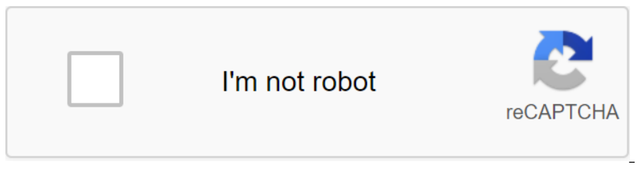
Foldit like games for android



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FolditScreenshot app Foldit, showing a folding puzzle in progressDeveloper (s)University of Washington, Center for Gaming Sciences, 12 years ago (2008-05-08)Preliminary releasePerpetual beta-operating systemCross platform: Windows, macOS, LinuxSize≈434 MBAvailable in13 LanguagesList of LanguagesCzech, Dutch, English, French, German, Hebrew, Indonesian, Italian, Polish, Romanian, Russian, Spanish, ScientistTypePuzzle video game, protein Licenseproprietary freeware for academic and non-commercial use. It is part of a pilot research project developed by the University of Washington, the Center for Gaming Sciences, in collaboration with the Department of Biochemistry at UW. The goal of Foldit is to fold the structures of the selected proteins as perfectly as possible using the tools provided in the game. The highest scoring solutions are analyzed by researchers, who determine whether there is a native structural configuration (native state) that can be applied to the corresponding proteins in the real world. Scientists can then use these solutions to target and eradicate disease and create biological innovation. In a 2010 paper published in the scientific journal Nature, 57,000 Foldit players received useful results that matched or surpassed algorithmically calculated solutions. David Baker, a researcher in protein research at the University of Washington, founded the Foldit project. Seth Cooper was the leading game designer. Before the project began, Baker and his lab colleagues relied on another research project called Rosetta to predict the native structures of different proteins using special algorithms to predict the structure of the computer protein. Rosetta was eventually expanded to harness the power of distributed computing: the program Rosetta@home was available for public download, and displayed its protein-folding progress as a screensaver. Its results were sent to the central server for verification. Some users Rosetta@home disappointed when they saw ways to solve protein structures, but were unable to interact with the program. Hoping that humans could improve computer attempts to solve protein structures, Baker turned to David Saalin and Soran Popovich, professors of computer science at the same university, to help conceptualize and build an interactive program, a video game that would appeal to the public and help find local protein structures. Many of the same people who created the Rosetta@home worked on Foldit. The public beta was released in May 2008 and has 240,000 registered players. Since 2008, Foldit has been involved in critical assessments of forecasting techniques белка (CASP), (CASP), solving problems based on unknown protein structures. CASP is an international program to evaluate methods for predicting protein structure and identifying the most productive. Predicting the structure of the target protein is important in several fields of science, including bioinformatics, molecular biology, and medicine. Identifying the structural configurations of natural proteins allows scientists to better understand them. This can lead to the creation of new proteins through design, advances in the treatment of diseases and solutions to other real problems such as invasive species, waste and pollution. The process by which living beings create the primary structure of proteins, protein biosynthesis, is well understood, as are the means by which proteins are encoded as DNA. However, it is more difficult to determine how the primary structure of this protein becomes a functioning three-dimensional structure, as the molecule folds up. The overall process is clear, but predicting a possible, functioning protein structure is computationally demanding. Similar to Rosetta@home, Foldit is a means of detecting local protein structures faster through distributed computing. However, Foldit pays more attention to collaboration with the community through its forums, where users can collaborate in certain folds. In addition, Foldit's crowdsourcing approach pays more attention to the user. Foldit's virtual interaction and gamification create a unique and innovative environment that can greatly advance the research of folding proteins. The Virtual Interaction Foldit tries to apply a three-dimensional pattern of human brain conformity and spatial reasoning abilities to help solve the problem of predicting the structure of the protein. 2016 puzzles are based on well-understood proteins. By analyzing how people intuitively approach these puzzles, the researchers hope to improve the algorithms used by the software to fold proteins. Foldit includes a series of tutorials where users manipulate a simple protein-like structure and a periodically updated set of puzzles based on real proteins. It shows a graphic representation of each protein that users can manipulate using a set of tools. The developers of Gamification Foldit wanted to attract as many people as possible to the reason for the folding of proteins. So instead of just creating a useful scientific tool, they used gamification (inclusion of game elements) to make Foldit attractive and appealing to the public. As the protein structure changes, the score is calculated based on how well the protein is complex, and the list of high scores for each puzzle is maintained. Foldit users can create and join groups, and groups can share puzzle solutions. The teams have proved useful for training new players. A separate list of group high scores is maintained. Achievement Results foldit have are included in a number of scientific publications. Foldit players have been cited collectively as Foldit players or Players, F. In some cases. Individual players were also listed as authors on at least one paper, and on four protein-related deposition pot data. In An August 2010 paper published in the journal Nature, 57,000 Foldit players received useful results that matched or surpassed algorithmically calculated solutions, stating, Layers are working together to develop a rich range of new strategies and algorithms; Unlike computational approaches, they explore not only the conformal space, but also the space of possible search strategies. In November 2011, an article in PNAS compared recipes developed by Foldit players to Rosetta scenarios developed by Baker Laboratory staff at the University of Washington. The blue fuse recipe developed by the player compares favorably with the algorithm of scientists Fast Rest. In 2011, Foldit players helped decipher the crystalline structure of the retroviral protease of the Mason-Pfizer monkey virus (M-PMV), a monkey virus that causes symptoms similar to HIV/AIDS, a scientific problem that has been unresolved for 15 years. While the puzzle was available for three weeks, players produced a 3D model of the enzyme in just ten days, which is accurate enough for a molecular replacement. In January 2012, Scientific American magazine reported that Foldit gamers had achieved the first crowdsourcing redesign of a protein, an enzyme that catalyzed Diels-Alder reactions, widely used in synthetic chemistry. The team, including David Baker at the Center for Game Sciences at the University of Washington in Seattle, computationally developed the enzyme from scratch, but found that its potency needed improvement. Foldit players reintroduce the enzyme by adding 13 amino acids, increasing its activity by more than 18 times. The article, published in September 2016 in the journal Nature Communications, details the competition for building crystallographers between trained crystallographers, students, Foldit players, and automatic model-building algorithms, in which the Foldit team has reached the most accurate structure suitable for protein, to the results of the X-ray crystallography experiment. In July 2018, the journal Nature Communications examined the collaboration of Foldit players and teams in the WeFold consortium in the two-year CASP CASP11 and CASP12 competitions. The letter, written in June 2019 in the journal Nature, describes an analysis of proteins developed by Foldit players. Four of the player's developed proteins were successfully grown in E. coli and then solved with X-ray crystallography. Proteins were added to the Protein Data Bank as 6MRR, 6MRS, 6MSP and 6NUK. In November 2019, in an article in the journal Biology reported that Foldit players were able to more accurately build protein structures into high-resolution crystallographic maps expert crystallographers or automated algorithms for building models using data from cryo EM experiments. The future development of Foldit's toolkit is mainly for the development of protein molecules. The game's creator announced a plan to add chemical building blocks to organic subcomponents by 2013 so that players could develop small molecules. Cm. also Civic Science Rosetta@home EteRNA Eyewire Folding@home Human-based computational game Molecular Graphics Comparison Software for Molecular Mechanics Modeling Predictor@home quantum moves protein structure prediction protein structure Protein structure prediction protein structure Of Serious Game Links - University of Washington, Center for Gaming Sciences - University of Washington, Department of Biochemistry - b c Mark J In a video game, combat the complexities of protein folding. The New York Times. Received on February 12, 2013. Cooper S, Khatib F, Treuille A, Barbero J, Lee J, Beenen M, et al (August 2010). Predicting protein structures with a multiplayer online game. Nature. 466 (7307): 756–60. Bibkod:2010Natur.466. 756C. doi:10.1038/nature09304. PMC 2956414. PMID 20686574. Rosetta Commons: Rosetta Simulation Software Center. RosettaCommons.org. RosettaCommons.org. 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