males. |
| 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 | 1,1,7,7,7 |

|  |  |
| --- | --- |
| ID | 3205(38) |
| 领域 | Bio-Medical |
| 用户问题 | Does RUNX2 inhibit astrocyte differentiation? |
| 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, RUNX2 does not inhibit astrocyte differentiation. In fact, RUNX2 is known to promote astrocyte differentiation. RUNX2 is a transcription factor that plays a crucial role in the development and differentiation of various cell types, including astrocytes. It has been found to be necessary for the generation of astrocytes from neural stem/progenitor cells. However, the exact mechanisms through which RUNX2 regulates astrocyte differentiation are still being studied. So, RUNX2 promotes, rather than inhibits, astrocyte differentiation. |
| 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. RUNX2 does not inhibit astrocyte differentiation. 2. RUNX2 is known to promote astrocyte differentiation. 3. RUNX2 is a transcription factor that is involved in the development and differentiation of various cell types. 4. RUNX2 has been found to be necessary for the generation of astrocytes from neural stem/progenitor cells. 5. The exact mechanisms through which RUNX2 regulates astrocyte differentiation are still being studied. |
| 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 | 2,2,1,7,1 |

|  |  |
| --- | --- |
| ID | 3209(39) |
| 领域 | Bio-Medical |
| 用户问题 | Where, in the body, would the Cobb-Stainsby excision arthroplasty be performed? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 4,4,4 |
| 模型回复 | The Cobb-Stainsby excision arthroplasty is a surgical procedure performed in the hand. Specifically, it is a surgical technique used to treat arthritis or dysfunction in the metacarpophalangeal (MCP) joint, which is the joint between the metacarpal bone in the hand and the proximal phalanx bone in the finger. |
| 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 Cobb-Stainsby excision arthroplasty is a surgical procedure performed in the hand. 2. This surgical procedure is used to treat arthritis or dysfunction. 3. The surgery is performed on the metacarpophalangeal (MCP) joint. 4. The metacarpophalangeal joint is positioned between the metacarpal bone in the hand and the proximal phalanx bone in the finger. |
| 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 |

|  |  |
| --- | --- |
| ID | 3243(40) |
| 领域 | Bio-Medical |
| 用户问题 | Does GRHL2 over-expression lead to EMT? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,3 |
| 模型回复 | Yes, over-expression of the GRHL2 gene has been found to lead to epithelial-mesenchymal transition (EMT) in several studies. EMT is a cellular process where epithelial cells lose their characteristics and adopt a mesenchymal cell-like phenotype, which is associated with increased migration and invasion abilities. GRHL2 is a transcription factor involved in the regulation of epithelial cell identity and differentiation. When GRHL2 is over-expressed, it can disrupt the balance of epithelial cell markers and induce EMT, promoting the invasive properties of cells. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. Over-expression of the GRHL2 gene can lead to epithelial-mesenchymal transition (EMT). 2. EMT is a cellular process in which epithelial cells lose their characteristics and turn into mesenchymal cells. 3. The epithelial-mesenchymal transition results in increased migration and invasion abilities of cells. 4. GRHL2 is a transcription factor that regulates epithelial cell identity and differentiation. 5. When overexpressed, GRHL2 can disrupt the balance of epithelial cell markers and induce EMT. |
| 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 | 3254(41) |
| 领域 | Bio-Medical |
| 用户问题 | Which T-UCRs have been implicated in lung cancer? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,5 |
| 模型回复 | Multiple T-UCRs (Tumor-Upregulated lncRNAs) have been implicated in lung cancer. Some of the notable T-UCRs associated with lung cancer include: 1. UCA1: Urothelial Carcinoma Associated 1. It is highly expressed in lung cancer tissues and has been shown to promote lung cancer cell growth, invasion, and metastasis. 2. HOTAIR: HOX Transcript Antisense RNA. It is upregulated in lung cancer and has been correlated with poorer prognosis. HOTAIR promotes tumor growth, invasion, and metastasis by interacting with various cellular signaling pathways. 3. CCAT2: Colon Cancer-Associated Transcript 2. Although initially associated with colon cancer, CCAT2 has also been found to be upregulated in lung cancer. It promotes lung cancer cell proliferation and invasion by regulating gene expression. 4. MALAT1: Metastasis-Associated Lung Adenocarcinoma Transcript 1. It is significantly upregulated in lung cancer tissues and is associated with advanced stages and poorer survival outcomes. MALAT1 promotes tumor growth and metastasis by regulating gene expression and promoting angiogenesis. These are just a few examples of the T-UCRs that have been implicated in lung cancer. Further research is being conducted to identify and understand the role of more T-UCRs in lung cancer development and progression. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. T-UCRs, or Tumor-Upregulated lncRNAs, have been implicated in lung cancer. 2. UCA1 is a T-UCR that promotes lung cancer cell growth, invasion, and metastasis. 3. HOTAIR, another T-UCR, promotes tumor growth, invasion, and metastasis in lung cancer. 4. CCAT2 has been found to be upregulated in lung cancer, despite its initial association with colon cancer. 5. MALAT1, a T-UCR, promotes tumor growth and metastasis in lung cancer and is associated with advanced stages and poorer survival outcomes. |
| 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 | 3268(42) |
| 领域 | Bio-Medical |
| 用户问题 | What is known about the orphan receptor GPR151? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,3,2 |
| 模型回复 | GPR151 is an orphan G protein-coupled receptor (GPCR), meaning its endogenous ligand and specific functions are still largely unknown. The receptor was first identified in 2001 through computational analysis of the human genome. Most of the available information about GPR151 comes from gene expression studies, primarily in the brain. GPR151 mRNA transcripts have been detected in various regions of the central nervous system, including the cerebral cortex, hippocampus, hypothalamus, and cerebellum. Studies have also highlighted the potential involvement of GPR151 in processes related to addiction and reward, as well as sleep regulation. GPR151 expression has been found to be altered in brain regions associated with drug addiction, suggesting a possible role in substance abuse and dependence. In addition, changes in GPR151 expression have been observed in the hypothalamus and brainstem during sleep deprivation, indicating its potential involvement in sleep-wake regulation. Despite these correlations, the specific ligands and downstream signaling pathways activated by GPR151 remain unknown. Further research is needed to characterize the endogenous ligands and to elucidate the functional roles of GPR151 in various biological processes. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. GPR151 is an orphan G protein-coupled receptor (GPCR). 2. The receptor GPR151 was first identified in 2001. 3. GPR151 mRNA transcripts have been detected in various regions of the central nervous system, including the cerebral cortex, hippocampus, hypothalamus, and cerebellum. 4. GPR151 expression has been found to be altered in brain regions associated with drug addiction. 5. Changes in GPR151 expression have been observed in the hypothalamus and brainstem during sleep deprivation. |
| 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 | 3285(43) |
| 领域 | Bio-Medical |
| 用户问题 | List the attenuated live viruses contained in the Fluzone intradermal quadrivalent vaccine. |
| 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 Fluzone intradermal quadrivalent vaccine contains attenuated live viruses for the following strains: 1. A/California/7/2009 (H1N1) 2. A/Hong Kong/2671/2019 (H3N2) 3. B/Washington/02/2019 (B/Victoria lineage) 4. B/Phuket/3073/2013 (B/Yamagata lineage) |
| 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 Fluzone intradermal quadrivalent vaccine includes an attenuated live virus for the A/California/7/2009 (H1N1) strain. 2. This vaccine also includes an attenuated live virus for the A/Hong Kong/2671/2019 (H3N2) strain. 3. An attenuated live virus for the B/Washington/02/2019 (B/Victoria lineage) strain is included in the Fluzone intradermal quadrivalent vaccine. 4. The vaccine also contains an attenuated virus for the B/Phuket/3073/2013 (B/Yamagata lineage) strain. 5. The Fluzone intradermal quadrivalent vaccine is used to protect against specific viral strains. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 2,2,2,2,1 |

|  |  |
| --- | --- |
| ID | 3345(44) |
| 领域 | Bio-Medical |
| 用户问题 | Which part of the TNFR2 gene is genetically associated with Systemic Lupus Erythematosus? |
| 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 TNFR2 gene, also known as tumor necrosis factor receptor superfamily member 1B (TNFRSF1B), has been shown to be associated with Systemic Lupus Erythematosus (SLE). Specifically, the single nucleotide polymorphism (SNP) rs1061622, which is located in the promoter region of the TNFR2 gene, has been identified as a potential genetic risk factor for SLE. |
| 回复标注（二选一）： 1-回复与问题相关 2-回复与问题不相关 | 1 |
| 提取的事实 | 1. The TNFR2 gene is also known as tumor necrosis factor receptor superfamily member 1B (TNFRSF1B). 2. The single nucleotide polymorphism (SNP) rs1061622 is located in the promoter region of the TNFR2 gene. 3. SNP rs1061622 has been identified as a potential genetic risk factor for Systemic Lupus Erythematosus (SLE). 4. The TNFR2 gene has been shown to be genetically associated with Systemic Lupus Erythematosus. |
| 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 |

|  |  |
| --- | --- |
| ID | 3353(45) |
| 领域 | Bio-Medical |
| 用户问题 | Is there a vaccine for peanut allergy? |
| 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 | As of now, there is no approved vaccine available for peanut allergy. However, there have been ongoing research and clinical trials exploring the development of a peanut allergy vaccine. These vaccine candidates aim to desensitize individuals to peanut allergens by gradually exposing them to increasing doses of peanut proteins. It is important to note that these vaccines are still in the experimental stages, and further studies are required to evaluate their effectiveness and safety. If you or someone you know has a peanut allergy, it is crucial to consult with a healthcare professional for appropriate management strategies. |
| 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. As of the given context time, there was no approved vaccine for a peanut allergy. 2. There is ongoing research and clinical trials for a peanut allergy vaccine. 3. The aim of these potential vaccines is to desensitize individuals to peanut allergens by gradually exposing them to increasing doses of peanut proteins. 4. The mentioned peanut allergy vaccines were still in the experimental stages at the time of this context. 5. It is crucial for people with a peanut allergy to consult a healthcare professional for management strategies. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 2,1,1,1,1 |

|  |  |
| --- | --- |
| ID | 3365(46) |
| 领域 | Bio-Medical |
| 用户问题 | What is particular about the mouse Fxy gene's chromosomal position? |
| 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 | The mouse Fxy gene is located on the X chromosome. This chromosomal position is significant because it makes the Fxy gene subject to X chromosome inactivation in females. X chromosome inactivation is a process in female mammals where one of the two X chromosomes is randomly inactivated in each cell to achieve dosage compensation between males and females. As a result, only one copy of the Fxy gene is active in female cells, while both copies are active in male cells. This has implications for the expression of the Fxy gene and its associated 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. The mouse Fxy gene is located on the X chromosome. 2. The chromosomal position of the Fxy gene makes it subject to X chromosome inactivation in females. 3. X chromosome inactivation is a process in female mammals where one of the two X chromosomes is randomly inactivated in each cell. 4. One copy of the Fxy gene is active in female cells due to X chromosome inactivation. 5. Both copies of the Fxy gene are active in male 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 | 7,7,1,1,7 |

|  |  |
| --- | --- |
| ID | 3397(47) |
| 领域 | Bio-Medical |
| 用户问题 | What is the basis of the methidiumpropyl-EDTA sequencing (MPE-seq) method? |
| 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 | The methidiumpropyl-EDTA sequencing (MPE-seq) method is based on the concept of sequencing DNA by incorporating reversible terminators. It employs a fluorescently labeled reversible terminator that blocks further DNA synthesis when incorporated into the growing DNA strand. In MPE-seq, the reversible terminator used is methidiumpropyl-EDTA (MPE), which is a reversible terminator with a fluorescent dye attached to it. The process starts with the template DNA being denatured into single strands. A DNA primer is then hybridized to the template strand, serving as the starting point for DNA synthesis. The sequencing reaction includes the DNA polymerase enzyme, dNTPs (deoxynucleotides), a fluorescently labeled MPE terminator, and divalent metal ions. During each sequencing cycle, a specific dNTP is added to the reaction mixture. If the complementary base is present in the template strand, the DNA polymerase will incorporate the dNTP and the fluorescently labeled MPE terminator. This incorporation halts further DNA synthesis. After each cycle, the reaction mixture is subjected to a laser excitation, causing the fluorescent dye attached to the MPE terminator to emit a signal. This signal is captured, and the fluorescent dye is removed, allowing the terminator to be cleaved off, enabling further DNA synthesis. By repeating this cycle for each base, the DNA sequence can be determined. The emitted fluorescent signals are detected and converted into nucleotide sequence information using specialized software and algorithms. |
| 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 methidiumpropyl-EDTA sequencing (MPE-seq) method is based on the concept of sequencing DNA by incorporating reversible terminators. 2. In MPE-seq, the reversible terminator used is methidiumpropyl-EDTA (MPE), which is a reversible terminator with a fluorescent dye attached to it. 3. The process of MPE-seq starts with the template DNA being denatured into single strands where a DNA primer then hybridizes to the template strand. 4. Each sequencing cycle in the MPE-seq method includes a DNA polymerase enzyme, dNTPs (deoxynucleotides), a fluorescently labeled MPE terminator, and divalent metal ions. 5. A laser excitation is used in MPE-seq to cause the fluorescent dye attached to the MPE terminator to emit a signal, which is then converted into nucleotide sequence information using specialized software and algorithms. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 7,7,7,7,7 |

|  |  |
| --- | --- |
| ID | 3400(48) |
| 领域 | Bio-Medical |
| 用户问题 | Which programming language has been used for implementing GWAR? |
| 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 GWAR (Generalized Word Alignment Repository) tool was implemented using the Python programming language. |
| 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. GWAR stands for Generalized Word Alignment Repository. 2. The Python programming language was used to implement GWAR. |
| 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 |

|  |  |
| --- | --- |
| ID | 3406(49) |
| 领域 | Bio-Medical |
| 用户问题 | Does xaliproden improve prognosis of amyotrophic lateral sclerosis? |
| 问题打分（逗号分隔）： 可读性（1-5） 规范性（1-5） 具体性（1-5） | 5,5,5 |
| 模型回复 | There is limited research and conflicting evidence regarding the effectiveness of xaliproden in improving the prognosis of amyotrophic lateral sclerosis (ALS). Xaliproden is a neuroprotective drug that has been studied as a potential treatment for ALS, but the results have been mixed. Some clinical trials have reported potential benefits of xaliproden, such as slowing the progression of disease and increasing survival rates. However, other studies have not found significant improvements in disease progression or survival. Overall, the current scientific evidence does not provide strong support for the use of xaliproden as a standard treatment for ALS. In most countries, xaliproden has not been approved for the treatment of ALS due to the lack of consistent evidence supporting its efficacy. It is important for individuals with ALS to consult with their healthcare providers for the most up-to-date and appropriate treatment options. |
| 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. Xaliproden is a neuroprotective drug that has been studied as a potential treatment for Amyotrophic Lateral Sclerosis (ALS). 2. Some clinical trials have reported that xaliproden may slow the progression of ALS and increase survival rates. 3. Other studies have reportedly not found significant improvements in disease progression or survival with the use of xaliproden. 4. Currently, scientific evidence does not firmly support the use of xaliproden as a standard treatment for ALS. 5. In most countries, xaliproden has not been approved for the treatment of ALS due to inconsistent evidence supporting its efficacy. |
| 事实标注 （每条事实八选一）： 1-完全正确事实 2-实体错误事实 3-关系错误事实 4-信息缺失事实 5-信息过时事实 6-表述绝对事实 7-无法验证事实 8-非事实表述 | 1,2,1,1,1 |