

**THE REPUBLIC OF TURKEY
MUGLA SITKI KOCMAN UNIVERSITY
GRADUATE SCHOOL OF NATURAL AND APPLIED
SCIENCES**

BIOINFORMATICS GRADUATE PROGRAM

**A COMPUTATIONAL APPROACH FOR PREDICTING
HOST SPECIFICITY OF ADENOVIRUSES**

MASTER THESIS

ONUR CAN KARABULUT

JUNE 2020

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MUGLA SITKI KOÇMAN ÜNİVERSİTESİ

Fen Bilimleri Enstitüsü

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ÖZET
ADENOVİRÜSLERİN KONAK ÖZGÜLLÜĞÜNÜ TAHMİN ETMEDE
KULLANILACAK BİR HESAPLAMA YÖNTEMİ

Onur Can KARABULUT

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Adenovirüsler, DNA sekansını ve çekirdek proteinlerini çevreleyen karmaşık bir protein kılıfından oluşan büyük virüslerdir. Adenoviridae adlı geniş bir aileye mensupturlar ve birçok omurgalıyı enfekte edebilen yüzlerce üyesi vardır. İnsan, insan olmayan primat, yarasa, kedi, köpek, domuz, koyun ve keçi türleri arasındaki adenovirüslerin bu türler arasındaki geçişleri bilinmektedir. Adenovirüs konakçı özgüllüğünü ve türler arası virüs bulaşma tahminini anlamak, adenovirüslerin neden olduğu enfeksiyonların tedavisinde önemlidir.

Bilinen adenovirüslerin yaklaşık elli tanesi insanı enfekte eder ve bazen ciddi, gastrointestinal, solunum, idrar ve kornea enfeksiyonlarına neden olabilir. Enfeksiyonun başlaması için adenovirüsler, tipik olarak bir konakçı hücre reseptörü ve AdV fiber proteini arasında bir bağlanma ile başlatılan, konakçı hücrelerle karmaşık bir etkileşim dizisi oluştururlar. Bu nedenle, reseptör ve lif proteinleri arasındaki protein-protein etkileşimlerini (PPE) anlamak, belirli bir adenovirüsün konakçı özgüllüğünü tahmin etmek için bir model geliştirmeye yönelik önemli bir adımdır.

Bu çalışmada amacımız, bir adenovirüsün konak özgüllüğünü tahmin etmek için bir çalışma dizini oluşturmaktır. Bu amaçla, önce bir literatür taraması yapılmıştır ve adenovirüslerin hücre içine alımına katılan tüm insan reseptörleri belirlenmiştir. Daha sonra, diğer adenovirüs konak türlerinden insan reseptör ortologları hesaplanmıştır. Ardından, farklı konak türleri enfekte eden çeşitli adenovirüslerden elde edilen bir lif proteinleri kütüphanesi oluşturuldu. Son olarak, adenovirüslerin konak özgüllüğünü öngören bir meta-sınıflandırıcı geliştirildi. Sınıflandırıcıda kullanılan veri nesneleri, mevcut PPE tahmin yöntemleri, yani VHPPI, HOPITOR ve DeNovo ile konak reseptör-fiber protein etkileşimleri için hesaplanan tahminlerdir. Bu veri nesneleri için, taksonomik düzey türleri, cinsi, ailesi ve takımında aynı taksayı paylaşan aday konak ve adenovirüs'ün bilinen konağına dayalı olarak dört farklı sınıf etiketi hesaplanmıştır.

Meta-sınıflandırmada birçok topluluk makinesi öğrenme yaklaşımı test edilmiştir. İstifleme grubu sınıflandırıcıları en iyi doğrulukları vermiştir. İstifleme için J48 karar

ağacı, Naive bayes, çok katmanlı algılayıcı, rastgele orman ve destek vektör makinesi algoritmaları test edildi. Sınıflandırıcıların performansı birbirine yakındır ve J48 karar ağacı biraz daha iyi olmuştur (Doğru pozitif oran:% 71.5, doğru negatif oran% 71.5 ve doğruluk % 71.0).

Bu çalışmada, adenovirüslerin konak özgüllüğünün öngörülmesinde bir grup PPE tahmin yöntemlerinin kullanılmasının potansiyelini ve doğruluğu gösterilmiştir. Adenoviridae fiber proteininin ve bilinen konak reseptör proteinlerinin çeşitliliği, çalışma dizininin geliştirilmesinde bir zorluk yaşatmıştır. Sonuçlarımız, daha doğru türler arası PPE tahminlerine ihtiyaç olduğunu göstermektedir. Gelecekte, konaklar arası geçişlerin erken tespiti veya adenovirüslerin konak özgüllüğünün değerlendirilmesi için çalışmalarımızın geliştirilebileceğini öngörüyoruz. Ayrıca, yaklaşımımız Adenoviridae dışındaki diğer virüs ailelerine yayılma potansiyeline sahiptir ve bu, özellikle son yıllardaki konaklar arası geçişlerle ilişkili viral hastalık salgınlarındaki artışı göz önüne alındığında, önem teşkil etmektedir.

Anahtar Kelimeler: Adenovirüs, Virüs Reseptörü, Protein-Protein Etkileşimi (PPE), Protein-Protein Etkileşim Tahmini, Konak-Virüs Etkileşimleri

ABSTRACT
**A COMPUTATIONAL APPROACH FOR PREDICTING HOST
SPECIFICITY OF ADENOVIRUSES**

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Adenoviruses are large viruses that consist of a complex protein cover enclosing its DNA sequence and core proteins. They belong to a large family called *Adenoviridae* with over hundred known members that can infect extensive range of vertebrates. The cross-species transmissions of adenoviruses between human, non-human primate, bat, cat, dog, pig, sheep and goat species are known. Understanding adenovirus host specificity and prediction of cross-species virus transmissions are important in the management of infections caused by adenoviruses.

Nearly fifty of known adenoviruses infect human and can cause, sometimes serious, gastrointestinal, respiratory, urinary, and corneal infections. For the infection to start, adenoviruses establish a complex set of interactions with host cells, typically initiated by a binding between a host cell receptor and adenovirus fiber protein. Hence, understanding protein-protein interactions (PPIs) between receptor and fiber proteins, is an essential step towards developing a model to predict host specificity of a given adenovirus.

In this work, our goal was to create a pipeline to predict host specificity of an adenovirus. For this purpose, we, first, conducted a literature review and identified all human receptors that are involved in the uptake of adenoviruses. Next, we computed human receptor orthologs from other adenovirus host species. Then, we computed a library of fiber proteins from various adenoviruses infecting different host species. Finally, we developed a meta-classifier predicting host specificity of adenoviruses. The data objects used in the classifier were the predictions computed for host receptor-fiber protein interactions by the existing PPI prediction methods, namely VHPPI, HOPITOR and DeNovo. For these data objects, four different class labels were computed based on candidate host and adenovirus's known host sharing the same taxa at taxonomic levels species, genus, family, and order.

Several ensemble machine learning approaches were tested in meta-classification. The stacking ensemble classifiers gave the best accuracies. For stacking, we tested J48 decision tree, naïve bayes, multilayer perceptron, random forest, and support vector machine algorithms. The performance of classifiers were close the each other

with J48 decision tree being slightly better (True positive rate:71.5%, true negative rate 71.5% and 71.0%).

In this work, we demonstrated the potential and accuracy of using an ensemble PPI prediction methods in prediction of host specificity of adenoviruses. The diversity of *Adenoviridae* fiber and known host receptor proteins posed a challenge in the development of the pipeline. Although our results are quite promising, they also suggest the need for more accurate cross-species PPI predictions. In the future, we anticipate our work can be leveraged and improved for early detection of host shifts or in assessment of host specificity of adenoviruses. Furthermore, our approach has the potential to be extended to other virus families beyond *Adenoviridae* and this is particularly significant, given the rise in viral disease epidemics involving host shifts in recent years.

Keywords: Adenovirus, Virus Receptor, Protein-Protein Interaction(PPI), Protein Protein Interaction Prediction, Host-Virus Interactions



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LIST OF ABBREVIATIONS AND SYMBOLS

PPI	Protein-Protein Interaction
UniProtKB	Universal Protein Knowledgebase
CAR	Coxsackievirus and Adenovirus Receptor
CD46	Cluster of Differentiation 46
CD80	Cluster of Differentiation 80
CD86	Cluster of Differentiation 86
ITAV	Integrin alpha-V
DNA	Deoxyribonucleic acid
WHO	World Health Organisation
CDC	Centers for Disease Control and Prevention
ITR	Inverted Terminal Repeat
SVM	Support Vector Machine
NCBI	National Center for Biotechnology Information
PDB	Protein Data Bank
AdV	Adenovirus

1. INTRODUCTION

Adenoviruses are large viruses that consist of a complex protein cover enclosing its DNA sequence and core proteins. The structure of the cover lately has been identified. The cover is icosahedral. The faces are consist of 240 hexons, each consist of three identical proteins, and 12 pentons takes part on the corners, each consists of five protein chains. A long fiber extends from each vertex, consist of three identical chains. These chains form a knob at the end.

Over 100 antigenic sorts of adenoviruses that can infect extensive range of vertebrates including mammals (mastadenoviruses), birds (aviadenoviruses), and even reptiles, are identified. There are 47 confirmed human adenovirus types and 5 more candidate types that are currently emphasized on. Adenoviruses infect various human tissues including gastrointestinal, respiratory, urinary, and corneal.

Adenoviruses entry into cells happens by direct influence of the plasma membrane by mechanisms of uptake into cells like endocytosis. They attach to a primary receptor such as the coxsackie virus AdV receptor (CAR) with the fiber protein. The CAR-related particles activate coreceptors and this precipitates a variety of cell responses (e.g. endocytosis). A second endocytic duration is stimulated synchronously with viral uptake, macropinocytosis. Together, these pathways are relevant to viral infection.

The variety of adenovirus receptors and fiber proteins that interacts with these receptors are associated with organism-specificity and tissue-specificity. Because, every adenovirus does not interact with every organism or tissue.

The main objective in this study was to determine host receptor-adenovirus fiber protein interactions that leads to adenoviruses' host organism-specificity. Our specific aims include:

- To identify host receptors and adenovirus fiber proteins spanning several host organisms and adenovirus strains

- To develop methods to predict host receptor-adenovirus fiber protein interactions and, through which, determining potential pathogenicity of an adenovirus strains for a given host

In relation to these specific aims, our final product includes:

- A list of host receptors contributing to adenovirus intake and their orthologs in other adenovirus host organisms.
- A list of fiber proteins from various adenovirus strains infecting different host organisms.
- An ensemble machine learning classifiers that predict host specificity of an adenovirus using PPI predictions computed for fiber protein and host receptors.

We anticipate this work will be the potential to be extended to other virus families beyond Adenoviriade and this is particularly significant, given the recent rise in viral disease epidemics involving host shifts.

2. SUBJECT AND SCOPE

In recent years, due to developments in high throughput experimental techniques and funding agencies' mandate for dissemination of data, large volumes of life sciences data in various formats spanning many experiment data types, experimental conditions and organisms became available through public databases. The abundance of data lead to opportunities to integrate, reanalyze and potentially discover new knowledge; *in silico life sciences research* where the term silico refers to silicon used in modern computer chips and *in silico* refers to tasks (or experiments) performed using computers. This new research area will become increasingly important with the pace of data expansion.

In silico studies in molecular biology have the potential to speed the rate of discovery while decreasing the need for costly lab work and clinical trials. Presence of proteome information of many organisms in public databases has increased the number of *in silico* studies. For example, viral diseases, which are very common in recent years, have become very dangerous for human health. It has led scientists to find solutions to diseases caused by these viruses. Viruses have a very large family. One of these families is Adenoviruses.

Adenoviruses are well characterized viruses and are gaining increasing interest, in recent years, due to their therapeutic/biotechnology uses and public health impact. For instance, only the Centers for Disease Control and Prevention (CDC) in United States, released over 2000 notices about adenovirus infection outbreaks. Similarly, the World Health Organization (WHO), reported thousands of adenovirus infection outbreaks worldwide. The increasing interest in adenoviruses is also reflected in, almost doubled number of in last two decades, PubMed indexed publications about Adenoviruses (Figure 1).

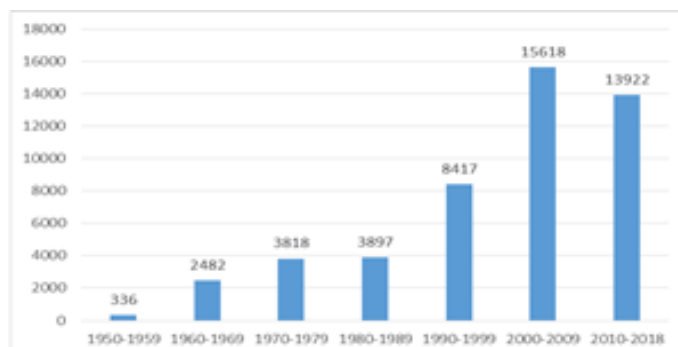


Figure 1. The number of PubMed-indexed publications about adenoviruses since 1950s

Although there is increasing interest in adenoviruses and the adenoviruses mechanism of infection is mostly known, there is still limited work on understanding the host specificity of adenoviruses in relation to host receptor and adenovirus protein interactions. Identification of key factors contributing to adenovirus host specificity and prediction of adenovirus pathogenicity for a host have public health impact. In this study, we will investigate host receptor- adenovirus fiber protein interactions that leads to adenoviruses' host organism-specificity. For this purpose, we will first identify host receptor and adenovirus fiber proteins spanning several host organisms and adenovirus strains. Then, we will identify sequential regions that play role in host receptor and adenovirus fiber protein interactions. Leveraging our findings on key sequential regions, we will develop methods to predict host receptor-adenovirus fiber protein interactions and we will determine potential pathogenicity of an adenovirus strains for a given host.

3. LITERATURE REVIEW

3.1 Adenovirus Overview

Adenoviruses are from the family *Adenoviridae*. They have icosahedral cover that composed of 240 non-vertex capsomers (hexons). It is 8-10 nm in diameter. Also, it has 12 vertex capsomers (penton bases) that each with a fiber sticking out from the virion surface (Figure 2). This situation gives the characteristic morphology to the virion. Penton base and fiber together form the penton. The studies so far revealed that the length of fibers between 9 and 77.5 nm. Adenoviruses (AdVs) are non-enveloped DNA viruses. The adenovirus genome is a single linear molecule of double helix DNA (26163–48395 bp). This DNA contains an inverted terminal repeat (ITR) of 30-371 base pairs at its termini, with the 5' ends of each DNA strand. The DNA strand that ends up with 5', linked covalently to a virus-coded terminal protein. Approximately 40 varied polypeptides are generated. Most of these polypeptides are part of the splicing mechanism. The nucleotide compounds consist of 33.6–67.6% guanine and cytosine. The central part of the genome is maintained throughout the family, however the terminal parts show large variations in length and gene substance (International Committee on Taxonomy of Viruses, 2017).

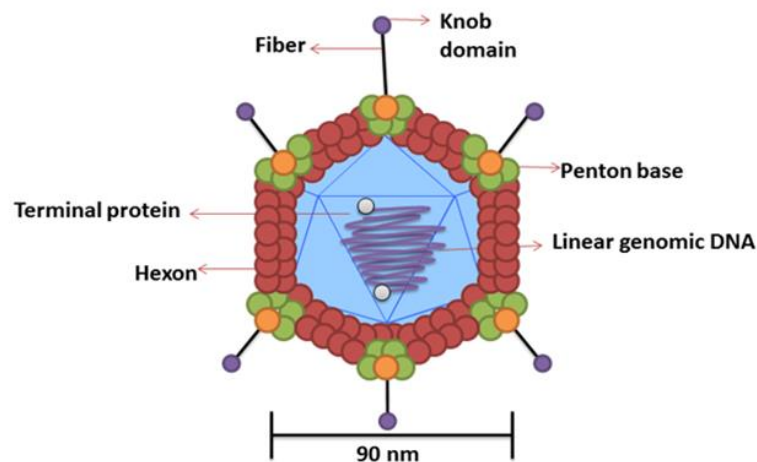


Figure 2. Cellular form of Adenovirus (International Committee on Taxonomy of Viruses, 2017)

Over 100 antigenic types of adenoviruses infect a diverse set of organisms including mammals (mastadenoviruses) and birds (aviadenoviruses). Specifically for human, there are 47 human adenovirus types that are classified, and there are also 5 more candidate types that are currently studied. There is a wide range of infection caused by adenoviruses in humans. For example; Bronchitis, colds and other respiratory diseases, croup, ear infection, pink eye, pneumonia, stomach and intestinal infection, swelling of the brain and spinal cord, urinary tract infections etc. They can be fatal, especially in immunocompromised (eg. organ transplant) or weak people (Wold et al. 2013). In addition to the negative health effects of adenoviruses, their medical use is gradually increasing. Adenovirus vectors have been evaluated as safe and tolerable in many clinical studies. They are immunogenic to support their medical use (Wold et al. 2013).

3.2 Mechanism of Adenovirus Infection

Human AdVs attachment to the host cells is triggered by a close interaction between a host cell receptor and AdV fiber knob domain Human AdV types interact with receptors such as CAR (coxsackie adenovirus receptor). It belongs to the immunoglobulin superfamily. (Coyne & Bergelson, 2005, 2006; Philipson & Pettersson, 2004). In a infection this will probably happen through an aerosol into either the respiratory or gastrointestinal tracts, the conjunctiva or oropharynx. AdV uptake happens via endocytosis supported by secondary interactions of the penton base with α v integrins (Wickham, 1993). Simultaneously, fractional disassembly of the virus particle in which the vertex proteins (e.g. penton base) are released into the acidified environment of the early or late endosome. The human Adenovirus disassembly is not extensively characterized yet. However scientists hypothesized the release of the internal capsid protein pVI at this phase ease the endosomalysis allowing entry of the uncoated particle into the cytoplasm. The N-terminal area of pI includes a predicted amphipathic α -helical domain. This area is a motif that is known to communicate with cell membranes. Pruning of this ~20 residue domain ablates membrane deterioration (Wiethoff, 2005). After endosomalysis, interaction between partly uncoated Ad particles and microtubule motors carry out vectorial transport to

the nucleus through microtubules (Suomalainen, 1999). Cell entry ends with the passage of the viral nucleic acid to the nuclear pore. In AdV infection mechanism, initial host receptor-and AdV fiber protein interaction (PPI) plays important role as the whole process starts with this critical interaction.

3.3 Protein-protein Interaction

Proteins usually act together. Many molecular processes within a cell are carried out by molecular machines that are built from numerous protein components organized by their PPIs. PPI networks are one of the most important source for understanding the biological processes, including cell-to-cell interplays and metabolic and developmental tracking. There are lots of experimental methods to determine these interactions. For example; affinity chromatography, tandem affinity purification, mass spectrometry, yeast-to-hybrid etc. These aforementioned methods are example of in vivo and in vitro methods. However, these methods have their own limitations like time, cost and so on. For this reason, scientists created in silico methods. These methods include sequence-based approaches, structure-based approaches and so on. (Zahiri, 2013) Clarifying of protein interaction networks also helps to understand analysis of signal transduction pathways. Thanks to computational methods, scientists have all the PPI networks for signaling pathways and protein complex identification in specific diseases.(Rao, 2014).

Databases were created to store PPIs that made large PPI data from various organisms available and accessible. There are more than 100 PPI related repositories that are available online. Some of the rather central and prominent examples includes;

- BioGRID - the General Repository for Interaction Database (<https://thebiogrid.org/>)
- DIP - The Database of Interacting Proteins (<https://dip.doe-mbi.ucla.edu/dip/Main.cgi>)
- BIND - The Biomolecular Interaction Network Database (<http://www.bind.ca/>)

- MINT - The Molecular Interaction Database (<https://mint.bio.uniroma2.it/>)
- HPRD - The Human Protein Reference Database (<http://www.hprd.org/>)
- IntAct - Molecular Interaction (<https://www.ebi.ac.uk/intact/>)

More or less, they serve the same purpose but in terms of functionality, number of proteins, number of organisms, number of experiments, and number of human interactions are different from each other. (Taghizadeh, 2015). Due to funding shortages, only protein-protein interactions with new organisms are added regularly to IntAct, STRINGDB and BioGRID. These databases, although partially contained, have not been specifically developed for virus-host PPIs. With the increasing importance of viruses, virus-host PPI databases such as Viruses.STRING (Cook et al. 2018), VirusMentha (Calderone et al. 2015) and VirHostNet (Girimand et al. 2015) have been developed.

PPI estimation tools have also been developed with the support of computable and up-to-date data. Approaches such as Struct2Net (Singh vd. 2010), Coev2Net (Hosur vd. 2012), PRISM (Tuncbag vd. 2011), which make PPI estimation using protein shapes (or models) in this area, as well as HomoMINT (Perciso et al. 2005) estimating PPIs based on the domain architecture of their existing proteins. These PPI prediction approaches focus more on predicting PPIs within an organism, but viral infections begin with inter-organism (virus and host) protein interactions. For this reason, methods of estimating PPIs between virus and host have recently become available.

3.4 Methods to Predict Protein-Protein Interaction Between Virus and Host

Viral infection contains numerous protein-protein interactions (PPIs) between virus and its targeted host. Hence, to understand mechanism of viral infections we should identify protein-protein interactions (PPIs) between virus and its host. In the past, several computational methods have been developed to predict PPIs. However, these developed methods aimed PPIs within species but not predicting inter-species PPIs. Recently, focus also shifted to computational methods have been developed to identify virus-host PPIs using by machine learning methods. For example, Beccera et

al. developed an algorithm that predicts human and HIV 1 virus interactions, assuming that the virus should naturally bind to the host receptor and mimic short linear motifs of host proteins. In addition, DeNovo virus-host PPI prediction model uses support vector machines (SVM) on amino acid sequence similarity-based features. However, the similarities between different types of viruses or hosts are relatively low. Therefore, the prediction sequence-similarity based predictions of virus-host PPIs has limitations. In an alternative method, for various viruses and host organisms, Naïve Bayes, Random Forest and SVM methods are employed on the feature vectors computed based on amino acid compositions of interacting host and virus proteins. (Zhou, 2018). Similarly, Barham et al. applied various machine learning classification algorithms and predicted PPI's with an accuracy of $> \sim 71\%$ to the attributes obtained from the amino acid compositions of proteins and the patterns in the interaction networks obtained from the VirusMINT database (Barham et al. 2014). Alguwaizani et al. has managed to predict PPI's in test sets with $\sim 84-92\%$ accuracy using SVM in the attributes it extracts from amino acid with repetitive patterns in proteins compositions (Alguwaizani et al. 2018).

4. ORIGINAL VALUE

Most of the emerging diseases in humans are zoonoses, that is, pathogens including viruses that cause infections are of animal origin (Taylor et al. 2001). In recent past, the cross-species transmission of viruses has created serious public health cases such as bird flu, HIV, SARS and Ebola. The identification of high-risk pathogens that can be passed on to human beings as hosts is important in the precautionary measures and management of the situation (avoidance, drug distribution, resource transfer, etc.) (Flanagan et al. 2012). Transition between species is very common in viruses and plays a significant role in the evolution of viruses (Geoghegan et al. 2017).

Adenoviruses belong to a family whose host cell-virus protein relationships and infection mechanisms are known. Transitions of adenoviruses between human, non-human primate, bat, cat, dog, pig, sheep and goat species have been identified and there is evidence that they will continue to cross species barriers (Borkenhagen 2019). The prediction of host specificity and cross-species transitions of adenoviruses is important in the management of infections caused by. On the other hand, in some cases, it may be desirable to know the transferability of Adenovirus. For example, in the last 40 years, Adenoviruses have been used as vectors in many clinical studies (Mennechett 2019). Adenoviruses that are used in humans and from other hosts (such as monkeys) can infect human cells, which may be important for their use, such as gene therapy. In both cases, as suggested in this project, a bioinformatics system needs to be developed to minimize the number of costly in vitro / vivo experiments to minimize the life of experimental creatures and / or to predict host specificity or interspecific transitions.

The novel aspects of the bioinformatics system to be developed in this project are as follows:

- There is no integrated system in the literature that provides estimation of host specificity or cross-species transitions of adenoviruses and even any virus. The

system developed in the project is the first study on this theme for Adenoviruses and is adaptable to other viruses.

- Current virus-host PPI prediction algorithms are not sufficient to reduce the number of false positive PPIs by making use of virus or host biology in PPI predictions. Limiting PPI predictions proposed in the project on Adenovirus fiber and host receptors is a unique approach to overcome this deficiency.
- There is no comprehensive dataset that includes Adenovirus host species, Adenovirus host receptors of these species, and Adenovirus fiber proteins that are probably to interact with these receptors. The project is unique in terms of compiling this dataset and the extensibility of the compilation process to additional host receptor or virus proteins.

5. METHODS

We developed a bioinformatics system to predict host specificity of adenoviruses in multiple steps (Figure 2); 1) the human adenoviruses are identified using public databases and the literature, 2) the known host organisms for adenoviruses are identified, 3) host adenoviruses from the known host organisms are identified, 4) fiber proteins in various adenoviruses are identified, 5) virus-host PPI's for receptor-fiber proteins pairs are computed using different prediction algorithms, finally 6) several techniques are applied to create a meta-predictor combining virus-host PPI predictions to assess host specificity (i.e. infection capacity for a given host) of a given adenovirus. The details of methods employed in these steps are detailed in following sections.

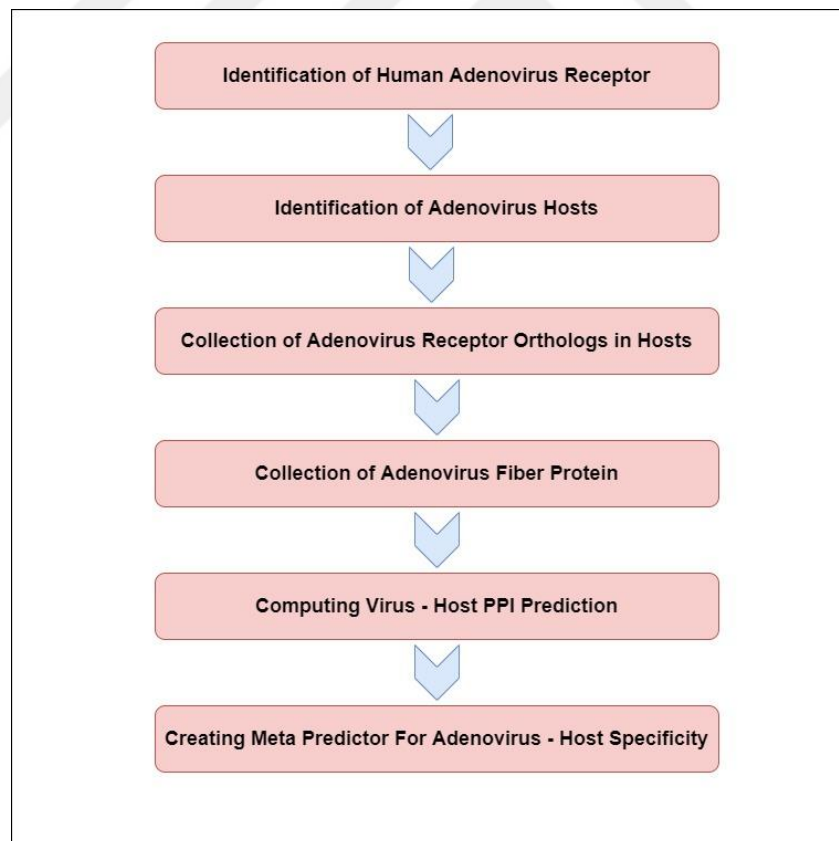


Figure 3. The steps followed in creation of the bioinformatics system

5.1 Identification of Human Adenovirus Receptors

Human Adenovirus receptors are better characterized than other hosts. Because this and the most striking result in our research are predictions of adenoviruses penetrating the human host, we began this work package by creating a cluster of Human Adenovirus receptors. Human Adenovirus receptors and their isoforms were searched in UniProt Knowledgebase (UniProt Consortium 2019) and NCBI RefSeq (O'Leary et al. 2016), which are public databases. Human proteins in these databases were searched with keywords such as "adenovirus", "adenovirus receptor", "adenovirus AND receptor." Among them, those with a cellular location of cell membranes were filtered and receptor candidates were identified. Candidate receptors have been confirmed by scanning the literature. In addition, PubMed was scanned with the "adenovirus receptor" and "human" keywords to cover the Adenovirus research results, which have taken place in the last 5 years and have not yet been curated in public databases. Isoforms (may be secreted isoforms) on the cell membrane of all identified receptors were found in the UniProt Knowledgebase and added to the list of receptors. As an intermediate output from this step, it is aimed to create a list containing all human Adenovirus receptor protein sequences and associated FASTA files.

5.2 Identification of Adenovirus Hosts

The species belonging to the "Adenoviriade" family in the UniProt Knowledgebase were used to identify host species. In UniProtKB, "Virus Hosts" information is curated in some of the proteins in the "Adenoviriade" family (eg. UniProt: P03286). In the absence of this information, parsers were written and used to find hosts from the name of the virus. There are cases when "Virus Hosts" information is usually given in old records at the "genus" level (eg. UniProt: Q64762) and they were excluded from the dataset. All proteins of the identified host species were downloaded from the UniProt Knowledgebase. A list of host species and FASTA files, each containing proteins, were created as intermediate output from this step.

5.3 Collection of Adenovirus Receptor Orthologs in Hosts

Ortholog databases OrthoDB (Zdobnov 2017) and OMA (Altenhoff 2018) were used to find the orthologs of human Adenovirus receptors in other hosts. However, we have evaluated the under-studied species and proteins of these databases and the possibility of not including orthologs of isoforms. In terms of inclusion, we used BLAST (Altschul et al. 1990) in Adenovirus host protein clusters that we compiled Human Adenovirus proteins at this step. At this point, we added proteins that were not caught in ortholog databases, aligned to human Adenovirus receptors, low e-value (Ex. $<1e-20$) and high overlap (Ex. $> 66\%$). To confirm this step, we checked the presence of the most known CAXR receptor in all mammals whose proteomas were completed. As an intermediate output from this step, it is aimed to create FASTA files containing the proteins of the host species taxonomy and adenovirus receptors. In the preliminary studies related to this work package, only 297 host organism candidates were identified in UniProtKB, including genus level taxa. Again, 200 receptor candidates were identified as a result of UniProtKB database searches, they were examined and a list containing five receptors named CXAR, CD46, CD80, CD86, ITAV and isoforms was prepared.

5.4 Creation of Adenovirus Fiber Protein Library

In this step, a comprehensive dataset containing 1) adenoviruses' fiber proteins interacting with host cell receptors that trigger virus's entry into the cell, 2) the respective host and host cell receptors is created.

The adenovirus fiber protein candidates are curated from the UniProt Knowledgebase and RefSeq protein databases. There were inconsistencies in the naming of Adenovirus fiber proteins in public protein databases. "Fiber", "Fiber", "Fiber protein", "Fiber homolog", "Fiber-1 protein", "protein fiber" etc. Therefore, in this step, keywords such as "fiber", "fiber protein", "fiber" were used to search for fiber protein candidates.

To account for unannotated fiber proteins (i.e. categorized as uncharacterized protein), BLAST is used to query a database of all adenovirus sequences using the curated fiber proteins using the same e-value and overlap thresholds described in Section 5.3.

5.5 Computing Virus-Host PPI Predictions

The output of this step is a tool that generates a final prediction by combining the results of multiple singular algorithms that predict PPI between two given proteins, one belonging to the Adenovirus fiber protein and the other to the host receptor.

The steps of this work package and the results of the related work we have done are as follows.

- We created a feature vector from the result of each virus - host PPI predictor. This feature vector is of size 15 (3 x 5; the number of PPI predictors X number of receptors). The three PPI predictors used were VHPPI (Alguwaizani et al. 2018), HOPITOR (Basit et al. 2018) and DeNovo (Eid et al. 2016). The five receptors used was CXAR, CD46, CD80, CD86 and ITAV. The vector is further extended with class labels computed based on adenovirus's known host and candidate host's sharing the same taxa at different taxonomic levels; species, genus, family and order. For instance; if the adenovirus is a human adenovirus and candidate host is human, then the class label at all taxonomic levels will be 1. In another example, for a simian adenovirus and host candidate being human, while organism and genus level class labels will be 0, family and order level class labels will be 1. The motivation behind using different taxonomic levels was to assess our systems' capacity in assessing cross-species, cross-genus, cross-family and cross-order host jumps.
- We also grouped and combined the PPI predictions for each of the 5 AdV receptors, namely CXAR, CD46, CD80, CD86 and ITAV in various ways.
 - **CXAR_ALL_ONE, CXAR_MAJORITY, CXAR_JUST_ONE**
 - **CD46_ALL_ONE, CD46_MAJORITY, CD46_JUST_ONE**

- **CD80_ALL_ONE, CD80_MAJORITY, CD80_JUST_ONE**
- **CD86_ALL_ONE, CD86_MAJORITY, CD86_JUST_ONE**
- **ITAV_ALL_ONE, ITAV_MAJORITY, ITAV_JUST_ONE**

where

- **[RECEPTOR]_ALL_ONE (e.g. CAXR_ALL_ONE):** These are the situations where the three predictors that we used find interaction between AdV receptor and fiber protein.
- **[RECEPTOR]_MAJORITY(e.g. CAXR_MAJORITY) :** These are the situations where at least two predictors that we used find interaction between AdV receptor and fiber protein.
- **[RECEPTOR]_JUST_ONE(e.g. CAXR_JUST_ONE):** These are the situations where just one predictor that we used find interaction between AdV receptor and fiber protein.

5.6 Creating Meta-Predictor for Adenovirus Host Specificity

We employed voting based approaches and machine learning based techniques to combine individual or grouped PPI predictions described in Section 5.5 to create a meta-predictor for adenovirus host specificity.

In the voting-based approach, the [RECEPTOR]_ALL_ONE, [RECEPTOR]_MAJORITY and [RECEPTOR]_JUST_A_ONE are evaluated as follows:

- **INFECTION_ALL_ONE:** If at least one [RECEPTOR]_ALL_ONE value is 1, then the adenovirus has the potential to infect the host. In other words, for at least one host receptor, if all of the PPI prediction tools support an interaction between a host receptor and adenovirus fiber protein, then the respective adenovirus has the potential to infect the host.
- **INFECTION_MAJORITY:** If at least one [RECEPTOR]_MAJORITY value is 1, then the adenovirus has the potential to infect the host. In other words, for at least one host receptor, if the majority of the PPI prediction tools support an interaction between a host receptor and adenovirus fiber protein, then the respective adenovirus has the potential to infect the host.

- **INFECTION_JUST_ONE:** If at least one [RECEPTOR]_JUST_ONE value is 1, then the adenovirus has the potential to infect the host. In other words, for at least one host receptor, if even one PPI prediction tool supports an interaction between a host receptor and adenovirus fiber protein, then the respective adenovirus has the potential to infect the host

Here **INFECTION_JUST_ONE** has the least and **INFECTION_ALL_ONE** has the most strictest criteria.

We also employed stacking ensemble machine learning to combine the PPI predictions from all the algorithms we used. The benefit of stacking is that it can harness the capabilities of a range of well-performing models on a classification and make predictions that have better performance than any single model in the ensemble. Given not all the PPI prediction algorithms are perfect, the stacking seemed to be a good fit our problem. For stacking, we tested J48 decision tree, naïve bayes, multilayer perceptron, random forest, and support vector machine algorithms.

The performances for individual approaches are assessed using several metrics that are typically used in machine learning including:

- **True Positive Rate(TPR):** The percentage of actual positives that are correctly classified (i.e. true positives or TP)..
- **True Negative Rate(TNR)** The percentage of actual negatives that are correctly classified (i.e. true negatives or TN).
- **Matthews correlation coefficient (MCC)** is used in machine learning. It's a measure of the quality of binary (two-class) classifications. The formula is;

$$\text{MCC} = \frac{TP * TN - FP * FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \quad (1)$$

- **Accuracy:** The percentage of correctly classified samples.

6. RESULTS

6.1 Identified Human Adenovirus Receptors

At this step, we searched UniProt Knowledgebase (UniProtKB) [The UniProt Consortium, 2017], for human proteins containing “adenovirus” keyword to identify 198 human receptor candidates. Then, we manually curated using literature and narrowed it down to five human proteins and included their 27 non-secreted isoforms using UniProtKB annotations. These receptors are CXAR, CD46, CD80, CD86 and ITAV.

Coxsackievirus and adenovirus receptor (CXAR) is a protein in humans. It is produced by the CXADR gene. CXAR protein is a type I membrane receptor. Group B coxsackie viruses and subgroup C adenoviruses interact with this protein. This protein is expressed in some tissues, including heart, brain, and, more commonly, epithelial and endothelial cells. CXAR has 40.0 kDa theoretically. It is composed of 365 amino acids. When interacting with extracellular matrix glycoproteins, it is used as a homophilic and heterophilic cell adhesion molecule (Figure 4).

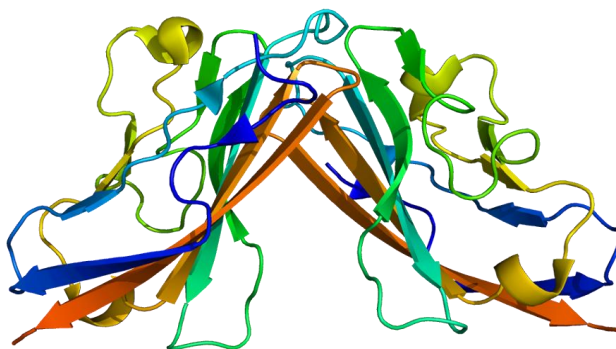


Figure 4. Structure of the CXAR protein (PDB accession 1EAJ)

CD46 also known as CD46 complement regulatory protein and membrane cofactor protein is a protein that in humans. It's encoded by CD46 gene. The protein encoded by this gene is a type I membrane protein. It's a regulatory part of the complement

system. The encoded protein can act as a receptor for group B adenoviruses (Figure 5).

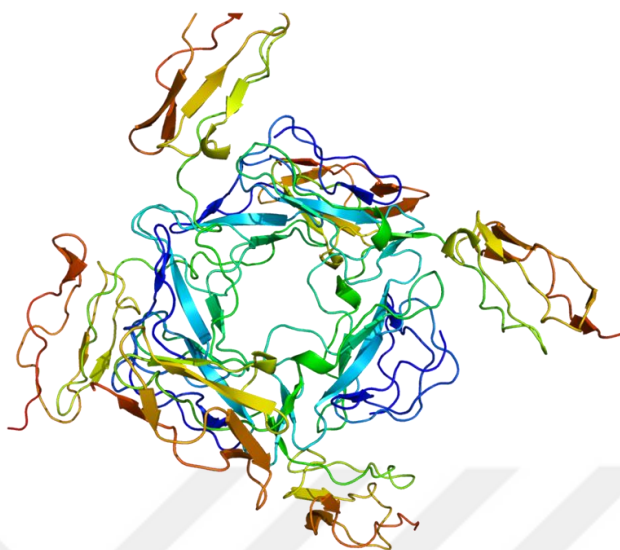


Figure 5. Structure of the CD46 protein (PDB accession 1CKL)

CD80 belongs to the immunoglobulin superfamily. It is a type I membrane protein. It has an extracellular immunoglobulin domain for receptor binding. This protein can be found on the surface of different immune cells. For example; dendritic cells, B cells, monocytes and antigen-presenting cells (Figure 6).

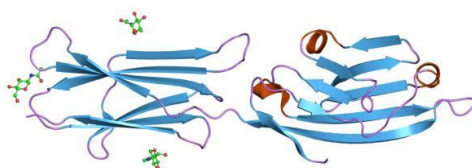


Figure 6. Structure of the CD80 protein (PDB accession 1DR9)

CD86 provides signals essential for T-cell activation and survival with CD80. CD86 can be used to signal for self-regulation and cell-cell association. This protein is found

on dendritic cells, macrophages, B-cells, and other antigen-presenting cells (Figure 7).

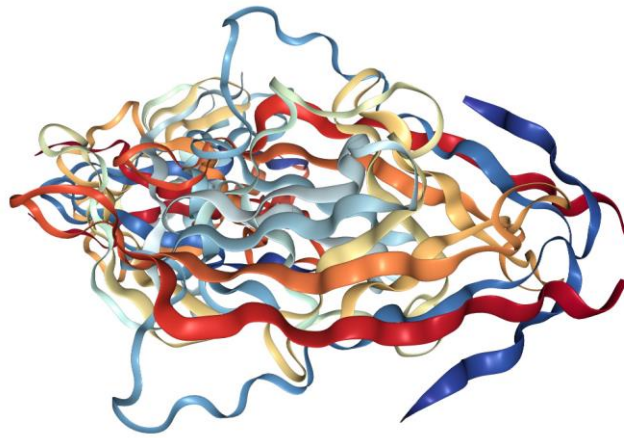


Figure 7. Structure of the CD86 protein (PDB accession 1I85)

ITAV is a protein that in humans. It's produced by the ITGAV gene. ITAV produces integrin alpha chain V. Integrins are heterodimeric integral membrane proteins. They come off an alpha chain and a beta chain. They are known to facilitate signal transduction (Figure 8).

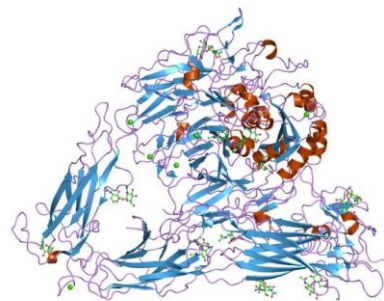


Figure 8. Structure of the ITAV protein (PDB accession 3VI4)

6.2 Identified Adenovirus Hosts

From 29,000 Adenoviridae proteins in UniProtKB, we identified 297 AdV host organisms spanning a wide range of taxa including mammals to birds. The hosts are either extracted from UniProtKB virtual host annotations, or, in their absence,

computed from AdV organism names. The host assignments were often problematic. The host naming were left at the different taxonomic levels higher than species. For instance; chicken written as Fowl, a taxa covering many birds. In such cases, we went back to nucleotide sequences and original submission to get the species level taxa. The hosts we have identified are provided in Appendix A. Adenovirus Host Organisms.

6.3 Collected Adenovirus Receptor Orthologs in Hosts

At this step, we managed to compute human adenovirus receptor orthologs in 48 out of 297 adenovirus hosts. The BLAST evalue and overlap thresholds were tried to increase the ortholog hits. Yet, in the majority of the cases the host organisms were not fully sequenced and the identified adenovirus host receptors, unfortunately, were not within the coverage of partial genomes sequenced. (Ex.<1e-20 and high overlap Ex.> 66%). All orthologs are available in the attached table. The host adenovirus receptors are provided in Appendix B. Human Adenovirus Receptors and Their Transmembrane Isoforms.

6.4 Identified Adenovirus Fiber Proteins

At this step, after removing multiple repeating fiber proteins, we had 424 unique Adenovirus fiber proteins. All identified AdV fiber proteins are available in Appendix D. Adenovirus Fiber Proteins.

In the searches made in UniProtKB, 424 fiber proteins of 5 different species (Figure 9) belonging to the Adenoviridae family were determined. In addition, the presence of critical areas of fiber-receptor interaction - "knob" in 807 and "C-terminal head domain" - in 196 - were confirmed in the vast majority of these proteins.

Adenoviridae					
Atadenovirus	Aviadenovirus	Ichadenovirus	Mastadenovirus	Siadenovirus	
Bovine AtV D Deer AtV A Duck AtV A Lizard AtV A Ovine AtV D Possum AtV A Psittacine AtV A Snake AtV A	Duck AvV B Falcon AvV A Fowl AvV A Fowl AvV B Fowl AvV C Fowl AvV D Fowl AvV E Goose AvV A Pigeon AvV A Pigeon AvV B Psittacine AvV B Turkey AvV B Turkey AvV C Turkey AvV D	Sturgeon IcV A	Bat MaV A Bat MaV B Bat MaV C Bat MaV D Bat MaV E Bat MaV F Bat MaV G Bovine MaV A Bovine MaV B Bovine MaV C Canine MaV A Deer MaV B Dolphin MaV A Dolphin MaV B Equine MaV A Equine MaV B Human MaV A Human MaV B Human MaV C Human MaV D Human MaV E Human MaV F Human MaV G	Murine MaV A Murine MaV B Murine MaV C Ovine MaV A Ovine MaV B Platyrrhini MaV A Porcine MaV A Porcine MaV B Porcine MaV C Sea lion MaV A Simian MaV A Simian MaV B Simian MaV C Simian MaV D Simian MaV E Simian MaV F Simian MaV G Simian MaV H Simian MaV I Skunk MaV A Squirrel MaV A Tree shrew MaV A	Frog SiV A Great tit SiV A Penguin SiV A Raptor SiV A Skua SiV A Turkey SiV A

Figure 9. Species in the Adenoviridae family with known fiber proteins

6.5 Comparison of Virus-Host PPI Prediction Tools

The PPI predictions by VHPPI, HOPITOR and DeNovo gave conflicting results for all the five receptors we have tested. The correlation coefficient between predictions of these tools for each tools is provided in Table 1.

Table 1. The correlation coefficient computed between PPI predictors

Receptor	Compared PPI Tools	Correlation Coefficient
CXAR	VHPPI vs. HOPITOR	0.6196
	VHPPI vs. DeNovo	0.8956
	HOPITOR vs. DeNovo	0.6824
CD86	VHPPI vs. HOPITOR	0.0745
	VHPPI vs. DeNovo	0.4127
	HOPITOR vs. DeNovo	0.3165
CD80	VHPPI vs. HOPITOR	0.0745
	VHPPI vs. DeNovo	0.4127
	HOPITOR vs. DeNovo	0.3165

Table 1. (cont'd)

Receptor	Compared PPI Tools	Correlation Coefficient
CD46	VHPPI vs. HOPITOR	0.0745
	VHPPI vs. DeNovo	0.4127
	HOPITOR vs. DeNovo	0.3165
ITAV	VHPPI vs. HOPITOR	0.0745
	VHPPI vs. DeNovo	0.4127
	HOPITOR vs. DeNovo	0.3165

VHPPI and DeNovo has the highest agreement in their predictions as reflected in the correlation coefficients. The disagreement between PPI algorithms further support the use a combined strategy in assessing the host specificity of adenoviruses.

6.6 Comparision of Meta-Predictions for Adenovirus Host Specificity

We have compared the different approaches (See Section 5.6) for combining PPI predictions (i.e. meta-predictors) in assessing adenovirus host specificity. Table 2. summarizes the comparision of meta-predictors at different taxonomic levels using different performance metrics.

Table 2. The performance of Meta-predictors

	Metrics	Organism Level	Genus Level	Family Level	Order Level
Stacking with J48	TPR	0.71	0.70	0.72	0.64
	TNR	0.71	0.70	0.72	0.64
	MCC	0.47	0.47	0.42	0.33
	Accuracy	0.71	0.70	0.73	0.65
Stacking with Naive Bayes	TPR	0.67	0.63	0.69	0.60
	TNR	0.67	0.63	0.69	0.60
	MCC	0.37	0.28	0.41	0.23
	Accuracy	0.67	0.63	0.69	0.60
Stacking with Multilayer Perceptron (Neural Network)	TPR	0.71	0.70	0.72	0.63
	TNR	0.71	0.70	0.72	0.63
	MCC	0.47	0.45	0.48	0.29
	Accuracy	0.71	0.70	0.73	0.64

Table 2. (cont'd)

	Metrics	Organism Level	Genus Level	Family Level	Order Level
Stacking with Random Forest	TPR	0.71	0.70	0.73	0.64
	TNR	0.71	0.70	0.73	0.64
	MCC	0.47	0.44	0.47	0.33
	Accuracy	0.71	0.70	0.73	0.65
Stacking with Support Vector Machines	TPR	0.68	0.66	0.72	0.63
	TNR	0.68	0.66	0.72	0.63
	MCC	0.40	0.345	0.46	0.29
	Accuracy	0.69	0.66	0.73	0.63
Voting with INFECTION_ALL_ONE	TPR	0.89	0.87	0.92	0.88
	TNR	0.23	0.23	0.23	0.27
	MCC	0.17	0.15	0.21	0.20
	Accuracy	0.57	0.56	0.58	0.58
Voting with INFECTION_MAJORITY	TPR	1	1	0.99	0.99
	TNR	0.006	0.006	0.007	0.008
	MCC	0.055	0.055	0.02	0.34
	Accuracy	0.50	0.50	0.50	0.50
Voting with INFECTION_JUST_A_ONE	TPR	0.89	1	1	1
	TNR	0.24	0	0	0
	MCC	0.17	0.15	0.21	0.20
	Accuracy	0.57	0.50	0.50	0.50

Overall the stacking-based ensemble learning techniques outperformed voting based techniques. This suggests, in alignment with the motivation behind ensemble learning, the shortcomings of one PPI prediction method is offset by others. Among the algorithms used to stack PPI predictions, decision tree based machine learning algorithm J48 seems to perform better based on metric used in comparison.

7. CONCLUSION

In this study, we developed a bioinformatics system to predict host specificity of adenoviruses in multiple steps; 1) the human adenoviruses are identified using public databases and the literature, 2) the known host organisms for adenoviruses are identified, 3) host adenoviruses from the known host organisms are identified, 4) fiber proteins in various adenoviruses are identified, 5) virus-host PPI's for receptor-fiber proteins pairs are computed using different prediction algorithms, finally 6) several techniques are applied to create a meta-predictor combining virus-host PPI predictions to assess host specificity (i.e. infection capacity for a given host) of a given adenovirus. The best performing meta-predictor, namely using stacking ensemble technique with J48 decision tree, achieved a true positive rate of 71.5%, a true negative rate 71.5% an accuracy of 71.0% in predicting whether an adenovirus can infect a given host.

Through this work, we also collected a comprehensive dataset of host receptor and adenovirus fiber proteins to support future adenovirus research. The dataset contains 424 fiber proteins from 5 adenovirus species that infect 297 host organisms.

Although our results are very promising, our system's performance relies on PPI predictions' accuracy and can be improved through development of better PPI prediction techniques. Given the limited agreement between PPI prediction algorithms VHPPI, HOPITOR ve DeNovo, we anticipate there is still room for development of more accurate cross-organism predictors.

In the future, we anticipate that our study could be serve in early detection of cross-species transtions (i.e. host jumps) or evaluation of host specificity of adenoviruses. In addition, our approach has the potential to be extended to virus families other than Adenoviriade that can have serious human health implications such as Coronaviridae.

REFERENCES

- Ahi YS, Mittal SK. Components of Adenovirus Genome Packaging. *Front Microbiol.* 2016 Sep 23;7:1503. eCollection 2016. Review.
- Alguwaizani S, Park B, Zhou X, Huang DS, Han K. Predicting Interactions between Virus and Host Proteins Using Repeat Patterns and Composition of Amino Acids. *J Healthc Eng.* 2018 May 9;2018:1391265. doi: 10.1155/2018/1391265. eCollection 2018.
- Altenhoff AM, Glover NM, Train CM, Kaleb K, Warwick Vesztrocy A, Dylus D, deFarias TM, Zile K, Stevenson C, Long J, Redestig H, Gonnet GH, Dessimoz C. The OMA orthology database in 2018: retrieving evolutionary relationships among all domains of life through richer web and programmatic interfaces. *Nucleic Acids Res.* 2018 Jan 4;46(D1):D477-D485. doi: 10.1093/nar/gkx1019. PubMed PMID: 29106550.
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. *J Mol Biol.* 1990 Oct 5;215(3):403-10. PubMed PMID: 2231712.
- Amberg A. (2013) In Silico Methods. In: Vogel H.G., Maas J., Hock F.J., Mayer D. (eds) *Drug Discovery and Evaluation: Safety and Pharmacokinetic Assays.* Springer, Berlin, Heidelberg
- Baker AT, Greenshields-Watson A, Coughlan L, Davies JA, Uusi-Kerttula H, Cole DK, Rizkallah PJ, Parker AL. Diversity within the adenovirus fiber knob hypervariable loops influences primary receptor interactions. *Nat Commun.* 2019 Feb 14;10(1):741. doi: 10.1038/s41467-019-08599-y.
- Barman RK, Saha S, Das S. Prediction of interactions between viral and host proteins using supervised machine learning methods. *PLoS One.* 2014 Nov 6;9(11):e112034. doi: 10.1371/journal.pone.0112034. eCollection 2014. PubMed PMID: 25375323.
- Basit AH, Abbasi WA, Asif A, Gull S, Minhas FUAA. Training host-pathogen protein-protein interaction predictors. *J Bioinform Comput Biol.* 2018 Aug;16(4):1850014.
- Becerra A, Bucheli VA, Moreno PA. Prediction of virus-host protein-protein interactions mediated by short linear motifs. *BMC Bioinformatics.* 2017 Mar 9;18(1):163. doi: 10.1186/s12859-017-1570-7. PubMed PMID: 28279163.
- Borkenhagen LK, Fieldhouse JK, Seto D, Gray GC. Are adenoviruses zoonotic? A systematic review of the evidence. *Emerg Microbes Infect.* 2019;8(1):1679-1687. doi: 10.1080/22221751.2019.1690953. PubMed PMID: 31749409.
- Calderone A, Licata L, Cesareni G. VirusMentha: a new resource for virus-host protein interactions. *Nucleic Acids Res.* 2015 Jan;43(Database issue):D588-92. doi: 10.1093/nar/gku830. Epub 2014 Sep 12. PubMed PMID: 25217587.

- Cook HV, Doncheva NT, Szklarczyk D, von Mering C, Jensen LJ. Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. *Viruses*. 2018 Sep 23;10(10). pii: E519. doi: 10.3390/v10100519. PubMed PMID: 30249048.
- Cook J, Radke J. Mechanisms of pathogenesis of emerging adenoviruses. *F1000Res*. 2017 Jan 30;6:90. doi: 10.12688/f1000research.10152.1. eCollection 2017. Review.
- Coyne CB, Bergelson JM. Virus-induced Abl and Fyn kinase signals permit coxsackievirus entry through epithelial tight junctions. *Cell*. 2006 Jan 13;124(1):119-31. PubMed PMID: 16413486.
- Deal C, Pekosz A, Ketner G. Prospects for oral replicating adenovirus-vectored vaccines. *Vaccine*. 2013 Jul 11;31(32):3236-43. doi: 10.1016/j.vaccine.2013.05.016. Epub 2013 May 22. Review. PubMed PMID: 23707160.
- Delcher AL, Bratke KA, Powers EC, Salzberg SL. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics*. 2007 Mar 15;23(6):673-9. Epub 2007 Jan 19. PubMed PMID: 17237039.
- Eid FE, ElHefnawi M, Heath LS. DeNovo: virus-host sequence-based protein-protein interaction prediction. *Bioinformatics*. 2016 Apr 15;32(8):1144-50. doi: 10.1093/bioinformatics/btv737. Epub 2015 Dec 16. PubMed PMID: 26677965.
- Flanagan ML, Parrish CR, Cobey S, Glass GE, Bush RM, Leighton TJ. Anticipating the species jump: surveillance for emerging viral threats. *Zoonoses Public Health*. 2012 May;59(3):155-63. doi: 10.1111/j.1863-2378.2011.01439.x. Epub 2011 Sep 14. Review. PubMed PMID: 21914152.
- Geoghegan JL, Duchêne S, Holmes EC. Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. *PLoS Pathog*. 2017 Feb 8;13(2):e1006215. doi: 10.1371/journal.ppat.1006215. eCollection 2017 Feb. PubMed PMID: 28178344.
- Guirimand T, Delmotte S, Navratil V. VirHostNet 2.0: surfing on the web of virus/host molecular interactions data. *Nucleic Acids Res*. 2015 Jan;43(Database issue):D583-7. doi: 10.1093/nar/gku1121. Epub 2014 Nov 11. PubMed PMID: 25392406.
- Heise C, Sampson-Johannes A, Williams A, McCormick F, Von Hoff DD, Kirn DH. ONYX-015, an E1B gene-attenuated adenovirus, causes tumor-specific cytolysis and antitumoral efficacy that can be augmented by standard chemotherapeutic agents. *Nat Med*. 1997 Jun;3(6):639-45. PubMed PMID: 9176490.
- Hosur R, Peng J, Vinayagam A, Stelzl U, Xu J, Perrimon N, Bienkowska J, Berger B. A computational framework for boosting confidence in high-throughput protein-protein interaction datasets. *Genome Biol*. 2012 Aug 31;13(8):R76. doi:10.1186/gb-2012-13-8-r76. PubMed PMID: 22937800.
- Howitt J, Bewley MC, Graziano V, Flanagan JM, Freimuth P. Structural basis for variation in adenovirus affinity for the cellular coxsackievirus and adenovirus receptor. *J Biol Chem*. 2003 Jul 11;278(28):26208-15. Epub 2003 Apr 25.

- Hunter S, Apweiler R, Attwood TK, Bairoch A, Bateman A, Binns D, Bork P, Das U, Daugherty L, Duquenne L, Finn RD, Gough J, Haft D, Hulo N, Kahn D, Kelly E, Laugraud A, Letunic I, Lonsdale D, Lopez R, Madera M, Maslen J, McAnulla C, McDowall J, Mistry J, Mitchell A, Mulder N, Natale D, Orengo C, Quinn AF, Selengut JD, Sigrist CJ, Thimma M, Thomas PD, Valentin F, Wilson D, Wu CH, Yeats C. InterPro: the integrative protein signature database. *Nucleic Acids Res.* 2009 Jan;37(Database issue):D211-5. doi: 10.1093/nar/gkn785. Epub 2008 Oct 21. PubMed PMID: 18940856.
- Ismail AM, Cui T, Dommaraju K, Singh G, Dehghan S, Seto J, Shrivastava S, Fedorova NB, Gupta N, Stockwell TB, Halpin R, Madupu R, Heim A, Kajon AE, Romanowski EG, Kowalski RP, Malathi J, Therese KL, Madhavan HN, Zhang Q, Ferreyra LJ, Jones MS, Rajaiya J, Dyer DW, Chodosh J, Seto D. Genomic analysis of a large set of currently-and historically-important human adenovirus pathogens. *Emerg Microbes Infect.* 2018 Feb 7;7(1):10. doi: 10.1038/s41426017-0004-y. Erratum in: *Emerg Microbes Infect.* 2018 Dec 8;7(1):208.
- Ismail AM, Lee JS, Lee JY, Singh G, Dyer DW, Seto D, Chodosh J, Rajaiya J. Adenoviromics: Mining the Human Adenovirus Species D Genome. *Front Microbiol.* 2018 Sep 11;9:2178. doi: 10.3389/fmicb.2018.02178. eCollection 2018. Review. Erratum in: *Front Microbiol.* 2018 Dec 04;9:3005.
- Lee CS, Bishop ES, Zhang R, Yu X, Farina EM, Yan S, Zhao C, Zheng Z, Shu Y, Wu X, Lei J, Li Y, Zhang W, Yang C, Wu K, Wu Y, Ho S, Athiviraham A, Lee MJ, Wolf JM, Reid RR, He TC. Adenovirus-Mediated Gene Delivery: Potential Applications for Gene and Cell-Based Therapies in the New Era of Personalized Medicine. *Genes Dis.* 2017 Jun;4(2):4363. doi: 10.1016/j.gendis.2017.04.001. Epub 2017 Apr 27. PubMed PMID: 28944281.
- Mennechet FJD, Paris O, Ouoba AR, Salazar Arenas S, Sirima SB, Takoudjou Dzomo GR, Diarra A, Traore IT, Kania D, Eichholz K, Weaver EA, Tuaillon E, Kremer EJ. A review of 65 years of human adenovirus seroprevalence. *Expert Rev Vaccines.* 2019 Jun;18(6):597-613. doi: 10.1080/14760584.2019.1588113. Epub 2019 May 27. PubMed PMID: 31132024.
- Mihara T, Nishimura Y, Shimizu Y, Nishiyama H, Yoshikawa G, Uehara H, Hingamp P, Goto S, Ogata H. Linking Virus Genomes with Host Taxonomy. *Viruses.* 2016 Mar 1;8(3):66. doi: 10.3390/v8030066. PubMed PMID: 2693855.
- Nemerow GR. Cell receptors involved in adenovirus entry. *Virology.* 2000 Aug 15;274(1):1-4. Review.
- Nemerow GR, Pache L, Reddy V, Stewart PL. Insights into adenovirus host cell interactions from structural studies. *Virology.* 2009 Feb 20;384(2):380-8. doi: 10.1016/j.virol.2008.10.016. Epub 2008 Nov 20. Review.
- Niemann J, Kühnel F. Oncolytic viruses: adenoviruses. *Virus Genes.* 2017 Oct;53(5):700-706. doi: 10.1007/s11262-0171488-1. Epub 2017 Jul 12. Review. PubMed PMID: 28702840.

- Persico M, Ceol A, Gavrilu C, Hoffmann R, Florio A, Cesareni G. HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. *BMC Bioinformatics*. 2005 Dec 1;6 Suppl 4:S21. PubMed PMID: 16351748.
- Radke JR, Cook JL. Human adenovirus infections: update and consideration of mechanisms of viral persistence. *Curr Opin Infect Dis*. 2018 Jun;31(3):251-256. doi: 10.1097/QCO.0000000000000451.
- Rao VS, Srinivas K, Sujini GN, Kumar GN. Protein-protein interaction detection: methods and analysis. *Int J Proteomics*. 2014;2014:147648. doi: 10.1155/2014/147648. Epub 2014 Feb 17. Review.
- O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, Rajput B, Robbertse B, Smith-White B, Ako-Adjei D, Astashyn A, Badretdin A, Bao Y, Blinkova O, Brover V, Chetvernin V, Choi J, Cox E, Ermolaeva O, Farrell CM, Goldfarb T, Gupta T, Haft D, Hatcher E, Hlavina W, Joardar VS, Kodali VK, Li W, Maglott D, Masterson P, McGarvey KM, Murphy MR, O'Neill K, Pujar S, Rangwala SH, Rausch D, Riddick LD, Schoch C, Shkeda A, Storz SS, Sun H, Thibaud-Nissen F, Tolstoy I, Tully RE, Vatsan AR, Wallin C, Webb D, Wu W, Landrum MJ, Kimchi A, Tatusova T, DiCuccio M, Kitts P, Murphy TD, Pruitt KD. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. *Nucleic Acids Res*. 2016 Jan 4;44(D1):D733-45. doi: 10.1093/nar/gkv1189. Epub 2015 Nov 8. PubMed PMID: 26553804.
- Roelvink PW, Lizonova A, Lee JG, Li Y, Bergelson JM, Finberg RW, Brough DE, Kovesdi I, Wickham TJ. The coxsackievirus-adenovirus receptor protein can function as a cellular attachment protein for adenovirus serotypes from subgroups A, C, D, E, and F. *J Virol*. 1998 Oct;72(10):7909-15.
- Short JJ, Pereboev AV, Kawakami Y, Vasu C, Holterman MJ, Curiel DT. Adenovirus serotype 3 utilizes CD80 (B7.1) and CD86 (B7.2) as cellular attachment receptors. *Virology*. 2004 May 1;322(2):349-59.
- Singh G, Ismail AM, Lee JY, Ramke M, Lee JS, Dyer DW, Seto D, Rajaiya J, Chodosh J. Divergent Evolution of E1A CR3 in Human Adenovirus Species D. *Viruses*. 2019 Feb 8;11(2). pii: E143. doi: 10.3390/v11020143.
- Singh R, Park D, Xu J, Hosur R, Berger B. Struct2Net: a web service to predict protein-protein interactions using a structure-based approach. *Nucleic Acids Res*. 2010 Jul;38(Web Server issue):W508-15. doi: 10.1093/nar/gkq481. Epub 2010 May 31. PubMed PMID: 20513650.
- Taylor LH, Latham SM, Woolhouse ME. Risk factors for human disease emergence. *Philos Trans R Soc Lond B Biol Sci*. 2001 Jul 29;356(1411):983-9. PubMed PMID: 11516376.

- Tuncbag N, Gursoy A, Nussinov R, Keskin O. Predicting protein-protein interactions on a proteome scale by matching evolutionary and structural similarities at interfaces using PRISM. *Nat Protoc.* 2011 Aug 11;6(9):1341-54.
- UniProt Consortium. UniProt: a worldwide hub of protein knowledge. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D506-D515. doi: 10.1093/nar/gky1049. PubMed PMID: 30395287.
- Wold WSM, Ison MG. Adenoviruses. In: Knipe DM, How-ley PM, editors. *Fields Virology*. Philadelphia, PA: Lippincott Williams & Wilkins; 2013. pp. 1732–1767.
- Zahiri J, Bozorgmehr JH, Masoudi-Nejad A. Computational Prediction of Protein-Protein Interaction Networks: Algorithms and Resources. *Curr Genomics.* 2013 Sep;14(6):397-414. doi: 10.2174/1389202911314060004.
- Zdobnov EM, Tegenfeldt F, Kuznetsov D, Waterhouse RM, Simão FA, Ioannidis P, Seppey M, Loetscher A, Kriventseva EV. OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. *Nucleic Acids Res.* 2017 Jan 4;45(D1):D744-D749. doi:10.1093/nar/gkw1119. Epub 2016 Nov 28. PubMed PMID: 27899580.
- Zhang Y, Bergelson JM. Adenovirus receptors. *J Virol.* 2005 Oct;79(19):12125-31. Review.
- Zhou X, Park B, Choi D, Han K. A generalized approach to predicting protein-protein interactions between virus and host. *BMC Genomics.* 2018 Aug 13;19(Suppl 6):568. doi: 10.1186/s12864-018-4924-2. PubMed PMID: 30367586.
- Zochowska M, Paca A, Schoehn G, Andrieu JP, Chroboczek J, Dublet B, Szolajska E. Adenovirus dodecahedron, as a drug delivery vector. *PLoS One.* 2009;4(5):e5569. doi: 10.1371/journal.pone.0005569. Epub 2009 May 15. PubMed PMID: 19440379.

APPENDICES



Appendix A. Adenovirus Host Organisms

Taxonomy Identifier	Scientific Name	Common Name
9606	Homo Sapiens	Human
10090	Mus Musculus	Mouse
10116	Rattus Norvegicus	Rat
9823	Sus Scrofa	Pig
9913	Bos Taurus	Bovine
29073	Ursus Maritimus	Polar Bear
9615	Canis Lupus Familiaris	Dog
9598	Pan Troglodytes	Chimpanzee
9544	Macaca Mulatta	Rhesus Macaque
9739	Tursiops Truncatus	Atlantic Bottle-nosed Dolphin
9796	Equus Caballus	Horse
9541	Macaca Fascicularis	Crab-eating Macaque
9685	Felis Catus	Cat
59463	Myotis Lucifugus	Little Brown Bat
9669	Mustela Putorius Furo	European Domestic Ferret
9595	Gorilla Gorilla Gorilla	Western Lowland Gorilla
9238	Pygoscelis Adeliae	Adelie Penguin
9233	Aptenodytes Forsteri	Emperor Penguin
60711	Chlorocebus Sabaeus	Green Monkey
28377	Anolis Carolinensis	Green Anole
9103	Meleagris Gallopavo	Wild Turkey
43179	Ictidomys Tridecemlineatus	Thirteen-lined Ground Squirrel
9940	Ovis Aries	Sheep
9925	Capra Hircus	Goat
8839	Anas Platyrhynchos	Mallard
8840	Anas Platyrhynchos Platyrhynchos	Northern Mallard
1752123	Acanthophis Cryptamydros	Kimberley Death Adder
412080	Acanthophis Sp.	Seram Death Adder
239748	Acanthophis Rugosus	Irian Jayan Death Adder
239746	Acanthophis Praelongus	Northern Death Adder
8605	Acanthophis Antarcticus	Common Death Adder
9407	Rousettus Aegyptiacus	Egyptian Fruit Bat
77220	Rousettus Aegyptiacus Aegyptiacus	Egyptian Fruit Bat
77221	Rousettus Aegyptiacus Princeps	Egyptian Fruit Bat
56349	Falco Femoralis	Aplomado Falcon
42254	Sorex Araneus	Eurasian Common Shrew

Taxonomy Identifier	Scientific Name	Common Name
9333	Pseudocheirus Peregrinus	Common Ring-tailed Possum
9337	Trichosurus Vulpecula	Brush-tailed Possum
38614	Distoechurus Pennatus	Feather-tailed Possum
38632	Tarsipes Rostratus	Honey Possum
128432	Trichosurus Caninus	Mountain Brushtail Possum
75566	Lophocebus Aterrimus	Black Crested Mangabey
164648	Piliocolobus Badius	Western Red Colobus
40233	Carollia Perspicillata	Seba's Short-tailed Bat
158814	Terrapene Carolina	Eastern Box Turtle
303588	Cercopithecus Campbelli	Campbell's Monkey
304410	Cercopithecus Campbelli Lowei	Lowe's Monkey
9858	Capreolus Capreolus	European Roe Deer
9860	Cervus Elaphus	Red Deer
9863	Cervus Nippon	Sika Deer
9888	Muntiacus Muntjak	Barking Deer
30532	Cervus Dama	Fallow Deer
36224	Cercopithecus Diana	Diana Monkey
9737	Delphinus Coeruleoalbus	Striped Dolphin
103589	Delphinus Clymene	Clymene Dolphin
118797	Lipotes Vexillifer	Yangtze River Dolphin
118798	Platanista Gangetica	Ganges River Dolphin
31138	Trachemys Scripta Elegans	Red-eared Slider Turtle
34903	Trachemys Scripta	Red-eared Slider Turtle
51298	Myotis Myotis	Greater Mouse-eared Bat
109482	Myotis Blythii	Lesser Mouse-eared Bat
412095	Myotis Oxygnathus	Lesser Mouse-eared Bat
77151	Mustela Nigripes	Black-footed Ferret
470562	Melogale Personata	Burmese Ferret-Badger
44316	Chloebia Gouldiae	Gouldian Finch
50047	Chelonoidis Carbonarius	Red-footed Tortoise
33548	Colobus Guereza	Mantled Guereza
9557	Papio Hamadryas	Hamadryas Baboon
36229	Papio Hamadryas Ursinus	Chacma Baboon
232645	Psittacula Cyanocephala	Plum-headed Parakeet
57374	Leontopithecus Chrysomelas	Golden-headed Lion Tamarin
77214	Eidolon Helvum	Straw-colored Fruit Bat
77218	Rhinolophus Hipposideros	Lesser Horseshoe Bat
169756	Rhinolophus Monoceros	Formosan Lesser Horseshoe Bat
59479	Rhinolophus Ferrumequinum	Greater Horseshoe Bat

Taxonomy Identifier	Scientific Name	Common Name
7902	Acipenser Gueldenstaedtii	Russian Sturgeon
7904	Acipenser Transmontanus	White Sturgeon
7906	Acipenser Ruthenus	Sterlet Sturgeon
7910	Acipenser Platyrhynchus	Shovelnose Sturgeon
61970	Acipenser Sinensis	Chinese Sturgeon
859983	Eulemur Rufus	Red-fronted Lemur
9455	Varecia Variegata	Black-and-white Ruffed Lemur
87289	Varecia Variegata Variegata	Black and White Ruffed Lemur
30602	Eulemur Macaco	Black Lemur
30603	Eulemur Macaco Macaco	Black Lemur
87288	Eulemur Flavifrons	Blue-eyed Black Lemur
13557	Hapalemur Griseus	Eastern Lesser Bamboo Lemur
13514	Eulemur Coronatus	Crowned Lemur
9447	Lemur Catta	Ring-tailed Lemur
30608	Microcebus Murinus	Gray Mouse Lemur
47178	Eulemur Fulvus Collaris	Collared Brown Lemur
482537	Galeopterus Variegatus	Malayan Flying Lemur
59465	Nyctalus Leisleri	Leisler's Bat
27660	Sturnira Lilium	Lesser yellow-shouldered Bat
27634	Artibeus Lituratus	Great Fruit-eating Bat
109483	Plecotus Austriacus	Grey Long-eared Bat
69075	Rattus Losea	Lesser Rice-field Rat
9483	Callithrix Jacchus	White-tufted-ear Marmoset
9485	Callithrix sp.	Marmoset
9495	Callimico goeldii	Goeldi's Marmoset
52232	Callithrix Humeralifera	Tassel-eared Marmoset
57378	Callithrix Penicillata	Black-pencilled Marmoset
8558	Varanus Albigularis	White-throated monitor
9502	Alouatta Caraya	Black Howler Monkey
9503	Alouatta Seniculus	Red Howler Monkey
30589	Alouatta Palliata	Mantled Howler Monkey
30590	Alouatta Belzebul	Red-handed Howler Monkey
121123	Alouatta Sara	Bolivian Red Howler Monkey
9523	Plecturocebus Moloch	Dusky Titi Monkey
30592	Cheracebus Torquatus	Collared Titi Monkey
230833	Plecturocebus Donacophilus	Bolivian Gray Titi Monkey
1812042	Plecturocebus Brunneus	Brown Titi Monkey
43147	Aotus Lemurinus	Gray-bellied Night

Taxonomy Identifier	Scientific Name	Common Name
		Monkey
1449913	Macaca Mulatta Lasiotus	Rhesus Macaque
1654737	Macaca Mulatta Brevicaudus	Rhesus Monkey
109481	Myotis Nattereri	Natterer's Bat
2510968	Myotis Nattereri Helverseni	Natterer's Bat
2510969	Myotis Nattereri Nattereri	Natterer's Bat
116115	Ctenophorus Nuchalis	Central Netted Dragon
34882	Enhydra Lutris	Sea Otter
281916	Poicephalus Meyeri	Meyer's Parrot
9538	Erythrocebus Patas	Red Guenon
9234	Aptenodytes Patagonicus	King Penguin
30457	Pygoscelis Papua	Gentoo Penguin
9825	Sus Scrofa Domesticus	Domestic Pig
59474	Pipistrellus Pipistrellus	Common Pipistrelle
246814	Pipistrellus Pygmaeus	Soprano Pipistrelle
395889	Catharacta Maccormicki	South Polar Skua
159858	Rhinolophus Pusillus	Least Horseshoe Bat
9493	Callithrix Pygmaea	Pygmy Marmoset
59485	Vespertilio Murinus	Particoloured Bat
9430	Desmodus Rotundus	Vampire Bat
38937	Anolis Sagrei	Brown Anole
8527	Tiliqua Rugosa	Shingleback Lizard
8552	Heloderma Horridum Horridum	Mexican Beaded Lizard
37197	Aspidoscelis Uniparens	Desert Grassland Whiptail Lizard
40250	Saara Hardwickii	Indian Spiny Tailed Lizard
9395	Tupaia Glis	Tree Shrew
37347	Tupaia Belangeri	Common Tree Shrew
70687	Tupaia Tana	Large Tree Shrew
246437	Tupaia Chinensis	Chinese Tree Shrew
320338	Ptilocercus Lowii	Pen-tailed Tree Shrew
9378	Suncus Murinus	Musk Shrew
28737	Elephantulus Edwardii	Cape Long-eared Elephant Shrew
9561	Mandrillus Sphinx	Papio Sphinx
9490	Saguinus Oedipus	Cotton-top Tamarin
35732	Rattus Tanezumi	Oriental House Rat
9157	Parus Major	Great Tit
86975	Testudo Graeca	Spur-thighed Tortoise
37012	Pan Troglodytes Verus	Western chimpanzee
37010	Pan Troglodyte Schweinfurthii	Eastern chimpanzee
756884	Pan Troglodytes Elliotti	Nigeria-Cameroon chimpanzee

Taxonomy Identifier	Scientific Name	Common Name
8843	Anser Anser	Domestic Goose
8844	Anser Anser Anser	Western Greylag Goose
8845	Anser Cygnoid	Swan Goose
103336	Agama Agama	Red-headed Rock Agama
118224	Phrynocephalus Interscapularis	Tajikistan Toadhead Agama
281410	Paralaudakia Caucasia	Caucasian Agama
1007066	Phrynocephalus Persicus	Persian Toad-headed Agama
118226	Pseudocalotes Brevipes	-
118236	Trapelus Persicus	Trapelus
1585939	Phrynocephalus Golubewii	Toadhead Agama
30538	Vicugna Pacos	Lama Pacos
52188	Bipes Biporus	Baja Worm Lizard
261503	Rhineura Floridana	Florida Worm Lizard
261506	Trogonophis Wiegmanni	Checkerboard Worm Lizard
302461	Amphisbaena Xera	Dry Worm Lizard
2024434	Amphisbaena Carli	Worm Lizard
141900	Anolis Reconditus	Blue Mountain Lizard
1235290	Anolis Distichus Vinosus	Lizard
1304629	Anolis Casildae	Casilda's Anole
1920713	Anolis Morazani	Honduras Lizard
74909	Cuora Amboinensis	Amboina Box Turtle
85611	Terrapene Ornata	Ornate Box Turtle
158815	Terrapene Coahuila	Coahuila Box Turtle
158816	Terrapene Nelsoni	Nelson's Box Turtle
13146	Melopsittacus Undulatus	Budgerigar
9543	Macaca Fuscata Fuscata	Japanese Macaque
9545	Macaca Nemestrina	Pig-tailed Macaque
91909	Chamaeleo Gracilis	Graceful Chameleon
179894	Brookesia Perarmata	Armored Leaf Chameleon
420386	Chamaeleo Calcaricarens	Awash Chameleon
9597	Pan Paniscus	Pygmy Chimpanzee
79643	Pygoscelis Antarcticus	Chinstrap Penguin
391345	Terrapene Carolina Carolina	Eastern Box Turtle
52435	Coleonyx Variegatus	Western Banded Gecko
96739	Goniurosaurus Kuroiwae	Tokashiki Gecko
302466	Eublepharis Turcmenicus	Turkmenistan Eyelid Gecko
449391	Coleonyx Mitratus	Central American Banded Gecko
481883	Eublepharis Macularius	Leopard Gecko
8951	Caracara Plancus	Southern Caracara

Taxonomy Identifier	Scientific Name	Common Name
8954	Falco Peregrinus	Peregrine Falcon
56345	Phalcoboenus Australis	Striated Caracara
56350	Falco Sparverius	American Kestrel
9031	Gallus Gallus	Chicken
30403	Polyplectron Napoleonis	Palawan Peacock-pheasant
30408	Crossoptilon Crossoptilon	White-eared Pheasant
1155787	Tetrastes Bonasia	Hazel Grouse
36310	Gekko Gecko	Tokay Gecko
143630	Paroedura Picta	Ocelot Gecko
221572	Narudasia Festiva	Rock-dwelling Gecko
357320	Ebenavia Inunguis	Madagascar nailless lizard
747216	Gehyra Punctata	Spotted gecko
109480	Myotis Emarginatus	Geoffroy's Bat
1159185	Gorilla Beringei Beringei	Eastern Mountain Gorilla
46359	Gorilla Beringei Graueri	Eastern Lowland Gorilla
9593	Gorilla Gorilla	Western Gorilla
499232	Gorilla Gorilla Beringei	Mountain Gorilla
109483	Plecotus Austriacus	Grey Long-eared Bat
10141	Cavia Porcellus	Guinea Pig
10144	Cavia Cutleri	Guinea Pig
37548	Cavia Aperea	Brazilian Guinea Pig
143287	Cavia Tschudii	Montane Guinea Pig
717921	Cavia Fulgida	Shiny Guinea Pig
8551	Heloderma Horridum	Mexican Beaded Lizard
8554	Heloderma Suspectum	Gila Monster
537493	Heloderma Suspectum Cinctum	Banded Gila Monster
709964	Heloderma Suspectum Suspectum	Reticulate Gila Monster
182253	Alouatta Pigra	Guatemalan Howler Monkey
32544	Dasyuroides Byrnei	Kowari
59472	Pipistrellus Kuhlii	Kuhl's Pipistrelle
8524	Zootoca Vivipara	Common Lizard
80465	Adolfus Jacksoni	Jackson's Forest Lizard
90065	Ophisops Elegans	Snake-eyed Lizard
947070	Eremias Scripta	Sand Racerunner
1588132	Eremias Strauchi Kopetdaghica	Kopet Dagh Racerunner
8404	Lithobates Pipiens	Northern leopard frog
38620	Lutreolina Crassicaudata	Lutrine Opossum
867363	Callithrix Kuhlii	Wied's Black-tufted-ear Marmoset
9659	Martes Foina	Beech Marten
9660	Martes Americana	American Marten
36721	Martes Melampus	Japanese Marten

Taxonomy Identifier	Scientific Name	Common Name
74864	Martes Flavigula	Yellow-throated Marten
10090	Mus musculus castaneus	Southeastern Asian house mouse
10092	Mus musculus domesticus	Western European house mouse
39442	Mus musculus musculus	Eastern European house mouse
57486	Mus musculus molossinus	Japanese house mouse
59451	Eptesicus nilssonii	Northern bat
9872	Odocoileus hemionus	Mule deer
9874	Odocoileus virginianus	White-tailed deer
9875	Odocoileus virginianus virginianus	Virginia white-tailed deer
598489	Odocoileus hemionus peninsulae	Deer
9938	Ovis aries musimon	Mouflon
94885	Pantherophis guttatus	Corn snake
412765	Pantherophis guttatus guttatus	Corn snake
91950	Pan troglodytes vellerosus	Central Chimpanzee
10041	Peromyscus leucopus	White-footed mouse
10042	Peromyscus maniculatus	North American deer mouse
57100	Peromyscus aztecus	Aztec mouse
89101	Peromyscus truei	Pinyon mouse
144755	Peromyscus fraterculus	Northern Baja deermouse
9742	Phocoena phocoena	Harbor porpoise
159324	Myotis dasycneme	Dutch pond bat
9986	Oryctolagus cuniculus	Rabbit
48083	Brachylagus idahoensis	Pygmy rabbit
48089	Romerolagus diazi	Volcano rabbit
218836	Rheomys raptor	Goldman's water mouse
9487	Saguinus fuscicollis	Brown-headed tamarin
9488	Saguinus mystax	Moustached tamarin
37588	Saguinus bicolor	Brazilian Bare-faced tamarin
78454	Saguinus labiatus	Red-chested mustached tamarin
111179	Trachylepis homalocephala	Red-sided skink
356595	Trachylepis variegata	Mottled skink
480717	Ctenotus ariadnae	Western Australia Skinks
754020	Trachylepis sulcata	Western rock skink
59452	Eptesicus serotinus	Serotine bat
110938	Neoromicia capensis	Cape serotine bat
159320	Eptesicus diminutus	Diminutive serotine bat
177184	Neoromicia brunneus	Dark-brown serotine bat
54056	Catharacta skua	Great skua

Taxonomy Identifier	Scientific Name	Common Name
54058	<i>Stercorarius longicaudus</i>	Long-tailed jaeger
30548	<i>Mephitis mephitis</i>	Striped skunk
8673	<i>Pseudonaja textilis</i>	Eastern brown snake
36307	<i>Deinagkistrodon acutus</i>	Hundred-pace snake
70142	<i>Notechis scutatus scutatus</i>	Mainland tiger snake
100989	<i>Tropidechis carinatus</i>	Australian rough-scaled snake
259325	<i>Gloydius brevicaudus</i>	Korean slamosa snake
61968	<i>Acipenser persicus</i>	Persian sturgeon
1331069	<i>Sturnira lilium paulsoni</i>	Yellow-shouldered bat
192726	<i>Urogale everetti</i>	Mindanao tree shrew
8559	<i>Varanus varius</i>	Lace monitor
52184	<i>Varanus griseus</i>	Desert monitor
62035	<i>Varanus acanthurus</i>	Ridge-tailed monitor
169837	<i>Varanus dumerilii</i>	Dumeril's monitor
153286	<i>Myotis nigricans</i>	Black myotis
159322	<i>Myotis albescens</i>	Silver-tipped myotis
159328	<i>Myotis macrotrichus</i>	Philippine large-footed myotis
225400	<i>Myotis davidii</i>	David's myotis
8723	<i>Bothrops insularis</i>	Lachesis insularis
8724	<i>Bothrops jararaca</i>	Jararaca
8726	<i>Bothrops jararacussu</i>	Jararacussu
8753	<i>Lachesis muta muta</i>	Bushmaster
242054	<i>Gloydius blomhoffii</i>	Mamushi
36238	<i>Mustela itatsi</i>	Japanese weasel
36239	<i>Mustela nivalis</i>	Least weasel
55048	<i>Mustela frenata</i>	Long-tailed weasel
92062	<i>Mustela altaica</i>	Mountain weasel

Appendix B. Human Adenovirus Receptors and Their Transmembrane Isoforms

Universal Protein Knowledgebase Accession	Protein Name
P42081	T-lymphocyte activation antigen CD86
P42081-3	Isoform 2 of T-lymphocyte activation antigen CD86
P42081-2	Isoform 3 of T-lymphocyte activation antigen CD86
P42081-4	Isoform 4 of T-lymphocyte activation antigen CD86
P42081-5	Isoform 5 of T-lymphocyte activation antigen CD86
P42081-6	Isoform 6 of T-lymphocyte activation antigen CD86
P06756	Integrin alpha-V
P06756-2	Isoform 2 of Integrin alpha-V
P06756-3	Isoform 3 of Integrin alpha-V
P33681	T-lymphocyte activation antigen CD80
P33681-2	Isoform 2 of T-lymphocyte activation antigen CD80
P33681-3	Isoform 3 of T-lymphocyte activation antigen CD80
P78310	Coxsackievirus and adenovirus receptor
P78310-2	Isoform 2 of Coxsackievirus and adenovirus receptor
P78310-6	Isoform 6 of Coxsackievirus and adenovirus receptor
P78310-7	Isoform 7 of Coxsackievirus and adenovirus receptor
P15529	Membrane cofactor protein (CD46)
P15529-2	Isoform B of Membrane cofactor protein (CD46)
P15529-11	Isoform C of Membrane cofactor protein (CD46)
P15529-3	Isoform D of Membrane cofactor protein (CD46)
P15529-12	Isoform E of Membrane cofactor protein (CD46)
P15529-4	Isoform F of Membrane cofactor protein (CD46)
P15529-13	Isoform G of Membrane cofactor protein (CD46)
P15529-5	Isoform H of Membrane cofactor protein (CD46)
P15529-14	Isoform I of Membrane cofactor protein (CD46)
P15529-6	Isoform J of Membrane cofactor protein (CD46)
P15529-15	Isoform K of Membrane cofactor protein (CD46)
P15529-7	Isoform L of Membrane cofactor protein (CD46)
P15529-8	Isoform M of Membrane cofactor protein (CD46)
P15529-9	Isoform N of Membrane cofactor protein (CD46)
P15529-10	Isoform 2 of Membrane cofactor protein (CD46)
P15529-16	Isoform 3 of Membrane cofactor protein (CD46)

Appendix C. Human Adenovirus Receptor Homologs

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
Q1JPC5	CD86 antigen	9913	Bos taurus
G3RSH3	Membrane cofactor protein	9595	Gorilla gorilla
A0A3Q2HQP9	Membrane cofactor protein	9796	Equus caballus
A0A2K5U3B6	Uncharacterized protein	9541	Macaca fascicularis
K7GL47	Ig-like domain-containing protein	9823	Sus scrofa
F7HAH2	CD86 molecule	9483	Callithrix jacchus
A0A3Q2UEZ7	Integrin alpha-V	9031	Gallus gallus
A0A337STB7	Uncharacterized protein	9685	Felis catus
P06756-2	Isoform 2 of Integrin alpha-V	9606	Homo sapiens
A0A2R8ZHS8	Uncharacterized protein	9597	Pan paniscus
A0A4X1TAW7	Ig-like domain-containing protein	9823	Sus scrofa
M3YH47	Uncharacterized protein	9669	Mustela putorius
O77684	B7 protein	9545	Macaca nemestrina
A0A2K5TTJ8	Ig-like domain-containing protein	9541	Macaca fascicularis
F7DT60	Membrane cofactor protein	9544	Macaca mulatta
Q6VE48	Membrane cofactor protein	9913	Bos taurus
A0A2K6B410	Membrane cofactor protein	9545	Macaca nemestrina
A0A2K6AUD1	Integrin_alpha2 domain-containing protein	9545	Macaca nemestrina
A0A1D5QAX6	Ig-like domain-containing protein	9544	Macaca mulatta
A0A340WSH3	T-lymphocyte activation antigen CD86 isoform X1	118797	Lipotes vexillifer
A0A2I3T9K7	Membrane cofactor protein	9598	Pan troglodytes
O19122	Membrane cofactor protein (Fragment)	9495	Callimico goeldii
A0A340XMJ7	Membrane cofactor protein	118797	Lipotes vexillifer
R0L494	T-lymphocyte activation antigen CD86 (Fragment)	8839	Anas platyrhynchos
A0A2K5WCD3	Integrin_alpha2 domain-containing protein	9541	Macaca fascicularis

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
K9J071	Putative vitronectin receptor alpha subunit	9430	Desmodus rotundus
A0A286ZW08	Membrane cofactor protein	9823	Sus scrofa
A0A2K6B3W1	Uncharacterized protein	9545	Macaca nemestrina
A5HJM2	T-lymphocyte activation antigen CD80 precursor	9483	Callithrix jacchus
G3RWI9	CD80 molecule	9595	Gorilla gorilla
F7FY16	Uncharacterized protein	9544	Macaca mulatta
P42081-2	Isoform 3 of T-lymphocyte activation antigen CD86	9606	Homo sapiens
M3W4G7	Integrin_alpha2 domain-containing protein	9685	Felis catus
H0VT70	Integrin_alpha2 domain-containing protein	10141	Cavia porcellus
A0A452E162	Integrin_alpha2 domain-containing protein	9925	Capra hircus
A0A2R8ZAN7	Membrane cofactor protein	9597	Pan paniscus
P42081-5	Isoform 5 of T-lymphocyte activation antigen CD86	9606	Homo sapiens
I3NHJ6	Uncharacterized protein	43179	Ictidomys tridecemlineatus
A0A493TA25	Uncharacterized protein	8840	Anas platyrhynchos
G3QZS4	CD86 molecule	9595	Gorilla gorilla
A0A287AH22	Membrane cofactor protein	9823	Sus scrofa
A0A493T590	Uncharacterized protein	8840	Anas platyrhynchos
A0A2R9B1B1	Ig-like domain-containing protein	9597	Pan paniscus
A0A087QPM6	Complement receptor type 2 (Fragment)	9233	Aptenodytes forsteri
G1SJ10	Uncharacterized protein	9986	Oryctolagus cuniculus
A0A384CY66	membrane cofactor protein-like isoform X3	29073	Ursus maritimus
F7DTG0	Membrane cofactor protein	9544	Macaca mulatta
A0A384CYU7	coxsackievirus and adenovirus receptor isoform X1	29073	Ursus maritimus
A2RQD8	Alpha v integrin subunit variant	9823	Sus scrofa
A0A384CXB8	Membrane cofactor protein	29073	Ursus maritimus
W5Q2S6	Uncharacterized protein	9940	Ovis aries
F1P3M9	Uncharacterized protein	9031	Gallus gallus

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
P15529-14	Isoform I of Membrane cofactor protein	9606	Homo sapiens
F6Y367	Uncharacterized protein	9483	Callithrix jacchus
Q00609	T-lymphocyte activation antigen CD80	10090	Mus musculus
A0A3Q1MNG5	Membrane cofactor protein	9913	Bos taurus
A0A2I3SXR1	Membrane cofactor protein	9598	Pan troglodytes
A0A3Q2GTA9	Membrane cofactor protein	9796	Equus caballus
G1KK56	Uncharacterized protein	28377	Anolis carolinensis
A0A384CX64	Membrane cofactor protein	29073	Ursus maritimus
A0A452FP52	Uncharacterized protein	9925	Capra hircus
A0A2K5WCR2	Uncharacterized protein	9541	Macaca fascicularis
U3KP03	Uncharacterized protein	9986	Oryctolagus cuniculus
O88174	Membrane cofactor protein	10090	Mus musculus
A0A2R9BU76	Uncharacterized protein	9597	Pan paniscus
A0A2K6BVH5	Ig-like domain-containing protein	9545	Macaca nemestrina
A0A2R9BBR1	Integrin_alpha2 domain-containing protein	9597	Pan paniscus
L8Y2N0	Integrin alpha-5	246437	Tupaia chinensis
A0A2K5TTJ9	Ig-like domain-containing protein	9541	Macaca fascicularis
F7DTF4	Membrane cofactor protein	9544	Macaca mulatta
A0A2I3SBD4	Membrane cofactor protein	9598	Pan troglodytes
K9IJ75	Putative coxsackievirus and adenovirus receptor	9430	Desmodus rotundus
G3SGB2	Membrane cofactor protein	9595	Gorilla gorilla
A0A2K5U3I1	Uncharacterized protein	9541	Macaca fascicularis
R0J934	Integrin alpha-V (Fragment)	8839	Anas platyrhynchos
A0A2R8ZA38	Uncharacterized protein	9597	Pan paniscus
A0A3Q1M522	Membrane cofactor protein	9913	Bos taurus
A0A493TIE6	Uncharacterized protein	8840	Anas platyrhynchos
P42081	T-lymphocyte activation antigen CD86	9606	Homo sapiens
A0A0G2K0F2	Cd80 molecule	10116	Rattus norvegicus
I3M227	Integrin_alpha2 domain-containing protein	43179	Ictidomys tridecemlineatus

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
P15529-16	Isoform 3 of Membrane cofactor protein	9606	Homo sapiens
U3DYD0	Integrin alpha-V isoform 1	9483	Callithrix jacchus
P15529-9	Isoform N of Membrane cofactor protein	9606	Homo sapiens
F7D1Y8	Coxsackievirus and adenovirus receptor isoform 5	9483	Callithrix jacchus
A0A3L8SJK6	Uncharacterized protein	44316	Chloebia gouldiae
P15529-13	Isoform G of Membrane cofactor protein	9606	Homo sapiens
A0A2K5V5I7	Uncharacterized protein	9541	Macaca fascicularis
F1P8Q0	Integrin subunit alpha V	9615	Canis lupus
P42081-3	Isoform 2 of T-lymphocyte activation antigen CD86	9606	Homo sapiens
A0A402EAK3	Uncharacterized protein	143630	Paroedura picta
G7NXR4	Ig-like domain-containing protein (Fragment)	9541	Macaca fascicularis
A0A2I3S1I7	CD86 isoform 6	9598	Pan troglodytes
P42082	T-lymphocyte activation antigen CD86	10090	Mus musculus
F7DTG7	Uncharacterized protein	9544	Macaca mulatta
A0A3Q1LW07	Membrane cofactor protein	9913	Bos taurus
A0A2I2Z745	CD80 molecule	9595	Gorilla gorilla
A0A4X1UHA3	Uncharacterized protein	9823	Sus scrofa
A0A2I3TQP4	ITGAV isoform 2	9598	Pan troglodytes
A0A0D9RJD3	Integrin_alpha2 domain-containing protein	60711	Chlorocebus sabaeus
L9JFJ1	Complement receptor type 1	246437	Tupaia chinensis
W5PX64	Uncharacterized protein	9940	Ovis aries
A0A2K5WCL8	Membrane cofactor protein	9541	Macaca fascicularis
A0A2K6B3Y0	Membrane cofactor protein	9545	Macaca nemestrina
P80746	Integrin alpha-V	9913	Bos taurus
A0A2K5TTP4	Ig-like domain-containing protein	9541	Macaca fascicularis
A0A2K6BVG0	Ig-like domain-containing protein	9545	Macaca nemestrina
O19124	Membrane cofactor protein (Fragment)	9488	Saguinus mystax
P15529-2	Isoform B of Membrane cofactor protein	9606	Homo sapiens

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
A0A444TZR0	Integrin alpha-V	7906	Acipenser ruthenus
U3BXX1	Coxsackievirus and adenovirus receptor isoform 1	9483	Callithrix jacchus
L5MFL6	C4b-binding protein alpha chain	225400	Myotis davidii
A0A2I2Y735	CXADR Ig-like cell adhesion molecule	9595	Gorilla gorilla
P33681-3	Isoform 3 of T-lymphocyte activation antigen CD80	9606	Homo sapiens
H2R6C3	ITGAV isoform 1	9598	Pan troglodytes
A0A340WKG2	T-lymphocyte activation antigen CD80 isoform X1	118797	Lipotes vexillifer
A0A384DHE3	T-lymphocyte activation antigen CD86 isoform X2	29073	Ursus maritimus
F1P992	CXADR Ig-like cell adhesion molecule	9615	Canis lupus
A0A2K5TTN7	Ig-like domain-containing protein	9541	Macaca fascicularis
A0A2R8ZKX0	Uncharacterized protein	9597	Pan paniscus
A0A402FE69	Uncharacterized protein	143630	Paroedura picta
A0A093NBR2	T-lymphocyte activation antigen CD86 (Fragment)	9238	Pygoscelis adeliae
A0A2K6E8Y6	Uncharacterized protein	9545	Macaca nemestrina
A0A2I2UQ66	Uncharacterized protein	9685	Felis catus
R0LYX6	Complement component receptor 1-like protein (Fragment)	8839	Anas platyrhynchos
A0SVL1	Coxsackie virus and adenovirus receptor	9986	Oryctolagus cuniculus
A0A3Q2I4N2	Family with sequence similarity 171 member B	9796	Equus caballus
A0A2I2ZH70	Membrane cofactor protein	9595	Gorilla gorilla
G3QQK9	Integrin subunit alpha V	9595	Gorilla gorilla
P42081-6	Isoform 6 of T-lymphocyte activation antigen CD86	9606	Homo sapiens
A0A3Q2TUR0	Uncharacterized protein	9031	Gallus gallus
A0A0D9R932	Uncharacterized protein	60711	Chlorocebus sabaeus
W5Q553	Integrin_alpha2 domain-containing protein	9940	Ovis aries
M3Y0B3	Ig-like domain-containing protein	9669	Mustela putorius
F6T6Z4	CD86 molecule	9796	Equus caballus
A0A287D3L3	Membrane cofactor protein	43179	Ictidomys tridecemlineatus

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
A0A452EU10	Ig-like domain-containing protein	9925	Capra hircus
A0A093NZ42	Complement component receptor 1-like (Fragment)	9238	Pygoscelis adeliae
P78310-7	Isoform 7 of Cocksackievirus and adenovirus receptor	9606	Homo sapiens
A0A2K5WCM2	Membrane cofactor protein	9541	Macaca fascicularis
K9IXH5	Membrane cofactor protein	9430	Desmodus rotundus
A0A384BS93	LOW QUALITY PROTEIN: integrin alpha-V	29073	Ursus maritimus
H2QKV2	CXADR isoform 2	9598	Pan troglodytes
A0A2R8ZAA9	Membrane cofactor protein	9597	Pan paniscus
A0A2U4AB13	coxsackievirus and adenovirus receptor isoform X2	9739	Tursiops truncatus
A0A340YJF8	integrin alpha-V	118797	Lipotes vexillifer
F6SQZ6	Membrane cofactor protein	9796	Equus caballus
P43406	Integrin alpha-V	10090	Mus musculus
A0A2K5V5I3	Uncharacterized protein	9541	Macaca fascicularis
A0A2R8ZGY4	Uncharacterized protein	9597	Pan paniscus
A0A2R9AV57	Ig-like domain-containing protein	9597	Pan paniscus
G1MZB7	Integrin_alpha2 domain-containing protein	9103	Meleagris gallopavo
A0A452E0E1	Uncharacterized protein	9925	Capra hircus
O62837	Membrane cofactor protein	9490	Saguinus oedipus
M3XG84	Ig-like domain-containing protein	9685	Felis catus
M3YAK3	CD80 molecule	9669	Mustela putorius
A0A286X8N9	Ig-like domain-containing protein	10141	Cavia porcellus
P06756-3	Isoform 3 of Integrin alpha-V	9606	Homo sapiens
A0A2K6BAK6	Uncharacterized protein	9545	Macaca nemestrina
A0A2I3RKR6	ITGAV isoform 3	9598	Pan troglodytes
A0A2I2YLN0	Membrane cofactor protein	9595	Gorilla gorilla
A0A286XTS1	Ig-like domain-containing protein	10141	Cavia porcellus

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
R0LKZ7	Coxsackievirus and adenovirus receptor-like protein (Fragment)	8839	Anas platyrhynchos
A0A493SW93	Uncharacterized protein	8840	Anas platyrhynchos
G1TE34	Integrin_alpha2 domain-containing protein	9986	Oryctolagus cuniculus
Q9R066	Coxsackievirus and adenovirus receptor homolog	10116	Rattus norvegicus
A0A287BA36	Membrane cofactor protein	9823	Sus scrofa
H0WAT0	Ig-like domain-containing protein	10141	Cavia porcellus
A0A452FK06	Membrane cofactor protein	9925	Capra hircus
P70105	Membrane cofactor protein	10141	Cavia porcellus
A0A2K5WC94	A0A2K5WC94_MACFA Integrin_alpha2 domain-containing protein	9541	Macaca fascicularis
U3IFY9	Integrin subunit alpha V	8840	Anas platyrhynchos
G1MYD5	Complement C3b/C4b receptor 1 (Knops blood group)	9103	Meleagris gallopavo
A0A402FHA7	Uncharacterized protein	143630	Paroedura picta
A0A2R8MEU5	Membrane cofactor protein	9483	Callithrix jacchus
A0A2U3V9J7	Membrane cofactor protein	9739	Tursiops truncatus
A0A2U4AD33	T-lymphocyte activation antigen CD86 isoform X5	9739	Tursiops truncatus
A0A0G2JXF7	CD86 molecule	10116	Rattus norvegicus
F6U6L8	CXADR Ig-like cell adhesion molecule	9796	Equus caballus
M3XUZ6	Uncharacterized protein	9669	Mustela putorius
A0A2I3SPE6	Membrane cofactor protein	9598	Pan troglodytes
A0A2K5WC83	Integrin_alpha2 domain-containing protein	9541	Macaca fascicularis
A0A3L8S9S0	Uncharacterized protein (Fragment)	44316	Chloebia gouldiae
F7GNK4	Uncharacterized protein	9544	Macaca mulatta
K7GMU1	T-lymphocyte activation antigen CD86 isoform 1	9823	Sus scrofa
A0A2I2YDQ9	Membrane cofactor protein	9595	Gorilla gorilla
A0A093PA37	Integrin alpha-V (Fragment)	9238	Pygoscelis adeliae

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
L5MDM5	T-lymphocyte activation antigen CD86	225400	Myotis davidii
A0A3Q2I090	CD86 molecule	9796	Equus caballus
P15529-11	Isoform C of Membrane cofactor protein	9606	Homo sapiens
A0A087RH78	T-lymphocyte activation antigen CD86 (Fragment)	9233	Aptenodytes forsteri
A0A2I2UI18	Ig-like domain-containing protein	9685	Felis catus
G3QD59	CD46 molecule	9595	Gorilla gorilla
O35531	CD86 molecule	10116	Rattus norvegicus
P78310-2	Isoform 2 of Cocksackievirus and adenovirus receptor	9606	Homo sapiens
L5LU13	Membrane cofactor protein	225400	Myotis davidii
A0A2K5WCV3	Membrane cofactor protein	9541	Macaca fascicularis
A0A452FP68	Uncharacterized protein	9925	Capra hircus
A0A384CY70	Membrane cofactor protein	29073	Ursus maritimus
F1P8Z7	Membrane cofactor protein	9615	Canis lupus
P97792	Cocksackievirus and adenovirus receptor homolog	10090	Mus musculus
P78310-6	Isoform 6 of Cocksackievirus and adenovirus receptor	9606	Homo sapiens
A0A087R9M1	Integrin alpha-V (Fragment)	9233	Aptenodytes forsteri
A0A2K6B3Y8	Membrane cofactor protein	9545	Macaca nemestrina
A0A287AU18	Uncharacterized protein	9823	Sus scrofa
P42081-4	Isoform 4 of T-lymphocyte activation antigen CD86	9606	Homo sapiens
A0A3Q1MGH4	Membrane cofactor protein	9913	Bos taurus
A0A2U3V2K6	integrin alpha-V isoform X1	9739	Tursiops truncatus
A0A2U4ADM4	T-lymphocyte activation antigen CD86 isoform X2	9739	Tursiops truncatus
A0A1D5QU78	Ig-like domain-containing protein	9544	Macaca mulatta
A0A2I2ZYV5	CD86 molecule	9595	Gorilla gorilla
G1PS43	IGv domain-containing protein	59463	Myotis lucifugus

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
A0A2K6AUD0	Integrin_alpha2 domain-containing protein	9545	Macaca nemestrina
A0A2I3T408	Membrane cofactor protein	9598	Pan troglodytes
F6QSK2	Integrin_alpha2 domain-containing protein	9544	Macaca mulatta
A0A2I3S9X7	CXADR isoform 1	9598	Pan troglodytes
W5Q2S5	Uncharacterized protein	9940	Ovis aries
A0A093NYC3	Coxsackievirus and adenovirus receptor (Fragment)	9238	Pygoscelis adeliae
A0A384CY69	Membrane cofactor protein	29073	Ursus maritimus
A0A2R9AVG5	Ig-like domain-containing protein	9597	Pan paniscus
F6ZPI6	Membrane cofactor protein	9796	Equus caballus
A0A2R9BBR5	Integrin_alpha2 domain-containing protein	9597	Pan paniscus
A0A3Q2H9C4	Membrane cofactor protein	9796	Equus caballus
A0A3Q1NCV9	CD86 molecule	9913	Bos taurus
H2QN76	CD86 isoform 3	9598	Pan troglodytes
G3QGF6	CXADR Ig-like cell adhesion molecule	9595	Gorilla gorilla
L9JBT2	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2	246437	Tupaia chinensis
A0A4X1TD61	Membrane cofactor protein	9823	Sus scrofa
U3EIU8	Membrane cofactor protein	9483	Callithrix jacchus
A0A3Q2HBD4	Uncharacterized protein	9796	Equus caballus
Q3BKZ5	CD86	9031	Gallus gallus
A0A384DH87	T-lymphocyte activation antigen CD86 isoform X3	29073	Ursus maritimus
A0A1D5Q8U5	Ig-like domain-containing protein	9544	Macaca mulatta
A0A2I2Z7U0	Integrin subunit alpha V	9595	Gorilla gorilla
A0A2R8ZED4	Membrane cofactor protein	9597	Pan paniscus
L5LNV3	Integrin alpha-V	225400	Myotis davidii
A0A337SQF7	Integrin_alpha2 domain-containing protein	9685	Felis catus
A0A2U4AB14	T-lymphocyte activation antigen CD80 isoform X3	9739	Tursiops truncatus
A0A2I2ZA62	Integrin subunit alpha V	9595	Gorilla gorilla
A0A2J8M3S7	CD86 isoform 7	9598	Pan troglodytes

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
G1P1A5	Uncharacterized protein	59463	Myotis lucifugus
P06756	Integrin alpha-V	9606	Homo sapiens
A0A337SXP9	Integrin_alpha2 domain-containing protein	9685	Felis catus
W5QFU6	Ig-like domain-containing protein	9940	Ovis aries
A0A2R9B7W7	Integrin_alpha2 domain-containing protein	9597	Pan paniscus
A0A1D5QDK0	Uncharacterized protein	9544	Macaca mulatta
A0A2I2Y3S6	Membrane cofactor protein	9595	Gorilla gorilla
H9GFU8	Uncharacterized protein	28377	Anolis carolinensis
A0A2K6BVG5	Ig-like domain-containing protein	9545	Macaca nemestrina
Q9TTF1	CD86 molecule	9615	Canis lupus
G1PLV3	Uncharacterized protein	59463	Myotis lucifugus
P15529-5	Isoform H of Membrane cofactor protein	9606	Homo sapiens
A0A2J8M3E9	CD80 isoform 1	9598	Pan troglodytes
G1NMI6	Uncharacterized protein	9103	Meleagris gallopavo
G1NNS6	Uncharacterized protein	9103	Meleagris gallopavo
Q9TQX1	B7-1 protein	9615	Canis lupus
A0A2K5WCS2	Membrane cofactor protein	9541	Macaca fascicularis
H2Q117	CD46 isoform 5	9598	Pan troglodytes
W5PWS0	Membrane cofactor protein	9940	Ovis aries
A0A2K5WCR4	Membrane cofactor protein	9541	Macaca fascicularis
A0A2U4AD29	T-lymphocyte activation antigen CD86 isoform X6	9739	Tursiops truncatus
H0VG28	Uncharacterized protein	10141	Cavia porcellus
P15529-10	Isoform 2 of Membrane cofactor protein	9606	Homo sapiens
G1T1I0	T-lymphocyte activation antigen CD86	9986	Oryctolagus cuniculus
F7CBS5	Integrin subunit alpha V	9483	Callithrix jacchus
A0A2U4AAN9	T-lymphocyte activation antigen CD80 isoform X1	9739	Tursiops truncatus
Q9GMZ8	B-lymphocyte activation antigen B7-1 (CD80)	9685	Felis catus
A0A2I2Y6M3	Membrane cofactor protein	9595	Gorilla gorilla
Q9TT71	CD80 protein	9823	Sus scrofa
A0A340X2P7	Membrane cofactor protein	118797	Lipotes vexillifer

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
P78310	Coxsackievirus and adenovirus receptor	9606	Homo sapiens
G1PZF1	Uncharacterized protein	59463	Myotis lucifugus
A0A2R8ZEB7	Membrane cofactor protein	9597	Pan paniscus
P15529-15	Isoform K of Membrane cofactor protein	9606	Homo sapiens
A0A2R8ZH17	Membrane cofactor protein	9597	Pan paniscus
F7HRG1	Uncharacterized protein	9544	Macaca mulatta
F6UTY5	Uncharacterized protein	9796	Equus caballus
A0A0X9R1W5	CD86 antigen	9031	Gallus gallus
A0A3Q2H388	Membrane cofactor protein	9796	Equus caballus
A0A2I2ZAI2	CD86 molecule	9595	Gorilla gorilla
A0A0D9RRP8	Membrane cofactor protein	60711	Chlorocebus sabaeus
A0A2K6AUD2	Integrin_alpha2 domain-containing protein	9545	Macaca nemestrina
A0A2I3RTP0	Membrane cofactor protein	9598	Pan troglodytes
P15529-6	Isoform J of Membrane cofactor protein	9606	Homo sapiens
H9G5P5	Integrin_alpha2 domain-containing protein	28377	Anolis carolinensis
F7DT48	Membrane cofactor protein	9544	Macaca mulatta
A0A2I3TEA5	Membrane cofactor protein	9598	Pan troglodytes
P15529-8	Isoform M of Membrane cofactor protein	9606	Homo sapiens
A0A1D5RJA5	Integrin_alpha2 domain-containing protein	9544	Macaca mulatta
P33681-2	Isoform 2 of T-lymphocyte activation antigen CD80	9606	Homo sapiens
F7IJZ6	Integrin subunit alpha V	9483	Callithrix jacchus
A0A2C9F1E0	Membrane cofactor protein	10141	Cavia porcellus
G1Q2I6	Membrane cofactor protein	59463	Myotis lucifugus
A0A384CZQ4	coxsackievirus and adenovirus receptor isoform X2	29073	Ursus maritimus
G1P9X0	Integrin_alpha2 domain-containing protein	59463	Myotis lucifugus
F7FY86	Integrin_alpha2 domain-containing protein	9544	Macaca mulatta

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
Q9TTF2	B7-2 protein	9615	Canis lupus
P15529-4	Isoform F of Membrane cofactor protein	9606	Homo sapiens
G1SXC4	T-lymphocyte activation antigen CD80	9986	Oryctolagus cuniculus
A0A087R8Z7	Coxsackievirus and adenovirus receptor (Fragment)	9233	Aptenodytes forsteri
A0A0D9R4U3	Ig-like domain-containing protein	60711	Chlorocebus sabaeus
Q8WMV3	Coxsackievirus and adenovirus receptor homolog	9913	Bos taurus
F7HAP5	CD86 molecule	9483	Callithrix jacchus
M3XWP9	Integrin subunit alpha V	9669	Mustela putorius
O19121	Membrane cofactor protein (Fragment)	9557	Papio hamadryas
Q9Z0M4	Membrane cofactor protein	10116	Rattus norvegicus
A0A384DHB6	T-lymphocyte activation antigen CD80	29073	Ursus maritimus
A0A493TJF9	CD86 molecule	8840	Anas platyrhynchos
L9KTN4	CXADR-like membrane protein	246437	Tupaia chinensis
A0A2I3S3E5	CD86 isoform 2	9598	Pan troglodytes
P15529-7	Isoform L of Membrane cofactor protein	9606	Homo sapiens
A0A2K6BVH6	Ig-like domain-containing protein	9545	Macaca nemestrina
I3M0T8	Ig-like domain-containing protein	43179	Ictidomys tridecemlineatus
A0A2I3T2N6	CD80 isoform 3	9598	Pan troglodytes
A0A337S2K2	Uncharacterized protein	9685	Felis catus
A0A3L8SFX0	Integrin_alpha2 domain-containing protein	44316	Chloebia gouldiae
A0A3Q1LT83	Coxsackievirus and adenovirus receptor homolog	9913	Bos taurus
A0A2K6E8Y5	Uncharacterized protein	9545	Macaca nemestrina
K9IJ17	Membrane cofactor protein	9430	Desmodus rotundus
P15529	Membrane cofactor protein	9606	Homo sapiens
P33681	T-lymphocyte activation antigen CD80	9606	Homo sapiens
P15529-12	Isoform E of Membrane cofactor protein	9606	Homo sapiens

Universal Protein Knowledgebase Accession	Protein Name	Host Taxonomy Identifier	Host Scientific Name
A0A2K6B3V3	Membrane cofactor protein	9545	Macaca nemestrina
A0A3L8RUJ1	Uncharacterized protein	44316	Chloebia gouldiae
A0A2U4CQ12	membrane cofactor protein-like	9739	Tursiops truncatus
A2AKI5	Integrin alpha-V	10090	Mus musculus
F1N4W4	Membrane cofactor protein	9913	Bos taurus
F7DTH4	Membrane cofactor protein	9544	Macaca mulatta
A0A0D9R3Y3	Ig-like domain-containing protein	60711	Chlorocebus sabaues
A0A287CYN8	Membrane cofactor protein	43179	Ictidomys tridecemlineatus
A0A340YI73	coxsackievirus and adenovirus receptor homolog	118797	Lipotes vexillifer
F1LZX9	Integrin subunit alpha V	10116	Rattus norvegicus
A0A2K6B3Z3	Membrane cofactor protein	9545	Macaca nemestrina
A0A2U4AB51	coxsackievirus and adenovirus receptor isoform X1	9739	Tursiops truncatus
W5QES9	Uncharacterized protein	9940	Ovis aries
A0A3L8S534	Uncharacterized protein	44316	Chloebia gouldiae
P15529-3	Isoform D of Membrane cofactor protein	9606	Homo sapiens
A0A2K5WCL7	Membrane cofactor protein	9541	Macaca fascicularis
A0A340WLZ1	T-lymphocyte activation antigen CD86 isoform X2	118797	Lipotes vexillifer
A0A3S5ZP81	CD80 molecule	9913	Bos taurus
A0A2R8PB83	Membrane cofactor protein	9483	Callithrix jacchus

Appendix D. Adenovirus Fiber Proteins

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A1Y0B6I6	Fiber protein	2170000	Deer mastadenovirus B
Q03553	Fiber protein	10510	Bovine adenovirus B serotype 3
G9HQI9	Fiber protein	10510	Bovine adenovirus B serotype
A0A1B0XBD0	Fiber protein	46916	Equine adenovirus A serotype 1
D6PSN1	Long fiber protein (Fragment)	10553	Fowl adenovirus A serotype 1 (strain CELO / Phelps)
A0A1L4BI69	Long fiber protein (Fragment)	190061	Fowl aviadenovirus A
A0A1L4BI74	Long fiber protein (Fragment)	190061	Fowl aviadenovirus A
E6YE24	Long fiber protein (Fragment)	190061	Fowl aviadenovirus A
E6YE23	Long fiber protein (Fragment)	190061	Fowl aviadenovirus A
A0A5H2WYN6	Fiber protein	2559941	Crane-associated adenovirus 1
Q64761	Fiber protein 1	10553	Fowl adenovirus A serotype 1 (strain CELO / Phelps)
A0A1L5YQN4	Long fiber protein	190061	Fowl aviadenovirus A
A0A5J6DCX8	Fiber protein	2608978	Siadenovirus IDL19-3602
S4TZF2	Fiber protein (Fragment)	130329	Duck adenovirus 1
S4TZF1	Fiber protein (Fragment)	130329	Duck adenovirus 1
S4TZM5	Fiber protein (Fragment)	130329	Duck adenovirus 1
A6N8P6	Fiber protein	130329	Duck adenovirus 1
S4TZI9	Fiber protein (Fragment)	130329	Duck adenovirus 1
S4TZH1	Fiber protein (Fragment)	130329	Duck adenovirus 1
A0A0D3MWP3	Fiber protein	130329	Duck adenovirus 1
S4TZM6	Fiber protein (Fragment)	130329	Duck adenovirus 1
O11424	Fiber protein	130329	Duck adenovirus 1
S4TZM1	Fiber protein (Fragment)	130329	Duck adenovirus 1
A1E166	Fiber protein	130329	Duck adenovirus 1
A0A0D3MW31	Fiber protein	130329	Duck adenovirus 1

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A348FKH7	Fiber protein	2039267	Eidolon helvum adenovirus
P19721	Fiber protein	10530	Murine adenovirus A serotype 1
P36711	Fiber protein	28282	Human adenovirus A serotype 12
D3JIU4	Fiber protein	10528	Human adenovirus A serotype 18
P03275	Fiber protein	10515	Human adenovirus C serotype 2
Q6R2L0	Fiber protein	114408	Feline adenovirus
Q911A0	Fiber protein	10515	Human adenovirus C serotype 2
Q911A1	Fiber protein	10515	Human adenovirus C serotype 2
A0A0E3STY8	Fiber protein	10515	Human adenovirus C serotype
Q53ZZ9	Fiber	10515	Human adenovirus C serotype 2
Q76DN7	Fiber protein	10533	Human adenovirus C serotype 1
Q910N0	Fiber protein	10515	Human adenovirus C serotype 2
P11818	Fiber protein	28285	Human adenovirus C serotype 5
Q6VGT5	Fiber protein	28285	Human adenovirus C serotype 5
A0A128A6F9	Fiber protein	1354736	Fowl adenovirus
A0A128A6E4	Fiber protein	1354736	Fowl adenovirus
M4GPH0	Fiber protein	172857	Fowl aviadenovirus 11
A0A128A6F1	Fiber protein	1354736	Fowl adenovirus
A0A291FDB0	Fiber protein	190064	Fowl aviadenovirus D
A0A096ZH22	Fiber	190064	Fowl aviadenovirus D
M4GQP9	Fiber protein	172857	Fowl aviadenovirus 11
Q77VH5	Fiber protein	172864	Fowl aviadenovirus 9
A0A128A6H0	Fiber protein	1354736	Fowl adenovirus
A0A128A6G4	Fiber protein	1354736	Fowl adenovirus
A0A128A6E1	Fiber protein	1354736	Fowl adenovirus
A0A128A6G8	Fiber protein	1354736	Fowl adenovirus
A0A128A6F3	Fiber protein	1354736	Fowl adenovirus
A0A128A6F5	Fiber protein	1354736	Fowl adenovirus
A0A128A6H1	Fiber protein	1354736	Fowl adenovirus
A0A128A6G7	Fiber protein	1354736	Fowl adenovirus
A0A128A6E0	Fiber protein	1354736	Fowl adenovirus
A0A128A6G9	Fiber protein	1354736	Fowl adenovirus
A0A128A6F2	Fiber protein	1354736	Fowl adenovirus

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A128A6E7	Fiber protein	1354736	Fowl adenovirus
A0A128A6E6	Fiber protein	1354736	Fowl adenovirus
P14267	Fiber protein 1	10524	Human adenovirus F serotype 4
F8WQR3	Long fiber protein	10524	Human adenovirus F serotype 4
A0A060ILR1	Long fiber protein	10524	Human adenovirus F serotype 4
A0A1S6EM21	Long fiber protein	10524	Human adenovirus F serotype 4
F8WQR2	Long fiber protein	10524	Human adenovirus F serotype 4
A0A1S6ELR1	Long fiber protein	10524	Human adenovirus F serotype 4
B5SNT7	Long fiber protein	10524	Human adenovirus F serotype 4
F8WQR6	Long fiber protein	10524	Human adenovirus F serotype 4
E2IJZ9	Long fiber protein	10524	Human adenovirus F serotype 4
F8WQR7	Long fiber protein	10524	Human adenovirus F serotype 4
Q9DL D8	Fiber protein	114429	Bovine adenovirus 2
P36848	Fiber protein	10529	Human adenovirus A serotype 31
A7LKA1	Fiber protein	10529	Human adenovirus A serotype 3
D0Z5U5	Fiber protein	10529	Human adenovirus A serotype 31
A0A2Z5DSR2	Fiber protein	190064	Fowl aviadenovirus D
A0A128A6E9	Fiber protein	1354736	Fowl adenovirus
A0A5H2QAI6	Fiber protein	10529	Human adenovirus A serotype 31
A0A128A6H2	Fiber protein	1354736	Fowl adenovirus
A0A128A6D9	Fiber protein	1354736	Fowl adenovirus
A0A128A6H4	Fiber protein	1354736	Fowl adenovirus
D3X7D1	Fiber protein	727977	Bat adenovirus TJM
H8WR01	Fiber protein	190062	Fowl aviadenovirus B
H8WG79	Fiber protein (Fragment)	190062	Fowl aviadenovirus B
Q8B4M4	Fiber protein subtype B	114429	Bovine adenovirus 2
P18047	Fiber protein 1	28284	Human adenovirus F serotype 4
F8WQR8	Long fiber protein	10524	Human adenovirus F serotype 4
F8WQR5	Long fiber protein	10524	Human adenovirus F serotype 4

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
Q96689	Fiber protein	69151	Canine adenovirus serotype 1 (strain RI261)
P22230	Fiber protein	10513	Canine adenovirus serotype 1 (strain Glaxo)
Q65961	Fiber protein	69150	Canine adenovirus serotype 1 (strain CLL)
Q65914	Fiber protein	69152	Canine adenovirus serotype 2 (strain Toronto A 26-61)
C7E2U3	Fiber protein	10537	Canine mastadenovirus
V9XSE0	Fiber protein	10514	Canine adenovirus serotype
A0A128A6G0	Fiber protein	1354736	Fowl adenovirus
A0A128A6H6	Fiber protein	1354736	Fowl adenovirus
A0A348FV83	Fiber protein	879186	Human adenovirus 57
W6A1S0	Fiber protein	879186	Human adenovirus 57
J7IEE1	Fiber	129951	Human mastadenovirus C
Q76DN6	Fiber	10534	Human adenovirus C serotype 6
A0A128A6F4	Fiber protein	1354736	Fowl adenovirus
A0A128A6G2	Fiber protein	1354736	Fowl adenovirus
A0A128A6F0	Fiber protein	1354736	Fowl adenovirus
A0A128A6G6	Fiber protein	1354736	Fowl adenovirus
A0A128A6H7	Fiber protein	1354736	Fowl adenovirus
A0A128A6F7	Fiber protein	1354736	Fowl adenovirus
A0A128A6E8	Fiber protein	1354736	Fowl adenovirus
A0A128A6G1	Fiber protein	1354736	Fowl adenovirus
A0A128A6I5	Fiber protein	1354736	Fowl adenovirus
A0A128A6F6	Fiber protein	1354736	Fowl adenovirus
A0A128A6I1	Fiber protein	1354736	Fowl adenovirus
M4GPG9	Fiber protein	66295	Avian adenovirus 8 (strain ATCC A-2A)
M4GQ34	Fiber protein	66295	Avian adenovirus 8 (strain ATCC A-2A)
E9KLB3	Fiber protein	190065	Fowl aviadenovirus E
A0A128A6G3	Fiber protein	1354736	Fowl adenovirus
A0A2H4WB13	Fiber protein	190065	Fowl aviadenovirus E
M4GPQ0	Fiber protein	66295	Avian adenovirus 8 (strain ATCC A-2A)
M4GQ32	Fiber protein	66295	Avian adenovirus 8 (strain ATCC A-2A)
A0A1B2TSK2	Fiber protein	190065	Fowl aviadenovirus E
A0A128A6I2	Fiber protein	1354736	Fowl adenovirus
A0A128A6H5	Fiber protein	1354736	Fowl adenovirus
A0A128A6F8	Fiber protein	1354736	Fowl adenovirus

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A128A6I3	Fiber protein	1354736	Fowl adenovirus
A0A128A6G5	Fiber protein	1354736	Fowl adenovirus
A0A1D8DE10	Fiber protein	190065	Fowl aviadenovirus E
A0A128A6D8	Fiber protein	1354736	Fowl adenovirus
A0A160CBM7	Fiber protein	586029	Fowl adenovirus 8b
Q994D4	Fiber protein	45370	Porcine adenovirus
A0A173ADT9	Fiber protein 2	130663	Fowl aviadenovirus 4
C5IK07	Fiber protein	130663	Fowl aviadenovirus 4
Q98XR5	Fiber	78522	Odocoileus adenovirus
A0A0K1DBU9	Fiber protein	67603	Equine adenovirus B serotype
A0A513PXU9	Fiber protein (Fragment)	114326	Porcine adenovirus
F4MI11	Fiber protein	1520002	Raptor adenovirus 1
O55281	Short fiber protein	10547	Fowl adenovirus C serotype 10 (strain SA2)
O56261	Fiber protein	41678	Turkey adenovirus
Q9YUQ4	Fiber protein	41678	Turkey adenovirus 3
Q83457	Fiber protein	35265	Porcine adenovirus A serotype 3
A0A1L1Z7M7	Fiber protein	10535	unidentified adenovirus
A0A1L1Z7J6	Fiber protein	10535	unidentified adenovirus
A0A162HSS4	Fiber protein	10535	unidentified adenovirus
A0A161CH96	Fiber protein	2005055	Penguin siadenovirus A
A0A173ADN4	Fiber protein 1	130663	Fowl aviadenovirus 4
Q96731	Fiber protein	66295	Avian adenovirus 8 (strain ATCC A-2A)
P36844	Fiber protein	28280	Human adenovirus E serotype 4
Q64855	Fiber protein	28280	Human adenovirus E serotype
Q6BEA6	Fiber protein	28280	Human adenovirus E serotype
Q6BEA4	Fiber protein	28280	Human adenovirus E serotype
Q6BEA5	Fiber protein	28280	Human adenovirus E serotype
A0A3G9K966	Fiber protein	35263	Human adenovirus 4a
A0A5H2V2M5	Fiber protein	35263	Human adenovirus 4a
A0A5H2V6T8	Fiber protein	35263	Human adenovirus 4a
A0A2R3WNY1	Fiber protein	130308	Human mastadenovirus E
A0A2R3WNN6	Fiber protein	130308	Human mastadenovirus E
A0A2L1F3D2	Fiber protein	130308	Human mastadenovirus E
A0A3G9JU55	Fiber protein	35263	Human adenovirus 4a
Q6BEA7	Fiber protein	28280	Human adenovirus E

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
			serotype
A0A3G9CMS6	Fiber protein	1643781	Human adenovirus 4p
Q2KSD3	Fiber	28280	Human adenovirus E serotype 4
A0A5H2V235	Fiber protein	35263	Human adenovirus 4a
A0A3G1S679	Fiber protein	28280	Human adenovirus E serotype 4
Q5VHA2	Fiber	28280	Human adenovirus E serotype 4
Q6H1A8	Fiber	130308	Human mastadenovirus E
Q2KSP0	Fiber	28280	Human adenovirus E serotype 4
A0A3G9JV37	Fiber protein	35263	Human adenovirus 4a
A0A3G9JZY5	Fiber protein	35263	Human adenovirus 4a
A9CB96	Fiber protein	189830	Snake adenovirus serotype 1
Q64762	Fiber protein 2	10553	Fowl adenovirus A serotype 1 (strain CELO / Phelps)
A0A1L5YQN3	L5 fiber 2	190061	Fowl aviadenovirus A
E6YE25	Short fiber protein (Fragment)	190061	Fowl aviadenovirus A
E6YE26	Short fiber protein (Fragment)	190061	Fowl aviadenovirus A
A0A0K0PX17	Fiber protein (Fragment)	108098	Human mastadenovirus B
E6YE27	Short fiber protein (Fragment)	190061	Fowl aviadenovirus A
P16883	Fiber protein 2	10524	Human adenovirus F serotype 4
P18048	Fiber protein 2	28284	Human adenovirus F serotype 4
A0A1S6EM08	Short fiber protein	10524	Human adenovirus F serotype 4
W0S1J1	Short fiber protein	10524	Human adenovirus F serotype 4
F8WQQ9	Short fiber protein	10524	Human adenovirus F serotype 4
A0A3G4W9B6	Short fiber protein	10524	Human adenovirus F serotype 4
F8WQQ4	Short fiber protein	10524	Human adenovirus F serotype 4
B5SNT6	Short fiber protein	10524	Human adenovirus F serotype 4
F8WQQ3	Short fiber protein	10524	Human adenovirus F serotype 4
E2IJZ8	Short fiber	10524	Human adenovirus F serotype 4

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
B8LFM5	Fiber protein	46922	Human adenovirus D serotype 1
D6PSN0	Short fiber protein (Fragment)	10553	Fowl adenovirus A serotype 1 (strain CELO / Phelps)
D2CH24	Fiber protein	433356	Human adenovirus 38H44
B5BQ06	Fiber protein	46924	Human adenovirus 2
A0A3S6PYI6	Fiber protein	130310	Human mastadenovirus D
C5HDT4	Fiber protein	46924	Human adenovirus 22
Q86843	Fiber protein	31545	Human adenovirus D serotype 8
Q8V2D0	Fiber protein	46932	Human adenovirus 3
G9JUY3	Fiber protein	1124795	Human adenovirus 63
Q76QY0	Fiber protein	28276	Human adenovirus D serotype 1
A0A291B0G3	Fiber protein	130310	Human mastadenovirus D
A0A0K0PXB3	Fiber protein (Fragment)	108098	Human mastadenovirus B
A0A0K0PXC4	Fiber protein	108098	Human mastadenovirus B
P36847	Fiber protein	28276	Human adenovirus D serotype 15
B5BQ05	Fiber	28275	Human adenovirus D10
O56783	Fiber	46922	Human adenovirus D serotype 17
A0A1Y1BYV9	Fiber protein	52275	Human adenovirus D37
A0A1Y1BYT6	Fiber protein	52275	Human adenovirus D37
Q5H8B4	Fiber	52275	Human adenovirus D37
A0A1Y1BYA0	Fiber protein	1907210	Human adenovirus sp.
M5A9G0	Fiber protein	88059	Human adenovirus 19
A0A1Y1C426	Fiber protein	52275	Human adenovirus D37
A0A1Y1BXS8	Fiber protein	1907210	Human adenovirus sp.
A0A1Y1C1Z8	Fiber protein	1907210	Human adenovirus sp.
E5RW25	Fiber	130310	Human mastadenovirus D
E5RW61	Fiber protein	130310	Human mastadenovirus D
Q76SK0	Fiber	28278	Human adenovirus 19
I0FX58	Fiber	130310	Human mastadenovirus D
Q64823	Fiber	52275	Human adenovirus D37
Q64822	Fiber	28278	Human adenovirus 19
A0A1Y1BYE1	Fiber protein	1907210	Human adenovirus sp.
H6WWB5	Fiber	1145295	Human adenovirus 64
A0A1U9XRC4	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRB6	Fiber protein (Fragment)	190065	Fowl aviadenovirus E

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A291L0X2	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRB0	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRA6	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRA3	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRB1	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A291L0W8	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRB7	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRC0	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A291L0W9	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A291L0X0	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
A0A1U9XRA8	Fiber protein (Fragment)	190065	Fowl aviadenovirus E
P68982	Fiber protein	10527	Human adenovirus D serotype 9
P68983	Fiber protein	308444	Human adenovirus D serotype 15/H9
P36845	Fiber protein	31545	Human adenovirus D serotype 8
Q75Q72	Fiber protein	31545	Human adenovirus D serotype 8
Q75Q71	Fiber protein	31545	Human adenovirus D serotype 8
A0A0P0HKP5	Fiber protein	31545	Human adenovirus D serotype
C8Z281	Fiber protein (Fragment)	10528	Human adenovirus A serotype 18
A0A481UJA1	Fiber protein	31545	Human adenovirus D serotype 8
Q5TIY8	39.3 kDa fiber protein	10527	Human adenovirus D serotype 9
A0A075TT07	Fiber protein	130310	Human mastadenovirus D
A0A0P0IE94	Fiber protein	31545	Human adenovirus D serotype
Q75Q70	Fiber	31545	Human adenovirus D serotype 8
A0A0N7IQH1	Fiber	31545	Human adenovirus D serotype 8
B5BQ11	Fiber	130310	Human mastadenovirus D
F2ZCA2	Fiber protein	216370	Human adenovirus 8E

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
F8UFS4	Fiber protein	130310	Human mastadenovirus D
A0A3G5BEE1	Fiber protein	130310	Human mastadenovirus D
A0A0P0IJM8	Fiber protein	31545	Human adenovirus D serotype
A0A1Y1C1I3	Fiber protein	31545	Human adenovirus D serotype 8
Q75Q69	Fiber protein	216370	Human adenovirus 8E
A0A4P2XI02	Fiber protein	130310	Human mastadenovirus D
A0A3G5BEE3	Fiber protein	130310	Human mastadenovirus D
E5RWD1	Fiber protein	556926	Human adenovirus 53
E1AI37	Fiber	880565	Human adenovirus 56
A0A1Y1BYZ2	Fiber protein	880565	Human adenovirus 56
Q6I7S0	Fiber protein	10527	Human adenovirus D serotype
A0A4P2XIT6	Fiber protein	130310	Human mastadenovirus D
B9A5P2	Fiber	651580	Human adenovirus 54
M0QVJ5	Fiber	46938	Human adenovirus 43
O56784	Fiber	46930	Human adenovirus 2
K7NG54	Fiber protein	1096763	Human adenovirus 68
R4HLF4	Fiber protein	31544	Human adenovirus B serotype 16
Q67711	Fiber protein	31544	Human adenovirus B serotype 16
P15141	Fiber protein	10519	Human adenovirus B serotype 7
A0A1L6C3Z6	Fiber protein (Fragment)	1354736	Fowl adenovirus
C8ZJU5	Fiber protein (Fragment)	650128	Human adenovirus D46H13
C8ZJU3	Fiber protein (Fragment)	650126	Human adenovirus D37H13
C8ZJU2	Fiber protein (Fragment)	650125	Human adenovirus D30H44
A0A0K0PY92	Fiber protein (Fragment)	108098	Human mastadenovirus B
P35773	Fiber protein	343463	Human adenovirus B serotype 11 (strain BC34)
P35774	Fiber protein	343462	Human adenovirus B serotype 11 (strain Slobiski)
Q76I92	Fiber protein	262789	Human adenovirus 35+11
A0A1L7NRL0	Fiber protein	108098	Human mastadenovirus B
A0A1B1CQI4	Fiber protein	10519	Human adenovirus B serotype 7
D6BP15	Fiber protein	693059	Human adenovirus 14p
A0A411EE39	Fiber protein	10519	Human adenovirus B

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
			serotype
A0A0K0PX16	Fiber protein (Fragment)	108098	Human mastadenovirus B
A0A219PCA0	L5 fiber protein	10519	Human adenovirus B serotype
Q508T0	L5 fiber protein	316517	Human adenovirus 7p
Q508S2	L5 fiber protein	310800	Human adenovirus 7l
Q508Q6	L5 fiber protein	101029	Human adenovirus 7d
S4UNB6	Fiber protein	714978	Human adenovirus 55
A0A219PCB6	L5 fiber protein	10521	Human adenovirus 1
D6BP12	Fiber protein	343463	Human adenovirus B serotype 11 (strain BC34)
Q5EY45	Fiber	10519	Human adenovirus B serotype 7
C7ED82	Fiber protein	10519	Human adenovirus B serotype
Q9PWU3	Fiber	10519	Human adenovirus B serotype 7
A0A1W6HVK2	Fiber protein	1907210	Human adenovirus sp.
Q6RK74	Fiber	10519	Human adenovirus B serotype 7
Q67713	Fiber protein	35261	Human adenovirus 34
C7ED85	Fiber protein	10519	Human adenovirus B serotype
Q77SK6	Fiber protein	101029	Human adenovirus 7d
Q9QL91	Fiber protein	85755	Human adenovirus 7a
Q2KS49	Fiber	10519	Human adenovirus B serotype 7
W6EK83	Fiber protein	1461395	Human adenovirus 11+34
Q75Q64	Fiber protein	10541	Human adenovirus 11
S4UM78	Fiber 35.3 kDa protein	714978	Human adenovirus 55
S5YS77	Fiber L5	565303	Human adenovirus B2
C7SRR8	353 kDa protein fiber	714978	Human adenovirus 55
Q508R4	Fiber protein	326124	Human adenovirus 7d2
C7ED83	Fiber protein	10519	Human adenovirus B serotype
Q508Q2	L5 fiber protein	101029	Human adenovirus 7d
A0A1L7NRN8	Fiber protein	1930638	Human adenovirus B79
A0A5F2P2A8	Fiber protein	10519	Human adenovirus B serotype 7
A0A3Q8D118	Fiber protein	1907210	Human adenovirus sp.
Q8V791	Fiber protein	10521	Human adenovirus 14
J7IAF2	Fiber	108098	Human mastadenovirus B
C6G826	Fiber	343463	Human adenovirus B serotype 11 (strain BC34)

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
D6BP11	Fiber protein	343463	Human adenovirus B serotype 11 (strain BC34)
C8ZJU0	Fiber protein (Fragment)	650123	Human adenovirus D17H29
A0A0K0PX90	Fiber protein	108098	Human mastadenovirus B
Q3ZKS7	Fiber protein	107462	Human adenovirus 50
Q67714	Fiber protein	35262	Human adenovirus type 35
A0A075IQB3	Fiber protein	1521028	Human adenovirus 21a
Q67712	Fiber protein	32608	Human adenovirus 2
Q3ZKX3	Fiber protein	10548	Human adenovirus 34
D7RGN5	Fiber protein	326124	Human adenovirus 7d2
Q91CL7	Fiber protein	10548	Human adenovirus 3
A0A219PCJ9	Fiber protein	714978	Human adenovirus 55
Q3T477	Fiber protein	321934	Human adenovirus 50 prototype strain Wan
D6BP13	Fiber protein	814922	Human adenovirus 14p1
C3UZM0	Fiber	10521	Human adenovirus 14
A0A2D1QVC8	Fiber protein	108098	Human mastadenovirus B
Q2KS96	Fiber protein	32608	Human adenovirus 21
A0A0B4SHV7	Fiber protein	32608	Human adenovirus 21
C8ZJU1	Fiber protein (Fragment)	650124	Human adenovirus D19H30
C8ZJU4	Fiber protein (Fragment)	650127	Human adenovirus D37H17
P04501	Fiber protein	45659	Human adenovirus B serotype 3
S4WZU2	Fiber protein	45659	Human adenovirus B serotype
A0A0K0PX23	Fiber protein (Fragment)	108098	Human mastadenovirus B
R4HLB2	Fiber protein	1337398	Human adenovirus 66
S4X4Y5	Fiber protein	45659	Human adenovirus B serotype
A0A1U9ALJ6	Fiber protein	45659	Human adenovirus B serotype 3
A0A3Q8CP90	Fiber protein	1907210	Human adenovirus sp.
Q2Y0F8	Fiber protein	45659	Human adenovirus B serotype 3
R4HLK2	Fiber protein	260047	Human adenovirus 3+7
A0A3Q8CF03	Fiber protein	1907210	Human adenovirus sp.
Q2KSJ2	Fiber protein	45659	Human adenovirus B serotype 3
C8ZJT9	Fiber protein (Fragment)	650122	Human adenovirus D15H9
A0A140KF94	Fiber protein (Fragment)	880565	Human adenovirus 56

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
A0A140KF92	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF96	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF91	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF90	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KFA2	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF95	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF85	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF87	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2Z0I6	Fiber protein (Fragment)	218120	Human adenovirus 49
A0A140KF89	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KFA5	Fiber protein (Fragment)	88059	Human adenovirus 19a
Q2Z0I4	Fiber protein (Fragment)	245072	Human adenovirus 51
A0A140KFA1	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2Z0J4	Fiber protein (Fragment)	46935	Human adenovirus 39
Q2Z0J5	Fiber protein (Fragment)	46943	Human adenovirus 38
A0A140KF88	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF93	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2Z0I8	Fiber protein (Fragment)	46942	Human adenovirus 47
Q2Z0J7	Fiber protein (Fragment)	46934	Human adenovirus 33
A0A140KF86	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2Z0J8	Fiber protein (Fragment)	46933	Human adenovirus 32
Q2Z0I9	Fiber protein (Fragment)	46941	Human adenovirus 46
Q2Z0K4	Fiber protein (Fragment)	46925	Human adenovirus 23
Q2Z0I7	Fiber protein (Fragment)	39641	Human adenovirus 48
Q2Z0K6	Fiber protein (Fragment)	46923	Human adenovirus 20

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
Q2Z0J1	Fiber protein (Fragment)	46939	Human adenovirus 44
Q2Z0I5	Fiber protein (Fragment)	107462	Human adenovirus 50
Q2Z0K2	Fiber protein (Fragment)	46927	Human adenovirus 25
Q2Z0J9	Fiber protein (Fragment)	46931	Human adenovirus 29
Q2Z0J6	Fiber protein (Fragment)	46936	Human adenovirus 36
Q2Z0K1	Fiber protein (Fragment)	46928	Human adenovirus 26
Q2Z0J0	Fiber protein (Fragment)	46940	Human adenovirus 45
A0A140KFB0	Fiber protein (Fragment)	52275	Human adenovirus D37
D0V1N4	Fiber protein (Fragment)	130310	Human mastadenovirus D
Q2Z0K0	Fiber protein (Fragment)	46929	Human adenovirus 27
Q2Z0J3	Fiber protein (Fragment)	46937	Human adenovirus 42
A0A140KFA0	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KFA3	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2Z0K5	Fiber protein (Fragment)	46924	Human adenovirus 22
A0A513PXW5	Fiber protein (Fragment)	114326	Porcine adenovirus
A0A140KF98	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KF97	Fiber protein (Fragment)	880565	Human adenovirus 56
Q2VTN6	Fiber protein (Fragment)	85755	Human adenovirus 7
Q2VTN8	Fiber protein (Fragment)	316517	Human adenovirus 7p
Q2Z0K8	Fiber protein (Fragment)	28275	Human adenovirus D10
Q2Z0J2	Fiber protein (Fragment)	46938	Human adenovirus 43
A0A140KFB1	Fiber protein (Fragment)	52275	Human adenovirus D37
Q2Z0H6	Fiber protein (Fragment)	10528	Human adenovirus A serotype 18
A0A140KFB6	Fiber protein (Fragment)	651580	Human adenovirus 54
Q2Z0H7	Fiber protein (Fragment)	46932	Human adenovirus 30

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
Q2Z0K7	Fiber protein (Fragment)	46921	Human adenovirus D13
Q2Z0K3	Fiber protein (Fragment)	46926	Human adenovirus 24
A0A482J640	Fiber protein (Fragment)	130329	Duck adenovirus 1
A0A140KF99	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A513PXX3	Fiber protein (Fragment)	114326	Porcine adenovirus
A0A140KFA9	Fiber protein (Fragment)	52275	Human adenovirus D37
A0A140KFF1	Fiber protein (Fragment)	10534	Human adenovirus C serotype 6
A0A140KFB5	Fiber protein (Fragment)	651580	Human adenovirus 54
A0A075IMH7	Fiber protein (Fragment)	1521028	Human adenovirus 21a
A0A140KFB2	Fiber protein (Fragment)	52275	Human adenovirus D37
A0A140KF80	Fiber protein (Fragment)	556926	Human adenovirus 53
A0A140KF84	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KFB4	Fiber protein (Fragment)	651580	Human adenovirus 54
A0A140KFB3	Fiber protein (Fragment)	651580	Human adenovirus 54
A0A140KF83	Fiber protein (Fragment)	556926	Human adenovirus 53
A0A140KFA8	Fiber protein (Fragment)	52275	Human adenovirus D37
A0A140KF81	Fiber protein (Fragment)	556926	Human adenovirus 53
Q5YKW0	Fiber protein (Fragment)	32608	Human adenovirus 2
Q5YKX1	Fiber protein (Fragment)	45659	Human adenovirus B serotype
A0A140KFA4	Fiber protein (Fragment)	880565	Human adenovirus 56
A0A140KFA7	Fiber protein (Fragment)	52275	Human adenovirus D37
Q5YKW4	Fiber protein (Fragment)	10519	Human adenovirus B serotype
A0A219PC25	L5 fiber protein	10519	Human adenovirus B serotype
Q80S15	Fiber protein (Fragment)	52275	Human adenovirus D3
Q80S16	Fiber protein (Fragment)	28278	Human adenovirus 1

Universal Protein Knowledgebase Accession	Protein Name	Virus Taxonomy Identifier	Virus Scientific Name
Q80S17	Fiber protein (Fragment)	28278	Human adenovirus 1
Q80S18	Fiber protein (Fragment)	28278	Human adenovirus 1
A0A2U8URG7	Fiber protein (Fragment)	32608	Human adenovirus 2
A0A140KF82	Fiber protein (Fragment)	556926	Human adenovirus 53
B3VKT9	Fiber protein (Fragment)	10524	Human adenovirus F serotype 4
A0A0F6PB57	Fiber protein (Fragment)	10515	Human adenovirus C serotype
A0A140KFA6	Fiber protein (Fragment)	52275	Human adenovirus D37
G1FBZ2	Fibre protein	1091197	Human adenovirus 62
W8CZP4	Fibre protein	46925	Human adenovirus 23
G1FC29	Fibre protein	1091198	Human adenovirus 60a
A0A1D8BAX4	Fibre protein	1354736	Fowl adenovirus
G5CZ95	Fibre protein	46916	Equine adenovirus A serotype 1

CURRICULUM VITAE

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Lisans	Muğla Sıtkı Koçman Üniversitesi	2016

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Yıl	Yer	Pozisyon/görev
2018-2018	IATI	Yazılım Mühendisi

Yabancı Dil(ler)

Dil (İngilizce, vs)	Başlangıç	Orta	İleri
Yazma			X
Konuşma		X	
Anlama			X
Okuma			X

Hobiler

1. Kitap Okumak
2. Müzik Dinlemek
3. Yeni Teknolojiler Öğrenmek