# *Prediction of PDZ interactions and classifications using Structures and Machine Learning Methods*

by

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**A Thesis Submitted to the**

**Graduate School of Sicence and Engineering**

**in Partial Fulfillment of the Requirements for**

**the Degree of**

**Master of Science**

**in**

**Computational Sciences and Engineering**

**Koc University**

**July 2014**

# Abstract

PDZ domains (PSD-95/Discs-large/ZO-1 homology) are one of the most abundant and evolutionary conserved domain families through uni- and multi-cellular organisms. As its abundance and high evolutinary conservation indicates, PDZ domains mediate a number of distinct functions in the cell including vesicular sorting, neuronal synaptic plasticity, development and neural guidance. Therefore, malfunction of the PDZ domain causes several crucial diseases such as Usher's syndrome, epilepsy, schizophrenia and types of cancer.

PDZ domains are 80-100 residues long and consist of two α-helices (αA- αB) and six β-sheets (βA to βF). The canonical interaction is the most common interaction type of PDZ domain where the PDZ domain binds the C-terminal of the target protein via the binding cavity. PDZ domains are categorized into three classes according to the motif of their binding partners as Class I, Class II and Class III. Altough, PDZ domains prefer to bind a particular class of peptides there are cases where the PDZ domain can interact with both Class I and Class II peptides, classified as Class I-II.

This study focuses on building prediction models for PDZ domain mediated interactions and PDZ domain classification by using their structural features. By utilizing the properties of the PDZ domains and their ligands, those have the available interaction experimental data, an interaction prediction and classification model was built via machine learning approaches. One of the most robust machine learning approach, support vector machine (SVM) algorithm, was selected to train the models. The interaction prediction and the classification models performances were evaluated by cross-fold validation test and validation of human proteome scanning results on experimentally known interactions data. The interaction prediction model and the classification model have area under ROC curve with a number of 0.99 and 0.91, respectively. Moreover, the human proteome scanning results showed that the interaction prediction model was able to predict the known PDZ domain mediated interactions correctly with a TP rate of 17 %. Additionally, the general knowledge of classification of PDZ domains were supported by our results. These models could be utilized by future experimental studies to narrow the search space of the novel binding partners of PDZ domains as well as drug discovery studies that target PDZ domain containing proteins.

# Özet

PDZ domain'i (PSD-95/Discs-large/ZO-1 homology) tek ve çok hücreli organizmalarda evrimsel süreç boyunca oldukça korunmuş ve en bol miktarda bulunan domain ailelerinden biridir. Evrimsel korunmuşluğun ve birçok organizmada yaygın olarak bulunuyor olmasının işaret ettiği gibi PDZ domain'inin önemli sayıda hücresel fonksiyonun yerine getirilmesinde rolü büyüktür. Bu fonksiyonlar arasında vesiküler taşınım, nöronal sinaptik bağlantılar, nöron gelişim ve dağılım örnek gösterilebilir. Dolayısıyla, PDZ domain işlevinde meydana gelecek bir aksama, Usher's sendromu, epilepsi, şizofreni ve bazı kanser türleri gibi oldukça ciddi hastalıklara sebebiyet verebilir.

PDZ domainleri 80-100 amino asit uzunluğunda, iki α-helix (αA- αB) ve six β-sheet (βA to βF) ten meydana gelir. PDZ domaininin en yaygın bağlanma şekli olarak bilinen 'canonical' etkileşimi, domain üzerinde bulunan bir bağlanma oluğu ile hedef proteinin C-terminal ucundaki 5 amino asitlik peptidler ile gerçekleşir. PDZ domainleri etkileşimlerindeni ligand seçimlerindeki özelleşmeye dayanarak Tip I, Tip II ve Tip III olmak üzere 3 sınıfa ayrılırlar. Genel olarak PDZ domainleri belirli bir sınıf peptide bağlansalar da, aralarında hem Tip I hem de Tip II ile etkileşebilen omainler olduğu bilinmektedir ve bunlar Tip I-II olarak sınıflandırılmaktadır.

Bu çalışma, PDZ domainlerinin yapısal özelliklerinden faydalanarak, onlara yeni ligandlar bulunması ve sınıflandırılması üzerine yoğunlaşmaktadır. Deneysel olarak etkileşim bilgileri bulunan domainlerin ve ligandlarının özelliklerinden faydalanarak, yapay öğrenme ile etkileşim tahmini ve sınıflandırma için modeller geliştirilmiştir. Bu modelleri geliştirmek için en güvenilir yapay öğrenme algoritmalarından biri olan 'support vector machine (SVM)' kullanılmıştır. Bu modellerin performans analizleri çapraz validasyon ('cross-validation') testlerinin yanı sıra insan proteomunun taranıp, doğru tahmin edilen etkileşimlerin istatistikleri kullanılarak yapılmıştır. Sonuç olarak, sırasıyla 0.99 ve 0.91 AUC değerlerine sahip etkileşim tahmin eden model ve sınıflandırma modeli geliştirilmiştir. Insan proteomu tarama sonuçlarına göre de etkileşim tahmin eden model, PDZ domainleri aracılığıyla gerçekleşen etkileşimleri 17 % lik doğruluk oranı ile tahmin etmiştir. Ayırca, PDZ domaini genel-geçer sınıflandırma sisteminin doğruluğunu da güçlendirmiştir. Bu modeller ileride PDZ domaini barındıran proteinlerin yeni ligandlarını bulmak ya da bu proteinleri hedefleyen ilaç molekülleri tasarlamak amacıyla yapılacak olan çalışmalarda, aday olacak peptidlerin sayıca aza indirgenmesinde kullanılabilir.

# Acknowledgements

I would like to thank my advisors Prof. Dr. Özlem Keskin and Prof. Dr. Attila Gürsoy for their guidance and support.

I would like to express my gratitude to all my friends who have shared the past two years or more with me, Kerem Fidan, Alper Başpınar, Engin Çukuroğlu, Güray Kuzu, Serena Muratçıoğlu, Emine Güven Mayorov, Yusuf D. Doğru, Deniz Demircioğlu, Emel Şen, Nilay Karahan, Derya Cavga and all of my past office mates.

Finally, no word exist to express the greatness of my gratitude to my family for their endless support and love. I am deeply pleased to dedicate this work to my dearest nephew Kaya 一男 Zeng Tümkaya.

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# Chapter 1

# INTRODUCTION

Protein-protein interactions are critical processes that are responsible for proper maintenance of cell functions. These interactions are mediated by conserved, specific interaction modules called domains [1]. The PDZ domain is one of the most abundant domains in the family among all other recognition domains from yeast to human. Their importance in a human cell is emphasized by their distinct functions such as epithelial polarity, phototransduction, vesicular sorting, and neuronal synaptic communication. Their malfunction causes several Mendalian human diseases such as Usher syndrome, Dejerine-Sottas neuropathy, some types of cancer and neurodegenerative diseases [2].

The inducement of such diseases in the case of PDZ domain malfunction and their role in several crucial cell processes make PDZ domain of great interest. The revelation of the interactions that are mediated by PDZ domain may shed light on several serious diseases mechanism and cellular processes, as well. The most common interaction type of PDZ domain is called 'canonical interaction' which occurs between the domain and the five-residue long C-terminal of the protein [4,5]. PDZ domain mediated interactions depend on several properties of the domain such as hydrophobicity, electrostatic potential, amino acid content and tertiary structure of the domain. Moreover, post-translational modifications are important modulators of these interactions. Furthermore, the classification (Class I, Class II, and Class III) of the domains is done based on C-terminal peptide's motif [6]. Altough the PDZ domains interact with a particular class of peptide, some PDZ domains may show promiscuous behavior and interact with distinct classes of peptide.

Currently, sequence-based and structure-based prediction models exist in the literature. For PDZ domain interaction prediction, sequence-based models were built by utilizing statictical approach [8,9,10] or machine learning approach [11]. These models made use of the primary sequence of the PDZ domains and generated features based on their amino acid types. A structure-based model was built by utilizing the support vector machine (SVM) algorithm, as well [12]. In this study, accessible surface area and hydrophobicity-electrostatic potential of the domains was used as features. For PDZ domain classification, Kalyoncu et al. [11] constructed a model based on general classification knowledge of PDZ domains by using primary sequence information.

In this study, we present a PDZ domain-peptide interaction prediction and classification model that is trained by using a both structural information of PDZ domains and sequential information of peptide ligands. Our model uses a combination of features that are known to mediate the PDZ domain-peptide interactions. To construct the interaction and classification models, a collection of known PDZ domain mediated interactions that available in the literature was used. SVM (support vector machine) algorithm was utilized to train models on the dataset. By testing the model with cross validation, we showed that a combination of features is more effective than using only one type of information. Moreover, we performed a human proteome scanning with the result of a high rate of true predicted interactions which proved the power of prediction model. Finally, the classification model was tested with 10-fold cross-validation for both multiple-classification (Class I / Class II / Class I-II) and binary classification of combinations of three classes (Class I / Class II , Class I / Class I-II, Class II / Class I-II). The results proved that classification model has a great differentiation ability on Class I, Class II and Class I-II PDZ domains.

Literature review related to the subject is provided in Chapter 2. In this section, background information including the structure and function of PDZ domains are given. Furthermore, previous studies of constructing machine learning models for prediction and classification of PDZ domain are reviewed as well as the support vector machine (SVM) algorithm.

In Chapter 3, the training dataset retrieving processes for both interaction and classification models are explained. The encoding steps and description of the features that are used in the study are given along with the performance measures definitions and training optimizations.

Chapter 4 represents the results for the interaction prediction and classification models, seperately. For classification part, both multi-classification and binary classification 10-fold cross-valdiation performance evaluation is achieved as the comparison of binary classification results. The performance evaluation for interaction prediction model is also showed. Moreover, the human proteome scanning process and the assesment are given in this chapter.

Finally, a brief summary of the study can be found in Chapter 5.

# Chapter 2

# LITERATURE REVIEW

In this chapter, background information of PDZ domain was given. The secondary structure data of PDZ domains and their interaction mechanism and the classification system were explained in detail. Moreover, the prediction models that exist in the literature also were discussed.

## 2.1 PDZ Domain (PSD-95, Discs large, Zona occludens 1)

PDZ domain is one of the most widespread protein-protein modulating domain which are specialized for binding to five-residue long C-terminal of partner proteins. Human genome encodes over 250 PDZ domains in over 100 proteins [7]. The name is derived from the three proteins in which it was first identified, namely postsynaptic density protein-95 (PDZ-95), disks large tumor suppresor (DLG) and zonula occludens-1 (ZO-1) [33-35]. PDZ domains are fewer in unicellular organisms than multicellular organism which indicates the co-evolution of the PDZ domain along with the multi-cellularity. PDZ domains are involved in several distinct functions that in the nervous system, excitatory synapses provide fascinating PDZ domain mediated functions [36-38].

PDZ domains are 80-100 residues long and consist of two α-helices (αA- αB) and six β-sheets (βA to βF) [3] (Figure 2.1.a). In the most common interaction type of PDZ domain, which is called canonical interaction, the PDZ domain binds the C-terminal of the target protein via the binding groove formed between the αB helix and the βB sheet [4,5]. Particular residues that are in close contact with their ligand (<4.5 angtroms) are crucial for PDZ domain mediated interactions. Previous studies used 16-residue and ten-residue binding site definitions. The ten-residue binding site definition was annotated by using nine PDZ domain-peptide complexes whereas the 16-residue binding site definition was identified only using one PDZ domain-peptide complex [9,10,12] (Figure 2.1.b).

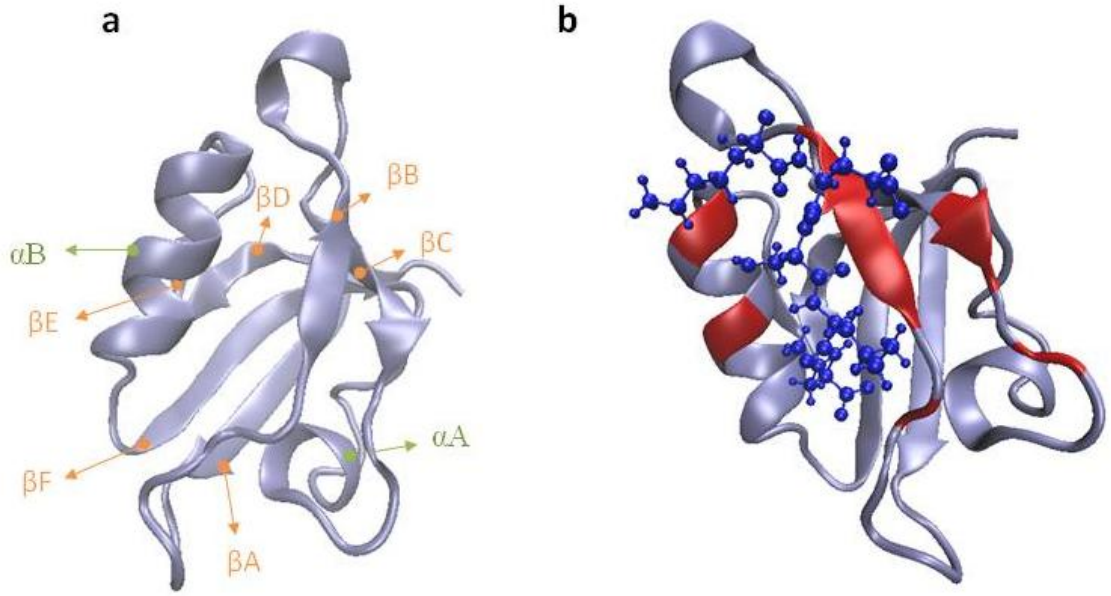


**Figure 2-1 Representative structure of a PDZ domain as free and bound form. (a)** The common respresentation of a PDZ domain (α-1 syntrophin) with labeled secondary structures (α helices and β sheets are colored as green and orange, respectively). **(b)** The canonical interaction of PDZ domain with five residues long C-terminal peptide (KESLV). The ten core binding residues of PDZ domain are highlighted in red whereas the peptide is colored blue.

The PDZ domain mediated interactions are regulated by post-translational modifications which include phosphorylation mechanism as the most common regulator. Experimental studies that have mutational approach (phospho-mimicing mutations) on binding residues of PDZ domains proved that phosphorylation has a dramatic reduction effect to the binding affinity [18, 24, 39]. Hydrophobicity, electrostatic potential, amino acid content and tertiary structure have also decisive role on PDZ domain-peptide interaction dynamics.

The specificity of PDZ domains for certain ligands led to the classification of PDZ domains into three classes according to the motif of their ligand. PDZ domain classes and their specific peptide selections are the following: Class I PDZ domains bind to the ligands with the motif of [ X-S/T-X-ϕ-COOH], Class II PDZ domains bind to the ligand with the motif of [X- ϕ-X- ϕ-COOH] and the Class III PDZ domains bind to the C-terminal motifs [ X-D/E-X- ϕ-COOH] [6] (X: any amino acid residue, ϕ: hydrophobic residue, S: serine, T: threonine, D: aspartate, E: glutamate). Although, PDZ domains prefer to bind a particular

class of peptides there are cases that the PDZ domain can interact with both Class I and Class II, which are classified as Class I-II.

## 2.2 Previous prediction models

High throughput experimental studies gave birth to a vast quantity of PDZ domain-peptide interaction information. One example for such high throughput study is from Stiffler et al. [7]. They scanned the billions of peptides to map binding specifity human and *Caenorhabditis elegans* PDZ domains, accurately. They used C-terminal peptide-phage display to conduct such a large-scale analysis of PDZ domain specifity. Moreover, both human and *Caenorhabditis elegans* PDZ domains were used in this study for comparison purposes. As a result, they mapped the binding specifity and identified partner preferences of half of the over 330 PDZ domains successfully. In another study Stiffler et al. [8] generated vast of experimental interaction information for mouse PDZ domains. This time they used 217 genome-encoded peptides instead of random peptides. Then they tested all possible interactions between 157 mouse PDZ domains and genome encoded-peptides via protein microarrays. Therefore, several computational prediction models have become possible to train by using experimental informations.

Chen et al.'s [9] study is one of the examples of computational models. In this study, it is reasoned that if the peptide ligand preferences of the PDZ domain are determined by the amino acid types at specific positions in the domain's three dimensional structure, it may be captured by integrating sequence and structural information. They constructed a multiple sequence alignment of mouse PDZ domain's primary sequences which have structural information in Protein Data Bank (PDB). After the elimination step of any residue position that has a gap in the alignment with the reference PDZ domain structure (α1-syntrophin in contact with GVKESLV peptide), a total of 38 position pairs were identified between 16 PDZ domain residues (referred as binding-site residues) and 5 peptide residues. Afterwards, an additive model comprising 38 scoring matrices per each domain-peptide pair was formulated. These matrices (20 x 20) include scores for amino acid pairs as one residue on the PDZ domain and the other on the peptide. To fit the model, they trained it by using interaction data that included 82 PDZ domais and 93 peptide ligands. Moreover, since the number of data points were much more less than the number of model parameters, which makes the model highly underdetermined, they utilized the Bayesian approach to circumvent this problem. As a

result, they had a statistical model that predicts PDZ domain-peptide interactions by using primary sequence information with an area under curve value of 0.87.

A model for sequence-based prediction was built by Stiffler et al. [8]. First, they cloned, expressed and purified 157 PDZ domains encoded in mouse genome. As distinct from their another study [7], they focused on genome-encoded peptide ligands instead of random peptides. After synthesizing and purifying 217 fluorescently labeled peptides, they designed a strategy that combines the throughput of protein microarray and the reliability of fluorescence polarization methods to investigate the biophysical interactions between 157 PDZ domains and 217 fluorescence peptides. Furthermore, to eliminate the false positive rate of the high-throughput method, they retested and quantified every array positive with solution-phase fluorescence polarization which was utilized as 'gold standart' in the study. The gold standart involved 85 PDZ domains that interact at least one peptide in the training set. Since the traditional position specific scoring matrix (PSSM) did not fit in one of their purposes, which were distinguishing one domain from another, they built a variation of PSSM. The model that includes many PDZ domains reffered as multidoman selectivity model (MDSM). To avoid the overfitting problem that may happen such a high-dimensional model, they implemented smoothing techniques. The trained model performes well on the microarray dataset with a true-positive rate of 96%. By considering the high agreement of the MDSM with the training-set data, they used the model to scan mouse proteome that involves 31,302 peptides to find 74 PDZ domain's binding partners. Finally, they provided these interaction predictions data (18,149 PDZ domain-peptide interactions) to help guide future biological investigations.

In another study a sequence-based prediction models is accomplished by Hui et al.[10]. Unlike the studies discussed above, a huge dataset from two independent high-throughput studies, which generated a vast of data by using protein microarray and phage display technologies, was utilized in this study [7,8]. Since the phage display method produces only positive data, they developed a method to generate artificial negative data. As it is referred, the commonly used random and shuffled peptides have not been resulted very well on predicted real negative inetactions in previous studies. Therefore, a position weight matrix (PWM) was trained on positive interactors and they used it to pick the negative interactors among a set of peptides those have a score below the threshold. In total, interaction data of 20 human and 82 mouse PDZ domains with over 3000 peptides were used to train the model. As primary sequence feature, the 16 binding-site residues definiton of PDZ domains from Chen et al.'s study was used. They encoded binary vectors with a length of 20 x 20 that represents

each type of amino acid for 38 residue pairs between 16 PDZ domain binding-site and 5 peptide ligand residues (in total, 38 x 400). Afterall, support vector machine (SVM) algorithm was used to train a model on the dataset with an AUC result of 0.89. Finally, the model was used to scan human, worm and fly proteomes to define 13 PDZ domain's interactors that have available validation data in PDZBase with a result of 85%, 25% and 37%, respectively.

One more computational study for building sequence-based predictor was conducted by Kalyoncu et al. [11]. They generated bigram and trigram amino acid frequencies of primary sequences of PDZ domains and peptides. For instance, a sequence of 'ABCDE' results in a trigram set of 'ABC', 'BCD', 'CDE' and a bigram dataset of 'AB', 'BC' , 'CD', 'DE'. Moreover, to reduce the dimension of the features they categorized 20 amino acid types into 7 classes with respect to their physicochemical properties. Eventually, a sequence-based PDZ domain interaction prediction model was created with an accuracy of 91.4 % by using random forest classifier. Additionally, a PDZ domain classification model was established in order to differentiate both multi-classes among them and binary classes. The multi-class differentiating model was achieved 90.7 % accuracy.

Since the structural features include more accurate information about protein-ligand interactions, Hui et al. [12] constructed a structure-based predictor. They used the dataset that has 2795 interaction infotmation (both binding and non-binding) of 83 PDZ domains that are related to human and mouse, and corresponding 871 peptides data. The electrostatic potential, hydrophobicity and accessible surface area properties were used as structural features. SVM (support vector machine) algorithm was used to train the model. The performance analysis of the model with cross validations gives an AUC value of 0.93. In addition, they used the model to scan the human proteome for 218 PDZ domains. As a result, they had true predictions for only 88 PDZ domains but not for remaining 130 domains. For 88 domains, they calculated an avarage TP rate with a value of over 21%.

# Chapter 3

# MATERIALS AND METHODS

In this chapter, the dataset that is used in the study was explained. The features description and the calculation process was given, as well. Moreover, the SVM classifier and the performance measures that we used in the study were described.

## 3.1 Dataset

A dataset which contains both positive (binding) and negative (non-binding) informations was needed to build the machine learning model. The PDZ domain interaction dataset, which is composed of 83 PDZ domains and 871 ligands, was retrieved from Hui et al. [12]. They collected the PDZ-peptide interactions from published high throughput phage display and protein microarray experiments for both human and mouse, respectively [7,8]. Since the phage display data contains only positive interactions, they used an established protocol and generated artificial negative interactions [10]. At the end, a PDZ domain-peptide interaction dataset with 942 binding and 1843 non-binding interactions between 83 PDZ domains and 871 ligands was generated (see Appendix: Table S1 for PDZ interaction data). The structures of the PDZ domains were collected from the web server of Bader Lab. The dataset contains one NMR and 17 X-ray structures for humans and five NMR structures for mice from the Protein Data Bank (PDB) [13]. We used only the first model was used for NMR structures as it was used in the previous study. Furthermore, 11 human and 54 mouse PDZ domain models in this dataset were modelled by SWISS-MODEL [14]. As it is referred in this study, homology models were used to increase the number of PDZ domain structures to build a robust prediction model. The quality of the homology models was estimated by template sequence ID and QMEAN score by Hui et al. [12]. Template sequence id is the measure of the identical residues between the domain and the template as a percentage where the QMEAN score is a scoring function that measures multiple geometrical aspects of protein structure, ranging from 0 to 1 with higher values indicate more qualified models.

For class prediction, PDZ domains were signed as Class I and Class II with respect to the C-terminal motif of interacting peptides, [ X-S/T-X-ϕ-COOH] for Class I and [X- ϕ-X- ϕ-COOH] for Class II, respectively. The domains that both interact with Class I and Class II peptides were annotated as Class I-II. All PDZ domains in our dataset were classified,

resulted in 12 Class I, 27 Class II and 27 Class I-II. These classes were determined by using the interaction informations of the PDZ domains with different classes of peptides in our dataset. The experimentally proved interactions were retrieved from IRefIndex [25], PDZBase server [40] and literature manually. However, 17 domains could not be classified due to the non-fitting of their interaction partners into any class pattern (see Appendix: Table S2 for class data of the domains). Since the peptides were used to label the classes of PDZ domains, the peptide's features (20 amino acid type x 5 residues) were removed from the feature vector space to avoid biased data.

## 3.2 Feature Encoding

Particular protein residues that are in close contact with their ligand (<4.5 angtroms) are crucial for PDZ domain mediated interactions. Previous studies used either 16-residue orten-residue binding site definitions. However, the ten-residue binding site definition was annotated by using nine PDZ domain-peptide complexes where the 16-residue binding site definition was identified only using one PDZ domain-peptide complex [9,10,12]. Therefore, in this study ten binding residues were identified for each of the PDZ domains. Four types of features that are responsible for protein-protein interactions and stability of proteins were computed to describe the PDZ domain. Then, the values corresponding to the ten binding residues were extracted and each PDZ domain was represented by a vector of length 301 features, in total.

The representation of the feature vector space of interaction is as following:

$$(X, Y, W) = \{(x_1, x_2, \ldots, x_{200}), (\Upsilon_1, \Upsilon_2, \ldots, \Upsilon_{100}), (\omega_1/\omega_2)\} \qquad (3.1)$$

where X is the vector space for PDZ domain information ( $x_1 - x_{90}$: electrostatic potential, $x_{91} - x_{180}$: hydrophobicity, $x_{181} - x_{190}$: relative accessible surface area, $x_{191} - x_{200}$: phosphorylation sites), Y is the vector space for peptide information ($\Upsilon_1 - \Upsilon_{100}$: binary vector

of 20 amino acid type for each of the five residues), and W is the label ($\omega_1$ : binding or $\omega_2$ : non-binding).

### 3.3 Relative Solvent Accessible Surface Area (rASA)

Relative accessible surface area is a simple measure, which is calculated by normalizing the residue's accessibility on the surface of a protein with its the standart ASA value. The rASA gives insight about the rate of the buried surface area and the accessible surface area for a residue. Furthermore, rASA can be utilized to define the magnitude of interaction-induced conformational changes of proteins. rASA of PDZ domains in our dataset were computed using the NACCESS software [16]. Each value corresponds to the ten binding sites of PDZ domains that were extracted, used to generate a feature vector with a length of 10 (1 feature x 10 binding residues).

### 3.4 Hydrophobicity and Electrostatic Potential

Electrostatic and hydrophobic characteristics of proteins have a major role in protein-protein interactions. Therefore, these properties were selected as the second and third features of the PDZ domains in the dataset. These features were generated by the VASCo software [17] and nine values were sampled for each of the ten binding residues as they were used and resulted well in one of the previous studies [12]. Sampling was done by extracting the hydrophobic and electrostatic potentials of the ten residues from the VASCo output which contains atom-based data. Afterwards, the atoms corresponded to the ten binding residues was ordered according to their x,y,z coordinates, and ninety values sampled that are equally far away from each other. By doing this calculation, we had a normalized sampling value for the ten binding domains that has different numbers of atoms. In the end, in a vector of length 90 (9 features x 10 binding residues) were generated for hydrophobic and electrostatic features, separately (18 features x 10 binding residue, in total).

### 3.5 Possible Phosphorylation Sites (PPS)

Post-translational modifications are known as the regulator of the protein-protein interactions [18]. In particular, phosphorylation of Ser, Thr, or Tyr residues within the PDZ domains have been proposed to modulate PDZ-mediated interactions and a recent study proves that the phosphorylation of PDZ domain binding site residue effected its binding ability dramatically [19,24,39]. Since the experimental phosphorylation data for all the PDZ domains in training dataset were not available, we used possible phosphorylation sites, the Ser, Thr and Tyr residues, in ten binding residues are marked as '1' in a binary vector of length 10 (1 feature x 10 binding residues).

### 3.6 Peptide Feature Encoding

We followed the literature and restricted the peptide length to five C-terminal residues. Since the primary sequence of the peptide is one of the decisive determinants of interaction, amino acid content of the peptides were converted to feature. As a sequential feature, each residue of the C-terminal of ligand was mapped into a binary vector with a length of 20 where each bit represents an aminoacid, resulting in a vector of length 100, in total (20 features x 5 C-terminal residues).

### 3.7 Model Training and Performance Measures

We prefered to train our model with the SVM (Support Vector Machine) algorithm among several machine learning approaches. The SVM algorithm maps the feature vector to a high-dimensional space and constructs a set of hyperplanes which can be used for classification or regression [20]. The LibSVM library was used for the application of SVM [21].

The support vector machine (SVM) algorithm is a supervised binary classification learning algorithm [20]. It is well suited on discriminative classification which is learning by utilizing example data and predicting on unseen data before. The algorithm needs three components to perform: a training set, corresponding class labels to training set and a test set.

SVM generates a hyper-plane that is maximally distant (known as 'the maximal margin hyper-plane') from each classes on training set. In the case of linear seperation is not possible, 'kernels' technique steps in and realizes the non-linear function to feature space [41].

The algorithm has been applied on various fields, including text categorization, image recognition and hand-written digit recognition [42]. Furthermore, SVM algorithm have been used in bioinformatics studies, including recognition of translation start sites, protein remote homology detection, protein folding issue, microarray gene expression analysis and prediction protein-protein interaction [43-47]. The popularity of the SVM stands on its flexibility and robustness as well as its accuracy even on relatively large datasets as evidenced by the listed studies. In this study, after optimization was done in a systematic manner, cost parameter, *C*, was choosed as 2.0, where 0.15 was picked as the Gamma parameter for interaction prediction model. Additionally, the Gamma and the cost parameter was selected as 0.05 and 2.0, respectively, for classification models.

The following statictical measurements were calculated to assess the model:

- *Sensitivity or Recall(TPR) = TP/(TP+FN)*
- *Precision = TP/(TP+FP)*
- *False Positive Rate(FPR) = FP/(FP+TN)*
- *Specificity = TN/(FP+TN)* *(3.2)*

where TP denotes true positive, FP denotes false positive, TN denotes true negative and FN represents false negative. We measure the performance of the model by using the receiver operating characteristics (ROC) curve which is obtained by plotting sensitivity (TPR) versus FPR and the area under the ROC curve (AUC).

# Chapter 4

# RESULTS

The results of this study were presented in two parts. First, the interaction prediction model's results were explained. Afterwards, the human proteome scanning test results were presented. Second, the classification model's results were presented. Then, the case study, which is based on the classification results, were discussed.

## 4.1 PDZ domain interaction prediction model

Significant differences in sample quantity of different classes cause imbalance problem and degenerate the performance of classifier [22]. Since the dataset we used have two times more non-binding information than binding information, we resampled our dataset before the SVM classifier was trained and optimized. Resampling is a supervised pre-process which generates samples by taking the class distribution into account. SVM classifier was optimized by altering the parameters of LibSVM systematically. To test the performance of the model we ran 10-fold cross-validation test and plotted ROC and PR curves to visualize the performance (Figure 4-1a and Figure 4-1b, respectively). The model achieved very high ROC and accuracy, namely 0.99 and 96.9 %, respectively. These results showed the model's performance is better than the previous sequence-based and structure-based models [8-12].

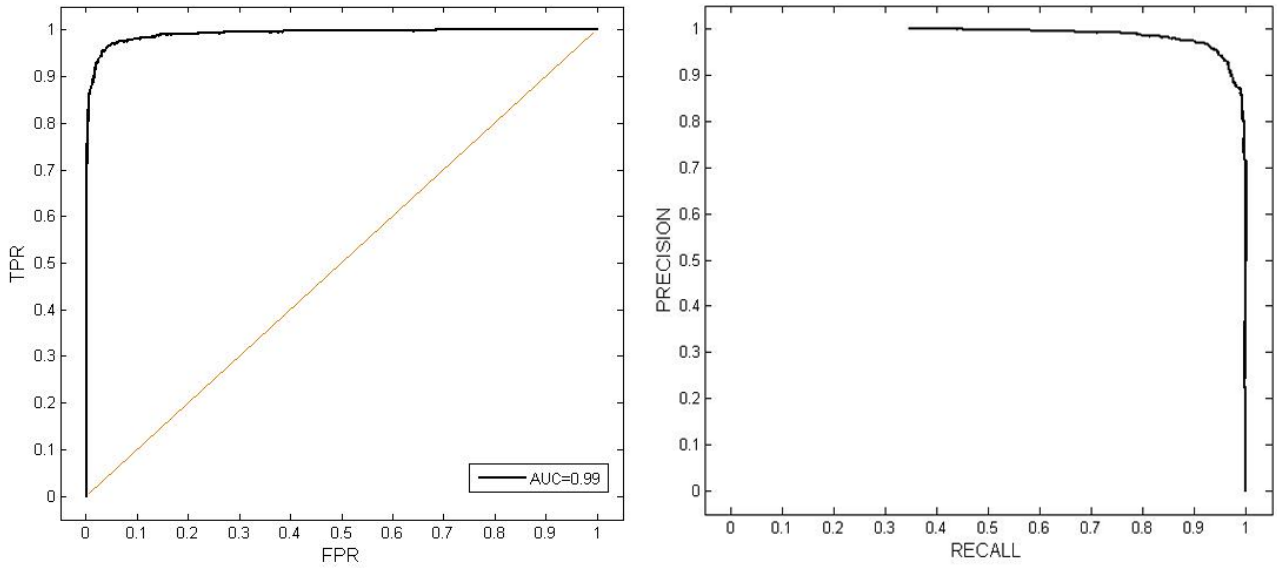


**Figure 4-1 (a)** ROC curve for interaction prediction model **(b)** Precision vs recall curve for interaction prediction model

ROC graphs are two-dimensional plots in which true positive rate (TPR) is plotted on the Y axis and false positive rate (FPR) is plotted on X axis. It is used to visualize the performance of a classifier. Basically, the ROC curve depicts the relative tradeoffs between benefits (TPR) and costs (FPR) of a classifier for distinct decision thresholds. Moreover, the area under the curve (AUC) is the measure of classifier performance. Since the AUC value is a portion of an unit square area, its value is always be between 0 and 1. Additionally, higher AUC value indicates a better classifier performance. Our model's ROC curve has an AUC value is 0.99. The previous structure-based interaction prediction model has an AUC value of 0.96 [12]. Even though the same dataset was used in both studies, the better performance of our model shows that the features we used are more descriptive on PDZ domain-peptide interaction. The contrubition of each feature to the model performance can be seen in Figure 4-2.

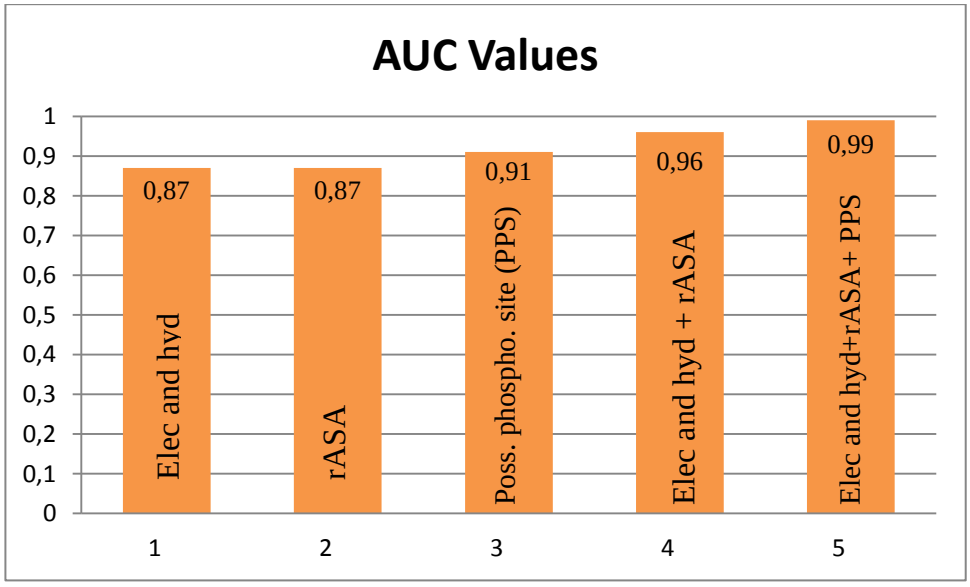


**Figure 4-2 Area under ROC curve (AUC) comparison chart.** AUC values for each of the features and combination of the features is showed (column number: 1- electrostatic potential and hydrophobicity, 2- relative accessible surface area, 3- possible phosphorylation sites, 4- electrostatic potential and hydrophobicity + relative accessible surface area, 5- electrostatic potential and hydrophobicity + relative accessible surface area + possible phosphorylation site)

Features has high AUC values when individually. However, even small improvements on the prediction model, with an AUC value in a certain interval (0.8-1.0), is a challenging task. By considering this fact, it is reasonable not to have dramatic AUC value differences between a single feature and a combination of them. Both the electrostatic potential-hydrophobicity and relative accessible surface area (rASA) features resulted 0.87 AUC value when they were used separately. However, when we integrate these two features, the model resulted with an AUC value of 0.96. Furthermore, when we added the possible phosphorylation sites (PPS) feature into our model, the AUC value increased from 0.96 to 0.99. Such an increase, while the model has already reached to 0.96, suggests that the PPS feature is highly informative on PDZ domain-peptide interactions.

In the study of Hui et al. [12], the electrostatic potential-hydrophobicity feature and accessible surface area were used to construct a structure-based model that resulted the AUC value of 0.96. By comparing Hui et al.'s prediction model with our model, that is represented in Figure 4-2 with a column number of 4, it can be seen that the AUC values of two are the same, namely 0.96. As we investigated the different features for these two models, it is noticed that the electrostatic potential-hydrophobicity feature is the same whereas we used relative accessible surface area (rASA) instead of accessible surface area (ASA). By considering that the two different models were utilized the same dataset, it can be said that rASA did not perform better than ASA, in this case.

Furthermore, when we compared the Hui et al.'s prediction model with our model, that is represented in Figure 4-2 with a column number of 5, the better performance of our model can be seen. In this model, we used an additional feature, possible phosphorylation sites (PPS) , as a difference from the previous model (in Figure 4-2 with a column number of 4). The PPS feature carried our prediction model's performance ahead of Hui et al.'s model, where the AUC value of our's is 0.99 as the other model's is 0.96. As this results indicated, the feature of PPS had a great improvement effect on our model and increased its AUC value over previous prediction model. It is reasonable to had such an improvement for this feature, by looking at previous experimental studies that have proved the phosphorylation role in PDZ domain mediated interactions [19,24,39].

In another study that is achieved by Chen et al. [9], an interaction prediction model was constructed by using primary sequence and structure information in a different manner resulted with an AUC value of 0.87. In this study, they conducted multiple-alignment for all

PDZ domains that have available three-dimensional structural data, and identified the conserved positions among all these domains and peptides. As a result, they defined 38 pairs of residues that include 16 domain and 5 peptide residues and the amino acid type of these specific positions were used as features. However, even if they were in specific aligned positions, it is not much likely to capture PDZ domain-peptide interactions just by looking at the residue's amino acid type, as the study's results indicate, as well. Moreover, they had to use a reference structure for the alignment purposes which made generalizing the model harder. Our model has superiorities including investigation of domains from distinct aspects and utilization of 2786 interaction data between 83 PDZ domains and 217 peptide ligands. As a result of the superiorities of our model, we achieved higher performance.

One another study of Hui et al. [10], they used Chen et al.'s [9] 16-binding residue site definition to generate sequence-based features for building an interaction prediction model which resulted with an AUC value of 0.89. In this study, they generated feature vectors that represents the amino acid types of each residue in the binding site. This study differs from Chen et al.'s due in usage of broader interaction dataset which helps the generalize the model. However, still the AUC value is much lower than our interaction prediction model, namely 0.89 and 0.99, respectively. The advantages of our model which are using structural and using more condensed 10-binding residue site definition, is showed much better than primary sequence-based information.

One more example of sequence-based interaction predictor construction is achieved by Kalyoncu et al. [11] which resulted with an AUC value of 0.97. In this study, novel sequence-based features, that is called bigram and trigram, were presented. Basically, bigram and trigram features represent the frequencies of the of two and three consecutive amino acids, respectively, in the primary sequence. As it is in most of the other studies, using only sequence-based information resulted a lower AUC value than our model's. Moreover, the classifier that was used in this study, which is random forest, has less robustness than SVM classifier which we used to construct the model.

Additionally, the confusion matrix and the detailed accuracy results of interaction prediction model can be seen in Table 4-1. As it represents, our interaction prediction model has quite high true positive rate (TPR), namely 0.969 and low false positive rate (FPR) with a value of 0.043. This values indicate the power of the model on predicting positive interactions. The model were able to predict 928 positive interactions out of 984 positives.

Moreover, it was able to predict 1771 negative interactions out of 1801 negatives which gives us an insight on the high specificity of the model.

**Table 4-1 Interaction prediction model's detalied accuracy and confusion matrix results**

| | | TP Rate | FP Rate | Precision | Recall | F-Measure | ROC Area |
|---|---|---|---|---|---|---|---|
| *Detailed Accuracy Results* | Binding | 0.943 | 0.017 | 0.969 | 0.943 | 0.956 | 0.993 |
| | Non-binding | 0.983 | 0.057 | 0.969 | 0.983 | 0.976 | 0.993 |
| | Weighted Avg. | 0.969 | 0.043 | 0.969 | 0.969 | 0.969 | 0.993 |
| *Confusion Matrix* | | | **Binding** | | **Non-binding** | | |
| | **Binding** | | 928 | | 56 | | |
| | **Non-binding** | | 30 | | 1771 | | |

Here we present a stable PDZ domain mediated interaction prediction model that is constructed by utilizing the structural and possible phosphorylation features of the domains with higher accuracy than previous models [8-12]. Moreover, it is concluded that using the combination of different types of features results better than using only one type information as it has been done so far [8-12]. Our model can be used to narrow the putative partner space of PDZ domains for experimental studies. The powerful predictions of our model on both experimentally determined (X-Ray, NMR) and homology modeled domains points that its ability to predict interactions even if the domain's crystal structure is not available.

Since the experimental information of phosphorylation for the most of PDZ domains is not available, only possible site phosphorylation site definition could be used in this study. However, the model may be improved by the addition of new interaction data of PDZ mediated interactions to our dataset and by using experimental phosphorylation information instead of possible phosphorylation sites.

## 4.2 PDZ domain class prediction model

Promiscuousity of PDZ domains cause a multi-classification problem for class prediction, because a number of PDZ domains bind to both Class I and Class II peptides which are labeled as Class I-II. Therefore, we trained our class prediction model on these classification dataset and used to discriminate both multi-classes (Class I/ Class II/ Class I-II) and binary classes (Class I/Class II, Class I/Class I-II, Class II/Class I-II) to have an insight on their pair wise classifications. ROC and PR curves were plotted to visualize class predictors' performance (Figure 4-3 and Figure 4-4, respectively). As the ROC plot represents, the area under ROC curve (AUC) is quite high, namely 0.91. The high AUC value shows the performance of the classification model, higher AUC value indicates more qualified model.

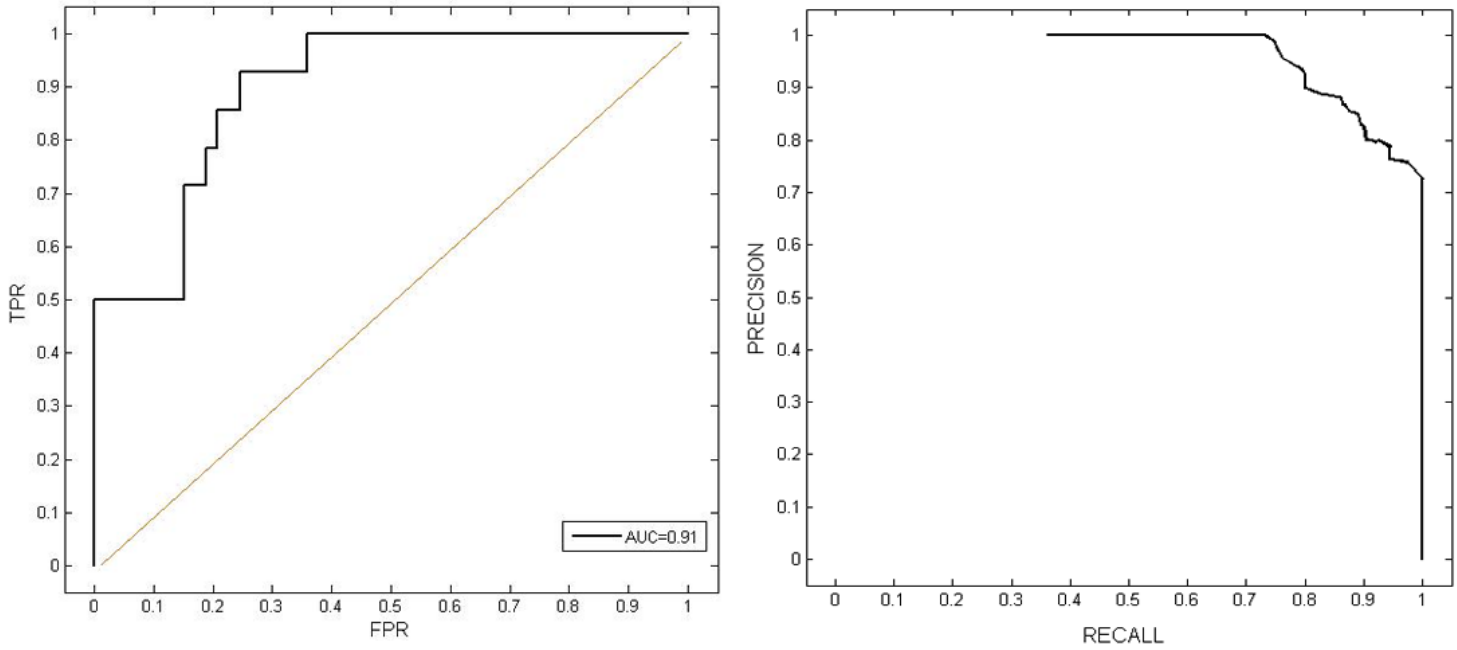


**Figure 4-3 (a)** ROC curve for multi-classification model **(b)** Presicion vs recall curve for multi-classification model

The multi-classification model correctly classifies 7 of 13 Class I, 19 of 27 Class II and 25 of 27 Class I-II PDZ domains as it is represented in Table 4-2.

**Table 4-2 Multi-classification model's detalied accuracy and confusion matrix results**

| | | **TP Rate** | **FP Rate** | **Precision** | **Recall** | **F-Measure** | **ROC Area** |
|---|---|---|---|---|---|---|---|
| *Detailed Accuracy Results* | Class I | 0.5 | 0.038 | 0.778 | 0.5 | 0.609 | 0.896 |
| | Class II | 0.792 | 0.163 | 0.731 | 0.792 | 0.76 | 0.907 |
| | Class I-II | 0.897 | 0.158 | 0.813 | 0.897 | 0.852 | 0.938 |
| | Weighted Avg. | 0.776 | 0.135 | 0.776 | 0.776 | 0.768 | 0.918 |

| *Confusion Matrix* | | **Class I** | **Class II** | **Class I-II** |
|---|---|---|---|---|
| | **Class I** | 7 | 1 | 5 |
| | **Class II** | 2 | 19 | 6 |
| | **Class I-II** | 1 | 1 | 25 |

One case of the multi-classification, that is the one between Class I and Class I-II, has the highest number of wrong classified Class I PDZ domains. Therefore, it was selected as a case study. A set of three-dimensional structures including: an originally Class I PDZ domain but predicted as Class I-II, an originally Class I PDZ domain and predicted as Class I, an originally Class I-II PDZ domain and classified as Class I-II, three structures per each category, in total 9 structures were examined (Figure 4-4). Originally Class I but predicted as Class I-II domains are LRRC7-1, SAP102-2 and SAP102-3 (Figure 4-4-a.d.g) and originally Class I and predicted as Class I domains are MAGI3-5, MASL2-1, PDZK1-1 (Figure 4-4-b.e.h), lastly, known as Class I-II and predicted as Class I-II domains are PSD95-2, PSD95-3, SAP97-3 (Figure 4-4-c.f.i) (see Appendix Table S3 for more details of PDZ domain structures). The structures investigated according to their hydrophobicity properties per residue. As the hydrophobic residues were highlighted in blue, a pattern recognized on the αB-helix of the domains (circled with dashed line in Figure 4-4). The hydrophobic residue content of αB-helix, which includes binding site of PDZ domain, is found more dense in the case of originally Class I domains that were classified as Class I-II (Figure 4-4-a.d.g). However, in the case of Class I domain predicted as Class I, the residue in the same position were hydrophilic for all three examples (Figure 4-4-b.e.h). Therefore, we conclude that if the residue in this exact position is hydrophobic in Class I PDZ domain, our multi-classification model predicted it as Class I-II. As a next step, we looked into three Class I-II domains that were predicted as Class I-II by our model. Interestingly, Class I-II domains had the same hydrophobic residue content with the wrong predicted Class I domains. Thus, these hydrophobic residues caused the wrong prediction of Class I PDZ domains which had this hydrophobic pattern.

The multiple-sequence alignment was conducted to identify the position of this hydrophobic residue (Figure 4-5). According to the alignment results, this particular residue position is detected as the 65th residue of the PDZ domain which corresponds to the 5th residue of αB-helix (marked on Figure 4-4). Futhermore, the 5th residue of αB-helix is one of the binding residues in ten-binding site definition (see Figure 2-1.b for correspondence).

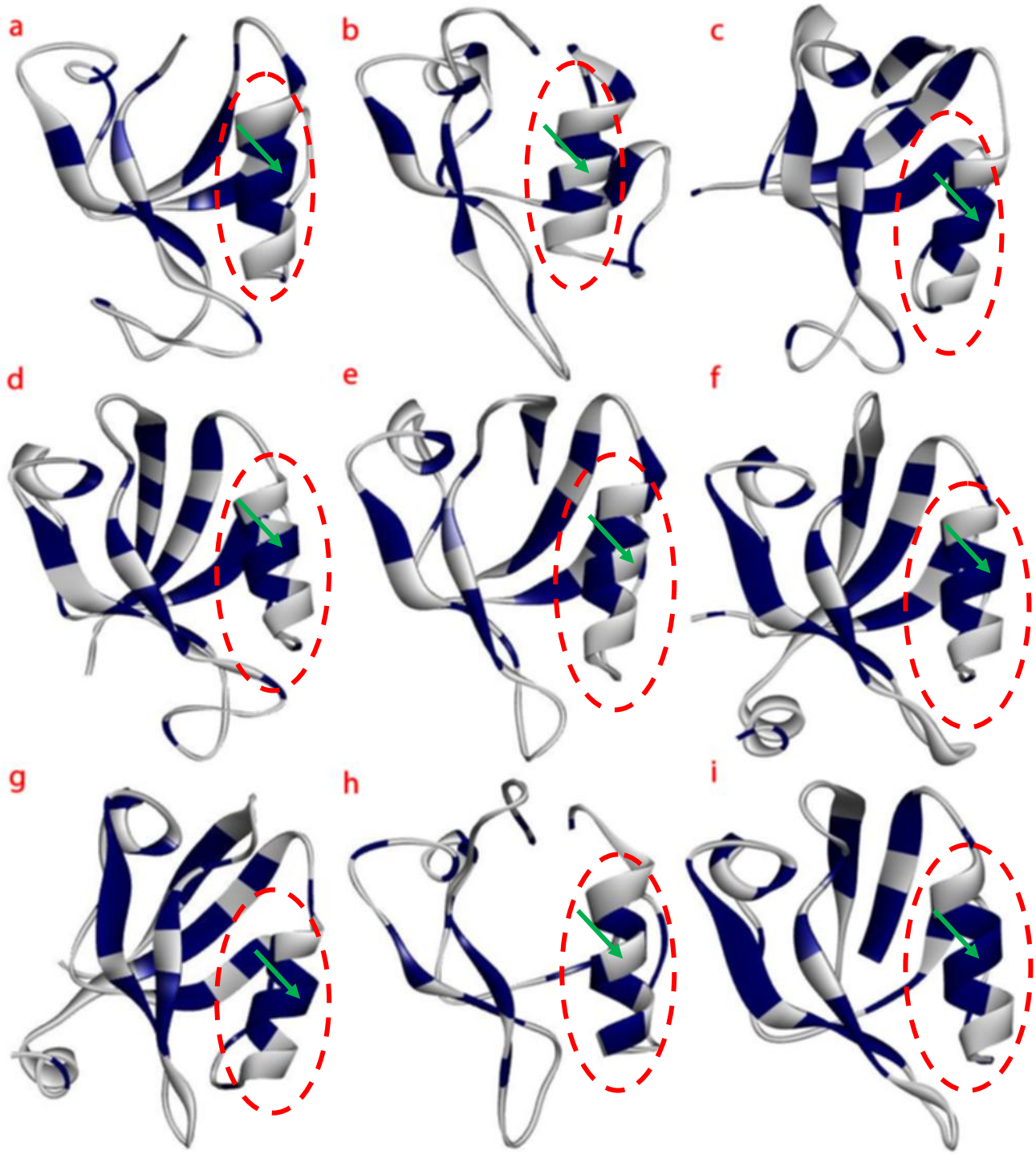


**Figure 4-4 Structural comarison of Class I but predicted as Class I-II (a-d-g), Class I and predicted as Class I (b-e-h) and Class I-II and predicted Class I-II domains (c-f-i)** Hydrophobic residues are highlighted in blue, αB-helices are circled with dashed line, 5th residue of the αB-helices marked with a gren pointer. (a: LRRC7-1, b: MAGI3-5, c: PSD95-2, d: SAP102-2, e: MASL2-1, f: PSD95-3, g: SAP102-3, h: PDZK1-1, i: SAP9703)

We concluded that the hydrophobicity properties of particular residues on PDZ domain structure has more important role than others on its binding preferences. As it is explained in *3.4 Hydrophobicity and Electrostatic Potential* section, we generated hydrophobicity value by considering PDZ domain as a whole. Instead, by using hydrophobicity feature per residue may contribute to the classification model's performance according to the case study.

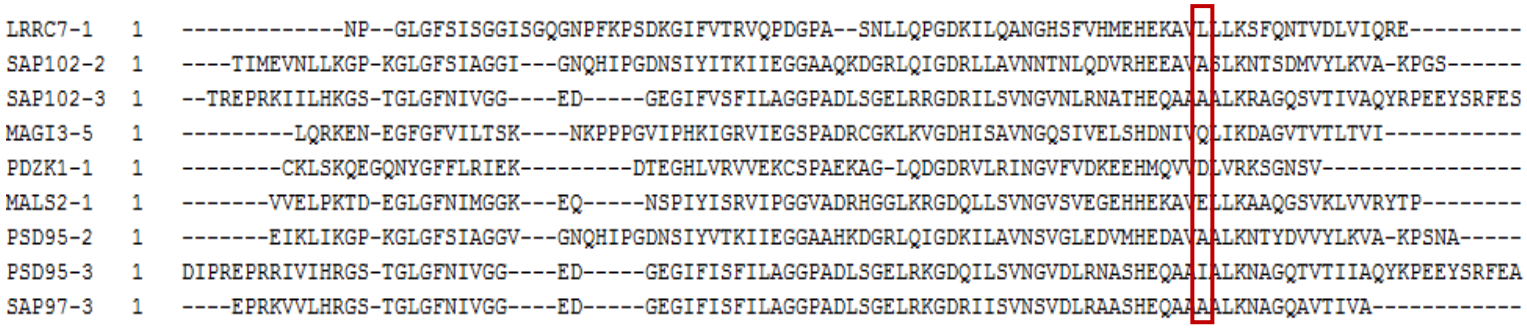


**Figure 4-5 Multiple-sequence alignment results** (the specific position of 65th residue of the domain is marked with a red box.)

As it can be seen in more detail in Table 4-3, Table 4-4 and Table 4-5, the binary classification models were able to differentiate most of the classes correctly. Differentiating Class I from Class II was achieved with an AUC value of 0.91 (Table 4-3).

**Table 4-3 Class I/Class II binary classification model's detalied accuracy and confusion matrix results**

| | | TP Rate | FP Rate | Precision | Recall | F-Measure | ROC Area |
|---|---|---|---|---|---|---|---|
| *Detailed Accuracy Results* | Class I | 0.538 | 0.037 | 0.875 | 0.538 | 0.667 | 0.915 |
| | Class II | 0.963 | 0.462 | 0.813 | 0.963 | 0.881 | 0.915 |
| | Weighted Avg. | 0.825 | 0.324 | 0.833 | 0.825 | 0.812 | 0.915 |

| *Confusion Matrix* | | **Class I** | **Class II** |
|---|---|---|---|
| | **Class I** | 7 | 6 |
| | **Class II** | 1 | 26 |

Another binary classification model, that discriminates Class I from Class I-II, has the lowest accuracy among all binary classifiers with an AUC value of 0.75 (Table 4-4). This results suggest that Class I is more similar to Class I-II than Class II. Surprisingly, in this binary classification model, Class I TP rate is lower than Class I-II TP rate. By considering the results of the case study for multi-classification model, it can be explained that if Class I domains had a hydrophobic residue at the aB-helix, the classifier TP rate for Class I decreased. This results are consistent wtih the case study very well.

**Table 4-4 Class I/Class I-II binary classification model's detalied accuracy and confusion matrix results**

| | | TP Rate | FP Rate | Precision | Recall | F-Measure | ROC Area |
|---|---|---|---|---|---|---|---|
| *Detailed Accuracy Results* | Class I | 0.308 | 0.037 | 0.8 | 0.308 | 0.444 | 0.752 |
| | Class I-II | 0.963 | 0.692 | 0.743 | 0.963 | 0.839 | 0.752 |
| | Weighted Avg. | 0.75 | 0.479 | 0.761 | 0.75 | 0.711 | 0.752 |

| *Confusion Matrix* | | **Class I** | **Class I-II** |
|---|---|---|---|
| | **Class I** | 4 | 9 |
| | **Class I-II** | 1 | 26 |

The last binary classification model, which is Class II/Class I-II classifier, has the highest accuracy among all binary classification models with an AUC value of 0.97 (Table 4-5). The succes on differentiating Class II from Class I-II suggests that Class II binding preferences and sturctural properties are quite different from Class I-II.

**Table 4-5 Class II/Class I-II binary classification model's detalied accuracy and confusion matrix results**

| | | TP Rate | FP Rate | Precision | Recall | F-Measure | ROC Area |
|---|---|---|---|---|---|---|---|
| *Detailed Accuracy Results* | Class II | 0.889 | 0.074 | 0.923 | 0.889 | 0.906 | 0.977 |
| | Class I-II | 0.926 | 0.111 | 0.893 | 0.926 | 0.909 | 0.977 |
| | Weighted Avg. | 0.907 | 0.093 | 0.908 | 0.907 | 0.907 | 0.977 |

| | | | |
|---|---|---|---|
| *Confusion Matrix* | | **Class II** | **Class I-II** |
| | **Class II** | 24 | 3 |
| | **Class I-II** | 2 | 25 |

To sum up with, the comparison of performances of binary classifications in Table 4-3 shows that Class II / Class I-II classification has the highest accuracy whereas Class I / Class I-II differentiation has the lowest accuracy. These results suggest that the peptide selections of Class II and Class I-II is more similar than any others and Class I-II may have its unique binding preferences. Moreover, the binary classification results are highly consistent with the multi-classification and the case study results.

**Table 4-6: Prediction results for multi-class learning and binary learning for pair wise combinations of three classes** (Weighted avarage results were shown.)

| | TP Rate | FP Rate | Precision | ROC Area | Accuracy(%) |
|---|---|---|---|---|---|
| Class I, Class II, Class I-II | 0.791 | 0.135 | 0.798 | 0.918 | 79.1 |
| Class I, Class II | 0.825 | 0.324 | 0.833 | 0.915 | 82.5 |
| Class I, Class I-II | 0.75 | 0.479 | 0.761 | 0.752 | 75 |
| Class II, Class I-II | 0.907 | 0.093 | 0.908 | 0.977 | 90.7 |

In the study of Kalyoncu et al.'s [11], the same classification definition, which includes Class I, Class II and Class I-II as a promiscuous class, was used to construct classification models. As it can be seen in Table 4-7, they had quite high accuracy for both multi-classification and binary classification models. In this study, a novel primary sequence based feature was used which are named as bigram and trigram. Additionally, the results of all classifer were shown separetly foe bigram and trigram features. As a difference from our classification models, they utilized Random Forest classifier to construct models. The lower accuracy of our model may be explained as the sequence-based features give more information about the classification of the PDZ domains. However, since we used different classifiers to constuct the models, testing these models on the same dataset would be more informative on the comparison of the model performances.

**Table 4-7 Multi-classification and binary classification weighted avarage results were shown for Kalyoncu et al.'s study [11]**

| | TP Rate | | FP Rate | | Precision | | Accuracy(%) | |
|---|---|---|---|---|---|---|---|---|
| | *Bigram - Trigram* | | *Bigram - Trigram* | | *Bigram - Trigram* | | *Bigram – Trigram* | |
| Class I, Class II, Class I-II | 0.895 | 0.907 | 0.093 | 0.081 | 0.902 | 0.911 | 89.5 | 90.7 |
| Class I, Class II | 0.956 | 0.918 | 0.200 | 0 | 0.915 | 1 | 90.8 | 93.8 |
| Class I, Class I-II | 0.955 | 0.900 | 0.227 | 0 | 0.894 | 1 | 89.4 | 92.4 |
| Class II, Class I-II | 0.813 | 1 | 0 | 0.107 | 1 | 0.812 | 92.7 | 92.7 |

The classification model that we have proposed in this study is based on the general knowledge of PDZ domain's classification issue . Although the PDZ domains show high interaction selectivity, there are PDZ domains that can interact both Class I and Class II which are named as Class I-II [11]. The high performance of discriminating this promiscuous class of PDZ domain among other classes suggest that there may be a pattern for Class I-II PDZ domains. This result supports the general classification knowledge of PDZ domains.

### 4.3 Human proteome scanning

To interrogate the reliability of the interaction prediction model, we scanned the human proteome for 218 PDZ domain interactions and compared them with the known interactions of these PDZ domains. For comparison purpose of the model with previous structure-based prediction model [12], we used the same human proteome C-terminals and human PDZ domains (defined by genome assembly Ensembl:GRCh37.64). In total, 61 XRAY and nine NMR structures were retrieved from PDB whereas 148 PDZ domains were modeled via SWISS-MODEL (see Appendix: Table S3 for more details, the same data was used with the Bader et. al study [12]). All models had a similarity above 22% (avarage 72%) with template sequence and QMEAN score of at least 0.36 (avarage 0.78). All of PDZ domain containing protein's interactions were obtained from IRefIndex [25] database that collects interactions from various databases including BioGRID [26], BIND [27] , IntAct[28], CORUM [29], DIP [30], HPRD [31] and MINT [32].

As a result, the model had positive interaction predictions for 101 domains out of 218, where the model could not predict any positive interactions for remaining 117 PDZ domains. Then, we validated these positive predicted interactions of 101 domains with their experimentally known interactions. To be consistent with the previous structure-based model's human proteome scanning results, an avarage value of TP rate's of 101 PDZ domains was calculated. The avarage of 101 PDZ domain TP rates was over 17 %. Previous structure-based interaction model's human proteome scanning resulted with positive predictions for 88 domains out of the same 218 PDZ domains that we used, and could not have positive interaction predictions for remaining 130 domains. Moreover, the same avarage calculation for 88 domain TP rates was ended up with a value of 21%. To be able to compare these two results, that are an avarage TP rate value of 17% for 101 PDZ domains and an avarage TP rate

value of 21% for 88 PDZ domains, we calculated the total avarages for the same 218 domains that we both used. The total avarages concluded with the value of 8% for both models. However, since our model had true positive predictions for 101 domains where the previous one had for 88 domsins, this results show that our model has more generalized rules than the previous one.

Afterwards, we investigated the common PDZ domains between 101 domains and 88 domains, that have true positive interaction predictions from our and the previous model, respectively. It is found for 69 common PDZ domains both models had true positive predicitions. Our model has a TP rate with a number of over 23% for 69 common PDZ domains.

There were some issues that might affect proteome scanning ability dramatically. First of all, known PPIs information is not specific to PDZ domains but to the protein as a whole that means the interaction might occur via other domains. Second, almost all the proteins that are scanned for PPIs have multiple PDZ domains, therefore, assigning an interaction to particular PDZ domain was not possible. In spite of the handicaps that effect the scanning results, correct predictions for 101 PDZ domains out of 218 with an avarage of greater than 17% shows the achivement of the predictor model.

**Table 4-8 Human proteome scanning results** (Number of experimentally proved interactions and number of the model predicted correctly for each domain.The first 69 domains are the mutual domains with the previous study [12])

| Row indices | PDZ Domain name | # of known interactions | # of correctly predicted interactions |
|---|---|---|---|
| **1** | APBA3-1 | 4 | 0 |
| **2** | APBA3-2 | 4 | 0 |
| **3** | CASK-1 | 54 | 4 |
| **4** | DLG1-1 | 77 | 25 |
| **5** | DLG1-2 | 77 | 25 |
| **6** | DLG1-3 | 77 | 25 |
| **7** | DLG2-1 | 43 | 19 |
| **8** | DLG2-2 | 43 | 24 |
| **9** | DLG2-3 | 43 | 27 |
| **10** | DLG3-1 | 50 | 13 |
| **11** | DLG3-2 | 50 | 19 |
| **12** | DLG3-3 | 50 | 12 |
| **13** | DLG4-1 | 119 | 36 |
| **14** | DLG4-2 | 119 | 33 |
| **15** | DLG4-3 | 119 | 41 |
| **16** | ERBB2IP-1 | 31 | 6 |
| **17** | IL16-1 | 24 | 4 |
| **18** | LIN7A-1 | 15 | 3 |
| **19** | LIN7B-1 | 14 | 3 |
| **20** | LIN7C-1 | 14 | 1 |
| **21** | LRRC7-1 | 12 | 2 |
| **22** | MAGI1-2 | 32 | 1 |
| **23** | MAGI1-4 | 32 | 1 |
| **24** | MAGI1-5 | 32 | 2 |
| **25** | MAGI1-6 | 32 | 4 |
| **26** | MAGI2-2 | 18 | 1 |
| **27** | MAGI2-4 | 18 | 0 |
| **28** | MAGI2-5 | 18 | 1 |
| **29** | MAGI2-6 | 18 | 3 |
| **30** | MAGI3-2 | 20 | 7 |
| **31** | MAGI3-4 | 20 | 0 |
| **32** | MAGI3-5 | 20 | 1 |
| **33** | MAGI3-6 | 20 | 6 |
| **34** | MAST2-1 | 13 | 0 |
| **35** | MPDZ-1 | 22 | 0 |

| | | | |
|---|---|---|---|
| **36** | MPDZ-2 | 22 | 0 |
| **37** | MPDZ-3 | 22 | 1 |
| **38** | MPDZ-4 | 22 | 0 |
| **39** | MPDZ-5 | 22 | 1 |
| **40** | MPDZ-7 | 22 | 1 |
| **41** | MPDZ-10 | 22 | 7 |
| **42** | MPDZ-12 | 22 | 2 |
| **43** | MPDZ-13 | 22 | 1 |
| **44** | MPP6-1 | 26 | 1 |
| **45** | PDZD3-1 | 13 | 0 |
| **46** | PDZK1-1 | 30 | 5 |
| **47** | PTPN3-1 | 13 | 0 |
| **48** | SCRIB-1 | 20 | 5 |
| **49** | SCRIB-2 | 20 | 6 |
| **50** | SCRIB-4 | 20 | 1 |
| **51** | SHANK2-1 | 21 | 5 |
| **52** | SLC9A3R2-2 | 41 | 22 |
| **53** | SNTA1-1 | 29 | 6 |
| **54** | SNTB1-1 | 11 | 6 |
| **55** | SNTB2-1 | 16 | 5 |
| **56** | SNTG2-1 | 4 | 1 |
| **57** | SYNJ2BP-1 | 9 | 1 |
| **58** | TJP1-1 | 62 | 10 |
| **59** | TJP2-1 | 20 | 1 |
| **60** | PDZD2-3 | 6 | 1 |
| **61** | PDZD2-5 | 6 | 0 |
| **62** | INADL-8 | 39 | 1 |
| **63** | INADL-9 | 39 | 0 |
| **64** | INADL-2 | 39 | 7 |
| **65** | INADL-3 | 39 | 1 |
| **66** | INADL-6 | 39 | 14 |
| **67** | PTPN4-1 | 16 | 0 |
| **68** | SCRIB-3 | 20 | 4 |
| **69** | PTPN13-1 | 26 | 0 |
| **70** | MAGI3-3 | 20 | 0 |
| **71** | PTPN13-2 | 26 | 0 |
| **72** | NOS1-1 | 31 | 0 |
| **73** | APBA2-2 | 12 | 0 |
| **74** | APBA2-1 | 12 | 0 |
| **75** | APBA1-2 | 24 | 0 |
| **76** | DVL1-1 | 32 | 0 |

| | | | |
|---|---|---|---|
| **77** | GRIP1-2 | 28 | 0 |
| **78** | LDB3-1 | 4 | 0 |
| **79** | PSCDBP-1 | 3 | 0 |
| **80** | PDZRN3-1 | 4 | 0 |
| **81** | PARD3B-2 | 10 | 1 |
| **82** | PDZD4-1 | 1 | 0 |
| **83** | INADL-5 | 39 | 6 |
| **84** | DVL1L1-1 | 2 | 0 |
| **85** | DVL2-1 | 63 | 0 |
| **86** | RGS3-1 | 20 | 0 |
| **87** | SHANK3-1 | 8 | 1 |
| **88** | ARHGEF12-1 | 11 | 0 |
| **89** | WHRN-1 | 1 | 0 |
| **90** | SHROOM3-1 | 2 | 0 |
| **91** | MAGI2-3 | 18 | 0 |
| **92** | PICK1-1 | 51 | 0 |
| **93** | PDLIM7-1 | 29 | 0 |
| **94** | MPP4-1 | 3 | 0 |
| **95** | PDLIM4-1 | 5 | 0 |
| **96** | PDZD11-1 | 3 | 1 |
| **97** | RADIL-1 | 10 | 0 |
| **98** | PTPN13-4 | 26 | 0 |
| **99** | IL16-3 | 24 | 3 |
| **100** | MPDZ-11 | 22 | 0 |
| **101** | DVL3-1 | 31 | 0 |
| | **TOTAL** | 2729 | 477 |

# Chapter 5

# CONCLUSION

PDZ domain's binding specificity preferences becomes more and more clear with the computational and high-throughput experimental studies. Since the PDZ domains are involved several cell processes, revealing PDZ domain mediated interactions and finding out its binding behaviour will contribute to many of the studies including PDZ related disease mechanisms and novel drug development.

This study aims to construct a powerful and robust model for prediction PDZ domain – peptide interactions and classification of PDZ domains. A model was trained on interaction dataset of PDZ domains which contains 83 PDZ domains with 871 ligands. To train such a model hydrophobicity, electrostatic potential and relatively accessible surface area were used as structural features whereas possible phosphorylation sites were used as post-translational feature of the PDZ domains. Peptides were converted into sequential information according to the amino acid types as a binary vector with a length of 20 per residue.

For interaction prediction, the model performance was tested on cross-validation set resulted a high area under ROC curve, namely, 0.99. Such high performance proved that utilizing structural and sequential features in the same model is more advantegous than using only one type of feature. Additionally, using the number of threonine, tyrosine and serine residues in the binding site of PDZ domain as possible phosphorylation sites feature, had a great contribution on the interaction prediction model performance which shows the important role of post-translational modifications on binding preferences of PDZ domais.

Both the multi-classification and the binary classification models achieved high performance on categorizing the PDZ domains. The multi-classification of the PDZ domains was one of the challenges because we did not want to discriminate only Class I and Class II PDZ domains, but also the promiscous PDZ domain class, namely Class I-II. Nevertheless, our model achieved very well performance on multi-classification issue with an area under ROC curve of 0.88. Since the model was constructed based on the general pattern of PDZ domain classification, these results encourages the current knowledge. Moreover, the comparison of the binary classifications of the pair wise combinations of three classes gave

insight about the diversity of the PDZ domain classes. As the results indicated, the most diverse classes were Class II/Class I-II where the most alike ones were Class I/Class I-II. Moreover, a case study that examines the differences between Class I and Class I-II in terms of the surface properties was accomplished. As the results indicated, Class I-II has a hydrophobic residue in the 5th position of αB-helix secondary structure. Additionally, it is also concluded that if Class I domains have a hydrophobic residue in this position, the classification models may classify the Class I PDZ domain as Class I-II.

Furthermore, we scanned the human proteome for 218 PDZ domains to be able to compare our model with the previous one that we used the same dataset and have an insight of the predictor's performance. All the PDZ domains that were possible to generate structural features, with a total number of 218 were used to scan the human proteome with a number of peptides of over 43000. After the scanning process, only the 101 domains that have positive predicted interactions were validated by using their experimentally known interactions. As a result of validation, the model predicted several human known PPIs succesfully with an avarage of TP rate of 101 domains greater than 17%.

Concerning the future directions, current study might have implications on finding novel binding partners of PDZ domains as well as drug discovery. The robustness and performance of the models may be improved by using experimental phosphorylation information for PDZ domain. The quality of the model may be increased by integrating the recent experimental data to the training set, as well. Lastly, a web server of the model may be developed to make it easier to use by others.

# APPENDIX

**Table S1.a PDZ domain interaction dataset** (PDZ domain name, Experiment(PM = Protein microarray, PD = Phage display), Organism(M = Mouse, H = Human), Domain ID(see Table S1.b), Peptide ID(see Table S1.c), Interaction).

| PDZ domain name | Experiment | Organism | Domain ID | Peptide ID | Interaction | PDZ domain name | Experiment | Organism | Domain ID | Peptide ID | Interaction |
|---|---|---|---|---|---|---|---|---|---|---|---|
| A1-SYNTROPHIN-1 | PM | M | 0 | 0 | Y | MAGI-3-1 | PM | M | 21 | 523 | N |
| A1-SYNTROPHIN-1 | PM | M | 0 | 1 | Y | MAGI-3-1 | PM | M | 21 | 564 | N |
| A1-SYNTROPHIN-1 | PM | M | 0 | 2 | Y | MAGI-3-1 | PM | M | 21 | 7 | N |
| A1-SYNTROPHIN-1 | PM | M | 0 | 3 | Y | MAGI-3-1 | PM | M | 21 | 565 | N |
| A1-SYNTROPHIN-1 | PM | M | 0 | 4 | Y | MAGI-3-1 | PM | M | 21 | 566 | N |
| A1-SYNTROPHIN-1 | PM | M | 0 | 5 | Y | MAGI-3-1 | PM | M | 21 | 567 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 5 | Y | MAGI-3-1 | PM | M | 21 | 454 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 6 | Y | MAGI-3-1 | PM | M | 21 | 496 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 7 | Y | MAGI-3-1 | PM | M | 21 | 568 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 3 | Y | MAGI-3-1 | PM | M | 21 | 569 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 5 | Y | MAGI-3-1 | PM | M | 21 | 570 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 8 | Y | MAGI-3-1 | PM | M | 21 | 571 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 9 | Y | MAGI-3-2 | PM | M | 22 | 25 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 10 | Y | MAGI-3-2 | PM | M | 22 | 21 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 2 | Y | MAGI-3-2 | PM | M | 22 | 1 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 4 | Y | MAGI-3-2 | PM | M | 22 | 519 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 11 | Y | MAGI-3-2 | PM | M | 22 | 508 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 12 | Y | MAGI-3-2 | PM | M | 22 | 23 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 0 | Y | MAGI-3-2 | PM | M | 22 | 6 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 13 | Y | MAGI-3-5 | PM | M | 23 | 572 | N |
| B1-SYNTROPHIN-1 | PM | M | 1 | 14 | Y | MAGI-3-5 | PM | M | 23 | 573 | N |
| CHAPSYN-110-2 | PM | M | 2 | 15 | Y | MAGI-3-5 | PM | M | 23 | 7 | N |
| CHAPSYN-110-2 | PM | M | 2 | 0 | Y | MAGI-3-5 | PM | M | 23 | 574 | N |
| CHAPSYN-110-2 | PM | M | 2 | 4 | Y | MAGI-3-5 | PM | M | 23 | 575 | N |
| CHAPSYN-110-2 | PM | M | 2 | 16 | Y | MAGI-3-5 | PM | M | 23 | 2 | N |
| CHAPSYN-110-2 | PM | M | 2 | 17 | Y | MAGI-3-5 | PM | M | 23 | 20 | N |
| CHAPSYN-110-2 | PM | M | 2 | 9 | Y | MAGI-3-5 | PM | M | 23 | 62 | N |
| CHAPSYN-110-2 | PM | M | 2 | 5 | Y | MAGI-3-5 | PM | M | 23 | 560 | N |
| CHAPSYN-110-2 | PM | M | 2 | 18 | Y | MAGI-3-5 | PM | M | 23 | 576 | N |
| CHAPSYN-110-2 | PM | M | 2 | 19 | Y | MAGI-3-5 | PM | M | 23 | 65 | N |
| CHAPSYN-110-2 | PM | M | 2 | 20 | Y | MAGI-3-5 | PM | M | 23 | 472 | N |
| CHAPSYN-110-2 | PM | M | 2 | 2 | Y | MAGI-3-5 | PM | M | 23 | 559 | N |
| CHAPSYN-110-2 | PM | M | 2 | 17 | Y | MAGI-3-5 | PM | M | 23 | 68 | N |
| CHAPSYN-110-2 | PM | M | 2 | 21 | Y | MAGI-3-5 | PM | M | 23 | 554 | N |
| CHAPSYN-110-2 | PM | M | 2 | 8 | Y | MAGI-3-5 | PM | M | 23 | 561 | N |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **CHAPSYN-110-2** | PM | M | 2 | 6 | Y | **MAGI-3-5** | PM | M | 23 | 577 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 5 | Y | **MAGI-3-5** | PM | M | 23 | 578 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 1 | Y | **MAGI-3-5** | PM | M | 23 | 67 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 11 | Y | **MAGI-3-5** | PM | M | 23 | 579 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 22 | Y | **MAGI-3-5** | PM | M | 23 | 534 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 0 | Y | **MAGI-3-5** | PM | M | 23 | 445 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 16 | Y | **MAGI-3-5** | PM | M | 23 | 580 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 14 | Y | **MAGI-3-5** | PM | M | 23 | 581 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 5 | Y | **MAGI-3-5** | PM | M | 23 | 555 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 5 | Y | **MAGI-3-5** | PM | M | 23 | 582 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 6 | Y | **MALS2-1** | PM | M | 24 | 583 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 20 | Y | **MALS2-1** | PM | M | 24 | 584 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 23 | Y | **MALS2-1** | PM | M | 24 | 506 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 24 | Y | **MALS2-1** | PM | M | 24 | 585 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 2 | Y | **MALS2-1** | PM | M | 24 | 586 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 8 | Y | **MALS2-1** | PM | M | 24 | 587 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 25 | Y | **MALS2-1** | PM | M | 24 | 567 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 15 | Y | **MALS2-1** | PM | M | 24 | 37 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 1 | Y | **MALS2-1** | PM | M | 24 | 588 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 9 | Y | **MALS2-1** | PM | M | 24 | 589 | N |
| **CIPP-10** | PM | M | 4 | 26 | Y | **MALS2-1** | PM | M | 24 | 502 | N |
| **CIPP-10** | PM | M | 4 | 22 | Y | **MALS2-1** | PM | M | 24 | 566 | N |
| **CIPP-10** | PM | M | 4 | 27 | Y | **MPP7-1** | PM | M | 25 | 474 | N |
| **CIPP-3** | PM | M | 5 | 26 | Y | **MPP7-1** | PM | M | 25 | 473 | N |
| **CIPP-3** | PM | M | 5 | 28 | Y | **MPP7-1** | PM | M | 25 | 475 | N |
| **CIPP-5** | PM | M | 6 | 29 | Y | **MPP7-1** | PM | M | 25 | 64 | N |
| **CIPP-5** | PM | M | 6 | 30 | Y | **MPP7-1** | PM | M | 25 | 472 | N |
| **CIPP-5** | PM | M | 6 | 31 | Y | **MPP7-1** | PM | M | 25 | 35 | N |
| **CIPP-5** | PM | M | 6 | 32 | Y | **MPP7-1** | PM | M | 25 | 15 | N |
| **CIPP-5** | PM | M | 6 | 32 | Y | **MPP7-1** | PM | M | 25 | 57 | N |
| **CIPP-8** | PM | M | 7 | 26 | Y | **MPP7-1** | PM | M | 25 | 463 | N |
| **CIPP-8** | PM | M | 7 | 21 | Y | **MPP7-1** | PM | M | 25 | 3 | N |
| **CIPP-8** | PM | M | 7 | 20 | Y | **MPP7-1** | PM | M | 25 | 73 | N |
| **CIPP-8** | PM | M | 7 | 23 | Y | **MPP7-1** | PM | M | 25 | 17 | N |
| **CIPP-8** | PM | M | 7 | 9 | Y | **MPP7-1** | PM | M | 25 | 23 | N |
| **CIPP-8** | PM | M | 7 | 33 | Y | **MPP7-1** | PM | M | 25 | 467 | N |
| **CIPP-8** | PM | M | 7 | 34 | Y | **MPP7-1** | PM | M | 25 | 465 | N |
| **CIPP-8** | PM | M | 7 | 35 | Y | **MPP7-1** | PM | M | 25 | 466 | N |
| **CIPP-8** | PM | M | 7 | 36 | Y | **MPP7-1** | PM | M | 25 | 45 | N |
| **CIPP-8** | PM | M | 7 | 25 | Y | **MPP7-1** | PM | M | 25 | 43 | N |
| **CIPP-9** | PM | M | 8 | 29 | Y | **MPP7-1** | PM | M | 25 | 26 | N |
| **CIPP-9** | PM | M | 8 | 37 | Y | **MPP7-1** | PM | M | 25 | 29 | N |
| **CIPP-9** | PM | M | 8 | 26 | Y | **MPP7-1** | PM | M | 25 | 16 | N |
| **CIPP-9** | PM | M | 8 | 38 | Y | **MPP7-1** | PM | M | 25 | 470 | N |
| **CIPP-9** | PM | M | 8 | 39 | Y | **MPP7-1** | PM | M | 25 | 476 | N |
| **CIPP-9** | PM | M | 8 | 40 | Y | **MPP7-1** | PM | M | 25 | 22 | N |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| **CIPP-9** | PM | M | 8 | 41 | Y | **MPP7-1** | PM | M | 25 | 13 | N |
| **CIPP-9** | PM | M | 8 | 42 | Y | **MPP7-1** | PM | M | 25 | 41 | N |
| **DVL1-1** | PM | M | 9 | 26 | Y | **MPP7-1** | PM | M | 25 | 65 | N |
| **DVL1-1** | PM | M | 9 | 30 | Y | **MPP7-1** | PM | M | 25 | 468 | N |
| **DVL1-1** | PM | M | 9 | 27 | Y | **MPP7-1** | PM | M | 25 | 469 | N |
| **DVL3-1** | PM | M | 10 | 30 | Y | **MPP7-1** | PM | M | 25 | 454 | N |
| **DVL3-1** | PM | M | 10 | 43 | Y | **MPP7-1** | PM | M | 25 | 63 | N |
| **DVL3-1** | PM | M | 10 | 26 | Y | **MUPP1-1** | PM | M | 26 | 64 | N |
| **DVL3-1** | PM | M | 10 | 27 | Y | **MUPP1-1** | PM | M | 26 | 473 | N |
| **ERBIN-1** | PM | M | 11 | 17 | Y | **MUPP1-1** | PM | M | 26 | 474 | N |
| **ERBIN-1** | PM | M | 11 | 9 | Y | **MUPP1-1** | PM | M | 26 | 65 | N |
| **GRIP1-6** | PM | M | 12 | 44 | Y | **MUPP1-1** | PM | M | 26 | 41 | N |
| **HARMONIN-2** | PM | M | 13 | 26 | Y | **MUPP1-1** | PM | M | 26 | 472 | N |
| **HARMONIN-2** | PM | M | 13 | 45 | Y | **MUPP1-1** | PM | M | 26 | 15 | N |
| **LARG-1** | PM | M | 14 | 8 | Y | **MUPP1-1** | PM | M | 26 | 57 | N |
| **LARG-1** | PM | M | 14 | 0 | Y | **MUPP1-1** | PM | M | 26 | 463 | N |
| **LARG-1** | PM | M | 14 | 20 | Y | **MUPP1-1** | PM | M | 26 | 23 | N |
| **LIN-7C-1** | PM | M | 15 | 15 | Y | **MUPP1-1** | PM | M | 26 | 465 | N |
| **LIN-7C-1** | PM | M | 15 | 1 | Y | **MUPP1-1** | PM | M | 26 | 13 | N |
| **LIN-7C-1** | PM | M | 15 | 2 | Y | **MUPP1-1** | PM | M | 26 | 2 | N |
| **LIN-7C-1** | PM | M | 15 | 7 | Y | **MUPP1-1** | PM | M | 26 | 467 | N |
| **LIN-7C-1** | PM | M | 15 | 14 | Y | **MUPP1-1** | PM | M | 26 | 468 | N |
| **LIN-7C-1** | PM | M | 15 | 9 | Y | **MUPP1-1** | PM | M | 26 | 17 | N |
| **LIN-7C-1** | PM | M | 15 | 5 | Y | **MUPP1-1** | PM | M | 26 | 475 | N |
| **LIN-7C-1** | PM | M | 15 | 0 | Y | **MUPP1-1** | PM | M | 26 | 43 | N |
| **LIN-7C-1** | PM | M | 15 | 46 | Y | **MUPP1-1** | PM | M | 26 | 3 | N |
| **LIN-7C-1** | PM | M | 15 | 47 | Y | **MUPP1-1** | PM | M | 26 | 29 | N |
| **LIN-7C-1** | PM | M | 15 | 12 | Y | **MUPP1-1** | PM | M | 26 | 454 | N |
| **LIN-7C-1** | PM | M | 15 | 13 | Y | **MUPP1-1** | PM | M | 26 | 45 | N |
| **LIN-7C-1** | PM | M | 15 | 24 | Y | **MUPP1-1** | PM | M | 26 | 73 | N |
| **LIN-7C-1** | PM | M | 15 | 10 | Y | **MUPP1-1** | PM | M | 26 | 470 | N |
| **LIN-7C-1** | PM | M | 15 | 19 | Y | **MUPP1-1** | PM | M | 26 | 16 | N |
| **LIN-7C-1** | PM | M | 15 | 5 | Y | **MUPP1-1** | PM | M | 26 | 469 | N |
| **LIN-7C-1** | PM | M | 15 | 4 | Y | **MUPP1-1** | PM | M | 26 | 466 | N |
| **LIN-7C-1** | PM | M | 15 | 8 | Y | **MUPP1-1** | PM | M | 26 | 476 | N |
| **LIN-7C-1** | PM | M | 15 | 6 | Y | **MUPP1-1** | PM | M | 26 | 22 | N |
| **LRRC7-1** | PM | M | 16 | 0 | Y | **MUPP1-1** | PM | M | 26 | 63 | N |
| **LRRC7-1** | PM | M | 16 | 14 | Y | **MUPP1-1** | PM | M | 26 | 35 | N |
| **LRRC7-1** | PM | M | 16 | 9 | Y | **MUPP1-1** | PM | M | 26 | 30 | N |
| **MAGI-1-6** | PM | M | 17 | 17 | Y | **MUPP1-10** | PM | M | 27 | 470 | N |
| **MAGI-1-6** | PM | M | 17 | 11 | Y | **MUPP1-10** | PM | M | 27 | 467 | N |
| **MAGI-1-6** | PM | M | 17 | 39 | Y | **MUPP1-10** | PM | M | 27 | 475 | N |
| **MAGI-1-6** | PM | M | 17 | 14 | Y | **MUPP1-10** | PM | M | 27 | 472 | N |
| **MAGI-1-6** | PM | M | 17 | 17 | Y | **MUPP1-10** | PM | M | 27 | 16 | N |
| **MAGI-1-6** | PM | M | 17 | 3 | Y | **MUPP1-10** | PM | M | 27 | 63 | N |
| **MAGI-1-6** | PM | M | 17 | 0 | Y | **MUPP1-10** | PM | M | 27 | 29 | N |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| **MAGI-1-6** | PM | M | 17 | 9 | Y | **MUPP1-10** | PM | M | 27 | 30 | N |
| **MAGI-1-6** | PM | M | 17 | 18 | Y | **MUPP1-10** | PM | M | 27 | 454 | N |
| **MAGI-1-6** | PM | M | 17 | 8 | Y | **MUPP1-10** | PM | M | 27 | 65 | N |
| **MAGI-1-6** | PM | M | 17 | 48 | Y | **MUPP1-10** | PM | M | 27 | 83 | N |
| **MAGI-1-6** | PM | M | 17 | 49 | Y | **MUPP1-10** | PM | M | 27 | 3 | N |
| **MAGI-2-2** | PM | M | 18 | 20 | Y | **MUPP1-10** | PM | M | 27 | 463 | N |
| **MAGI-2-2** | PM | M | 18 | 6 | Y | **MUPP1-10** | PM | M | 27 | 476 | N |
| **MAGI-2-2** | PM | M | 18 | 15 | Y | **MUPP1-10** | PM | M | 27 | 466 | N |
| **MAGI-2-2** | PM | M | 18 | 16 | Y | **MUPP1-10** | PM | M | 27 | 469 | N |
| **MAGI-2-2** | PM | M | 18 | 16 | Y | **MUPP1-10** | PM | M | 27 | 22 | N |
| **MAGI-2-2** | PM | M | 18 | 1 | Y | **MUPP1-10** | PM | M | 27 | 473 | N |
| **MAGI-2-2** | PM | M | 18 | 21 | Y | **MUPP1-10** | PM | M | 27 | 508 | N |
| **MAGI-2-2** | PM | M | 18 | 0 | Y | **MUPP1-10** | PM | M | 27 | 64 | N |
| **MAGI-2-2** | PM | M | 18 | 17 | Y | **MUPP1-10** | PM | M | 27 | 465 | N |
| **MAGI-2-2** | PM | M | 18 | 4 | Y | **MUPP1-10** | PM | M | 27 | 17 | N |
| **MAGI-2-2** | PM | M | 18 | 9 | Y | **MUPP1-10** | PM | M | 27 | 41 | N |
| **MAGI-2-2** | PM | M | 18 | 2 | Y | **MUPP1-10** | PM | M | 27 | 474 | N |
| **MAGI-2-2** | PM | M | 18 | 5 | Y | **MUPP1-10** | PM | M | 27 | 73 | N |
| **MAGI-2-2** | PM | M | 18 | 50 | Y | **MUPP1-10** | PM | M | 27 | 11 | N |
| **MAGI-2-2** | PM | M | 18 | 51 | Y | **MUPP1-10** | PM | M | 27 | 468 | N |
| **MAGI-2-5** | PM | M | 19 | 15 | Y | **MUPP1-10** | PM | M | 27 | 13 | N |
| **MAGI-2-5** | PM | M | 19 | 5 | Y | **MUPP1-11** | PM | M | 28 | 40 | N |
| **MAGI-2-6** | PM | M | 20 | 18 | Y | **MUPP1-11** | PM | M | 28 | 473 | N |
| **MAGI-2-6** | PM | M | 20 | 17 | Y | **MUPP1-11** | PM | M | 28 | 476 | N |
| **MAGI-2-6** | PM | M | 20 | 20 | Y | **MUPP1-11** | PM | M | 28 | 73 | N |
| **MAGI-2-6** | PM | M | 20 | 49 | Y | **MUPP1-11** | PM | M | 28 | 23 | N |
| **MAGI-2-6** | PM | M | 20 | 11 | Y | **MUPP1-11** | PM | M | 28 | 3 | N |
| **MAGI-2-6** | PM | M | 20 | 48 | Y | **MUPP1-11** | PM | M | 28 | 45 | N |
| **MAGI-2-6** | PM | M | 20 | 52 | Y | **MUPP1-11** | PM | M | 28 | 15 | N |
| **MAGI-2-6** | PM | M | 20 | 26 | Y | **MUPP1-11** | PM | M | 28 | 57 | N |
| **MAGI-2-6** | PM | M | 20 | 9 | Y | **MUPP1-11** | PM | M | 28 | 463 | N |
| **MAGI-2-6** | PM | M | 20 | 3 | Y | **MUPP1-11** | PM | M | 28 | 472 | N |
| **MAGI-2-6** | PM | M | 20 | 0 | Y | **MUPP1-11** | PM | M | 28 | 7 | N |
| **MAGI-2-6** | PM | M | 20 | 27 | Y | **MUPP1-11** | PM | M | 28 | 470 | N |
| **MAGI-2-6** | PM | M | 20 | 17 | Y | **MUPP1-11** | PM | M | 28 | 474 | N |
| **MAGI-3-1** | PM | M | 21 | 15 | Y | **MUPP1-11** | PM | M | 28 | 13 | N |
| **MAGI-3-1** | PM | M | 21 | 0 | Y | **MUPP1-11** | PM | M | 28 | 32 | N |
| **MAGI-3-1** | PM | M | 21 | 4 | Y | **MUPP1-11** | PM | M | 28 | 467 | N |
| **MAGI-3-1** | PM | M | 21 | 16 | Y | **MUPP1-11** | PM | M | 28 | 468 | N |
| **MAGI-3-1** | PM | M | 21 | 17 | Y | **MUPP1-11** | PM | M | 28 | 17 | N |
| **MAGI-3-1** | PM | M | 21 | 2 | Y | **MUPP1-11** | PM | M | 28 | 475 | N |
| **MAGI-3-1** | PM | M | 21 | 5 | Y | **MUPP1-11** | PM | M | 28 | 19 | N |
| **MAGI-3-1** | PM | M | 21 | 53 | Y | **MUPP1-11** | PM | M | 28 | 43 | N |
| **MAGI-3-1** | PM | M | 21 | 6 | Y | **MUPP1-11** | PM | M | 28 | 35 | N |
| **MAGI-3-1** | PM | M | 21 | 5 | Y | **MUPP1-11** | PM | M | 28 | 42 | N |
| **MAGI-3-1** | PM | M | 21 | 51 | Y | **MUPP1-11** | PM | M | 28 | 454 | N |

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| **MAGI-3-1** | PM | M | 21 | 21 | Y | **MUPP1-11** | PM | M | 28 | 65 | N |
| **MAGI-3-1** | PM | M | 21 | 23 | Y | **MUPP1-11** | PM | M | 28 | 508 | N |
| **MAGI-3-1** | PM | M | 21 | 19 | Y | **MUPP1-11** | PM | M | 28 | 64 | N |
| **MAGI-3-1** | PM | M | 21 | 9 | Y | **MUPP1-11** | PM | M | 28 | 16 | N |
| **MAGI-3-1** | PM | M | 21 | 20 | Y | **MUPP1-11** | PM | M | 28 | 469 | N |
| **MAGI-3-1** | PM | M | 21 | 1 | Y | **MUPP1-11** | PM | M | 28 | 14 | N |
| **MAGI-3-1** | PM | M | 21 | 12 | Y | **MUPP1-11** | PM | M | 28 | 466 | N |
| **MAGI-3-2** | PM | M | 22 | 20 | Y | **MUPP1-11** | PM | M | 28 | 465 | N |
| **MAGI-3-5** | PM | M | 23 | 47 | Y | **MUPP1-11** | PM | M | 28 | 22 | N |
| **MAGI-3-5** | PM | M | 23 | 17 | Y | **MUPP1-11** | PM | M | 28 | 63 | N |
| **MAGI-3-5** | PM | M | 23 | 54 | Y | **MUPP1-11** | PM | M | 28 | 26 | N |
| **MAGI-3-5** | PM | M | 23 | 8 | Y | **MUPP1-11** | PM | M | 28 | 30 | N |
| **MAGI-3-5** | PM | M | 23 | 49 | Y | **MUPP1-12** | PM | M | 29 | 476 | N |
| **MAGI-3-5** | PM | M | 23 | 10 | Y | **MUPP1-12** | PM | M | 29 | 29 | N |
| **MAGI-3-5** | PM | M | 23 | 26 | Y | **MUPP1-12** | PM | M | 29 | 65 | N |
| **MAGI-3-5** | PM | M | 23 | 36 | Y | **MUPP1-12** | PM | M | 29 | 73 | N |
| **MAGI-3-5** | PM | M | 23 | 9 | Y | **MUPP1-12** | PM | M | 29 | 17 | N |
| **MAGI-3-5** | PM | M | 23 | 4 | Y | **MUPP1-12** | PM | M | 29 | 23 | N |
| **MAGI-3-5** | PM | M | 23 | 0 | Y | **MUPP1-12** | PM | M | 29 | 463 | N |
| **MAGI-3-5** | PM | M | 23 | 48 | Y | **MUPP1-12** | PM | M | 29 | 57 | N |
| **MAGI-3-5** | PM | M | 23 | 34 | Y | **MUPP1-12** | PM | M | 29 | 467 | N |
| **MAGI-3-5** | PM | M | 23 | 13 | Y | **MUPP1-12** | PM | M | 29 | 41 | N |
| **MAGI-3-5** | PM | M | 23 | 18 | Y | **MUPP1-12** | PM | M | 29 | 22 | N |
| **MAGI-3-5** | PM | M | 23 | 55 | Y | **MUPP1-12** | PM | M | 29 | 45 | N |
| **MAGI-3-5** | PM | M | 23 | 25 | Y | **MUPP1-12** | PM | M | 29 | 63 | N |
| **MAGI-3-5** | PM | M | 23 | 14 | Y | **MUPP1-12** | PM | M | 29 | 466 | N |
| **MAGI-3-5** | PM | M | 23 | 27 | Y | **MUPP1-12** | PM | M | 29 | 473 | N |
| **MAGI-3-5** | PM | M | 23 | 17 | Y | **MUPP1-12** | PM | M | 29 | 16 | N |
| **MAGI-3-5** | PM | M | 23 | 3 | Y | **MUPP1-12** | PM | M | 29 | 469 | N |
| **MAGI-3-5** | PM | M | 23 | 56 | Y | **MUPP1-12** | PM | M | 29 | 470 | N |
| **MAGI-3-5** | PM | M | 23 | 11 | Y | **MUPP1-12** | PM | M | 29 | 64 | N |
| **MAGI-3-5** | PM | M | 23 | 46 | Y | **MUPP1-12** | PM | M | 29 | 15 | N |
| **MAGI-3-5** | PM | M | 23 | 52 | Y | **MUPP1-12** | PM | M | 29 | 472 | N |
| **MALS2-1** | PM | M | 24 | 16 | Y | **MUPP1-12** | PM | M | 29 | 5 | N |
| **MALS2-1** | PM | M | 24 | 9 | Y | **MUPP1-12** | PM | M | 29 | 35 | N |
| **MALS2-1** | PM | M | 24 | 15 | Y | **MUPP1-12** | PM | M | 29 | 474 | N |
| **MALS2-1** | PM | M | 24 | 0 | Y | **MUPP1-12** | PM | M | 29 | 468 | N |
| **MALS2-1** | PM | M | 24 | 16 | Y | **MUPP1-12** | PM | M | 29 | 475 | N |
| **MALS2-1** | PM | M | 24 | 19 | Y | **MUPP1-12** | PM | M | 29 | 26 | N |
| **MALS2-1** | PM | M | 24 | 8 | Y | **MUPP1-12** | PM | M | 29 | 30 | N |
| **MALS2-1** | PM | M | 24 | 7 | Y | **MUPP1-12** | PM | M | 29 | 13 | N |
| **MALS2-1** | PM | M | 24 | 1 | Y | **MUPP1-12** | PM | M | 29 | 465 | N |
| **MALS2-1** | PM | M | 24 | 46 | Y | **MUPP1-12** | PM | M | 29 | 454 | N |
| **MALS2-1** | PM | M | 24 | 2 | Y | **MUPP1-12** | PM | M | 29 | 43 | N |
| **MALS2-1** | PM | M | 24 | 6 | Y | **MUPP1-12** | PM | M | 29 | 3 | N |
| **MPP7-1** | PM | M | 25 | 30 | Y | **MUPP1-12** | PM | M | 29 | 436 | N |

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| **MPP7-1** | PM | M | 25 | 28 | Y | **MUPP1-13** | PM | M | 30 | 445 | N |
| **MUPP1-1** | PM | M | 26 | 26 | Y | **MUPP1-13** | PM | M | 30 | 446 | N |
| **MUPP1-10** | PM | M | 27 | 23 | Y | **MUPP1-13** | PM | M | 30 | 0 | N |
| **MUPP1-10** | PM | M | 27 | 45 | Y | **MUPP1-13** | PM | M | 30 | 23 | N |
| **MUPP1-10** | PM | M | 27 | 43 | Y | **MUPP1-13** | PM | M | 30 | 20 | N |
| **MUPP1-10** | PM | M | 27 | 15 | Y | **MUPP1-13** | PM | M | 30 | 52 | N |
| **MUPP1-10** | PM | M | 27 | 35 | Y | **MUPP1-13** | PM | M | 30 | 68 | N |
| **MUPP1-10** | PM | M | 27 | 26 | Y | **MUPP1-13** | PM | M | 30 | 67 | N |
| **MUPP1-10** | PM | M | 27 | 33 | Y | **MUPP1-13** | PM | M | 30 | 48 | N |
| **MUPP1-10** | PM | M | 27 | 57 | Y | **MUPP1-13** | PM | M | 30 | 26 | N |
| **MUPP1-11** | PM | M | 28 | 41 | Y | **MUPP1-13** | PM | M | 30 | 25 | N |
| **MUPP1-11** | PM | M | 28 | 29 | Y | **MUPP1-13** | PM | M | 30 | 449 | N |
| **MUPP1-12** | PM | M | 29 | 27 | Y | **MUPP1-13** | PM | M | 30 | 19 | N |
| **MUPP1-13** | PM | M | 30 | 9 | Y | **MUPP1-13** | PM | M | 30 | 27 | N |
| **MUPP1-13** | PM | M | 30 | 8 | Y | **MUPP1-13** | PM | M | 30 | 21 | N |
| **MUPP1-13** | PM | M | 30 | 13 | Y | **MUPP1-5** | PM | M | 31 | 590 | N |
| **MUPP1-13** | PM | M | 30 | 1 | Y | **MUPP1-5** | PM | M | 31 | 591 | N |
| **MUPP1-13** | PM | M | 30 | 6 | Y | **MUPP1-5** | PM | M | 31 | 592 | N |
| **MUPP1-5** | PM | M | 31 | 29 | Y | **MUPP1-5** | PM | M | 31 | 593 | N |
| **MUPP1-5** | PM | M | 31 | 42 | Y | **MUPP1-5** | PM | M | 31 | 14 | N |
| **MUPP1-5** | PM | M | 31 | 32 | Y | **MUPP1-5** | PM | M | 31 | 37 | N |
| **MUPP1-5** | PM | M | 31 | 32 | Y | **MUPP1-5** | PM | M | 31 | 594 | N |
| **NHERF-2-2** | PM | M | 32 | 8 | Y | **MUPP1-5** | PM | M | 31 | 595 | N |
| **NHERF-2-2** | PM | M | 32 | 55 | Y | **MUPP1-5** | PM | M | 31 | 596 | N |
| **NHERF-2-2** | PM | M | 32 | 58 | Y | **MUPP1-5** | PM | M | 31 | 508 | N |
| **NHERF-2-2** | PM | M | 32 | 59 | Y | **MUPP1-5** | PM | M | 31 | 597 | N |
| **NNOS-1** | PM | M | 33 | 43 | Y | **MUPP1-5** | PM | M | 31 | 598 | N |
| **NNOS-1** | PM | M | 33 | 45 | Y | **MUPP1-5** | PM | M | 31 | 447 | N |
| **NNOS-1** | PM | M | 33 | 15 | Y | **MUPP1-5** | PM | M | 31 | 599 | N |
| **OMP25-1** | PM | M | 34 | 6 | Y | **MUPP1-5** | PM | M | 31 | 600 | N |
| **OMP25-1** | PM | M | 34 | 5 | Y | **NHERF-2-2** | PM | M | 32 | 61 | N |
| **OMP25-1** | PM | M | 34 | 25 | Y | **NHERF-2-2** | PM | M | 32 | 601 | N |
| **OMP25-1** | PM | M | 34 | 19 | Y | **NHERF-2-2** | PM | M | 32 | 17 | N |
| **OMP25-1** | PM | M | 34 | 21 | Y | **NHERF-2-2** | PM | M | 32 | 574 | N |
| **OMP25-1** | PM | M | 34 | 23 | Y | **NHERF-2-2** | PM | M | 32 | 602 | N |
| **OMP25-1** | PM | M | 34 | 47 | Y | **NHERF-2-2** | PM | M | 32 | 603 | N |
| **OMP25-1** | PM | M | 34 | 60 | Y | **NHERF-2-2** | PM | M | 32 | 604 | N |
| **OMP25-1** | PM | M | 34 | 20 | Y | **NHERF-2-2** | PM | M | 32 | 605 | N |
| **OMP25-1** | PM | M | 34 | 2 | Y | **NHERF-2-2** | PM | M | 32 | 606 | N |
| **OMP25-1** | PM | M | 34 | 5 | Y | **NHERF-2-2** | PM | M | 32 | 5 | N |
| **OMP25-1** | PM | M | 34 | 48 | Y | **NHERF-2-2** | PM | M | 32 | 607 | N |
| **OMP25-1** | PM | M | 34 | 17 | Y | **NHERF-2-2** | PM | M | 32 | 19 | N |
| **OMP25-1** | PM | M | 34 | 34 | Y | **NHERF-2-2** | PM | M | 32 | 608 | N |
| **OMP25-1** | PM | M | 34 | 15 | Y | **NHERF-2-2** | PM | M | 32 | 609 | N |
| **OMP25-1** | PM | M | 34 | 7 | Y | **NNOS-1** | PM | M | 33 | 16 | N |
| **OMP25-1** | PM | M | 34 | 9 | Y | **NNOS-1** | PM | M | 33 | 473 | N |

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| **OMP25-1** | PM | M | 34 | 14 | Y | **NNOS-1** | PM | M | 33 | 22 | N |
| **OMP25-1** | PM | M | 34 | 50 | Y | **NNOS-1** | PM | M | 33 | 468 | N |
| **OMP25-1** | PM | M | 34 | 0 | Y | **NNOS-1** | PM | M | 33 | 13 | N |
| **OMP25-1** | PM | M | 34 | 17 | Y | **NNOS-1** | PM | M | 33 | 41 | N |
| **OMP25-1** | PM | M | 34 | 57 | Y | **NNOS-1** | PM | M | 33 | 470 | N |
| **OMP25-1** | PM | M | 34 | 4 | Y | **NNOS-1** | PM | M | 33 | 474 | N |
| **OMP25-1** | PM | M | 34 | 61 | Y | **NNOS-1** | PM | M | 33 | 463 | N |
| **OMP25-1** | PM | M | 34 | 1 | Y | **NNOS-1** | PM | M | 33 | 57 | N |
| **OMP25-1** | PM | M | 34 | 24 | Y | **NNOS-1** | PM | M | 33 | 464 | N |
| **OMP25-1** | PM | M | 34 | 62 | Y | **NNOS-1** | PM | M | 33 | 466 | N |
| **OMP25-1** | PM | M | 34 | 11 | Y | **NNOS-1** | PM | M | 33 | 26 | N |
| **OMP25-1** | PM | M | 34 | 12 | Y | **NNOS-1** | PM | M | 33 | 475 | N |
| **OMP25-1** | PM | M | 34 | 46 | Y | **NNOS-1** | PM | M | 33 | 452 | N |
| **OMP25-1** | PM | M | 34 | 16 | Y | **NNOS-1** | PM | M | 33 | 63 | N |
| **OMP25-1** | PM | M | 34 | 63 | Y | **NNOS-1** | PM | M | 33 | 17 | N |
| **OMP25-1** | PM | M | 34 | 16 | Y | **NNOS-1** | PM | M | 33 | 467 | N |
| **OMP25-1** | PM | M | 34 | 8 | Y | **NNOS-1** | PM | M | 33 | 448 | N |
| **PAR6B-1** | PM | M | 35 | 64 | Y | **NNOS-1** | PM | M | 33 | 469 | N |
| **PAR6B-1** | PM | M | 35 | 65 | Y | **NNOS-1** | PM | M | 33 | 65 | N |
| **PDZK1-1** | PM | M | 36 | 8 | Y | **NNOS-1** | PM | M | 33 | 465 | N |
| **PDZK1-1** | PM | M | 36 | 27 | Y | **NNOS-1** | PM | M | 33 | 546 | N |
| **PDZK1-1** | PM | M | 36 | 58 | Y | **NNOS-1** | PM | M | 33 | 462 | N |
| **PDZK1-1** | PM | M | 36 | 23 | Y | **NNOS-1** | PM | M | 33 | 551 | N |
| **PDZK1-1** | PM | M | 36 | 13 | Y | **NNOS-1** | PM | M | 33 | 29 | N |
| **PDZK1-1** | PM | M | 36 | 58 | Y | **NNOS-1** | PM | M | 33 | 472 | N |
| **PDZK1-1** | PM | M | 36 | 66 | Y | **NNOS-1** | PM | M | 33 | 73 | N |
| **PDZK1-1** | PM | M | 36 | 64 | Y | **NNOS-1** | PM | M | 33 | 72 | N |
| **PDZK1-1** | PM | M | 36 | 0 | Y | **NNOS-1** | PM | M | 33 | 476 | N |
| **PDZK1-1** | PM | M | 36 | 9 | Y | **NNOS-1** | PM | M | 33 | 3 | N |
| **PDZK1-1** | PM | M | 36 | 67 | Y | **NNOS-1** | PM | M | 33 | 30 | N |
| **PDZK1-3** | PM | M | 37 | 64 | Y | **NNOS-1** | PM | M | 33 | 64 | N |
| **PDZK1-3** | PM | M | 37 | 68 | Y | **NNOS-1** | PM | M | 33 | 553 | N |
| **PDZK1-3** | PM | M | 37 | 58 | Y | **NNOS-1** | PM | M | 33 | 454 | N |
| **PDZK1-3** | PM | M | 37 | 13 | Y | **NNOS-1** | PM | M | 33 | 35 | N |
| **PDZK1-3** | PM | M | 37 | 58 | Y | **NNOS-1** | PM | M | 33 | 436 | N |
| **PDZK1-3** | PM | M | 37 | 66 | Y | **NNOS-1** | PM | M | 33 | 23 | N |
| **PDZK1-3** | PM | M | 37 | 67 | Y | **NNOS-1** | PM | M | 33 | 471 | N |
| **PDZK11-1** | PM | M | 38 | 7 | Y | **OMP25-1** | PM | M | 34 | 529 | N |
| **PSD95-2** | PM | M | 39 | 17 | Y | **OMP25-1** | PM | M | 34 | 610 | N |
| **PSD95-2** | PM | M | 39 | 17 | Y | **OMP25-1** | PM | M | 34 | 436 | N |
| **PSD95-2** | PM | M | 39 | 9 | Y | **OMP25-1** | PM | M | 34 | 457 | N |
| **PSD95-2** | PM | M | 39 | 5 | Y | **OMP25-1** | PM | M | 34 | 446 | N |
| **PSD95-2** | PM | M | 39 | 5 | Y | **OMP25-1** | PM | M | 34 | 37 | N |
| **PSD95-2** | PM | M | 39 | 1 | Y | **OMP25-1** | PM | M | 34 | 611 | N |
| **PSD95-2** | PM | M | 39 | 2 | Y | **OMP25-1** | PM | M | 34 | 53 | N |
| **PSD95-2** | PM | M | 39 | 11 | Y | **OMP25-1** | PM | M | 34 | 612 | N |

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| **PSD95-2** | PM | M | 39 | 20 | Y | **OMP25-1** | PM | M | 34 | 613 | N |
| **PSD95-2** | PM | M | 39 | 4 | Y | **OMP25-1** | PM | M | 34 | 454 | N |
| **PSD95-2** | PM | M | 39 | 15 | Y | **OMP25-1** | PM | M | 34 | 476 | N |
| **PSD95-2** | PM | M | 39 | 6 | Y | **OMP25-1** | PM | M | 34 | 614 | N |
| **PSD95-3** | PM | M | 40 | 15 | Y | **OMP25-1** | PM | M | 34 | 615 | N |
| **PSD95-3** | PM | M | 40 | 0 | Y | **OMP25-1** | PM | M | 34 | 3 | N |
| **PSD95-3** | PM | M | 40 | 16 | Y | **OMP25-1** | PM | M | 34 | 445 | N |
| **PSD95-3** | PM | M | 40 | 5 | Y | **OMP25-1** | PM | M | 34 | 26 | N |
| **PSD95-3** | PM | M | 40 | 1 | Y | **OMP25-1** | PM | M | 34 | 28 | N |
| **PSD95-3** | PM | M | 40 | 9 | Y | **OMP25-1** | PM | M | 34 | 35 | N |
| **PSD95-3** | PM | M | 40 | 5 | Y | **OMP25-1** | PM | M | 34 | 515 | N |
| **PSD95-3** | PM | M | 40 | 23 | Y | **OMP25-1** | PM | M | 34 | 524 | N |
| **PSD95-3** | PM | M | 40 | 6 | Y | **OMP25-1** | PM | M | 34 | 544 | N |
| **PSD95-3** | PM | M | 40 | 2 | Y | **OMP25-1** | PM | M | 34 | 442 | N |
| **PSD95-3** | PM | M | 40 | 20 | Y | **PAR6B-1** | PM | M | 35 | 26 | N |
| **PSD95-3** | PM | M | 40 | 8 | Y | **PAR6B-1** | PM | M | 35 | 29 | N |
| **PSD95-3** | PM | M | 40 | 14 | Y | **PAR6B-1** | PM | M | 35 | 474 | N |
| **PTP-BL-2** | PM | M | 41 | 5 | Y | **PAR6B-1** | PM | M | 35 | 454 | N |
| **PTP-BL-2** | PM | M | 41 | 47 | Y | **PAR6B-1** | PM | M | 35 | 3 | N |
| **PTP-BL-2** | PM | M | 41 | 33 | Y | **PAR6B-1** | PM | M | 35 | 52 | N |
| **PTP-BL-2** | PM | M | 41 | 57 | Y | **PAR6B-1** | PM | M | 35 | 17 | N |
| **PTP-BL-2** | PM | M | 41 | 4 | Y | **PAR6B-1** | PM | M | 35 | 27 | N |
| **PTP-BL-2** | PM | M | 41 | 17 | Y | **PAR6B-1** | PM | M | 35 | 476 | N |
| **PTP-BL-2** | PM | M | 41 | 9 | Y | **PAR6B-1** | PM | M | 35 | 15 | N |
| **PTP-BL-2** | PM | M | 41 | 60 | Y | **PAR6B-1** | PM | M | 35 | 57 | N |
| **PTP-BL-2** | PM | M | 41 | 20 | Y | **PAR6B-1** | PM | M | 35 | 463 | N |
| **PTP-BL-2** | PM | M | 41 | 13 | Y | **PAR6B-1** | PM | M | 35 | 446 | N |
| **PTP-BL-2** | PM | M | 41 | 5 | Y | **PAR6B-1** | PM | M | 35 | 23 | N |
| **PTP-BL-2** | PM | M | 41 | 14 | Y | **PAR6B-1** | PM | M | 35 | 6 | N |
| **PTP-BL-2** | PM | M | 41 | 25 | Y | **PAR6B-1** | PM | M | 35 | 465 | N |
| **PTP-BL-2** | PM | M | 41 | 34 | Y | **PAR6B-1** | PM | M | 35 | 445 | N |
| **PTP-BL-2** | PM | M | 41 | 19 | Y | **PAR6B-1** | PM | M | 35 | 13 | N |
| **PTP-BL-2** | PM | M | 41 | 11 | Y | **PAR6B-1** | PM | M | 35 | 25 | N |
| **PTP-BL-2** | PM | M | 41 | 15 | Y | **PAR6B-1** | PM | M | 35 | 467 | N |
| **PTP-BL-2** | PM | M | 41 | 26 | Y | **PAR6B-1** | PM | M | 35 | 41 | N |
| **PTP-BL-2** | PM | M | 41 | 8 | Y | **PAR6B-1** | PM | M | 35 | 63 | N |
| **PTP-BL-2** | PM | M | 41 | 17 | Y | **PAR6B-1** | PM | M | 35 | 470 | N |
| **SAP102-2** | PM | M | 42 | 15 | Y | **PAR6B-1** | PM | M | 35 | 73 | N |
| **SAP102-2** | PM | M | 42 | 0 | Y | **PAR6B-1** | PM | M | 35 | 468 | N |
| **SAP102-2** | PM | M | 42 | 23 | Y | **PAR6B-1** | PM | M | 35 | 0 | N |
| **SAP102-2** | PM | M | 42 | 16 | Y | **PAR6B-1** | PM | M | 35 | 9 | N |
| **SAP102-2** | PM | M | 42 | 16 | Y | **PAR6B-1** | PM | M | 35 | 67 | N |
| **SAP102-2** | PM | M | 42 | 2 | Y | **PAR6B-1** | PM | M | 35 | 473 | N |
| **SAP102-2** | PM | M | 42 | 25 | Y | **PAR6B-1** | PM | M | 35 | 449 | N |
| **SAP102-2** | PM | M | 42 | 5 | Y | **PAR6B-1** | PM | M | 35 | 475 | N |
| **SAP102-2** | PM | M | 42 | 18 | Y | **PAR6B-1** | PM | M | 35 | 16 | N |

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| **SAP102-2** | PM | M | 42 | 4 | Y | **PAR6B-1** | PM | M | 35 | 472 | N |
| **SAP102-2** | PM | M | 42 | 19 | Y | **PAR6B-1** | PM | M | 35 | 22 | N |
| **SAP102-2** | PM | M | 42 | 20 | Y | **PAR6B-1** | PM | M | 35 | 48 | N |
| **SAP102-2** | PM | M | 42 | 21 | Y | **PAR6B-1** | PM | M | 35 | 466 | N |
| **SAP102-2** | PM | M | 42 | 11 | Y | **PAR6B-1** | PM | M | 35 | 30 | N |
| **SAP102-2** | PM | M | 42 | 9 | Y | **PAR6B-1** | PM | M | 35 | 19 | N |
| **SAP102-2** | PM | M | 42 | 8 | Y | **PAR6B-1** | PM | M | 35 | 469 | N |
| **SAP102-2** | PM | M | 42 | 6 | Y | **PAR6B-1** | PM | M | 35 | 35 | N |
| **SAP102-2** | PM | M | 42 | 5 | Y | **PAR6B-1** | PM | M | 35 | 21 | N |
| **SAP102-2** | PM | M | 42 | 17 | Y | **PAR6B-1** | PM | M | 35 | 45 | N |
| **SAP102-2** | PM | M | 42 | 1 | Y | **PAR6B-1** | PM | M | 35 | 43 | N |
| **SAP102-2** | PM | M | 42 | 17 | Y | **PAR6B-1** | PM | M | 35 | 68 | N |
| **SAP102-3** | PM | M | 43 | 15 | Y | **PAR6B-1** | PM | M | 35 | 8 | N |
| **SAP102-3** | PM | M | 43 | 14 | Y | **PDZK11-1** | PM | M | 38 | 448 | N |
| **SAP102-3** | PM | M | 43 | 0 | Y | **PDZK11-1** | PM | M | 38 | 26 | N |
| **SAP102-3** | PM | M | 43 | 9 | Y | **PDZK11-1** | PM | M | 38 | 21 | N |
| **SAP102-3** | PM | M | 43 | 8 | Y | **PDZK11-1** | PM | M | 38 | 63 | N |
| **SAP102-3** | PM | M | 43 | 20 | Y | **PDZK11-1** | PM | M | 38 | 59 | N |
| **SAP102-3** | PM | M | 43 | 1 | Y | **PDZK11-1** | PM | M | 38 | 6 | N |
| **SAP102-3** | PM | M | 43 | 2 | Y | **PDZK1-1** | PM | M | 36 | 446 | N |
| **SAP102-3** | PM | M | 43 | 6 | Y | **PDZK1-1** | PM | M | 36 | 21 | N |
| **SAP97-1** | PM | M | 44 | 18 | Y | **PDZK1-1** | PM | M | 36 | 574 | N |
| **SAP97-1** | PM | M | 44 | 17 | Y | **PDZK1-1** | PM | M | 36 | 52 | N |
| **SAP97-1** | PM | M | 44 | 20 | Y | **PDZK1-1** | PM | M | 36 | 440 | N |
| **SAP97-1** | PM | M | 44 | 15 | Y | **PDZK1-1** | PM | M | 36 | 616 | N |
| **SAP97-1** | PM | M | 44 | 11 | Y | **PDZK1-1** | PM | M | 36 | 617 | N |
| **SAP97-1** | PM | M | 44 | 14 | Y | **PDZK1-1** | PM | M | 36 | 6 | N |
| **SAP97-1** | PM | M | 44 | 6 | Y | **PDZK1-1** | PM | M | 36 | 449 | N |
| **SAP97-1** | PM | M | 44 | 4 | Y | **PDZK1-1** | PM | M | 36 | 618 | N |
| **SAP97-1** | PM | M | 44 | 2 | Y | **PDZK1-1** | PM | M | 36 | 619 | N |
| **SAP97-1** | PM | M | 44 | 3 | Y | **PDZK1-1** | PM | M | 36 | 26 | N |
| **SAP97-1** | PM | M | 44 | 1 | Y | **PDZK1-1** | PM | M | 36 | 68 | N |
| **SAP97-1** | PM | M | 44 | 9 | Y | **PDZK1-1** | PM | M | 36 | 620 | N |
| **SAP97-1** | PM | M | 44 | 17 | Y | **PDZK1-1** | PM | M | 36 | 621 | N |
| **SAP97-2** | PM | M | 45 | 20 | Y | **PDZK1-1** | PM | M | 36 | 445 | N |
| **SAP97-2** | PM | M | 45 | 6 | Y | **PDZK1-1** | PM | M | 36 | 19 | N |
| **SAP97-2** | PM | M | 45 | 15 | Y | **PDZK1-1** | PM | M | 36 | 25 | N |
| **SAP97-2** | PM | M | 45 | 17 | Y | **PDZK1-1** | PM | M | 36 | 614 | N |
| **SAP97-2** | PM | M | 45 | 5 | Y | **PDZK1-1** | PM | M | 36 | 48 | N |
| **SAP97-2** | PM | M | 45 | 8 | Y | **PDZK1-1** | PM | M | 36 | 622 | N |
| **SAP97-2** | PM | M | 45 | 9 | Y | **PDZK1-3** | PM | M | 37 | 606 | N |
| **SAP97-2** | PM | M | 45 | 0 | Y | **PDZK1-3** | PM | M | 37 | 623 | N |
| **SAP97-2** | PM | M | 45 | 3 | Y | **PDZK1-3** | PM | M | 37 | 533 | N |
| **SAP97-2** | PM | M | 45 | 17 | Y | **PDZK1-3** | PM | M | 37 | 51 | N |
| **SAP97-2** | PM | M | 45 | 21 | Y | **PDZK1-3** | PM | M | 37 | 624 | N |
| **SAP97-2** | PM | M | 45 | 1 | Y | **PDZK1-3** | PM | M | 37 | 590 | N |

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| **SAP97-2** | PM | M | 45 | 11 | Y | **PDZK1-3** | PM | M | 37 | 50 | N |
| **SAP97-2** | PM | M | 45 | 2 | Y | **PDZK1-3** | PM | M | 37 | 625 | N |
| **SAP97-3** | PM | M | 40 | 1 | Y | **PDZK1-3** | PM | M | 37 | 626 | N |
| **SAP97-3** | PM | M | 40 | 6 | Y | **PDZK1-3** | PM | M | 37 | 627 | N |
| **SAP97-3** | PM | M | 40 | 20 | Y | **PDZK1-3** | PM | M | 37 | 628 | N |
| **SAP97-3** | PM | M | 40 | 15 | Y | **PDZK1-3** | PM | M | 37 | 629 | N |
| **SAP97-3** | PM | M | 40 | 46 | Y | **PDZK1-3** | PM | M | 37 | 608 | N |
| **SAP97-3** | PM | M | 40 | 24 | Y | **PSD95-2** | PM | M | 39 | 630 | N |
| **SAP97-3** | PM | M | 40 | 8 | Y | **PSD95-2** | PM | M | 39 | 19 | N |
| **SAP97-3** | PM | M | 40 | 23 | Y | **PSD95-2** | PM | M | 39 | 62 | N |
| **SAP97-3** | PM | M | 40 | 9 | Y | **PSD95-2** | PM | M | 39 | 604 | N |
| **SAP97-3** | PM | M | 40 | 2 | Y | **PSD95-2** | PM | M | 39 | 454 | N |
| **SAP97-3** | PM | M | 40 | 0 | Y | **PSD95-2** | PM | M | 39 | 631 | N |
| **SAP97-3** | PM | M | 40 | 69 | Y | **PSD95-2** | PM | M | 39 | 632 | N |
| **SAP97-3** | PM | M | 40 | 14 | Y | **PSD95-2** | PM | M | 39 | 633 | N |
| **SCRB1-1** | PM | M | 46 | 1 | Y | **PSD95-2** | PM | M | 39 | 634 | N |
| **SCRB1-1** | PM | M | 46 | 10 | Y | **PSD95-2** | PM | M | 39 | 593 | N |
| **SCRB1-1** | PM | M | 46 | 0 | Y | **PSD95-2** | PM | M | 39 | 635 | N |
| **SCRB1-1** | PM | M | 46 | 8 | Y | **PSD95-2** | PM | M | 39 | 636 | N |
| **SCRB1-1** | PM | M | 46 | 9 | Y | **PSD95-2** | PM | M | 39 | 637 | N |
| **SCRB1-2** | PM | M | 47 | 0 | Y | **PSD95-3** | PM | M | 40 | 464 | N |
| **SCRB1-2** | PM | M | 47 | 9 | Y | **PSD95-3** | PM | M | 40 | 436 | N |
| **SCRB1-2** | PM | M | 47 | 11 | Y | **PSD95-3** | PM | M | 40 | 57 | N |
| **SCRB1-3** | PM | M | 48 | 1 | Y | **PSD95-3** | PM | M | 40 | 462 | N |
| **SCRB1-3** | PM | M | 48 | 46 | Y | **PSD95-3** | PM | M | 40 | 549 | N |
| **SCRB1-3** | PM | M | 48 | 12 | Y | **PSD95-3** | PM | M | 40 | 465 | N |
| **SCRB1-3** | PM | M | 48 | 0 | Y | **PSD95-3** | PM | M | 40 | 452 | N |
| **SCRB1-3** | PM | M | 48 | 2 | Y | **PSD95-3** | PM | M | 40 | 7 | N |
| **SCRB1-3** | PM | M | 48 | 61 | Y | **PSD95-3** | PM | M | 40 | 551 | N |
| **SCRB1-3** | PM | M | 48 | 9 | Y | **PSD95-3** | PM | M | 40 | 28 | N |
| **SCRB1-3** | PM | M | 48 | 7 | Y | **PSD95-3** | PM | M | 40 | 72 | N |
| **SCRB1-3** | PM | M | 48 | 63 | Y | **PSD95-3** | PM | M | 40 | 19 | N |
| **SCRB1-3** | PM | M | 48 | 3 | Y | **PSD95-3** | PM | M | 40 | 61 | N |
| **SCRB1-3** | PM | M | 48 | 67 | Y | **PSD95-3** | PM | M | 40 | 471 | N |
| **SCRB1-3** | PM | M | 48 | 10 | Y | **PSD95-3** | PM | M | 40 | 476 | N |
| **SCRB1-3** | PM | M | 48 | 24 | Y | **PSD95-3** | PM | M | 40 | 37 | N |
| **SCRB1-3** | PM | M | 48 | 27 | Y | **PTP-BL-2** | PM | M | 41 | 0 | N |
| **SCRB1-3** | PM | M | 48 | 56 | Y | **PTP-BL-2** | PM | M | 41 | 3 | N |
| **SCRB1-3** | PM | M | 48 | 52 | Y | **PTP-BL-2** | PM | M | 41 | 638 | N |
| **SCRB1-3** | PM | M | 48 | 13 | Y | **PTP-BL-2** | PM | M | 41 | 29 | N |
| **SCRB1-3** | PM | M | 48 | 8 | Y | **PTP-BL-2** | PM | M | 41 | 6 | N |
| **SCRB1-3** | PM | M | 48 | 14 | Y | **PTP-BL-2** | PM | M | 41 | 470 | N |
| **SCRB1-3** | PM | M | 48 | 6 | Y | **PTP-BL-2** | PM | M | 41 | 83 | N |
| **SCRB1-3** | PM | M | 48 | 11 | Y | **PTP-BL-2** | PM | M | 41 | 475 | N |
| **SEMCAP3-1** | PM | M | 49 | 14 | Y | **PTP-BL-2** | PM | M | 41 | 63 | N |
| **SEMCAP3-1** | PM | M | 49 | 0 | Y | **PTP-BL-2** | PM | M | 41 | 64 | N |

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| **SEMCAP3-1** | PM | M | 49 | 46 | Y | **PTP-BL-2** | PM | M | 41 | 639 | N |
| **SEMCAP3-1** | PM | M | 49 | 16 | Y | **PTP-BL-2** | PM | M | 41 | 22 | N |
| **SEMCAP3-1** | PM | M | 49 | 2 | Y | **PTP-BL-2** | PM | M | 41 | 473 | N |
| **SEMCAP3-1** | PM | M | 49 | 8 | Y | **PTP-BL-2** | PM | M | 41 | 562 | N |
| **SEMCAP3-1** | PM | M | 49 | 13 | Y | **PTP-BL-2** | PM | M | 41 | 7 | N |
| **SHANK1-1** | PM | M | 50 | 0 | Y | **PTP-BL-2** | PM | M | 41 | 21 | N |
| **SHANK1-1** | PM | M | 50 | 58 | Y | **PTP-BL-2** | PM | M | 41 | 468 | N |
| **SHANK1-1** | PM | M | 50 | 70 | Y | **PTP-BL-2** | PM | M | 41 | 502 | N |
| **SHANK1-1** | PM | M | 50 | 51 | Y | **PTP-BL-2** | PM | M | 41 | 508 | N |
| **SHANK1-1** | PM | M | 50 | 58 | Y | **PTP-BL-2** | PM | M | 41 | 35 | N |
| **SHANK1-1** | PM | M | 50 | 15 | Y | **PTP-BL-2** | PM | M | 41 | 474 | N |
| **SHANK1-1** | PM | M | 50 | 8 | Y | **PTP-BL-2** | PM | M | 41 | 67 | N |
| **SHANK1-1** | PM | M | 50 | 67 | Y | **PTP-BL-2** | PM | M | 41 | 555 | N |
| **SHANK1-1** | PM | M | 50 | 10 | Y | **PTP-BL-2** | PM | M | 41 | 463 | N |
| **SHANK1-1** | PM | M | 50 | 68 | Y | **PTP-BL-2** | PM | M | 41 | 454 | N |
| **SHANK1-1** | PM | M | 50 | 64 | Y | **PTP-BL-2** | PM | M | 41 | 53 | N |
| **SHANK1-1** | PM | M | 50 | 13 | Y | **PTP-BL-2** | PM | M | 41 | 65 | N |
| **SHANK1-1** | PM | M | 50 | 27 | Y | **PTP-BL-2** | PM | M | 41 | 73 | N |
| **SHANK1-1** | PM | M | 50 | 9 | Y | **PTP-BL-2** | PM | M | 41 | 519 | N |
| **SHANK1-1** | PM | M | 50 | 66 | Y | **PTP-BL-2** | PM | M | 41 | 466 | N |
| **SHANK1-1** | PM | M | 50 | 71 | Y | **PTP-BL-2** | PM | M | 41 | 41 | N |
| **SHANK1-1** | PM | M | 50 | 50 | Y | **PTP-BL-2** | PM | M | 41 | 43 | N |
| **SHANK3-1** | PM | M | 51 | 70 | Y | **PTP-BL-2** | PM | M | 41 | 476 | N |
| **SHANK3-1** | PM | M | 51 | 58 | Y | **PTP-BL-2** | PM | M | 41 | 18 | N |
| **SHANK3-1** | PM | M | 51 | 72 | Y | **PTP-BL-2** | PM | M | 41 | 472 | N |
| **SHANK3-1** | PM | M | 51 | 7 | Y | **PTP-BL-2** | PM | M | 41 | 51 | N |
| **SHANK3-1** | PM | M | 51 | 51 | Y | **PTP-BL-2** | PM | M | 41 | 446 | N |
| **SHANK3-1** | PM | M | 51 | 64 | Y | **PTP-BL-2** | PM | M | 41 | 1 | N |
| **SHANK3-1** | PM | M | 51 | 55 | Y | **PTP-BL-2** | PM | M | 41 | 62 | N |
| **SHANK3-1** | PM | M | 51 | 8 | Y | **PTP-BL-2** | PM | M | 41 | 30 | N |
| **SHANK3-1** | PM | M | 51 | 67 | Y | **PTP-BL-2** | PM | M | 41 | 544 | N |
| **SHANK3-1** | PM | M | 51 | 10 | Y | **PTP-BL-2** | PM | M | 41 | 16 | N |
| **SHANK3-1** | PM | M | 51 | 68 | Y | **PTP-BL-2** | PM | M | 41 | 465 | N |
| **SHANK3-1** | PM | M | 51 | 50 | Y | **PTP-BL-2** | PM | M | 41 | 2 | N |
| **SHANK3-1** | PM | M | 51 | 58 | Y | **PTP-BL-2** | PM | M | 41 | 467 | N |
| **SHANK3-1** | PM | M | 51 | 13 | Y | **PTP-BL-2** | PM | M | 41 | 23 | N |
| **SHANK3-1** | PM | M | 51 | 52 | Y | **PTP-BL-2** | PM | M | 41 | 48 | N |
| **SHANK3-1** | PM | M | 51 | 66 | Y | **PTP-BL-2** | PM | M | 41 | 469 | N |
| **SHANK3-1** | PM | M | 51 | 71 | Y | **PTP-BL-2** | PM | M | 41 | 40 | N |
| **SHANK3-1** | PM | M | 51 | 27 | Y | **PTP-BL-2** | PM | M | 41 | 45 | N |
| **SHROOM-1** | PM | M | 52 | 8 | Y | **PTP-BL-2** | PM | M | 41 | 28 | N |
| **SHROOM-1** | PM | M | 52 | 0 | Y | **PTP-BL-2** | PM | M | 41 | 46 | N |
| **SHROOM-1** | PM | M | 52 | 13 | Y | **PTP-BL-2** | PM | M | 41 | 16 | N |
| **SLIM-1** | PM | M | 53 | 49 | Y | **PTP-BL-2** | PM | M | 41 | 36 | N |
| **ZO-1-1** | PM | M | 54 | 73 | Y | **PTP-BL-2** | PM | M | 41 | 32 | N |
| **ZO-1-1** | PM | M | 54 | 38 | Y | **SAP102-2** | PM | M | 42 | 640 | N |

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| **ZO-1-1** | PM | M | 54 | 45 | Y | **SAP102-2** | PM | M | 42 | 641 | N |
| **ZO-1-1** | PM | M | 54 | 74 | Y | **SAP102-2** | PM | M | 42 | 642 | N |
| **ZO-1-1** | PM | M | 54 | 75 | Y | **SAP102-2** | PM | M | 42 | 53 | N |
| **ZO-1-1** | PM | M | 54 | 32 | Y | **SAP102-2** | PM | M | 42 | 643 | N |
| **ZO-1-1** | PM | M | 54 | 76 | Y | **SAP102-2** | PM | M | 42 | 644 | N |
| **ZO-1-1** | PM | M | 54 | 77 | Y | **SAP102-2** | PM | M | 42 | 62 | N |
| **ZO-1-1** | PM | M | 54 | 78 | Y | **SAP102-2** | PM | M | 42 | 637 | N |
| **ZO-1-1** | PM | M | 54 | 79 | Y | **SAP102-2** | PM | M | 42 | 454 | N |
| **ZO-1-1** | PM | M | 54 | 80 | Y | **SAP102-2** | PM | M | 42 | 566 | N |
| **ZO-1-1** | PM | M | 54 | 41 | Y | **SAP102-2** | PM | M | 42 | 645 | N |
| **ZO-1-1** | PM | M | 54 | 81 | Y | **SAP102-2** | PM | M | 42 | 646 | N |
| **ZO-1-1** | PM | M | 54 | 82 | Y | **SAP102-2** | PM | M | 42 | 40 | N |
| **ZO-1-1** | PM | M | 54 | 50 | Y | **SAP102-2** | PM | M | 42 | 647 | N |
| **ZO-1-1** | PM | M | 54 | 83 | Y | **SAP102-3** | PM | M | 43 | 47 | N |
| **ZO-1-1** | PM | M | 54 | 43 | Y | **SAP102-3** | PM | M | 43 | 19 | N |
| **ZO-1-1** | PM | M | 54 | 26 | Y | **SAP102-3** | PM | M | 43 | 7 | N |
| **ZO-1-1** | PM | M | 54 | 27 | Y | **SAP102-3** | PM | M | 43 | 23 | N |
| **ZO-1-1** | PM | M | 54 | 83 | Y | **SAP102-3** | PM | M | 43 | 22 | N |
| **ZO-2-1** | PM | M | 55 | 15 | Y | **SAP102-3** | PM | M | 43 | 476 | N |
| **ZO-2-1** | PM | M | 55 | 83 | Y | **SAP102-3** | PM | M | 43 | 11 | N |
| **ZO-2-1** | PM | M | 55 | 74 | Y | **SAP102-3** | PM | M | 43 | 46 | N |
| **ZO-2-1** | PM | M | 55 | 77 | Y | **SAP102-3** | PM | M | 43 | 648 | N |
| **ZO-2-1** | PM | M | 55 | 78 | Y | **SAP102-3** | PM | M | 43 | 3 | N |
| **ZO-2-1** | PM | M | 55 | 76 | Y | **SAP102-3** | PM | M | 43 | 69 | N |
| **ZO-2-1** | PM | M | 55 | 43 | Y | **SAP102-3** | PM | M | 43 | 12 | N |
| **ZO-2-1** | PM | M | 55 | 45 | Y | **SAP102-3** | PM | M | 43 | 555 | N |
| **ZO-2-1** | PM | M | 55 | 83 | Y | **SAP102-3** | PM | M | 43 | 13 | N |
| **ZO-2-1** | PM | M | 55 | 82 | Y | **SAP102-3** | PM | M | 43 | 472 | N |
| **ZO-2-1** | PM | M | 55 | 73 | Y | **SAP97-1** | PM | M | 44 | 7 | N |
| **ZO-2-1** | PM | M | 55 | 79 | Y | **SAP97-1** | PM | M | 44 | 65 | N |
| **ZO-2-1** | PM | M | 55 | 41 | Y | **SAP97-1** | PM | M | 44 | 546 | N |
| **ZO-3-1** | PM | M | 56 | 41 | Y | **SAP97-1** | PM | M | 44 | 545 | N |
| **CASK-1** | PD | H | 57 | 84 | Y | **SAP97-1** | PM | M | 44 | 22 | N |
| **CASK-1** | PD | H | 57 | 85 | Y | **SAP97-1** | PM | M | 44 | 19 | N |
| **CASK-1** | PD | H | 57 | 86 | Y | **SAP97-1** | PM | M | 44 | 462 | N |
| **CASK-1** | PD | H | 57 | 87 | Y | **SAP97-1** | PM | M | 44 | 555 | N |
| **CASK-1** | PD | H | 57 | 88 | Y | **SAP97-1** | PM | M | 44 | 23 | N |
| **CASK-1** | PD | H | 57 | 89 | Y | **SAP97-1** | PM | M | 44 | 551 | N |
| **CASK-1** | PD | H | 57 | 90 | Y | **SAP97-1** | PM | M | 44 | 12 | N |
| **CASK-1** | PD | H | 57 | 91 | Y | **SAP97-1** | PM | M | 44 | 472 | N |
| **CASK-1** | PD | H | 57 | 92 | Y | **SAP97-1** | PM | M | 44 | 436 | N |
| **CASK-1** | PD | H | 57 | 93 | Y | **SAP97-1** | PM | M | 44 | 639 | N |
| **CASK-1** | PD | H | 57 | 94 | Y | **SAP97-1** | PM | M | 44 | 648 | N |
| **CASK-1** | PD | H | 57 | 95 | Y | **SAP97-2** | PM | M | 45 | 649 | N |
| **CASK-1** | PD | H | 57 | 96 | Y | **SAP97-2** | PM | M | 45 | 19 | N |
| **CASK-1** | PD | H | 57 | 97 | Y | **SAP97-2** | PM | M | 45 | 64 | N |

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| **CASK-1** | PD | H | 57 | 98 | Y | **SAP97-2** | PM | M | 45 | 4 | N |
| **CASK-1** | PD | H | 57 | 99 | Y | **SAP97-2** | PM | M | 45 | 454 | N |
| **CASK-1** | PD | H | 57 | 100 | Y | **SAP97-3** | PM | M | 40 | 3 | N |
| **CASK-1** | PD | H | 57 | 101 | Y | **SAP97-3** | PM | M | 40 | 11 | N |
| **CASK-1** | PD | H | 57 | 102 | Y | **SAP97-3** | PM | M | 40 | 7 | N |
| **CASK-1** | PD | H | 57 | 103 | Y | **SAP97-3** | PM | M | 40 | 555 | N |
| **DLG3-2** | PD | H | 58 | 104 | Y | **SAP97-3** | PM | M | 40 | 65 | N |
| **DLG3-2** | PD | H | 58 | 105 | Y | **SAP97-3** | PM | M | 40 | 10 | N |
| **DLG3-2** | PD | H | 58 | 106 | Y | **SAP97-3** | PM | M | 40 | 472 | N |
| **DLG3-2** | PD | H | 58 | 107 | Y | **SAP97-3** | PM | M | 40 | 22 | N |
| **DLG3-2** | PD | H | 58 | 108 | Y | **SAP97-3** | PM | M | 40 | 436 | N |
| **DLG3-2** | PD | H | 58 | 109 | Y | **SAP97-3** | PM | M | 40 | 650 | N |
| **DLG3-2** | PD | H | 58 | 110 | Y | **SAP97-3** | PM | M | 40 | 12 | N |
| **DLG3-2** | PD | H | 58 | 111 | Y | **SAP97-3** | PM | M | 40 | 13 | N |
| **DLG3-2** | PD | H | 58 | 112 | Y | **SCRB1-1** | PM | M | 46 | 464 | N |
| **DLG3-2** | PD | H | 58 | 113 | Y | **SCRB1-1** | PM | M | 46 | 465 | N |
| **DLG3-2** | PD | H | 58 | 114 | Y | **SCRB1-1** | PM | M | 46 | 473 | N |
| **DLG3-2** | PD | H | 58 | 115 | Y | **SCRB1-1** | PM | M | 46 | 551 | N |
| **DLG3-2** | PD | H | 58 | 116 | Y | **SCRB1-1** | PM | M | 46 | 462 | N |
| **DLG3-2** | PD | H | 58 | 117 | Y | **SCRB1-1** | PM | M | 46 | 488 | N |
| **DLG3-2** | PD | H | 58 | 118 | Y | **SCRB1-1** | PM | M | 46 | 7 | N |
| **DLG3-2** | PD | H | 58 | 119 | Y | **SCRB1-1** | PM | M | 46 | 553 | N |
| **DLG3-2** | PD | H | 58 | 120 | Y | **SCRB1-1** | PM | M | 46 | 471 | N |
| **DLG3-2** | PD | H | 58 | 121 | Y | **SCRB1-1** | PM | M | 46 | 59 | N |
| **DLG3-2** | PD | H | 58 | 122 | Y | **SCRB1-1** | PM | M | 46 | 547 | N |
| **DLG3-2** | PD | H | 58 | 123 | Y | **SCRB1-1** | PM | M | 46 | 515 | N |
| **DLG3-2** | PD | H | 58 | 124 | Y | **SCRB1-1** | PM | M | 46 | 552 | N |
| **DLG3-2** | PD | H | 58 | 125 | Y | **SCRB1-1** | PM | M | 46 | 72 | N |
| **DLG3-2** | PD | H | 58 | 126 | Y | **SCRB1-1** | PM | M | 46 | 546 | N |
| **DLG3-2** | PD | H | 58 | 127 | Y | **SCRB1-1** | PM | M | 46 | 436 | N |
| **DLG3-2** | PD | H | 58 | 128 | Y | **SCRB1-1** | PM | M | 46 | 452 | N |
| **DLG3-2** | PD | H | 58 | 129 | Y | **SCRB1-2** | PM | M | 47 | 15 | N |
| **DLG3-2** | PD | H | 58 | 130 | Y | **SCRB1-2** | PM | M | 47 | 436 | N |
| **DLG3-2** | PD | H | 58 | 131 | Y | **SCRB1-2** | PM | M | 47 | 8 | N |
| **ERBB2IP-1** | PD | H | 59 | 132 | Y | **SCRB1-2** | PM | M | 47 | 7 | N |
| **ERBB2IP-1** | PD | H | 59 | 133 | Y | **SCRB1-2** | PM | M | 47 | 2 | N |
| **ERBB2IP-1** | PD | H | 59 | 134 | Y | **SCRB1-2** | PM | M | 47 | 63 | N |
| **ERBB2IP-1** | PD | H | 59 | 135 | Y | **SCRB1-2** | PM | M | 47 | 17 | N |
| **ERBB2IP-1** | PD | H | 59 | 136 | Y | **SCRB1-2** | PM | M | 47 | 534 | N |
| **ERBB2IP-1** | PD | H | 59 | 137 | Y | **SCRB1-3** | PM | M | 48 | 651 | N |
| **ERBB2IP-1** | PD | H | 59 | 138 | Y | **SCRB1-3** | PM | M | 48 | 69 | N |
| **ERBB2IP-1** | PD | H | 59 | 139 | Y | **SCRB1-3** | PM | M | 48 | 436 | N |
| **ERBB2IP-1** | PD | H | 59 | 140 | Y | **SCRB1-3** | PM | M | 48 | 54 | N |
| **ERBB2IP-1** | PD | H | 59 | 141 | Y | **SCRB1-3** | PM | M | 48 | 509 | N |
| **ERBB2IP-1** | PD | H | 59 | 142 | Y | **SCRB1-3** | PM | M | 48 | 652 | N |
| **ERBB2IP-1** | PD | H | 59 | 143 | Y | **SCRB1-3** | PM | M | 48 | 579 | N |

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| **ERBB2IP-1** | PD | H | 59 | 144 | Y | **SCRB1-3** | PM | M | 48 | 653 | N |
| **ERBB2IP-1** | PD | H | 59 | 145 | Y | **SCRB1-3** | PM | M | 48 | 65 | N |
| **ERBB2IP-1** | PD | H | 59 | 146 | Y | **SCRB1-3** | PM | M | 48 | 68 | N |
| **ERBB2IP-1** | PD | H | 59 | 147 | Y | **SCRB1-3** | PM | M | 48 | 654 | N |
| **ERBB2IP-1** | PD | H | 59 | 148 | Y | **SCRB1-3** | PM | M | 48 | 655 | N |
| **ERBB2IP-1** | PD | H | 59 | 149 | Y | **SCRB1-3** | PM | M | 48 | 66 | N |
| **ERBB2IP-1** | PD | H | 59 | 150 | Y | **SCRB1-3** | PM | M | 48 | 656 | N |
| **ERBB2IP-1** | PD | H | 59 | 151 | Y | **SCRB1-3** | PM | M | 48 | 58 | N |
| **ERBB2IP-1** | PD | H | 59 | 152 | Y | **SCRB1-3** | PM | M | 48 | 657 | N |
| **ERBB2IP-1** | PD | H | 59 | 153 | Y | **SCRB1-3** | PM | M | 48 | 658 | N |
| **ERBB2IP-1** | PD | H | 59 | 154 | Y | **SCRB1-3** | PM | M | 48 | 35 | N |
| **ERBB2IP-1** | PD | H | 59 | 155 | Y | **SCRB1-3** | PM | M | 48 | 58 | N |
| **ERBB2IP-1** | PD | H | 59 | 156 | Y | **SCRB1-3** | PM | M | 48 | 64 | N |
| **ERBB2IP-1** | PD | H | 59 | 157 | Y | **SCRB1-3** | PM | M | 48 | 472 | N |
| **ERBB2IP-1** | PD | H | 59 | 158 | Y | **SCRB1-3** | PM | M | 48 | 71 | N |
| **ERBB2IP-1** | PD | H | 59 | 159 | Y | **SEMCAP3-1** | PM | M | 49 | 7 | N |
| **ERBB2IP-1** | PD | H | 59 | 160 | Y | **SEMCAP3-1** | PM | M | 49 | 28 | N |
| **ERBB2IP-1** | PD | H | 59 | 161 | Y | **SEMCAP3-1** | PM | M | 49 | 3 | N |
| **ERBB2IP-1** | PD | H | 59 | 162 | Y | **SEMCAP3-1** | PM | M | 49 | 9 | N |
| **ERBB2IP-1** | PD | H | 59 | 163 | Y | **SEMCAP3-1** | PM | M | 49 | 476 | N |
| **ERBB2IP-1** | PD | H | 59 | 164 | Y | **SEMCAP3-1** | PM | M | 49 | 61 | N |
| **MPDZ-1** | PD | H | 60 | 165 | Y | **SEMCAP3-1** | PM | M | 49 | 19 | N |
| **MPDZ-1** | PD | H | 60 | 166 | Y | **SEMCAP3-1** | PM | M | 49 | 47 | N |
| **MPDZ-1** | PD | H | 60 | 167 | Y | **SEMCAP3-1** | PM | M | 49 | 5 | N |
| **MPDZ-1** | PD | H | 60 | 168 | Y | **SHANK1-1** | PM | M | 50 | 659 | N |
| **MPDZ-1** | PD | H | 60 | 169 | Y | **SHANK1-1** | PM | M | 50 | 465 | N |
| **MPDZ-1** | PD | H | 60 | 170 | Y | **SHANK1-1** | PM | M | 50 | 660 | N |
| **MPDZ-1** | PD | H | 60 | 171 | Y | **SHANK1-1** | PM | M | 50 | 661 | N |
| **MPDZ-1** | PD | H | 60 | 172 | Y | **SHANK1-1** | PM | M | 50 | 475 | N |
| **MPDZ-1** | PD | H | 60 | 173 | Y | **SHANK1-1** | PM | M | 50 | 662 | N |
| **MPDZ-1** | PD | H | 60 | 174 | Y | **SHANK1-1** | PM | M | 50 | 454 | N |
| **MPDZ-1** | PD | H | 60 | 175 | Y | **SHANK1-1** | PM | M | 50 | 663 | N |
| **MPDZ-1** | PD | H | 60 | 176 | Y | **SHANK1-1** | PM | M | 50 | 26 | N |
| **MPDZ-1** | PD | H | 60 | 177 | Y | **SHANK1-1** | PM | M | 50 | 638 | N |
| **MPDZ-10** | PD | H | 61 | 178 | Y | **SHANK1-1** | PM | M | 50 | 664 | N |
| **MPDZ-10** | PD | H | 61 | 179 | Y | **SHANK1-1** | PM | M | 50 | 2 | N |
| **MPDZ-10** | PD | H | 61 | 180 | Y | **SHANK1-1** | PM | M | 50 | 472 | N |
| **MPDZ-10** | PD | H | 61 | 181 | Y | **SHANK1-1** | PM | M | 50 | 533 | N |
| **MPDZ-10** | PD | H | 61 | 182 | Y | **SHANK1-1** | PM | M | 50 | 665 | N |
| **MPDZ-10** | PD | H | 61 | 183 | Y | **SHANK1-1** | PM | M | 50 | 468 | N |
| **MPDZ-10** | PD | H | 61 | 184 | Y | **SHANK1-1** | PM | M | 50 | 476 | N |
| **MPDZ-10** | PD | H | 61 | 185 | Y | **SHANK1-1** | PM | M | 50 | 470 | N |
| **MPDZ-10** | PD | H | 61 | 186 | Y | **SHANK1-1** | PM | M | 50 | 6 | N |
| **MPDZ-10** | PD | H | 61 | 187 | Y | **SHANK1-1** | PM | M | 50 | 17 | N |
| **MPDZ-10** | PD | H | 61 | 188 | Y | **SHANK1-1** | PM | M | 50 | 16 | N |
| **MPDZ-10** | PD | H | 61 | 189 | Y | **SHANK1-1** | PM | M | 50 | 30 | N |

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| **MPDZ-10** | PD | H | 61 | 190 | Y | **SHANK1-1** | PM | M | 50 | 23 | N |
| **MPDZ-10** | PD | H | 61 | 191 | Y | **SHANK1-1** | PM | M | 50 | 666 | N |
| **MPDZ-10** | PD | H | 61 | 192 | Y | **SHANK1-1** | PM | M | 50 | 7 | N |
| **MPDZ-10** | PD | H | 61 | 193 | Y | **SHANK1-1** | PM | M | 50 | 473 | N |
| **MPDZ-12** | PD | H | 62 | 194 | Y | **SHANK1-1** | PM | M | 50 | 45 | N |
| **MPDZ-12** | PD | H | 62 | 195 | Y | **SHANK1-1** | PM | M | 50 | 628 | N |
| **MPDZ-12** | PD | H | 62 | 196 | Y | **SHANK1-1** | PM | M | 50 | 22 | N |
| **MPDZ-12** | PD | H | 62 | 197 | Y | **SHANK1-1** | PM | M | 50 | 41 | N |
| **MPDZ-12** | PD | H | 62 | 198 | Y | **SHANK1-1** | PM | M | 50 | 11 | N |
| **MPDZ-12** | PD | H | 62 | 199 | Y | **SHANK1-1** | PM | M | 50 | 57 | N |
| **MPDZ-12** | PD | H | 62 | 200 | Y | **SHANK1-1** | PM | M | 50 | 463 | N |
| **MPDZ-12** | PD | H | 62 | 201 | Y | **SHANK1-1** | PM | M | 50 | 65 | N |
| **MPDZ-12** | PD | H | 62 | 202 | Y | **SHANK1-1** | PM | M | 50 | 667 | N |
| **MPDZ-12** | PD | H | 62 | 203 | Y | **SHANK1-1** | PM | M | 50 | 467 | N |
| **MPDZ-12** | PD | H | 62 | 204 | Y | **SHANK1-1** | PM | M | 50 | 12 | N |
| **SCRIB-1** | PD | H | 63 | 205 | Y | **SHANK1-1** | PM | M | 50 | 668 | N |
| **SCRIB-1** | PD | H | 63 | 206 | Y | **SHANK1-1** | PM | M | 50 | 46 | N |
| **SCRIB-1** | PD | H | 63 | 3 | Y | **SHANK1-1** | PM | M | 50 | 466 | N |
| **SCRIB-1** | PD | H | 63 | 207 | Y | **SHANK1-1** | PM | M | 50 | 469 | N |
| **SCRIB-1** | PD | H | 63 | 208 | Y | **SHANK1-1** | PM | M | 50 | 55 | N |
| **SCRIB-1** | PD | H | 63 | 209 | Y | **SHANK1-1** | PM | M | 50 | 669 | N |
| **SCRIB-1** | PD | H | 63 | 210 | Y | **SHANK1-1** | PM | M | 50 | 52 | N |
| **SCRIB-1** | PD | H | 63 | 211 | Y | **SHANK1-1** | PM | M | 50 | 560 | N |
| **SCRIB-1** | PD | H | 63 | 212 | Y | **SHANK1-1** | PM | M | 50 | 29 | N |
| **SCRIB-1** | PD | H | 63 | 213 | Y | **SHANK1-1** | PM | M | 50 | 474 | N |
| **SCRIB-1** | PD | H | 63 | 214 | Y | **SHANK1-1** | PM | M | 50 | 73 | N |
| **SCRIB-1** | PD | H | 63 | 215 | Y | **SHANK1-1** | PM | M | 50 | 35 | N |
| **SCRIB-1** | PD | H | 63 | 216 | Y | **SHANK1-1** | PM | M | 50 | 63 | N |
| **SCRIB-1** | PD | H | 63 | 217 | Y | **SHANK1-1** | PM | M | 50 | 670 | N |
| **SCRIB-1** | PD | H | 63 | 218 | Y | **SHANK1-1** | PM | M | 50 | 3 | N |
| **SCRIB-1** | PD | H | 63 | 219 | Y | **SHANK1-1** | PM | M | 50 | 43 | N |
| **SCRIB-1** | PD | H | 63 | 220 | Y | **SHANK3-1** | PM | M | 51 | 560 | N |
| **SCRIB-1** | PD | H | 63 | 221 | Y | **SHANK3-1** | PM | M | 51 | 671 | N |
| **SCRIB-1** | PD | H | 63 | 152 | Y | **SHANK3-1** | PM | M | 51 | 3 | N |
| **SCRIB-1** | PD | H | 63 | 222 | Y | **SHANK3-1** | PM | M | 51 | 0 | N |
| **SCRIB-1** | PD | H | 63 | 223 | Y | **SHANK3-1** | PM | M | 51 | 672 | N |
| **SCRIB-1** | PD | H | 63 | 224 | Y | **SHANK3-1** | PM | M | 51 | 673 | N |
| **SCRIB-1** | PD | H | 63 | 8 | Y | **SHANK3-1** | PM | M | 51 | 674 | N |
| **SCRIB-1** | PD | H | 63 | 137 | Y | **SHANK3-1** | PM | M | 51 | 675 | N |
| **SCRIB-1** | PD | H | 63 | 225 | Y | **SHANK3-1** | PM | M | 51 | 664 | N |
| **SCRIB-1** | PD | H | 63 | 226 | Y | **SHANK3-1** | PM | M | 51 | 26 | N |
| **SCRIB-1** | PD | H | 63 | 227 | Y | **SHANK3-1** | PM | M | 51 | 676 | N |
| **DLG1-2** | PD | H | 64 | 228 | Y | **SHANK3-1** | PM | M | 51 | 21 | N |
| **DLG1-2** | PD | H | 64 | 229 | Y | **SHANK3-1** | PM | M | 51 | 533 | N |
| **DLG1-2** | PD | H | 64 | 230 | Y | **SHANK3-1** | PM | M | 51 | 677 | N |
| **DLG1-2** | PD | H | 64 | 231 | Y | **SHANK3-1** | PM | M | 51 | 534 | N |

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| **DLG1-2** | PD | H | 64 | 232 | Y | **SHANK3-1** | PM | M | 51 | 678 | N |
| **DLG1-2** | PD | H | 64 | 233 | Y | **SHANK3-1** | PM | M | 51 | 638 | N |
| **DLG1-2** | PD | H | 64 | 124 | Y | **SHANK3-1** | PM | M | 51 | 679 | N |
| **DLG1-2** | PD | H | 64 | 234 | Y | **SHANK3-1** | PM | M | 51 | 680 | N |
| **DLG1-2** | PD | H | 64 | 235 | Y | **SHANK3-1** | PM | M | 51 | 681 | N |
| **DLG1-2** | PD | H | 64 | 236 | Y | **SHANK3-1** | PM | M | 51 | 682 | N |
| **DLG1-2** | PD | H | 64 | 237 | Y | **SHANK3-1** | PM | M | 51 | 683 | N |
| **DLG1-2** | PD | H | 64 | 238 | Y | **SHANK3-1** | PM | M | 51 | 684 | N |
| **DLG1-2** | PD | H | 64 | 239 | Y | **SHANK3-1** | PM | M | 51 | 669 | N |
| **DLG1-2** | PD | H | 64 | 240 | Y | **SHANK3-1** | PM | M | 51 | 668 | N |
| **DLG1-2** | PD | H | 64 | 241 | Y | **SHANK3-1** | PM | M | 51 | 6 | N |
| **DLG1-2** | PD | H | 64 | 136 | Y | **SHROOM-1** | PM | M | 52 | 6 | N |
| **DLG1-2** | PD | H | 64 | 242 | Y | **SHROOM-1** | PM | M | 52 | 27 | N |
| **DLG1-2** | PD | H | 64 | 243 | Y | **SHROOM-1** | PM | M | 52 | 19 | N |
| **DLG1-2** | PD | H | 64 | 168 | Y | **SHROOM-1** | PM | M | 52 | 23 | N |
| **DLG1-2** | PD | H | 64 | 244 | Y | **SHROOM-1** | PM | M | 52 | 445 | N |
| **DLG1-2** | PD | H | 64 | 245 | Y | **SHROOM-1** | PM | M | 52 | 446 | N |
| **DLG1-2** | PD | H | 64 | 246 | Y | **SHROOM-1** | PM | M | 52 | 68 | N |
| **DLG1-2** | PD | H | 64 | 127 | Y | **SHROOM-1** | PM | M | 52 | 52 | N |
| **DLG1-2** | PD | H | 64 | 123 | Y | **SHROOM-1** | PM | M | 52 | 48 | N |
| **DLG1-2** | PD | H | 64 | 247 | Y | **SHROOM-1** | PM | M | 52 | 26 | N |
| **DLG1-2** | PD | H | 64 | 248 | Y | **SHROOM-1** | PM | M | 52 | 9 | N |
| **DLG1-2** | PD | H | 64 | 249 | Y | **SHROOM-1** | PM | M | 52 | 449 | N |
| **DLG1-2** | PD | H | 64 | 250 | Y | **SHROOM-1** | PM | M | 52 | 67 | N |
| **DLG1-2** | PD | H | 64 | 251 | Y | **SHROOM-1** | PM | M | 52 | 25 | N |
| **DLG1-2** | PD | H | 64 | 252 | Y | **SHROOM-1** | PM | M | 52 | 21 | N |
| **DLG1-2** | PD | H | 64 | 253 | Y | **SLIM-1** | PM | M | 53 | 448 | N |
| **DLG1-2** | PD | H | 64 | 254 | Y | **SLIM-1** | PM | M | 53 | 470 | N |
| **DLG1-2** | PD | H | 64 | 255 | Y | **SLIM-1** | PM | M | 53 | 447 | N |
| **DLG1-2** | PD | H | 64 | 256 | Y | **SLIM-1** | PM | M | 53 | 16 | N |
| **DLG1-2** | PD | H | 64 | 257 | Y | **SLIM-1** | PM | M | 53 | 61 | N |
| **DLG1-2** | PD | H | 64 | 258 | Y | **ZO-1-1** | PM | M | 54 | 16 | N |
| **DLG1-2** | PD | H | 64 | 259 | Y | **ZO-1-1** | PM | M | 54 | 603 | N |
| **DLG1-2** | PD | H | 64 | 260 | Y | **ZO-1-1** | PM | M | 54 | 685 | N |
| **DLG1-2** | PD | H | 64 | 261 | Y | **ZO-1-1** | PM | M | 54 | 649 | N |
| **DLG1-2** | PD | H | 64 | 116 | Y | **ZO-1-1** | PM | M | 54 | 686 | N |
| **DLG1-2** | PD | H | 64 | 262 | Y | **ZO-1-1** | PM | M | 54 | 664 | N |
| **DLG1-2** | PD | H | 64 | 263 | Y | **ZO-1-1** | PM | M | 54 | 32 | N |
| **DLG1-2** | PD | H | 64 | 264 | Y | **ZO-1-1** | PM | M | 54 | 687 | N |
| **DLG1-2** | PD | H | 64 | 265 | Y | **ZO-1-1** | PM | M | 54 | 508 | N |
| **DLG1-2** | PD | H | 64 | 266 | Y | **ZO-1-1** | PM | M | 54 | 545 | N |
| **DLG1-2** | PD | H | 64 | 267 | Y | **ZO-1-1** | PM | M | 54 | 688 | N |
| **DLG1-2** | PD | H | 64 | 268 | Y | **ZO-1-1** | PM | M | 54 | 689 | N |
| **DLG4-3** | PD | H | 65 | 208 | Y | **ZO-1-1** | PM | M | 54 | 35 | N |
| **DLG4-3** | PD | H | 65 | 269 | Y | **ZO-1-1** | PM | M | 54 | 561 | N |
| **DLG4-3** | PD | H | 65 | 270 | Y | **ZO-1-1** | PM | M | 54 | 449 | N |

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| **DLG4-3** | PD | H | 65 | 108 | Y | **ZO-1-1** | PM | M | 54 | 690 | N |
| **DLG4-3** | PD | H | 65 | 271 | Y | **ZO-1-1** | PM | M | 54 | 691 | N |
| **DLG4-3** | PD | H | 65 | 272 | Y | **ZO-1-1** | PM | M | 54 | 436 | N |
| **DLG4-3** | PD | H | 65 | 273 | Y | **ZO-1-1** | PM | M | 54 | 448 | N |
| **DLG4-3** | PD | H | 65 | 274 | Y | **ZO-1-1** | PM | M | 54 | 521 | N |
| **DLG4-3** | PD | H | 65 | 275 | Y | **ZO-1-1** | PM | M | 54 | 692 | N |
| **DLG4-3** | PD | H | 65 | 261 | Y | **ZO-1-1** | PM | M | 54 | 693 | N |
| **DLG4-3** | PD | H | 65 | 241 | Y | **ZO-1-1** | PM | M | 54 | 11 | N |
| **DLG4-3** | PD | H | 65 | 276 | Y | **ZO-1-1** | PM | M | 54 | 694 | N |
| **DLG4-3** | PD | H | 65 | 277 | Y | **ZO-1-1** | PM | M | 54 | 522 | N |
| **DLG4-3** | PD | H | 65 | 205 | Y | **ZO-1-1** | PM | M | 54 | 562 | N |
| **DLG4-3** | PD | H | 65 | 278 | Y | **ZO-1-1** | PM | M | 54 | 4 | N |
| **DLG4-3** | PD | H | 65 | 279 | Y | **ZO-1-1** | PM | M | 54 | 649 | N |
| **SCRIB-2** | PD | H | 66 | 139 | Y | **ZO-1-1** | PM | M | 54 | 695 | N |
| **SCRIB-2** | PD | H | 66 | 135 | Y | **ZO-2-1** | PM | M | 55 | 454 | N |
| **SCRIB-2** | PD | H | 66 | 156 | Y | **ZO-2-1** | PM | M | 55 | 29 | N |
| **SCRIB-2** | PD | H | 66 | 140 | Y | **ZO-2-1** | PM | M | 55 | 475 | N |
| **SCRIB-2** | PD | H | 66 | 149 | Y | **ZO-2-1** | PM | M | 55 | 16 | N |
| **SCRIB-2** | PD | H | 66 | 280 | Y | **ZO-2-1** | PM | M | 55 | 32 | N |
| **SCRIB-2** | PD | H | 66 | 238 | Y | **ZO-2-1** | PM | M | 55 | 446 | N |
| **SCRIB-2** | PD | H | 66 | 281 | Y | **ZO-2-1** | PM | M | 55 | 696 | N |
| **SCRIB-2** | PD | H | 66 | 282 | Y | **ZO-2-1** | PM | M | 55 | 64 | N |
| **SCRIB-2** | PD | H | 66 | 283 | Y | **ZO-2-1** | PM | M | 55 | 80 | N |
| **SCRIB-2** | PD | H | 66 | 284 | Y | **ZO-2-1** | PM | M | 55 | 463 | N |
| **SCRIB-2** | PD | H | 66 | 163 | Y | **ZO-2-1** | PM | M | 55 | 57 | N |
| **SCRIB-2** | PD | H | 66 | 219 | Y | **ZO-2-1** | PM | M | 55 | 467 | N |
| **SCRIB-2** | PD | H | 66 | 285 | Y | **ZO-2-1** | PM | M | 55 | 466 | N |
| **SCRIB-2** | PD | H | 66 | 133 | Y | **ZO-2-1** | PM | M | 55 | 649 | N |
| **SCRIB-2** | PD | H | 66 | 203 | Y | **ZO-2-1** | PM | M | 55 | 452 | N |
| **INADL-2** | PD | H | 67 | 286 | Y | **ZO-2-1** | PM | M | 55 | 649 | N |
| **INADL-2** | PD | H | 67 | 287 | Y | **ZO-2-1** | PM | M | 55 | 518 | N |
| **INADL-2** | PD | H | 67 | 288 | Y | **ZO-2-1** | PM | M | 55 | 17 | N |
| **INADL-2** | PD | H | 67 | 289 | Y | **ZO-2-1** | PM | M | 55 | 474 | N |
| **INADL-2** | PD | H | 67 | 290 | Y | **ZO-2-1** | PM | M | 55 | 473 | N |
| **INADL-2** | PD | H | 67 | 291 | Y | **ZO-2-1** | PM | M | 55 | 35 | N |
| **INADL-2** | PD | H | 67 | 292 | Y | **ZO-2-1** | PM | M | 55 | 13 | N |
| **INADL-2** | PD | H | 67 | 293 | Y | **ZO-2-1** | PM | M | 55 | 470 | N |
| **INADL-2** | PD | H | 67 | 294 | Y | **ZO-2-1** | PM | M | 55 | 447 | N |
| **INADL-2** | PD | H | 67 | 295 | Y | **ZO-2-1** | PM | M | 55 | 22 | N |
| **INADL-2** | PD | H | 67 | 296 | Y | **ZO-2-1** | PM | M | 55 | 436 | N |
| **DLG1-3** | PD | H | 68 | 208 | Y | **ZO-2-1** | PM | M | 55 | 685 | N |
| **DLG1-3** | PD | H | 68 | 297 | Y | **ZO-2-1** | PM | M | 55 | 65 | N |
| **DLG1-3** | PD | H | 68 | 1 | Y | **ZO-2-1** | PM | M | 55 | 5 | N |
| **DLG1-3** | PD | H | 68 | 298 | Y | **ZO-2-1** | PM | M | 55 | 32 | N |
| **DLG1-3** | PD | H | 68 | 261 | Y | **ZO-2-1** | PM | M | 55 | 81 | N |
| **DLG1-3** | PD | H | 68 | 299 | Y | **ZO-2-1** | PM | M | 55 | 468 | N |

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| **DLG1-3** | PD | H | 68 | 300 | Y | **ZO-2-1** | PM | M | 55 | 26 | N |
| **DLG1-3** | PD | H | 68 | 277 | Y | **ZO-2-1** | PM | M | 55 | 465 | N |
| **DLG1-3** | PD | H | 68 | 237 | Y | **ZO-2-1** | PM | M | 55 | 522 | N |
| **DLG1-3** | PD | H | 68 | 301 | Y | **ZO-2-1** | PM | M | 55 | 472 | N |
| **DLG1-3** | PD | H | 68 | 302 | Y | **ZO-2-1** | PM | M | 55 | 469 | N |
| **DLG1-3** | PD | H | 68 | 303 | Y | **ZO-2-1** | PM | M | 55 | 476 | N |
| **DLG1-3** | PD | H | 68 | 2 | Y | **ZO-2-1** | PM | M | 55 | 38 | N |
| **DLG1-1** | PD | H | 69 | 267 | Y | **ZO-2-1** | PM | M | 55 | 4 | N |
| **DLG1-1** | PD | H | 69 | 304 | Y | **ZO-2-1** | PM | M | 55 | 3 | N |
| **DLG1-1** | PD | H | 69 | 305 | Y | **ZO-2-1** | PM | M | 55 | 75 | N |
| **DLG1-1** | PD | H | 69 | 168 | Y | **ZO-2-1** | PM | M | 55 | 63 | N |
| **DLG1-1** | PD | H | 69 | 197 | Y | **ZO-2-1** | PM | M | 55 | 23 | N |
| **DLG1-1** | PD | H | 69 | 306 | Y | **ZO-2-1** | PM | M | 55 | 30 | N |
| **DLG1-1** | PD | H | 69 | 307 | Y | **ZO-3-1** | PM | M | 56 | 436 | N |
| **DLG1-1** | PD | H | 69 | 308 | Y | **CASK-1** | PD | H | 57 | 335 | N |
| **DLG1-1** | PD | H | 69 | 244 | Y | **CASK-1** | PD | H | 57 | 353 | N |
| **DLG1-1** | PD | H | 69 | 309 | Y | **CASK-1** | PD | H | 57 | 407 | N |
| **DLG1-1** | PD | H | 69 | 124 | Y | **CASK-1** | PD | H | 57 | 347 | N |
| **LRRC7-1** | PD | H | 70 | 152 | Y | **CASK-1** | PD | H | 57 | 363 | N |
| **LRRC7-1** | PD | H | 70 | 135 | Y | **CASK-1** | PD | H | 57 | 170 | N |
| **LRRC7-1** | PD | H | 70 | 163 | Y | **CASK-1** | PD | H | 57 | 382 | N |
| **LRRC7-1** | PD | H | 70 | 310 | Y | **CASK-1** | PD | H | 57 | 398 | N |
| **LRRC7-1** | PD | H | 70 | 311 | Y | **CASK-1** | PD | H | 57 | 313 | N |
| **LRRC7-1** | PD | H | 70 | 312 | Y | **CASK-1** | PD | H | 57 | 413 | N |
| **LRRC7-1** | PD | H | 70 | 137 | Y | **CASK-1** | PD | H | 57 | 378 | N |
| **LRRC7-1** | PD | H | 70 | 140 | Y | **CASK-1** | PD | H | 57 | 174 | N |
| **LRRC7-1** | PD | H | 70 | 284 | Y | **CASK-1** | PD | H | 57 | 328 | N |
| **LRRC7-1** | PD | H | 70 | 313 | Y | **CASK-1** | PD | H | 57 | 266 | N |
| **LRRC7-1** | PD | H | 70 | 280 | Y | **CASK-1** | PD | H | 57 | 428 | N |
| **LRRC7-1** | PD | H | 70 | 133 | Y | **CASK-1** | PD | H | 57 | 385 | N |
| **LRRC7-1** | PD | H | 70 | 139 | Y | **CASK-1** | PD | H | 57 | 421 | N |
| **LRRC7-1** | PD | H | 70 | 314 | Y | **CASK-1** | PD | H | 57 | 418 | N |
| **LRRC7-1** | PD | H | 70 | 315 | Y | **CASK-1** | PD | H | 57 | 350 | N |
| **LRRC7-1** | PD | H | 70 | 143 | Y | **CASK-1** | PD | H | 57 | 390 | N |
| **LRRC7-1** | PD | H | 70 | 195 | Y | **DLG3-2** | PD | H | 58 | 377 | N |
| **LRRC7-1** | PD | H | 70 | 161 | Y | **DLG3-2** | PD | H | 58 | 417 | N |
| **LRRC7-1** | PD | H | 70 | 316 | Y | **DLG3-2** | PD | H | 58 | 697 | N |
| **LRRC7-1** | PD | H | 70 | 149 | Y | **DLG3-2** | PD | H | 58 | 401 | N |
| **LRRC7-1** | PD | H | 70 | 317 | Y | **DLG3-2** | PD | H | 58 | 402 | N |
| **LRRC7-1** | PD | H | 70 | 132 | Y | **DLG3-2** | PD | H | 58 | 408 | N |
| **LRRC7-1** | PD | H | 70 | 136 | Y | **DLG3-2** | PD | H | 58 | 325 | N |
| **LRRC7-1** | PD | H | 70 | 281 | Y | **DLG3-2** | PD | H | 58 | 170 | N |
| **LRRC7-1** | PD | H | 70 | 318 | Y | **DLG3-2** | PD | H | 58 | 698 | N |
| **LRRC7-1** | PD | H | 70 | 319 | Y | **DLG3-2** | PD | H | 58 | 97 | N |
| **MPP6-1** | PD | H | 71 | 320 | Y | **DLG3-2** | PD | H | 58 | 174 | N |
| **MPP6-1** | PD | H | 71 | 321 | Y | **DLG3-2** | PD | H | 58 | 287 | N |

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| **MPP6-1** | PD | H | 71 | 322 | Y | **DLG3-2** | PD | H | 58 | 382 | N |
| **MPP6-1** | PD | H | 71 | 323 | Y | **DLG3-2** | PD | H | 58 | 699 | N |
| **MPP6-1** | PD | H | 71 | 324 | Y | **DLG3-2** | PD | H | 58 | 399 | N |
| **MPP6-1** | PD | H | 71 | 325 | Y | **DLG3-2** | PD | H | 58 | 397 | N |
| **MPP6-1** | PD | H | 71 | 326 | Y | **DLG3-2** | PD | H | 58 | 700 | N |
| **MPP6-1** | PD | H | 71 | 327 | Y | **DLG3-2** | PD | H | 58 | 371 | N |
| **MPP6-1** | PD | H | 71 | 328 | Y | **DLG3-2** | PD | H | 58 | 294 | N |
| **MPP6-1** | PD | H | 71 | 329 | Y | **DLG3-2** | PD | H | 58 | 701 | N |
| **MPP6-1** | PD | H | 71 | 330 | Y | **DLG3-2** | PD | H | 58 | 404 | N |
| **MPP6-1** | PD | H | 71 | 331 | Y | **DLG3-2** | PD | H | 58 | 428 | N |
| **MPP6-1** | PD | H | 71 | 332 | Y | **DLG3-2** | PD | H | 58 | 369 | N |
| **MPP6-1** | PD | H | 71 | 333 | Y | **DLG3-2** | PD | H | 58 | 702 | N |
| **MPP6-1** | PD | H | 71 | 334 | Y | **DLG3-2** | PD | H | 58 | 373 | N |
| **PDZK1-1** | PD | H | 72 | 335 | Y | **DLG3-2** | PD | H | 58 | 378 | N |
| **PDZK1-1** | PD | H | 72 | 336 | Y | **DLG3-2** | PD | H | 58 | 415 | N |
| **PDZK1-1** | PD | H | 72 | 337 | Y | **DLG3-2** | PD | H | 58 | 703 | N |
| **PDZK1-1** | PD | H | 72 | 338 | Y | **DLG3-2** | PD | H | 58 | 403 | N |
| **PDZK1-1** | PD | H | 72 | 339 | Y | **DLG3-2** | PD | H | 58 | 407 | N |
| **PDZK1-1** | PD | H | 72 | 340 | Y | **DLG3-2** | PD | H | 58 | 160 | N |
| **PDZK1-1** | PD | H | 72 | 341 | Y | **DLG3-2** | PD | H | 58 | 419 | N |
| **PDZK1-1** | PD | H | 72 | 342 | Y | **DLG3-2** | PD | H | 58 | 704 | N |
| **PDZK1-1** | PD | H | 72 | 343 | Y | **DLG3-2** | PD | H | 58 | 705 | N |
| **PDZK1-1** | PD | H | 72 | 344 | Y | **DLG3-2** | PD | H | 58 | 349 | N |
| **PDZK1-1** | PD | H | 72 | 345 | Y | **DLG3-2** | PD | H | 58 | 425 | N |
| **PDZK1-1** | PD | H | 72 | 346 | Y | **DLG3-2** | PD | H | 58 | 385 | N |
| **PDZK1-1** | PD | H | 72 | 347 | Y | **DLG3-2** | PD | H | 58 | 706 | N |
| **PDZK1-1** | PD | H | 72 | 348 | Y | **ERBB2IP-1** | PD | H | 59 | 385 | N |
| **PDZK1-1** | PD | H | 72 | 349 | Y | **ERBB2IP-1** | PD | H | 59 | 342 | N |
| **PDZK1-1** | PD | H | 72 | 350 | Y | **ERBB2IP-1** | PD | H | 59 | 176 | N |
| **PDZK1-1** | PD | H | 72 | 351 | Y | **ERBB2IP-1** | PD | H | 59 | 348 | N |
| **PDZK1-1** | PD | H | 72 | 352 | Y | **ERBB2IP-1** | PD | H | 59 | 378 | N |
| **PDZK1-1** | PD | H | 72 | 353 | Y | **ERBB2IP-1** | PD | H | 59 | 131 | N |
| **PDZK1-1** | PD | H | 72 | 354 | Y | **ERBB2IP-1** | PD | H | 59 | 399 | N |
| **PDZK1-1** | PD | H | 72 | 355 | Y | **ERBB2IP-1** | PD | H | 59 | 415 | N |
| **PDZK1-1** | PD | H | 72 | 356 | Y | **ERBB2IP-1** | PD | H | 59 | 340 | N |
| **PDZK1-1** | PD | H | 72 | 357 | Y | **ERBB2IP-1** | PD | H | 59 | 428 | N |
| **PDZK1-1** | PD | H | 72 | 358 | Y | **ERBB2IP-1** | PD | H | 59 | 192 | N |
| **PDZK1-1** | PD | H | 72 | 359 | Y | **ERBB2IP-1** | PD | H | 59 | 371 | N |
| **PDZK1-1** | PD | H | 72 | 360 | Y | **ERBB2IP-1** | PD | H | 59 | 416 | N |
| **PDZK1-1** | PD | H | 72 | 361 | Y | **ERBB2IP-1** | PD | H | 59 | 332 | N |
| **PDZK1-1** | PD | H | 72 | 362 | Y | **ERBB2IP-1** | PD | H | 59 | 193 | N |
| **PDZK1-1** | PD | H | 72 | 363 | Y | **ERBB2IP-1** | PD | H | 59 | 291 | N |
| **PDZK1-1** | PD | H | 72 | 364 | Y | **ERBB2IP-1** | PD | H | 59 | 298 | N |
| **MAGI1-5** | PD | H | 73 | 365 | Y | **ERBB2IP-1** | PD | H | 59 | 417 | N |
| **MAGI1-5** | PD | H | 73 | 366 | Y | **ERBB2IP-1** | PD | H | 59 | 174 | N |
| **MAGI1-5** | PD | H | 73 | 367 | Y | **ERBB2IP-1** | PD | H | 59 | 374 | N |

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| **MAGI1-5** | PD | H | 73 | 368 | Y | **ERBB2IP-1** | PD | H | 59 | 389 | N |
| **MAGI1-5** | PD | H | 73 | 369 | Y | **ERBB2IP-1** | PD | H | 59 | 407 | N |
| **MAGI1-5** | PD | H | 73 | 370 | Y | **ERBB2IP-1** | PD | H | 59 | 405 | N |
| **MAGI1-5** | PD | H | 73 | 371 | Y | **ERBB2IP-1** | PD | H | 59 | 382 | N |
| **MAGI1-5** | PD | H | 73 | 372 | Y | **ERBB2IP-1** | PD | H | 59 | 96 | N |
| **MAGI1-5** | PD | H | 73 | 373 | Y | **ERBB2IP-1** | PD | H | 59 | 383 | N |
| **MAGI1-5** | PD | H | 73 | 374 | Y | **ERBB2IP-1** | PD | H | 59 | 170 | N |
| **MAGI1-5** | PD | H | 73 | 375 | Y | **ERBB2IP-1** | PD | H | 59 | 103 | N |
| **MAGI1-5** | PD | H | 73 | 376 | Y | **ERBB2IP-1** | PD | H | 59 | 404 | N |
| **MAGI3-5** | PD | H | 74 | 376 | Y | **ERBB2IP-1** | PD | H | 59 | 275 | N |
| **MAGI3-5** | PD | H | 74 | 377 | Y | **ERBB2IP-1** | PD | H | 59 | 369 | N |
| **MAGI3-5** | PD | H | 74 | 370 | Y | **ERBB2IP-1** | PD | H | 59 | 87 | N |
| **PSCDBP-1** | PD | H | 75 | 173 | Y | **ERBB2IP-1** | PD | H | 59 | 388 | N |
| **PSCDBP-1** | PD | H | 75 | 378 | Y | **MPDZ-1** | PD | H | 60 | 707 | N |
| **PSCDBP-1** | PD | H | 75 | 379 | Y | **MPDZ-1** | PD | H | 60 | 369 | N |
| **PSCDBP-1** | PD | H | 75 | 380 | Y | **MPDZ-1** | PD | H | 60 | 421 | N |
| **PSCDBP-1** | PD | H | 75 | 381 | Y | **MPDZ-1** | PD | H | 60 | 373 | N |
| **PSCDBP-1** | PD | H | 75 | 382 | Y | **MPDZ-1** | PD | H | 60 | 345 | N |
| **DVL2-1** | PD | H | 76 | 383 | Y | **MPDZ-1** | PD | H | 60 | 708 | N |
| **DVL2-1** | PD | H | 76 | 384 | Y | **MPDZ-1** | PD | H | 60 | 709 | N |
| **DVL2-1** | PD | H | 76 | 385 | Y | **MPDZ-1** | PD | H | 60 | 327 | N |
| **DVL2-1** | PD | H | 76 | 386 | Y | **MPDZ-1** | PD | H | 60 | 87 | N |
| **DLG2-3** | PD | H | 77 | 108 | Y | **MPDZ-1** | PD | H | 60 | 371 | N |
| **DLG2-3** | PD | H | 77 | 241 | Y | **MPDZ-1** | PD | H | 60 | 407 | N |
| **DLG2-3** | PD | H | 77 | 261 | Y | **MPDZ-1** | PD | H | 60 | 710 | N |
| **DLG2-3** | PD | H | 77 | 1 | Y | **MPDZ-1** | PD | H | 60 | 711 | N |
| **DLG2-3** | PD | H | 77 | 387 | Y | **MPDZ-1** | PD | H | 60 | 266 | N |
| **DLG2-3** | PD | H | 77 | 388 | Y | **MPDZ-1** | PD | H | 60 | 712 | N |
| **DLG2-3** | PD | H | 77 | 270 | Y | **MPDZ-1** | PD | H | 60 | 385 | N |
| **DLG2-3** | PD | H | 77 | 389 | Y | **MPDZ-1** | PD | H | 60 | 713 | N |
| **DLG2-3** | PD | H | 77 | 390 | Y | **MPDZ-1** | PD | H | 60 | 714 | N |
| **DLG2-3** | PD | H | 77 | 391 | Y | **MPDZ-1** | PD | H | 60 | 715 | N |
| **DLG2-3** | PD | H | 77 | 392 | Y | **MPDZ-1** | PD | H | 60 | 298 | N |
| **DLG2-3** | PD | H | 77 | 393 | Y | **MPDZ-1** | PD | H | 60 | 716 | N |
| **DLG2-3** | PD | H | 77 | 394 | Y | **MPDZ-1** | PD | H | 60 | 270 | N |
| **DLG2-3** | PD | H | 77 | 395 | Y | **MPDZ-1** | PD | H | 60 | 423 | N |
| **MPDZ-3** | PD | H | 78 | 396 | Y | **MPDZ-10** | PD | H | 61 | 717 | N |
| **MPDZ-3** | PD | H | 78 | 397 | Y | **MPDZ-10** | PD | H | 61 | 399 | N |
| **MPDZ-3** | PD | H | 78 | 398 | Y | **MPDZ-10** | PD | H | 61 | 380 | N |
| **MPDZ-3** | PD | H | 78 | 399 | Y | **MPDZ-10** | PD | H | 61 | 718 | N |
| **MPDZ-3** | PD | H | 78 | 400 | Y | **MPDZ-10** | PD | H | 61 | 719 | N |
| **MPDZ-3** | PD | H | 78 | 401 | Y | **MPDZ-10** | PD | H | 61 | 378 | N |
| **MPDZ-3** | PD | H | 78 | 402 | Y | **MPDZ-10** | PD | H | 61 | 402 | N |
| **MPDZ-3** | PD | H | 78 | 403 | Y | **MPDZ-10** | PD | H | 61 | 344 | N |
| **MPDZ-3** | PD | H | 78 | 404 | Y | **MPDZ-10** | PD | H | 61 | 405 | N |
| **MPDZ-3** | PD | H | 78 | 405 | Y | **MPDZ-10** | PD | H | 61 | 412 | N |

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| **MPDZ-3** | PD | H | 78 | 406 | Y | **MPDZ-10** | PD | H | 61 | 423 | N |
| **MPDZ-3** | PD | H | 78 | 407 | Y | **MPDZ-10** | PD | H | 61 | 720 | N |
| **PDLIM4-1** | PD | H | 79 | 408 | Y | **MPDZ-10** | PD | H | 61 | 721 | N |
| **PDLIM4-1** | PD | H | 79 | 409 | Y | **MPDZ-10** | PD | H | 61 | 353 | N |
| **PDLIM4-1** | PD | H | 79 | 410 | Y | **MPDZ-10** | PD | H | 61 | 398 | N |
| **PDLIM4-1** | PD | H | 79 | 411 | Y | **MPDZ-10** | PD | H | 61 | 377 | N |
| **PDLIM4-1** | PD | H | 79 | 412 | Y | **MPDZ-10** | PD | H | 61 | 407 | N |
| **PDLIM4-1** | PD | H | 79 | 413 | Y | **MPDZ-10** | PD | H | 61 | 408 | N |
| **PDLIM4-1** | PD | H | 79 | 316 | Y | **MPDZ-10** | PD | H | 61 | 722 | N |
| **PDLIM4-1** | PD | H | 79 | 414 | Y | **MPDZ-10** | PD | H | 61 | 723 | N |
| **PDLIM4-1** | PD | H | 79 | 415 | Y | **MPDZ-10** | PD | H | 61 | 724 | N |
| **PDLIM4-1** | PD | H | 79 | 416 | Y | **MPDZ-10** | PD | H | 61 | 385 | N |
| **SLC9A3R2-2** | PD | H | 80 | 417 | Y | **MPDZ-10** | PD | H | 61 | 404 | N |
| **SLC9A3R2-2** | PD | H | 80 | 418 | Y | **MPDZ-10** | PD | H | 61 | 397 | N |
| **SLC9A3R2-2** | PD | H | 80 | 419 | Y | **MPDZ-10** | PD | H | 61 | 725 | N |
| **SLC9A3R2-2** | PD | H | 80 | 420 | Y | **MPDZ-10** | PD | H | 61 | 726 | N |
| **SLC9A3R2-2** | PD | H | 80 | 421 | Y | **MPDZ-12** | PD | H | 62 | 384 | N |
| **SLC9A3R2-2** | PD | H | 80 | 422 | Y | **MPDZ-12** | PD | H | 62 | 399 | N |
| **SLC9A3R2-2** | PD | H | 80 | 423 | Y | **MPDZ-12** | PD | H | 62 | 386 | N |
| **SLC9A3R2-2** | PD | H | 80 | 424 | Y | **MPDZ-12** | PD | H | 62 | 400 | N |
| **SLC9A3R2-2** | PD | H | 80 | 425 | Y | **MPDZ-12** | PD | H | 62 | 385 | N |
| **SLC9A3R2-2** | PD | H | 80 | 426 | Y | **MPDZ-12** | PD | H | 62 | 369 | N |
| **SLC9A3R2-2** | PD | H | 80 | 427 | Y | **MPDZ-12** | PD | H | 62 | 287 | N |
| **SLC9A3R2-2** | PD | H | 80 | 428 | Y | **MPDZ-12** | PD | H | 62 | 407 | N |
| **SNTA1-1** | PD | H | 81 | 429 | Y | **MPDZ-12** | PD | H | 62 | 371 | N |
| **SNTA1-1** | PD | H | 81 | 430 | Y | **MPDZ-12** | PD | H | 62 | 170 | N |
| **SNTA1-1** | PD | H | 81 | 431 | Y | **MPDZ-12** | PD | H | 62 | 405 | N |
| **SNTA1-1** | PD | H | 81 | 357 | Y | **SCRIB-1** | PD | H | 63 | 371 | N |
| **SNTA1-1** | PD | H | 81 | 205 | Y | **SCRIB-1** | PD | H | 63 | 369 | N |
| **SNTA1-1** | PD | H | 81 | 432 | Y | **SCRIB-1** | PD | H | 63 | 170 | N |
| **SNTA1-1** | PD | H | 81 | 108 | Y | **SCRIB-1** | PD | H | 63 | 293 | N |
| **SNTA1-1** | PD | H | 81 | 270 | Y | **SCRIB-1** | PD | H | 63 | 407 | N |
| **SNTA1-1** | PD | H | 81 | 433 | Y | **SCRIB-1** | PD | H | 63 | 87 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 58 | N | **SCRIB-1** | PD | H | 63 | 406 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 434 | N | **SCRIB-1** | PD | H | 63 | 287 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 435 | N | **SCRIB-1** | PD | H | 63 | 187 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 436 | N | **SCRIB-1** | PD | H | 63 | 405 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 437 | N | **SCRIB-1** | PD | H | 63 | 96 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 56 | N | **SCRIB-1** | PD | H | 63 | 233 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 438 | N | **SCRIB-1** | PD | H | 63 | 377 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 439 | N | **SCRIB-1** | PD | H | 63 | 412 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 440 | N | **SCRIB-1** | PD | H | 63 | 400 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 441 | N | **SCRIB-1** | PD | H | 63 | 380 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 442 | N | **SCRIB-1** | PD | H | 63 | 385 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 443 | N | **SCRIB-1** | PD | H | 63 | 350 | N |
| **A1-SYNTROPHIN-1** | PM | M | 0 | 444 | N | **SCRIB-1** | PD | H | 63 | 404 | N |

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| **B1-SYNTROPHIN-1** | PM | M | 1 | 445 | N | **SCRIB-1** | PD | H | 63 | 374 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 446 | N | **SCRIB-1** | PD | H | 63 | 155 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 447 | N | **SCRIB-1** | PD | H | 63 | 171 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 26 | N | **SCRIB-1** | PD | H | 63 | 399 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 48 | N | **SCRIB-1** | PD | H | 63 | 408 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 436 | N | **SCRIB-1** | PD | H | 63 | 381 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 52 | N | **SCRIB-1** | PD | H | 63 | 382 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 25 | N | **SCRIB-1** | PD | H | 63 | 375 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 67 | N | **DLG1-2** | PD | H | 64 | 727 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 448 | N | **DLG1-2** | PD | H | 64 | 385 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 21 | N | **DLG1-2** | PD | H | 64 | 430 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 27 | N | **DLG1-2** | PD | H | 64 | 380 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 68 | N | **DLG1-2** | PD | H | 64 | 419 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 23 | N | **DLG1-2** | PD | H | 64 | 287 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 19 | N | **DLG1-2** | PD | H | 64 | 401 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 69 | N | **DLG1-2** | PD | H | 64 | 728 | N |
| **B1-SYNTROPHIN-1** | PM | M | 1 | 449 | N | **DLG1-2** | PD | H | 64 | 176 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 436 | N | **DLG1-2** | PD | H | 64 | 729 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 450 | N | **DLG1-2** | PD | H | 64 | 416 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 451 | N | **DLG1-2** | PD | H | 64 | 399 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 452 | N | **DLG1-2** | PD | H | 64 | 724 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 453 | N | **DLG1-2** | PD | H | 64 | 193 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 454 | N | **DLG1-2** | PD | H | 64 | 218 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 455 | N | **DLG1-2** | PD | H | 64 | 103 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 456 | N | **DLG1-2** | PD | H | 64 | 382 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 457 | N | **DLG1-2** | PD | H | 64 | 421 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 458 | N | **DLG1-2** | PD | H | 64 | 730 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 459 | N | **DLG1-2** | PD | H | 64 | 731 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 460 | N | **DLG1-2** | PD | H | 64 | 366 | N |
| **CHAPSYN-110-2** | PM | M | 2 | 461 | N | **DLG1-2** | PD | H | 64 | 378 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 452 | N | **DLG1-2** | PD | H | 64 | 423 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 29 | N | **DLG1-2** | PD | H | 64 | 87 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 65 | N | **DLG1-2** | PD | H | 64 | 369 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 46 | N | **DLG1-2** | PD | H | 64 | 699 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 17 | N | **DLG1-2** | PD | H | 64 | 170 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 462 | N | **DLG1-2** | PD | H | 64 | 377 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 463 | N | **DLG1-2** | PD | H | 64 | 94 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 57 | N | **DLG1-2** | PD | H | 64 | 397 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 464 | N | **DLG1-2** | PD | H | 64 | 732 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 41 | N | **DLG1-2** | PD | H | 64 | 352 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 465 | N | **DLG1-2** | PD | H | 64 | 389 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 45 | N | **DLG1-2** | PD | H | 64 | 415 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 63 | N | **DLG1-2** | PD | H | 64 | 325 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 466 | N | **DLG1-2** | PD | H | 64 | 289 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 467 | N | **DLG1-2** | PD | H | 64 | 398 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 468 | N | **DLG1-2** | PD | H | 64 | 407 | N |

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| **CHAPSYN-110-3** | PM | M | 3 | 469 | N | **DLG1-2** | PD | H | 64 | 275 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 470 | N | **DLG1-2** | PD | H | 64 | 733 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 64 | N | **DLG1-2** | PD | H | 64 | 174 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 471 | N | **DLG1-2** | PD | H | 64 | 342 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 472 | N | **DLG1-2** | PD | H | 64 | 294 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 473 | N | **DLG1-2** | PD | H | 64 | 404 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 35 | N | **DLG1-2** | PD | H | 64 | 371 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 474 | N | **DLG1-2** | PD | H | 64 | 374 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 73 | N | **DLG1-2** | PD | H | 64 | 396 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 475 | N | **DLG1-2** | PD | H | 64 | 734 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 26 | N | **DLG4-3** | PD | H | 65 | 112 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 30 | N | **DLG4-3** | PD | H | 65 | 382 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 13 | N | **DLG4-3** | PD | H | 65 | 170 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 476 | N | **DLG4-3** | PD | H | 65 | 735 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 454 | N | **DLG4-3** | PD | H | 65 | 736 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 43 | N | **DLG4-3** | PD | H | 65 | 368 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 3 | N | **DLG4-3** | PD | H | 65 | 737 | N |
| **CHAPSYN-110-3** | PM | M | 3 | 436 | N | **DLG4-3** | PD | H | 65 | 738 | N |
| **CIPP-10** | PM | M | 4 | 64 | N | **DLG4-3** | PD | H | 65 | 739 | N |
| **CIPP-10** | PM | M | 4 | 473 | N | **DLG4-3** | PD | H | 65 | 401 | N |
| **CIPP-10** | PM | M | 4 | 474 | N | **DLG4-3** | PD | H | 65 | 294 | N |
| **CIPP-10** | PM | M | 4 | 65 | N | **DLG4-3** | PD | H | 65 | 371 | N |
| **CIPP-10** | PM | M | 4 | 466 | N | **DLG4-3** | PD | H | 65 | 400 | N |
| **CIPP-10** | PM | M | 4 | 472 | N | **DLG4-3** | PD | H | 65 | 381 | N |
| **CIPP-10** | PM | M | 4 | 15 | N | **DLG4-3** | PD | H | 65 | 740 | N |
| **CIPP-10** | PM | M | 4 | 57 | N | **DLG4-3** | PD | H | 65 | 741 | N |
| **CIPP-10** | PM | M | 4 | 463 | N | **DLG4-3** | PD | H | 65 | 396 | N |
| **CIPP-10** | PM | M | 4 | 23 | N | **DLG4-3** | PD | H | 65 | 174 | N |
| **CIPP-10** | PM | M | 4 | 465 | N | **DLG4-3** | PD | H | 65 | 369 | N |
| **CIPP-10** | PM | M | 4 | 469 | N | **DLG4-3** | PD | H | 65 | 728 | N |
| **CIPP-10** | PM | M | 4 | 41 | N | **DLG4-3** | PD | H | 65 | 384 | N |
| **CIPP-10** | PM | M | 4 | 467 | N | **DLG4-3** | PD | H | 65 | 97 | N |
| **CIPP-10** | PM | M | 4 | 468 | N | **DLG4-3** | PD | H | 65 | 404 | N |
| **CIPP-10** | PM | M | 4 | 13 | N | **DLG4-3** | PD | H | 65 | 415 | N |
| **CIPP-10** | PM | M | 4 | 475 | N | **DLG4-3** | PD | H | 65 | 742 | N |
| **CIPP-10** | PM | M | 4 | 436 | N | **DLG4-3** | PD | H | 65 | 176 | N |
| **CIPP-10** | PM | M | 4 | 3 | N | **DLG4-3** | PD | H | 65 | 743 | N |
| **CIPP-10** | PM | M | 4 | 29 | N | **SCRIB-2** | PD | H | 66 | 377 | N |
| **CIPP-10** | PM | M | 4 | 448 | N | **SCRIB-2** | PD | H | 66 | 399 | N |
| **CIPP-10** | PM | M | 4 | 45 | N | **SCRIB-2** | PD | H | 66 | 402 | N |
| **CIPP-10** | PM | M | 4 | 73 | N | **SCRIB-2** | PD | H | 66 | 407 | N |
| **CIPP-10** | PM | M | 4 | 470 | N | **SCRIB-2** | PD | H | 66 | 405 | N |
| **CIPP-10** | PM | M | 4 | 454 | N | **SCRIB-2** | PD | H | 66 | 398 | N |
| **CIPP-10** | PM | M | 4 | 63 | N | **SCRIB-2** | PD | H | 66 | 345 | N |
| **CIPP-10** | PM | M | 4 | 17 | N | **SCRIB-2** | PD | H | 66 | 378 | N |
| **CIPP-10** | PM | M | 4 | 476 | N | **SCRIB-2** | PD | H | 66 | 404 | N |

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| **CIPP-10** | PM | M | 4 | 16 | N | **SCRIB-2** | PD | H | 66 | 371 | N |
| **CIPP-10** | PM | M | 4 | 30 | N | **SCRIB-2** | PD | H | 66 | 170 | N |
| **CIPP-10** | PM | M | 4 | 35 | N | **SCRIB-2** | PD | H | 66 | 323 | N |
| **CIPP-10** | PM | M | 4 | 43 | N | **SCRIB-2** | PD | H | 66 | 316 | N |
| **CIPP-3** | PM | M | 5 | 477 | N | **SCRIB-2** | PD | H | 66 | 385 | N |
| **CIPP-3** | PM | M | 5 | 478 | N | **SCRIB-2** | PD | H | 66 | 369 | N |
| **CIPP-3** | PM | M | 5 | 479 | N | **SCRIB-2** | PD | H | 66 | 368 | N |
| **CIPP-3** | PM | M | 5 | 480 | N | **INADL-2** | PD | H | 67 | 342 | N |
| **CIPP-3** | PM | M | 5 | 481 | N | **INADL-2** | PD | H | 67 | 744 | N |
| **CIPP-3** | PM | M | 5 | 482 | N | **INADL-2** | PD | H | 67 | 430 | N |
| **CIPP-3** | PM | M | 5 | 483 | N | **INADL-2** | PD | H | 67 | 399 | N |
| **CIPP-3** | PM | M | 5 | 484 | N | **INADL-2** | PD | H | 67 | 390 | N |
| **CIPP-3** | PM | M | 5 | 485 | N | **INADL-2** | PD | H | 67 | 266 | N |
| **CIPP-3** | PM | M | 5 | 486 | N | **INADL-2** | PD | H | 67 | 745 | N |
| **CIPP-3** | PM | M | 5 | 487 | N | **INADL-2** | PD | H | 67 | 746 | N |
| **CIPP-3** | PM | M | 5 | 488 | N | **INADL-2** | PD | H | 67 | 707 | N |
| **CIPP-5** | PM | M | 6 | 489 | N | **INADL-2** | PD | H | 67 | 369 | N |
| **CIPP-5** | PM | M | 6 | 490 | N | **INADL-2** | PD | H | 67 | 747 | N |
| **CIPP-5** | PM | M | 6 | 491 | N | **INADL-2** | PD | H | 67 | 748 | N |
| **CIPP-5** | PM | M | 6 | 492 | N | **INADL-2** | PD | H | 67 | 749 | N |
| **CIPP-5** | PM | M | 6 | 493 | N | **INADL-2** | PD | H | 67 | 402 | N |
| **CIPP-5** | PM | M | 6 | 494 | N | **INADL-2** | PD | H | 67 | 750 | N |
| **CIPP-5** | PM | M | 6 | 495 | N | **INADL-2** | PD | H | 67 | 371 | N |
| **CIPP-5** | PM | M | 6 | 496 | N | **INADL-2** | PD | H | 67 | 751 | N |
| **CIPP-5** | PM | M | 6 | 497 | N | **INADL-2** | PD | H | 67 | 385 | N |
| **CIPP-5** | PM | M | 6 | 498 | N | **INADL-2** | PD | H | 67 | 425 | N |
| **CIPP-5** | PM | M | 6 | 499 | N | **INADL-2** | PD | H | 67 | 396 | N |
| **CIPP-8** | PM | M | 7 | 500 | N | **INADL-2** | PD | H | 67 | 752 | N |
| **CIPP-8** | PM | M | 7 | 501 | N | **DLG1-3** | PD | H | 68 | 174 | N |
| **CIPP-8** | PM | M | 7 | 0 | N | **DLG1-3** | PD | H | 68 | 728 | N |
| **CIPP-8** | PM | M | 7 | 83 | N | **DLG1-3** | PD | H | 68 | 401 | N |
| **CIPP-8** | PM | M | 7 | 472 | N | **DLG1-3** | PD | H | 68 | 753 | N |
| **CIPP-8** | PM | M | 7 | 19 | N | **DLG1-3** | PD | H | 68 | 380 | N |
| **CIPP-8** | PM | M | 7 | 502 | N | **DLG1-3** | PD | H | 68 | 402 | N |
| **CIPP-8** | PM | M | 7 | 503 | N | **DLG1-3** | PD | H | 68 | 754 | N |
| **CIPP-8** | PM | M | 7 | 445 | N | **DLG1-3** | PD | H | 68 | 368 | N |
| **CIPP-8** | PM | M | 7 | 48 | N | **DLG1-3** | PD | H | 68 | 170 | N |
| **CIPP-8** | PM | M | 7 | 504 | N | **DLG1-3** | PD | H | 68 | 755 | N |
| **CIPP-8** | PM | M | 7 | 446 | N | **DLG1-3** | PD | H | 68 | 383 | N |
| **CIPP-8** | PM | M | 7 | 449 | N | **DLG1-3** | PD | H | 68 | 369 | N |
| **CIPP-8** | PM | M | 7 | 8 | N | **DLG1-3** | PD | H | 68 | 39 | N |
| **CIPP-8** | PM | M | 7 | 505 | N | **DLG1-3** | PD | H | 68 | 756 | N |
| **CIPP-8** | PM | M | 7 | 27 | N | **DLG1-3** | PD | H | 68 | 396 | N |
| **CIPP-8** | PM | M | 7 | 506 | N | **DLG1-3** | PD | H | 68 | 404 | N |
| **CIPP-8** | PM | M | 7 | 6 | N | **DLG1-3** | PD | H | 68 | 757 | N |
| **CIPP-8** | PM | M | 7 | 507 | N | **DLG1-3** | PD | H | 68 | 382 | N |

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| **CIPP-8** | PM | M | 7 | 508 | N | **DLG1-3** | PD | H | 68 | 758 | N |
| **CIPP-8** | PM | M | 7 | 509 | N | **DLG1-3** | PD | H | 68 | 759 | N |
| **CIPP-8** | PM | M | 7 | 510 | N | **DLG1-3** | PD | H | 68 | 760 | N |
| **CIPP-8** | PM | M | 7 | 67 | N | **DLG1-3** | PD | H | 68 | 378 | N |
| **CIPP-8** | PM | M | 7 | 511 | N | **DLG1-3** | PD | H | 68 | 415 | N |
| **CIPP-8** | PM | M | 7 | 68 | N | **DLG1-1** | PD | H | 69 | 761 | N |
| **CIPP-8** | PM | M | 7 | 512 | N | **DLG1-1** | PD | H | 69 | 407 | N |
| **CIPP-8** | PM | M | 7 | 13 | N | **DLG1-1** | PD | H | 69 | 762 | N |
| **CIPP-8** | PM | M | 7 | 4 | N | **DLG1-1** | PD | H | 69 | 369 | N |
| **CIPP-8** | PM | M | 7 | 52 | N | **DLG1-1** | PD | H | 69 | 763 | N |
| **CIPP-9** | PM | M | 8 | 446 | N | **DLG1-1** | PD | H | 69 | 764 | N |
| **CIPP-9** | PM | M | 8 | 513 | N | **DLG1-1** | PD | H | 69 | 403 | N |
| **CIPP-9** | PM | M | 8 | 514 | N | **DLG1-1** | PD | H | 69 | 404 | N |
| **CIPP-9** | PM | M | 8 | 515 | N | **DLG1-1** | PD | H | 69 | 765 | N |
| **CIPP-9** | PM | M | 8 | 45 | N | **DLG1-1** | PD | H | 69 | 402 | N |
| **CIPP-9** | PM | M | 8 | 53 | N | **DLG1-1** | PD | H | 69 | 371 | N |
| **CIPP-9** | PM | M | 8 | 23 | N | **DLG1-1** | PD | H | 69 | 766 | N |
| **CIPP-9** | PM | M | 8 | 516 | N | **DLG1-1** | PD | H | 69 | 397 | N |
| **CIPP-9** | PM | M | 8 | 5 | N | **DLG1-1** | PD | H | 69 | 399 | N |
| **CIPP-9** | PM | M | 8 | 517 | N | **DLG1-1** | PD | H | 69 | 756 | N |
| **CIPP-9** | PM | M | 8 | 18 | N | **DLG1-1** | PD | H | 69 | 767 | N |
| **CIPP-9** | PM | M | 8 | 0 | N | **DLG1-1** | PD | H | 69 | 385 | N |
| **CIPP-9** | PM | M | 8 | 83 | N | **DLG1-1** | PD | H | 69 | 768 | N |
| **CIPP-9** | PM | M | 8 | 447 | N | **DLG1-1** | PD | H | 69 | 170 | N |
| **CIPP-9** | PM | M | 8 | 17 | N | **DLG1-1** | PD | H | 69 | 380 | N |
| **CIPP-9** | PM | M | 8 | 32 | N | **DLG1-1** | PD | H | 69 | 697 | N |
| **CIPP-9** | PM | M | 8 | 445 | N | **LRRC7-1** | PD | H | 70 | 769 | N |
| **CIPP-9** | PM | M | 8 | 80 | N | **LRRC7-1** | PD | H | 70 | 94 | N |
| **CIPP-9** | PM | M | 8 | 34 | N | **LRRC7-1** | PD | H | 70 | 193 | N |
| **CIPP-9** | PM | M | 8 | 1 | N | **LRRC7-1** | PD | H | 70 | 298 | N |
| **CIPP-9** | PM | M | 8 | 51 | N | **LRRC7-1** | PD | H | 70 | 404 | N |
| **CIPP-9** | PM | M | 8 | 518 | N | **LRRC7-1** | PD | H | 70 | 371 | N |
| **CIPP-9** | PM | M | 8 | 20 | N | **LRRC7-1** | PD | H | 70 | 398 | N |
| **CIPP-9** | PM | M | 8 | 7 | N | **LRRC7-1** | PD | H | 70 | 375 | N |
| **CIPP-9** | PM | M | 8 | 469 | N | **LRRC7-1** | PD | H | 70 | 266 | N |
| **CIPP-9** | PM | M | 8 | 16 | N | **LRRC7-1** | PD | H | 70 | 427 | N |
| **CIPP-9** | PM | M | 8 | 62 | N | **LRRC7-1** | PD | H | 70 | 421 | N |
| **CIPP-9** | PM | M | 8 | 519 | N | **LRRC7-1** | PD | H | 70 | 385 | N |
| **CIPP-9** | PM | M | 8 | 78 | N | **LRRC7-1** | PD | H | 70 | 770 | N |
| **CIPP-9** | PM | M | 8 | 520 | N | **LRRC7-1** | PD | H | 70 | 114 | N |
| **CIPP-9** | PM | M | 8 | 43 | N | **LRRC7-1** | PD | H | 70 | 87 | N |
| **CIPP-9** | PM | M | 8 | 521 | N | **LRRC7-1** | PD | H | 70 | 397 | N |
| **CIPP-9** | PM | M | 8 | 67 | N | **LRRC7-1** | PD | H | 70 | 771 | N |
| **CIPP-9** | PM | M | 8 | 4 | N | **LRRC7-1** | PD | H | 70 | 407 | N |
| **CIPP-9** | PM | M | 8 | 21 | N | **LRRC7-1** | PD | H | 70 | 342 | N |
| **CIPP-9** | PM | M | 8 | 74 | N | **LRRC7-1** | PD | H | 70 | 405 | N |

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| **CIPP-9** | PM | M | 8 | 32 | N | **LRRC7-1** | PD | H | 70 | 772 | N |
| **CIPP-9** | PM | M | 8 | 70 | N | **LRRC7-1** | PD | H | 70 | 773 | N |
| **CIPP-9** | PM | M | 8 | 508 | N | **LRRC7-1** | PD | H | 70 | 399 | N |
| **CIPP-9** | PM | M | 8 | 35 | N | **LRRC7-1** | PD | H | 70 | 369 | N |
| **CIPP-9** | PM | M | 8 | 6 | N | **LRRC7-1** | PD | H | 70 | 774 | N |
| **CIPP-9** | PM | M | 8 | 9 | N | **LRRC7-1** | PD | H | 70 | 368 | N |
| **CIPP-9** | PM | M | 8 | 15 | N | **LRRC7-1** | PD | H | 70 | 775 | N |
| **CIPP-9** | PM | M | 8 | 77 | N | **LRRC7-1** | PD | H | 70 | 411 | N |
| **CIPP-9** | PM | M | 8 | 514 | N | **LRRC7-1** | PD | H | 70 | 776 | N |
| **CIPP-9** | PM | M | 8 | 522 | N | **LRRC7-1** | PD | H | 70 | 378 | N |
| **CIPP-9** | PM | M | 8 | 50 | N | **LRRC7-1** | PD | H | 70 | 777 | N |
| **CIPP-9** | PM | M | 8 | 523 | N | **LRRC7-1** | PD | H | 70 | 103 | N |
| **CIPP-9** | PM | M | 8 | 2 | N | **LRRC7-1** | PD | H | 70 | 332 | N |
| **CIPP-9** | PM | M | 8 | 76 | N | **LRRC7-1** | PD | H | 70 | 170 | N |
| **CIPP-9** | PM | M | 8 | 524 | N | **LRRC7-1** | PD | H | 70 | 176 | N |
| **DVL1-1** | PM | M | 9 | 525 | N | **LRRC7-1** | PD | H | 70 | 778 | N |
| **DVL1-1** | PM | M | 9 | 526 | N | **MPP6-1** | PD | H | 71 | 176 | N |
| **DVL1-1** | PM | M | 9 | 527 | N | **MPP6-1** | PD | H | 71 | 779 | N |
| **DVL1-1** | PM | M | 9 | 528 | N | **MPP6-1** | PD | H | 71 | 371 | N |
| **DVL1-1** | PM | M | 9 | 482 | N | **MPP6-1** | PD | H | 71 | 780 | N |
| **DVL1-1** | PM | M | 9 | 529 | N | **MPP6-1** | PD | H | 71 | 415 | N |
| **DVL1-1** | PM | M | 9 | 530 | N | **MPP6-1** | PD | H | 71 | 378 | N |
| **DVL1-1** | PM | M | 9 | 531 | N | **MPP6-1** | PD | H | 71 | 781 | N |
| **DVL1-1** | PM | M | 9 | 456 | N | **MPP6-1** | PD | H | 71 | 782 | N |
| **DVL1-1** | PM | M | 9 | 532 | N | **MPP6-1** | PD | H | 71 | 380 | N |
| **DVL1-1** | PM | M | 9 | 62 | N | **MPP6-1** | PD | H | 71 | 783 | N |
| **DVL3-1** | PM | M | 10 | 45 | N | **MPP6-1** | PD | H | 71 | 138 | N |
| **DVL3-1** | PM | M | 10 | 473 | N | **MPP6-1** | PD | H | 71 | 430 | N |
| **DVL3-1** | PM | M | 10 | 470 | N | **MPP6-1** | PD | H | 71 | 369 | N |
| **DVL3-1** | PM | M | 10 | 475 | N | **MPP6-1** | PD | H | 71 | 784 | N |
| **DVL3-1** | PM | M | 10 | 23 | N | **MPP6-1** | PD | H | 71 | 388 | N |
| **DVL3-1** | PM | M | 10 | 454 | N | **MPP6-1** | PD | H | 71 | 785 | N |
| **DVL3-1** | PM | M | 10 | 15 | N | **MPP6-1** | PD | H | 71 | 428 | N |
| **DVL3-1** | PM | M | 10 | 57 | N | **MPP6-1** | PD | H | 71 | 263 | N |
| **DVL3-1** | PM | M | 10 | 463 | N | **MPP6-1** | PD | H | 71 | 342 | N |
| **DVL3-1** | PM | M | 10 | 35 | N | **MPP6-1** | PD | H | 71 | 375 | N |
| **DVL3-1** | PM | M | 10 | 65 | N | **MPP6-1** | PD | H | 71 | 382 | N |
| **DVL3-1** | PM | M | 10 | 466 | N | **MPP6-1** | PD | H | 71 | 417 | N |
| **DVL3-1** | PM | M | 10 | 3 | N | **MPP6-1** | PD | H | 71 | 786 | N |
| **DVL3-1** | PM | M | 10 | 467 | N | **MPP6-1** | PD | H | 71 | 787 | N |
| **DVL3-1** | PM | M | 10 | 476 | N | **MPP6-1** | PD | H | 71 | 788 | N |
| **DVL3-1** | PM | M | 10 | 41 | N | **PDZK1-1** | PD | H | 72 | 153 | N |
| **DVL3-1** | PM | M | 10 | 63 | N | **PDZK1-1** | PD | H | 72 | 381 | N |
| **DVL3-1** | PM | M | 10 | 16 | N | **PDZK1-1** | PD | H | 72 | 389 | N |
| **DVL3-1** | PM | M | 10 | 29 | N | **PDZK1-1** | PD | H | 72 | 275 | N |
| **DVL3-1** | PM | M | 10 | 468 | N | **PDZK1-1** | PD | H | 72 | 417 | N |

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| **DVL3-1** | PM | M | 10 | 64 | N | **PDZK1-1** | PD | H | 72 | 216 | N |
| **DVL3-1** | PM | M | 10 | 465 | N | **PDZK1-1** | PD | H | 72 | 288 | N |
| **DVL3-1** | PM | M | 10 | 17 | N | **PDZK1-1** | PD | H | 72 | 789 | N |
| **DVL3-1** | PM | M | 10 | 472 | N | **PDZK1-1** | PD | H | 72 | 790 | N |
| **DVL3-1** | PM | M | 10 | 474 | N | **PDZK1-1** | PD | H | 72 | 388 | N |
| **DVL3-1** | PM | M | 10 | 73 | N | **PDZK1-1** | PD | H | 72 | 157 | N |
| **DVL3-1** | PM | M | 10 | 13 | N | **PDZK1-1** | PD | H | 72 | 791 | N |
| **DVL3-1** | PM | M | 10 | 22 | N | **PDZK1-1** | PD | H | 72 | 256 | N |
| **DVL3-1** | PM | M | 10 | 469 | N | **PDZK1-1** | PD | H | 72 | 430 | N |
| **ERBIN-1** | PM | M | 11 | 465 | N | **PDZK1-1** | PD | H | 72 | 380 | N |
| **ERBIN-1** | PM | M | 11 | 29 | N | **PDZK1-1** | PD | H | 72 | 371 | N |
| **ERBIN-1** | PM | M | 11 | 73 | N | **PDZK1-1** | PD | H | 72 | 765 | N |
| **ERBIN-1** | PM | M | 11 | 508 | N | **PDZK1-1** | PD | H | 72 | 407 | N |
| **ERBIN-1** | PM | M | 11 | 11 | N | **PDZK1-1** | PD | H | 72 | 177 | N |
| **ERBIN-1** | PM | M | 11 | 41 | N | **PDZK1-1** | PD | H | 72 | 403 | N |
| **ERBIN-1** | PM | M | 11 | 533 | N | **PDZK1-1** | PD | H | 72 | 401 | N |
| **ERBIN-1** | PM | M | 11 | 475 | N | **PDZK1-1** | PD | H | 72 | 399 | N |
| **ERBIN-1** | PM | M | 11 | 15 | N | **PDZK1-1** | PD | H | 72 | 412 | N |
| **ERBIN-1** | PM | M | 11 | 57 | N | **PDZK1-1** | PD | H | 72 | 402 | N |
| **ERBIN-1** | PM | M | 11 | 463 | N | **PDZK1-1** | PD | H | 72 | 792 | N |
| **ERBIN-1** | PM | M | 11 | 466 | N | **PDZK1-1** | PD | H | 72 | 194 | N |
| **ERBIN-1** | PM | M | 11 | 468 | N | **PDZK1-1** | PD | H | 72 | 369 | N |
| **ERBIN-1** | PM | M | 11 | 45 | N | **PDZK1-1** | PD | H | 72 | 404 | N |
| **ERBIN-1** | PM | M | 11 | 65 | N | **PDZK1-1** | PD | H | 72 | 793 | N |
| **ERBIN-1** | PM | M | 11 | 63 | N | **PDZK1-1** | PD | H | 72 | 794 | N |
| **ERBIN-1** | PM | M | 11 | 534 | N | **PDZK1-1** | PD | H | 72 | 374 | N |
| **ERBIN-1** | PM | M | 11 | 467 | N | **PDZK1-1** | PD | H | 72 | 795 | N |
| **ERBIN-1** | PM | M | 11 | 454 | N | **PDZK1-1** | PD | H | 72 | 796 | N |
| **ERBIN-1** | PM | M | 11 | 13 | N | **PDZK1-1** | PD | H | 72 | 382 | N |
| **ERBIN-1** | PM | M | 11 | 64 | N | **PDZK1-1** | PD | H | 72 | 385 | N |
| **ERBIN-1** | PM | M | 11 | 1 | N | **PDZK1-1** | PD | H | 72 | 396 | N |
| **ERBIN-1** | PM | M | 11 | 20 | N | **PDZK1-1** | PD | H | 72 | 248 | N |
| **ERBIN-1** | PM | M | 11 | 23 | N | **PDZK1-1** | PD | H | 72 | 96 | N |
| **ERBIN-1** | PM | M | 11 | 470 | N | **PDZK1-1** | PD | H | 72 | 797 | N |
| **ERBIN-1** | PM | M | 11 | 473 | N | **PDZK1-1** | PD | H | 72 | 292 | N |
| **ERBIN-1** | PM | M | 11 | 35 | N | **MAGI1-5** | PD | H | 73 | 381 | N |
| **ERBIN-1** | PM | M | 11 | 447 | N | **MAGI1-5** | PD | H | 73 | 390 | N |
| **ERBIN-1** | PM | M | 11 | 16 | N | **MAGI1-5** | PD | H | 73 | 302 | N |
| **ERBIN-1** | PM | M | 11 | 476 | N | **MAGI1-5** | PD | H | 73 | 798 | N |
| **ERBIN-1** | PM | M | 11 | 3 | N | **MAGI1-5** | PD | H | 73 | 174 | N |
| **ERBIN-1** | PM | M | 11 | 30 | N | **MAGI1-5** | PD | H | 73 | 799 | N |
| **ERBIN-1** | PM | M | 11 | 474 | N | **MAGI1-5** | PD | H | 73 | 734 | N |
| **ERBIN-1** | PM | M | 11 | 17 | N | **MAGI1-5** | PD | H | 73 | 421 | N |
| **ERBIN-1** | PM | M | 11 | 22 | N | **MAGI1-5** | PD | H | 73 | 406 | N |
| **ERBIN-1** | PM | M | 11 | 26 | N | **MAGI1-5** | PD | H | 73 | 428 | N |
| **ERBIN-1** | PM | M | 11 | 43 | N | **MAGI1-5** | PD | H | 73 | 800 | N |

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| **ERBIN-1** | PM | M | 11 | 472 | N | **MAGI1-5** | PD | H | 73 | 801 | N |
| **ERBIN-1** | PM | M | 11 | 469 | N | **MAGI1-5** | PD | H | 73 | 352 | N |
| **GRIP1-6** | PM | M | 12 | 535 | N | **MAGI1-5** | PD | H | 73 | 802 | N |
| **GRIP1-6** | PM | M | 12 | 536 | N | **MAGI1-5** | PD | H | 73 | 417 | N |
| **GRIP1-6** | PM | M | 12 | 537 | N | **MAGI1-5** | PD | H | 73 | 803 | N |
| **GRIP1-6** | PM | M | 12 | 538 | N | **MAGI1-5** | PD | H | 73 | 804 | N |
| **GRIP1-6** | PM | M | 12 | 539 | N | **MAGI1-5** | PD | H | 73 | 416 | N |
| **GRIP1-6** | PM | M | 12 | 540 | N | **MAGI1-5** | PD | H | 73 | 430 | N |
| **GRIP1-6** | PM | M | 12 | 541 | N | **MAGI1-5** | PD | H | 73 | 415 | N |
| **GRIP1-6** | PM | M | 12 | 479 | N | **MAGI1-5** | PD | H | 73 | 731 | N |
| **GRIP1-6** | PM | M | 12 | 542 | N | **MAGI1-5** | PD | H | 73 | 805 | N |
| **GRIP1-6** | PM | M | 12 | 462 | N | **MAGI3-5** | PD | H | 74 | 806 | N |
| **GRIP1-6** | PM | M | 12 | 543 | N | **MAGI3-5** | PD | H | 74 | 807 | N |
| **HARMONIN-2** | PM | M | 13 | 474 | N | **MAGI3-5** | PD | H | 74 | 170 | N |
| **HARMONIN-2** | PM | M | 13 | 473 | N | **MAGI3-5** | PD | H | 74 | 422 | N |
| **HARMONIN-2** | PM | M | 13 | 475 | N | **MAGI3-5** | PD | H | 74 | 808 | N |
| **HARMONIN-2** | PM | M | 13 | 64 | N | **MAGI3-5** | PD | H | 74 | 809 | N |
| **HARMONIN-2** | PM | M | 13 | 41 | N | **MAGI3-5** | PD | H | 74 | 810 | N |
| **HARMONIN-2** | PM | M | 13 | 3 | N | **MAGI3-5** | PD | H | 74 | 431 | N |
| **HARMONIN-2** | PM | M | 13 | 15 | N | **MAGI3-5** | PD | H | 74 | 811 | N |
| **HARMONIN-2** | PM | M | 13 | 57 | N | **MAGI3-5** | PD | H | 74 | 717 | N |
| **HARMONIN-2** | PM | M | 13 | 463 | N | **MAGI3-5** | PD | H | 74 | 734 | N |
| **HARMONIN-2** | PM | M | 13 | 23 | N | **MAGI3-5** | PD | H | 74 | 812 | N |
| **HARMONIN-2** | PM | M | 13 | 73 | N | **MAGI3-5** | PD | H | 74 | 813 | N |
| **HARMONIN-2** | PM | M | 13 | 13 | N | **PSCDBP-1** | PD | H | 75 | 814 | N |
| **HARMONIN-2** | PM | M | 13 | 472 | N | **PSCDBP-1** | PD | H | 75 | 815 | N |
| **HARMONIN-2** | PM | M | 13 | 467 | N | **PSCDBP-1** | PD | H | 75 | 371 | N |
| **HARMONIN-2** | PM | M | 13 | 465 | N | **PSCDBP-1** | PD | H | 75 | 407 | N |
| **HARMONIN-2** | PM | M | 13 | 17 | N | **PSCDBP-1** | PD | H | 75 | 385 | N |
| **HARMONIN-2** | PM | M | 13 | 470 | N | **PSCDBP-1** | PD | H | 75 | 816 | N |
| **HARMONIN-2** | PM | M | 13 | 43 | N | **PSCDBP-1** | PD | H | 75 | 427 | N |
| **HARMONIN-2** | PM | M | 13 | 35 | N | **PSCDBP-1** | PD | H | 75 | 817 | N |
| **HARMONIN-2** | PM | M | 13 | 29 | N | **PSCDBP-1** | PD | H | 75 | 266 | N |
| **HARMONIN-2** | PM | M | 13 | 16 | N | **PSCDBP-1** | PD | H | 75 | 818 | N |
| **HARMONIN-2** | PM | M | 13 | 476 | N | **PSCDBP-1** | PD | H | 75 | 819 | N |
| **HARMONIN-2** | PM | M | 13 | 22 | N | **PSCDBP-1** | PD | H | 75 | 820 | N |
| **HARMONIN-2** | PM | M | 13 | 469 | N | **PSCDBP-1** | PD | H | 75 | 738 | N |
| **HARMONIN-2** | PM | M | 13 | 466 | N | **PSCDBP-1** | PD | H | 75 | 821 | N |
| **HARMONIN-2** | PM | M | 13 | 65 | N | **PSCDBP-1** | PD | H | 75 | 822 | N |
| **HARMONIN-2** | PM | M | 13 | 468 | N | **PSCDBP-1** | PD | H | 75 | 390 | N |
| **HARMONIN-2** | PM | M | 13 | 63 | N | **DVL2-1** | PD | H | 76 | 823 | N |
| **HARMONIN-2** | PM | M | 13 | 454 | N | **DVL2-1** | PD | H | 76 | 190 | N |
| **HARMONIN-2** | PM | M | 13 | 30 | N | **DVL2-1** | PD | H | 76 | 824 | N |
| **LARG-1** | PM | M | 14 | 33 | N | **DVL2-1** | PD | H | 76 | 825 | N |
| **LARG-1** | PM | M | 14 | 12 | N | **DVL2-1** | PD | H | 76 | 826 | N |
| **LIN-7C-1** | PM | M | 15 | 468 | N | **DVL2-1** | PD | H | 76 | 827 | N |

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| **LIN-7C-1** | PM | M | 15 | 29 | N | **DVL2-1** | PD | H | 76 | 389 | N |
| **LIN-7C-1** | PM | M | 15 | 470 | N | **DVL2-1** | PD | H | 76 | 828 | N |
| **LIN-7C-1** | PM | M | 15 | 16 | N | **DVL2-1** | PD | H | 76 | 430 | N |
| **LIN-7C-1** | PM | M | 15 | 62 | N | **DVL2-1** | PD | H | 76 | 829 | N |
| **LIN-7C-1** | PM | M | 15 | 17 | N | **DVL2-1** | PD | H | 76 | 371 | N |
| **LIN-7C-1** | PM | M | 15 | 466 | N | **DVL2-1** | PD | H | 76 | 830 | N |
| **LIN-7C-1** | PM | M | 15 | 475 | N | **DVL2-1** | PD | H | 76 | 831 | N |
| **LIN-7C-1** | PM | M | 15 | 69 | N | **DVL2-1** | PD | H | 76 | 832 | N |
| **LIN-7C-1** | PM | M | 15 | 463 | N | **DLG2-3** | PD | H | 77 | 170 | N |
| **LIN-7C-1** | PM | M | 15 | 60 | N | **DLG2-3** | PD | H | 77 | 368 | N |
| **LIN-7C-1** | PM | M | 15 | 467 | N | **DLG2-3** | PD | H | 77 | 174 | N |
| **LIN-7C-1** | PM | M | 15 | 68 | N | **DLG2-3** | PD | H | 77 | 402 | N |
| **LIN-7C-1** | PM | M | 15 | 26 | N | **DLG2-3** | PD | H | 77 | 735 | N |
| **LIN-7C-1** | PM | M | 15 | 64 | N | **DLG2-3** | PD | H | 77 | 814 | N |
| **LIN-7C-1** | PM | M | 15 | 66 | N | **DLG2-3** | PD | H | 77 | 378 | N |
| **LIN-7C-1** | PM | M | 15 | 63 | N | **DLG2-3** | PD | H | 77 | 396 | N |
| **LIN-7C-1** | PM | M | 15 | 11 | N | **DLG2-3** | PD | H | 77 | 833 | N |
| **LIN-7C-1** | PM | M | 15 | 45 | N | **DLG2-3** | PD | H | 77 | 404 | N |
| **LIN-7C-1** | PM | M | 15 | 473 | N | **DLG2-3** | PD | H | 77 | 415 | N |
| **LIN-7C-1** | PM | M | 15 | 3 | N | **DLG2-3** | PD | H | 77 | 834 | N |
| **LIN-7C-1** | PM | M | 15 | 469 | N | **DLG2-3** | PD | H | 77 | 371 | N |
| **LIN-7C-1** | PM | M | 15 | 476 | N | **DLG2-3** | PD | H | 77 | 835 | N |
| **LIN-7C-1** | PM | M | 15 | 22 | N | **DLG2-3** | PD | H | 77 | 836 | N |
| **LIN-7C-1** | PM | M | 15 | 53 | N | **DLG2-3** | PD | H | 77 | 401 | N |
| **LIN-7C-1** | PM | M | 15 | 41 | N | **DLG2-3** | PD | H | 77 | 837 | N |
| **LIN-7C-1** | PM | M | 15 | 474 | N | **DLG2-3** | PD | H | 77 | 838 | N |
| **LIN-7C-1** | PM | M | 15 | 57 | N | **DLG2-3** | PD | H | 77 | 382 | N |
| **LIN-7C-1** | PM | M | 15 | 472 | N | **DLG2-3** | PD | H | 77 | 839 | N |
| **LIN-7C-1** | PM | M | 15 | 465 | N | **DLG2-3** | PD | H | 77 | 384 | N |
| **LIN-7C-1** | PM | M | 15 | 544 | N | **DLG2-3** | PD | H | 77 | 369 | N |
| **LIN-7C-1** | PM | M | 15 | 73 | N | **DLG2-3** | PD | H | 77 | 377 | N |
| **LIN-7C-1** | PM | M | 15 | 17 | N | **DLG2-3** | PD | H | 77 | 713 | N |
| **LIN-7C-1** | PM | M | 15 | 30 | N | **MPDZ-3** | PD | H | 78 | 430 | N |
| **LIN-7C-1** | PM | M | 15 | 65 | N | **MPDZ-3** | PD | H | 78 | 840 | N |
| **LIN-7C-1** | PM | M | 15 | 52 | N | **MPDZ-3** | PD | H | 78 | 835 | N |
| **LIN-7C-1** | PM | M | 15 | 454 | N | **MPDZ-3** | PD | H | 78 | 841 | N |
| **LIN-7C-1** | PM | M | 15 | 35 | N | **MPDZ-3** | PD | H | 78 | 248 | N |
| **LIN-7C-1** | PM | M | 15 | 43 | N | **MPDZ-3** | PD | H | 78 | 388 | N |
| **LIN-7C-1** | PM | M | 15 | 23 | N | **MPDZ-3** | PD | H | 78 | 207 | N |
| **LIN-7C-1** | PM | M | 15 | 70 | N | **MPDZ-3** | PD | H | 78 | 842 | N |
| **LRRC7-1** | PM | M | 16 | 473 | N | **MPDZ-3** | PD | H | 78 | 294 | N |
| **LRRC7-1** | PM | M | 16 | 545 | N | **MPDZ-3** | PD | H | 78 | 268 | N |
| **LRRC7-1** | PM | M | 16 | 59 | N | **MPDZ-3** | PD | H | 78 | 843 | N |
| **LRRC7-1** | PM | M | 16 | 471 | N | **MPDZ-3** | PD | H | 78 | 786 | N |
| **LRRC7-1** | PM | M | 16 | 488 | N | **MPDZ-3** | PD | H | 78 | 193 | N |
| **LRRC7-1** | PM | M | 16 | 546 | N | **MPDZ-3** | PD | H | 78 | 390 | N |

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| **LRRC7-1** | PM | M | 16 | 4 | N | **MPDZ-3** | PD | H | 78 | 844 | N |
| **LRRC7-1** | PM | M | 16 | 533 | N | **MPDZ-3** | PD | H | 78 | 845 | N |
| **LRRC7-1** | PM | M | 16 | 466 | N | **MPDZ-3** | PD | H | 78 | 846 | N |
| **LRRC7-1** | PM | M | 16 | 72 | N | **MPDZ-3** | PD | H | 78 | 231 | N |
| **LRRC7-1** | PM | M | 16 | 464 | N | **MPDZ-3** | PD | H | 78 | 371 | N |
| **LRRC7-1** | PM | M | 16 | 547 | N | **MPDZ-3** | PD | H | 78 | 234 | N |
| **LRRC7-1** | PM | M | 16 | 548 | N | **MPDZ-3** | PD | H | 78 | 847 | N |
| **LRRC7-1** | PM | M | 16 | 436 | N | **MPDZ-3** | PD | H | 78 | 200 | N |
| **LRRC7-1** | PM | M | 16 | 508 | N | **PDLIM4-1** | PD | H | 79 | 848 | N |
| **LRRC7-1** | PM | M | 16 | 549 | N | **PDLIM4-1** | PD | H | 79 | 773 | N |
| **LRRC7-1** | PM | M | 16 | 550 | N | **PDLIM4-1** | PD | H | 79 | 144 | N |
| **LRRC7-1** | PM | M | 16 | 551 | N | **PDLIM4-1** | PD | H | 79 | 701 | N |
| **LRRC7-1** | PM | M | 16 | 552 | N | **PDLIM4-1** | PD | H | 79 | 849 | N |
| **LRRC7-1** | PM | M | 16 | 534 | N | **PDLIM4-1** | PD | H | 79 | 369 | N |
| **LRRC7-1** | PM | M | 16 | 462 | N | **PDLIM4-1** | PD | H | 79 | 850 | N |
| **LRRC7-1** | PM | M | 16 | 452 | N | **PDLIM4-1** | PD | H | 79 | 229 | N |
| **LRRC7-1** | PM | M | 16 | 553 | N | **PDLIM4-1** | PD | H | 79 | 176 | N |
| **LRRC7-1** | PM | M | 16 | 465 | N | **PDLIM4-1** | PD | H | 79 | 398 | N |
| **LRRC7-1** | PM | M | 16 | 63 | N | **PDLIM4-1** | PD | H | 79 | 851 | N |
| **MAGI-1-6** | PM | M | 17 | 554 | N | **PDLIM4-1** | PD | H | 79 | 852 | N |
| **MAGI-1-6** | PM | M | 17 | 555 | N | **PDLIM4-1** | PD | H | 79 | 430 | N |
| **MAGI-1-6** | PM | M | 17 | 51 | N | **PDLIM4-1** | PD | H | 79 | 853 | N |
| **MAGI-1-6** | PM | M | 17 | 556 | N | **PDLIM4-1** | PD | H | 79 | 232 | N |
| **MAGI-1-6** | PM | M | 17 | 534 | N | **PDLIM4-1** | PD | H | 79 | 817 | N |
| **MAGI-1-6** | PM | M | 17 | 557 | N | **PDLIM4-1** | PD | H | 79 | 388 | N |
| **MAGI-1-6** | PM | M | 17 | 54 | N | **PDLIM4-1** | PD | H | 79 | 778 | N |
| **MAGI-2-2** | PM | M | 18 | 63 | N | **PDLIM4-1** | PD | H | 79 | 112 | N |
| **MAGI-2-2** | PM | M | 18 | 446 | N | **PDLIM4-1** | PD | H | 79 | 184 | N |
| **MAGI-2-2** | PM | M | 18 | 68 | N | **SLC9A3R2-2** | PD | H | 80 | 854 | N |
| **MAGI-2-2** | PM | M | 18 | 502 | N | **SLC9A3R2-2** | PD | H | 80 | 91 | N |
| **MAGI-2-2** | PM | M | 18 | 67 | N | **SLC9A3R2-2** | PD | H | 80 | 407 | N |
| **MAGI-2-2** | PM | M | 18 | 26 | N | **SLC9A3R2-2** | PD | H | 80 | 855 | N |
| **MAGI-2-2** | PM | M | 18 | 448 | N | **SLC9A3R2-2** | PD | H | 80 | 856 | N |
| **MAGI-2-2** | PM | M | 18 | 27 | N | **SLC9A3R2-2** | PD | H | 80 | 371 | N |
| **MAGI-2-2** | PM | M | 18 | 23 | N | **SLC9A3R2-2** | PD | H | 80 | 294 | N |
| **MAGI-2-2** | PM | M | 18 | 19 | N | **SLC9A3R2-2** | PD | H | 80 | 389 | N |
| **MAGI-2-2** | PM | M | 18 | 508 | N | **SLC9A3R2-2** | PD | H | 80 | 369 | N |
| **MAGI-2-2** | PM | M | 18 | 454 | N | **SLC9A3R2-2** | PD | H | 80 | 97 | N |
| **MAGI-2-5** | PM | M | 19 | 447 | N | **SLC9A3R2-2** | PD | H | 80 | 857 | N |
| **MAGI-2-5** | PM | M | 19 | 558 | N | **SLC9A3R2-2** | PD | H | 80 | 858 | N |
| **MAGI-2-5** | PM | M | 19 | 448 | N | **SLC9A3R2-2** | PD | H | 80 | 177 | N |
| **MAGI-2-5** | PM | M | 19 | 436 | N | **SLC9A3R2-2** | PD | H | 80 | 114 | N |
| **MAGI-2-6** | PM | M | 20 | 39 | N | **SLC9A3R2-2** | PD | H | 80 | 748 | N |
| **MAGI-2-6** | PM | M | 20 | 50 | N | **SLC9A3R2-2** | PD | H | 80 | 300 | N |
| **MAGI-2-6** | PM | M | 20 | 21 | N | **SLC9A3R2-2** | PD | H | 80 | 859 | N |
| **MAGI-2-6** | PM | M | 20 | 23 | N | **SLC9A3R2-2** | PD | H | 80 | 860 | N |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **MAGI-2-6** | PM | M | 20 | 8 | N | **SLC9A3R2-2** | PD | H | 80 | 368 | N |
| **MAGI-2-6** | PM | M | 20 | 559 | N | **SLC9A3R2-2** | PD | H | 80 | 193 | N |
| **MAGI-2-6** | PM | M | 20 | 555 | N | **SLC9A3R2-2** | PD | H | 80 | 861 | N |
| **MAGI-2-6** | PM | M | 20 | 2 | N | **SLC9A3R2-2** | PD | H | 80 | 862 | N |
| **MAGI-2-6** | PM | M | 20 | 67 | N | **SNTA1-1** | PD | H | 81 | 863 | N |
| **MAGI-2-6** | PM | M | 20 | 68 | N | **SNTA1-1** | PD | H | 81 | 294 | N |
| **MAGI-2-6** | PM | M | 20 | 34 | N | **SNTA1-1** | PD | H | 81 | 864 | N |
| **MAGI-2-6** | PM | M | 20 | 554 | N | **SNTA1-1** | PD | H | 81 | 865 | N |
| **MAGI-2-6** | PM | M | 20 | 6 | N | **SNTA1-1** | PD | H | 81 | 866 | N |
| **MAGI-2-6** | PM | M | 20 | 514 | N | **SNTA1-1** | PD | H | 81 | 867 | N |
| **MAGI-2-6** | PM | M | 20 | 445 | N | **SNTA1-1** | PD | H | 81 | 398 | N |
| **MAGI-2-6** | PM | M | 20 | 54 | N | **SNTA1-1** | PD | H | 81 | 415 | N |
| **MAGI-2-6** | PM | M | 20 | 560 | N | **SNTA1-1** | PD | H | 81 | 868 | N |
| **MAGI-2-6** | PM | M | 20 | 561 | N | **SNTA1-1** | PD | H | 81 | 869 | N |
| **MAGI-2-6** | PM | M | 20 | 65 | N | **SNTA1-1** | PD | H | 81 | 369 | N |
| **MAGI-2-6** | PM | M | 20 | 7 | N | **SNTA1-1** | PD | H | 81 | 378 | N |
| **MAGI-2-6** | PM | M | 20 | 446 | N | **SNTA1-1** | PD | H | 81 | 247 | N |
| **MAGI-2-6** | PM | M | 20 | 449 | N | **SNTA1-1** | PD | H | 81 | 374 | N |
| **MAGI-2-6** | PM | M | 20 | 25 | N | **SNTA1-1** | PD | H | 81 | 870 | N |
| **MAGI-2-6** | PM | M | 20 | 19 | N | **SNTA1-1** | PD | H | 81 | 835 | N |
| **MAGI-2-6** | PM | M | 20 | 13 | N | **SNTA1-1** | PD | H | 81 | 380 | N |
| **MAGI-2-6** | PM | M | 20 | 22 | N | **SNTA1-1** | PD | H | 81 | 99 | N |
| **MAGI-2-6** | PM | M | 20 | 562 | N | **SNTA1-1** | PD | H | 81 | 871 | N |
| **MAGI-3-1** | PM | M | 21 | 563 | N | | | | | | |

**Table S1.b PDZ Domain sequences** (Domain ID, Sequence in FASTA format)

| Domain ID | PDZ Domain Sequence |
|---|---|
| **0** | GGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSSATHDEAVQALKKT GKEVVLEVKYMK |
| **1** | GGLGISIKGGKENKMPILISKIFKGLAADQTQALYVGDAILSVNGADLRDATHDEAVQALKR AGKEVLLEVKYMR |
| **2** | KGLGFSIAGGVGDQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSLEEVTHEEA VAILKNTSDVVYLKVGKPT |
| **3** | TGLGFNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGA GQTVTIIAQYQP |
| **4** | DALGISIAGGKGSPLGDIPIFIAMIQANGVAARTQKLKVGDRIVSINGQPLDGLSHTDAVNLL KNAFGRIILQVVADT |
| **5** | QSLGIRIVGYVGTAHPGEASGIYVKSIIPGSAAYHNGQIQVNDKIVAVDGVNIQGFANQDVV EVLRNAGQVVHLTLVRRK |
| **6** | KGLGFSILDYQDPLDPTRSVIVIRSLVADGVAERSGELLPGDRLVSVNEFSLDNATLAEAVEV LKAVPPGVVHLGICKPL |
| **7** | SGLGLSIVGGKDTPLDAIVIHEVYEEGAAARDGRLWAGDQILEVNGVDLRSSSHEEAITALR QTPQKVRLVVYRDE |
| **8** | RGLGLSIVGKRSGSGVFISDIVKGGAADLDGRLIRGDQILSVNGEDMRHASQETVATILKCV QGLVQLEIGRLR |
| **9** | HFLGISIVGQSNDRGDGGIYIGSIMKGGAVAADGRIEPGDMLLQVNDVNFENMSNDDAVRV |

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|---|---|
| | LREIVSQTGPISLTVAK |
| **10** | NFLGISIVGQSNERGDGGIYIGSIMKGGAVAADGRIEPGDMLLQVNEINFENMSNDDAVRVL REIVHKPGPITLTVAKCW |
| **11** | PELGFSISGGVGGRGNPFRPDDDGIFVTRVQPEGPASKLLQPGDKIIQANGYSFINIEHGQAVS LLKTFHNAVDLIIVREV |
| **12** | GPLGITISGTEEPFDPIIISSLTKGGLAERTGAIHIGDRILAINSSSLKGKPLSEAIHLLQMAGETV TLKIKKQT |
| **13** | RGLGCSISSGPIQKPGIFVSHVKPGSLSAEVGLETGDQIVEVNGIDFTNLDHKEAVNVLKSSRS LTISIVAGA |
| **14** | NGFGLTVSGDNPVFVQSVKEDGAAMRAGVQTGDRIIKVNGTLVTHSNHLEVVKLIRSGSYV ALTVQGRP |
| **15** | EGLGFNIMGGKEQNSPIYISRIIPGGIADRHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKA AQGKVKLVVRYTP |
| **16** | PGLGFSISGGISGQGNPFKPSDKGIFVTRVQPDGPASNLLQPGDKILQANGHSFVHMEHEKA VLLLKSFQNTVDLVIQREL |
| **17** | KGFGFSLRGGREYNMDLYVLRLAEDGPAERCGKMRIGDEILEINGETTKNMKHSRAIELIKN GGRRVRLFLRRGD |
| **18** | MGFGFTIIGGDEPDEFLQVKSVIPDGPAAQDGKMETGDVIVYINEVCVLGHTHADVVKLFQS VPIGQSVNLVLCRGY |
| **19** | EGFGFVIISSLNRPESGATITVPHKIGRIIDGSPADRCAKLKVGDRILAVNGQSIINMPHADIVK LIKDAGLSVTLRIIPQE |
| **20** | KGFGFSIRGGREYKMDLYVLRLAEDGPAIRNGRMRVGDQIIEINGESTRDMTHARAIELIKS GGRRVRLLLKRGT |
| **21** | MGFGFTIIGGDRPDEFLQVKNVLKDGPAAQDGKIAPGDVIVDINGNCVLGHTHADVVQMFQ LVPVNQYVNLTLCRGY |
| **22** | KGFGFAIADSPTGQKVKMILDSQWCQGLQKGDIIKEIYHQNVQNLTHLQVVEVLKQFPVGA DVPLLILRGG |
| **23** | RGFGFSLRGGKEYNMGLFILRLAEDGPAIKDGRIHVGDQIVEINGEPTQGITHTRAIELIQAGG NKVLLLLRPGT |
| **24** | EGLGFNIMGGKEQNSPIYISRVIPGGVADRHGGLKRGDQLLSVNGVSVEGEHHEKAVELLK AAQGSVKLVVRYTP |
| **25** | EPLGATIKKDEQTGAITVARIMRGGAADRSGLIHVGDELREVNGIPVEDKRPEEIIKILSQSKG AITFKIIPST |
| **26** | GGLGFSVVGLRSENRGELGIFVQEIQEGSVAHRDGRLKETDQILAINGQVLDQTITHQQAISI LQKAKDTVQLVIARGS |
| **27** | TGLGLSIVGGSDTLLGAIIIHEVYEEGAACKDGRLWAGDQILEVNGIDLRKATHDEAINVLR QTPQRVRLTLYRDE |
| **28** | KGLGLSIVGKRNDTGVFVSDIVKGGIADADGRLMQGDQILMVNGEDVRHATQEAVAALLK CSLGAVTLEVGRVK |
| **29** | DSLGLSIAGGVGSPLGDVPIFIAMMHPNGVAAQTQKLRVGDRIVTICGTSTDGMTHTQAVN LMKNASGSIEVQVVAGG |
| **30** | DGLGFSIVGGYGSPHGDLPIYVKTVFAKGAAAEDGRLKRGDQIIAVNGQSLEGVTHEEAVAI LKRTKGTVTLMVLS |
| **31** | RGLGFSILDYQDPIDPANTVIVIRSLVPGGIAEKDGRLFPGDRLMFVNDINLENSTLEEAVEAL KGAPSGMVRIGVAKPL |
| **32** | QGYGFNLHSDKSRPGQYIRSVDPGSPASHSGLRAQDRLIEVNGQNVEGLRHAEVVARIKAQ EDEARLLVVDPE |
| **33** | GGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYDSALEVLRGIAS ETHVVLILRGP |
| **34** | SGLGFNIVGGTDQQYVSNDSGIYVSRIKEDGAAAQDGRLQEGDKILSVNGQDLKNLLHQDA VDLFRNAGCAVSLRVQHRL |
| **35** | KPLGFYIRDGSSVRVTPHGLEKVPGIFISRLVPGGLAQSTGLLAVNDEVLEVNGIEVSGKSLD QVTDMMIANSRNLIITVRPAN |
| **36** | QNYGFFLRIEKDTDGHLIRVIEEGSPAEKAGLLDGDRVLRINGVFVDKEEHAQVVELVRKSG NSVTLLVLDGD |
| **37** | NGYGFYLRAGPEQKGQIIKDIEPGSPAEAAGLKNNDLVVAVNGKSVEALDHDGVVEMIRKG GDQTTLLVLDKE |
| **38** | AQLGFNIRGGKASQLGIFISKVIPDSDAHRAGLQEGDQVLAVNDVDFQDIEHSKAVEILKTA REISMRVRFFP |
| **39** | KGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKILAVNSVGLEDVMHEDAV |

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|---|---|
| | AALKNTYDVVYLKVAKPS |
| **40** | TGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAG QTVTIIAQYKP |
| **41** | GSLGISVTGGVNTSVRHGGIYVKAIIPKGAAESDGRIHKGDRVLAVNGVSLEGATHKQAVET LRNTGQVVHLLLEKGQ |
| **42** | KGLGFSIAGGIGNQHIPGDNSIYITKIIEGGAAQKDGRLQIGDRLLAVNNTNLQDVRHEEAVA SLKNTSDMVYLKVAKPG |
| **43** | TGLGFNIVGGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRNATHEQAAAALKRA GQSVTIVAQYRP |
| **44** | SGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILRVNEADVRDVTHSKAVE ALKEAGSIVRLYVKRRK |
| **45** | KGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNSVCLEEVTHEEAV TALKNTSDFVYLKVAKPT |
| **46** | GGLGISIAGGKGSTPYKGDDEGIFISRVSEEGPAARAGVRVGDKLLEVNGVALQDAEHHEA VEALRGAGAAVQMRVWRER |
| **47** | KGLGFSIAGGKGSTPYRAGDGGIFISRIAEGGAAHRAGTLQVGDRVLSINGVDMTEARHDH AVSLLTAASPTISLLLERET |
| **48** | GPLGLSIVGGSDHSSHPFGVQDPGVFISKVLPRGLAARCGLRVGDRILAVNGQDVREATHQE AVSALLRPCLELCLLVRRDP |
| **49** | GSLGFNIIGGRPCVDNQDGSSSEGIFVSKIVDSGPAAKEGGLQIHDRIIEVNGKDLSRATHDQ AVEAFKTAKEPIVVQVLRRT |
| **50** | EGFGFVLRGAKAQTPIEEFTPTPAFPALQYLESVDEGGVAWRAGLRMGDFLIEVNGQNVVK VGHRQVVNMIRQGGNTLMVKVVMVTRHPD |
| **51** | EGFGFVLRGAKAETPIEEFTPTPAFPALQYLESVDVEGVAWRAGLRTGDFLIEVNGVNVVK VGHKQVVGLIRQGGNRLVMKVVSVT |
| **52** | APWGFTLKGGLERGEPLIISKIEEGGKADSVSSGLQAGDEVIHINEVALSSPRREAVSLVKGS YKTLRLVVRRDV |
| **53** | APWGFRISGGRDFHTPIIVTKVTERGKAEAADLRPGDIIVAINGQSAENMLHAEAQSKIRQSA SPLRLQLDRSQ |
| **54** | FGFGIAISGGRDNPHFQSGETSIVISDVLKGGPAEGQLQENDRVAMVNGVSMDNVEHAFAV QQLRKSGKNAKITIRRKK |
| **55** | RGFGIAVSGGRDNPHFENGETSIVISDVLPGGPADGLLQENDRVVMVNGTPMEDVLHSFAV QQLRKSGKIAAIVVKRPR |
| **56** | RGFGIAVSGGHDRASGSVVVSDVVPGGPAEGRLRTGDHIVMVNGVSVENVTSAFAIQILKT CTKTANVTVKRPR |
| **57** | LVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGDEIREINGISVANQTVEQ LQKMLREMRGSITFKI |
| **58** | EVNLLKGPKGLGFSIAGGIGNQHIPGDNSIYITKIIEGGAAQKDGRLQIGDRLLAVNNTNLQD VRHEEAVASLKNTSDMVYLKV |
| **59** | RVRVEKDPELGFSISGGVGGRGNPFRPDDDGIFVTRVQPEGPASKLLQPGDKIIQANGYSFINI EHGQAVSLLKTFQNTVELII |
| **60** | VFELLKPPSGGLGFSVVGLRSENRGELGIFVQEIQEGSVAHRDGRLKETDQILAINGQALDQT ITHQQAISILQKAKDTVQLVI |
| **61** | TIEISKGRTGLGLSIVGGSDTLLGAIIIHEVYEEGAACKDGRLWAGDQILEVNGIDLRKATHD EAINVLRQTPQRVRLTL |
| **62** | TVEMKKGPTDSLGISIAGGVGSPLGDVPIFIAMMHPTGVAAQTQKLRVGDRIVTICGTSTEG MTHTQAVNLLKNASGSIEMQV |
| **63** | TLTILRQTGGLGISIAGGKGSTPYKGDDEGIFISRVSEEGPAARAGVRVGDKLLEVNGVALQ GAEHHEAVEALRGAGTAVQMRV |
| **64** | EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEE VTHEEAVTALKNTSDFVYLKV |
| **65** | RIVIHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAA IALKNAGQTVTIIA |
| **66** | VACLARSERGLGFSIAGGKGSTPYRAGDAGIFVSRIAEGGAAHRAGTLQVGDRVLSINGVD VTEARHDHAVSLLTAASPTIALLL |
| **67** | EVELINDGSGLGFGIVGGKTSGVVVRTIVPGGLADRDGRLQTGDHILKIGGTNVQGMTSEQV AQVLRNCGNSVRMLV |
| **68** | KVVLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQA AAALKNAGQAVTIVA |
| **69** | EITLERGNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILRVNEVDVRDV |

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|---|---|
| | THSKAVEALKEAGSIVRLYV |
| **70** | CVRIEKNPGLGFSISGGISGQGNPFKPSDKGIFVTRVQPDGPASNLLQPGDKILQANGHSFVH MEHEKAVLLLKSFQNTVDLVI |
| **71** | ILGIHKRAGEPLGVTFRVENNDLVIARILHGGMIDRQGLLHVGDIIKEVNGHEVGNNPKELQ ELLKNISGSVTLKI |
| **72** | ECKLSKQEGQNYGFFLRIEKDTEGHLVRVVEKCSPAEKAGLQDGDRVLRINGVFVDKEEHM QVVDLVRKSGNSVTLLV |
| **73** | DVEIRRGENEGFGFVIVSSVSRPEAGTTFAGNACVAMPHKIGRIIEGSPADRCGKLKVGDRIL AVNGCSITNKSHSDIVNLIKEAGNTVTLRI |
| **74** | DVFLRKQESGFGFRVLGGDGPDQSIYIGAIIPLGAAEKDGRLRAADELMCIDGIPVKGKSHK QVLDLMTTAARNGHVLLTV |
| **75** | LVTVEKQDNETFGFEIQSYRPQNQNACSSEMFTLICKIQEDSPAHCAGLQAGDVLANINGVS TEGFTYKQVVDLIRSSGNLLTIET |
| **76** | TVTLNMEKYNFLGISIVGQSNERGDGGIYIGSIMKGGAVAADGRIEPGDMLLQVNDMNFEN MSNDDAVRVLRDIVHKPGPIVLTV |
| **77** | KVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQ AAAALKGAGQTVTIIA |
| **78** | DVELTKNVQGLGITIAGYIGDKKLEPSGIFVKSITKSSAVEHDGRIQIGDQIIAVDGTNLQGFT NQQAVEVLRHTGQTVLLTL |
| **79** | SVTLRGPSPWGFRLVGGRDFSAPLTISRVHAGSKAALAALCPGDLIQAINGESTELMTHLEA QNRIKGCHDHLTLSV |
| **80** | LCHLRKGPQGYGFNLHSDKSRPGQYIRSVDPGSPAARSGLRAQDRLIEVNGQNVEGLRHAE VVASIKAREDEARLLV |
| **81** | RVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSSATHD EAVQVLKKTGKEVVLEV |

**Table S1.c Peptide sequences** (Peptide ID, Peptide sequence in FASTA format)

| Peptide ID | Peptide Sequence | Peptide ID | Peptide Sequence | Peptide ID | Peptide Sequence |
|---|---|---|---|---|---|
| **0** | KETAL | **301** | KNTSV | **602** | CTSLM |
| **1** | KQTSV | **302** | RQTSL | **603** | YCQFF |
| **2** | RETTV | **303** | RTTRV | **604** | NVVFT |
| **3** | RETDL | **304** | WETDV | **605** | YDILR |
| **4** | RESIV | **305** | WETMV | **606** | IKGLF |
| **5** | LESEV | **306** | FETLV | **607** | YEAVL |
| **6** | GETTV | **307** | YETLV | **608** | YVGDL |
| **7** | DETSI | **308** | RETWV | **609** | CCTCV |
| **8** | LETSL | **309** | WSTDV | **610** | YYMYF |
| **9** | IETHV | **310** | GDTWV | **611** | SWTTC |
| **10** | DETNL | **311** | FETWI | **612** | FIHYM |
| **11** | VETDV | **312** | VETWV | **613** | CTTPA |
| **12** | SETQV | **313** | LESWL | **614** | DHSVV |
| **13** | QETRL | **314** | RETWL | **615** | FCKYE |
| **14** | PETSV | **315** | PETWV | **616** | YFSWQ |
| **15** | KESLV | **316** | ESDWL | **617** | KFVYL |
| **16** | RESEI | **317** | LETWI | **618** | FCVEP |
| **17** | IESDV | **318** | WETWV | **619** | KDSAW |
| **18** | IFTDV | **319** | VETWL | **620** | IVVEF |
| **19** | LESMV | **320** | KEWFL | **621** | MTSHN |

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|---|---|---|---|---|---|
| **20** | MVTEV | **321** | VEYFL | **622** | LMTEC |
| **21** | RTTPV | **322** | HEWFL | **623** | NDLEL |
| **22** | MLTEV | **323** | DEYFL | **624** | IIGRC |
| **23** | LQSAV | **324** | REYYL | **625** | FSSFV |
| **24** | KESSI | **325** | REYWL | **626** | ARSSL |
| **25** | RISSV | **326** | REWFL | **627** | KIDNC |
| **26** | IIAWV | **327** | REYFL | **628** | LERLI |
| **27** | FLTWL | **328** | QEYFL | **629** | FNVML |
| **28** | KEWLI | **329** | LEYFL | **630** | RQGEL |
| **29** | TGIQV | **330** | QEWFL | **631** | CKGWK |
| **30** | KEYFF | **331** | KEWFI | **632** | WEPEP |
| **31** | KEYFI | **332** | IEYFL | **633** | ITIYS |
| **32** | KEYYV | **333** | REWFI | **634** | WWTSN |
| **33** | LVSIC | **334** | GEWFL | **635** | IIDAI |
| **34** | RISNV | **335** | WETYL | **636** | PISSW |
| **35** | KVDSV | **336** | WSTWL | **637** | YVKEI |
| **36** | KISSL | **337** | RSTLL | **638** | LPSIL |
| **37** | QSVEV | **338** | SSTYL | **639** | MESQM |
| **38** | LGAYV | **339** | YSTFL | **640** | FAIFE |
| **39** | HWFDV | **340** | YSSWL | **641** | FVIQY |
| **40** | GSVEV | **341** | FSTWL | **642** | LDVCN |
| **41** | KSQYV | **342** | YSTRM | **643** | QEGWA |
| **42** | LPVQV | **343** | FSTYL | **644** | LSTRW |
| **43** | RKDYV | **344** | WSTFL | **645** | TIWIQ |
| **44** | GHFNF | **345** | WSSRM | **646** | HENYW |
| **45** | LNDYV | **346** | KSTRL | **647** | NLTTK |
| **46** | KESSL | **347** | KQTWL | **648** | SVHTV |
| **47** | EESSV | **348** | WSTYL | **649** | EEFYA |
| **48** | EDSDV | **349** | HQTWL | **650** | RTYSC |
| **49** | CDSDL | **350** | FSSRL | **651** | NLVAD |
| **50** | VDTRV | **351** | WSTLL | **652** | HWMSP |
| **51** | STTRV | **352** | KSTFL | **653** | RIFSS |
| **52** | GDTSL | **353** | FSTWM | **654** | QVTEE |
| **53** | GEAAV | **354** | FETFL | **655** | AATTF |
| **54** | LLTDV | **355** | FETLL | **656** | NVEEG |
| **55** | YVSNL | **356** | RSTYL | **657** | WSSYP |
| **56** | RVSAL | **357** | FSTRL | **658** | RFLWE |
| **57** | RDSVV | **358** | LSTWL | **659** | HSFRH |
| **58** | VTTRL | **359** | YSSRL | **660** | SPCLL |
| **59** | EDSFL | **360** | RGTWL | **661** | MGTWG |
| **60** | NESKV | **361** | LSTYL | **662** | CAKCL |
| **61** | HGTSI | **362** | ESTWL | **663** | DADYL |
| **62** | QQSNV | **363** | HSTFL | **664** | FYPRN |
| **63** | RGTSI | **364** | KSTWL | **665** | TDIYF |
| **64** | AQTRL | **365** | WWLDV | **666** | FEGGD |
| **65** | IQTQI | **366** | WWMDV | **667** | ISVGN |

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|---|---|---|---|---|---|
| **66** | DHTRL | **367** | WFLDV | **668** | DDAPL |
| **67** | NATRL | **368** | WWYDA | **669** | EESRR |
| **68** | LPTRL | **369** | TYSDW | **670** | ESDGV |
| **69** | KETVA | **370** | WFIDV | **671** | TELRI |
| **70** | SSSTL | **371** | RVADA | **672** | SQTVT |
| **71** | GATGL | **372** | WFFDA | **673** | PAKLR |
| **72** | TTSSL | **373** | WWFDA | **674** | TCSNK |
| **73** | AREYV | **374** | WFYDA | **675** | YVWRF |
| **74** | KYDYV | **375** | WYLDV | **676** | QSSWR |
| **75** | KKNYV | **376** | WWFDV | **677** | KDYRS |
| **76** | ASNYV | **377** | WSFWI | **678** | TGSFP |
| **77** | SKEYV | **378** | TSGWF | **679** | GGPRT |
| **78** | GKDYV | **379** | HSFWV | **680** | NVSVC |
| **79** | KRDYV | **380** | LDFWF | **681** | LSGTV |
| **80** | KSAHV | **381** | SSGWF | **682** | YSEYC |
| **81** | TKNYV | **382** | FKLWF | **683** | HHKGC |
| **82** | LTGYV | **383** | LLGFF | **684** | VWPSD |
| **83** | KNAYV | **384** | LLGIF | **685** | ANNIK |
| **84** | TFFDV | **385** | YFGGL | **686** | HGPYL |
| **85** | RFFDV | **386** | FFGFF | **687** | AIVAA |
| **86** | VFFDV | **387** | LETRV | **688** | FHMHG |
| **87** | RYFDI | **388** | LCTRV | **689** | ALNTV |
| **88** | QFFDV | **389** | WTLRV | **690** | ADVIK |
| **89** | KYFDV | **390** | KVTSI | **691** | FVPWP |
| **90** | SFFDV | **391** | KCTRV | **692** | FCAIL |
| **91** | LYFDV | **392** | NETSV | **693** | PCMWL |
| **92** | RYFDV | **393** | KVTRV | **694** | TKACF |
| **93** | FYFDV | **394** | MTTRV | **695** | CIWEF |
| **94** | IFFDV | **395** | LETSV | **696** | NYDEY |
| **95** | TYFDV | **396** | WTFLL | **697** | CHTDT |
| **96** | FFFDV | **397** | FSYYL | **698** | KLNKV |
| **97** | QFFNV | **398** | ILGIF | **699** | KMRSV |
| **98** | MYFDV | **399** | LFFRL | **700** | LSHSV |
| **99** | HFFDV | **400** | FYFYL | **701** | ENTDQ |
| **100** | VYFDV | **401** | TLFHL | **702** | NYPDV |
| **101** | WFFDV | **402** | IYFYL | **703** | SDCGV |
| **102** | TWFDV | **403** | FLGLF | **704** | GEFTV |
| **103** | VYFYV | **404** | FSFFF | **705** | KERDR |
| **104** | RQTDV | **405** | WDFHL | **706** | ICLLV |
| **105** | RWTTV | **406** | TLGHF | **707** | YCCFV |
| **106** | KSTTV | **407** | NFWRI | **708** | QARRV |
| **107** | TSTDV | **408** | ESPGL | **709** | FAHDH |
| **108** | RETRV | **409** | ESAWL | **710** | FEERK |
| **109** | KWSDV | **410** | ESPWL | **711** | RTREV |
| **110** | IWTDV | **411** | ESPWM | **712** | PKTRV |
| **111** | YSTDV | **412** | ETDWL | **713** | DGAHV |

| | | | | | |
|---|---|---|---|---|---|
| **112** | IWSDV | **413** | ESEWL | **714** | GAHWG |
| **113** | RMTDV | **414** | ESGWL | **715** | FYWHL |
| **114** | FWSDV | **415** | ESDWM | **716** | CDFWI |
| **115** | KETRV | **416** | EPPWL | **717** | FRYVV |
| **116** | RETDV | **417** | CDTKF | **718** | DKRAV |
| **117** | KETLV | **418** | FDTRF | **719** | RQSML |
| **118** | KNTWV | **419** | GSSWL | **720** | KFSRS |
| **119** | VWTDV | **420** | CSTFL | **721** | SASRW |
| **120** | RWTSV | **421** | GSTYF | **722** | PVPLV |
| **121** | RSTIV | **422** | FDTRL | **723** | LKPEV |
| **122** | KWTDV | **423** | CDTYL | **724** | SETRF |
| **123** | RETVV | **424** | FTTWL | **725** | HGNIV |
| **124** | RETLV | **425** | LDTYL | **726** | YNYQV |
| **125** | KSTVV | **426** | WSSWL | **727** | CGTPE |
| **126** | TWTDV | **427** | CTTRL | **728** | TWTQD |
| **127** | RHTDV | **428** | NNTWF | **729** | SGGLV |
| **128** | RSTVV | **429** | RETIL | **730** | RSEKV |
| **129** | KSTDV | **430** | RDTRP | **731** | KGENV |
| **130** | RETQV | **431** | RETRS | **732** | RGSPW |
| **131** | THTLV | **432** | RSTRL | **733** | KVSCV |
| **132** | FDSWV | **433** | RSTSL | **734** | IWCMV |
| **133** | TDTWV | **434** | KCDEV | **735** | VRTWS |
| **134** | NDTWV | **435** | TKSEV | **736** | CFTSH |
| **135** | FETWV | **436** | GDEPV | **737** | VEKGK |
| **136** | RDTWV | **437** | AEEDF | **738** | RMIQV |
| **137** | FETWL | **438** | GGTVV | **739** | KMIPG |
| **138** | FDDWV | **439** | EEGEE | **740** | ECTPT |
| **139** | YDTWV | **440** | QRTWP | **741** | AEDCI |
| **140** | MDTWV | **441** | QEPAL | **742** | TEKRR |
| **141** | FQTWV | **442** | KEPTF | **743** | PEHLI |
| **142** | RDSWV | **443** | FWHED | **744** | GDPIV |
| **143** | IDTWV | **444** | TIIFL | **745** | QEVNA |
| **144** | WDTFV | **445** | VLSSV | **746** | RARMF |
| **145** | SDTWV | **446** | KVELV | **747** | VEMPT |
| **146** | WDSWV | **447** | GQYWV | **748** | QPIWQ |
| **147** | LATWV | **448** | KAMAI | **749** | ESVWA |
| **148** | YDDWV | **449** | TSDQL | **750** | NLEEV |
| **149** | WDTWV | **450** | LFGPQ | **751** | TNIQF |
| **150** | ADTWV | **451** | AKHYI | **752** | CFWWG |
| **151** | FDTWL | **452** | IPKGQ | **753** | QFIGV |
| **152** | LETWL | **453** | NRFWA | **754** | SCIMV |
| **153** | YDEWV | **454** | APRSV | **755** | ALTED |
| **154** | VDTWV | **455** | AGILQ | **756** | SGTFQ |
| **155** | HDSWV | **456** | RVGQF | **757** | PNISI |
| **156** | LDTWV | **457** | PERSK | **758** | ASTMH |
| **157** | FESWV | **458** | VGLWW | **759** | PATAR |

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|---|---|---|---|---|---|
| **158** | DDTWV | **459** | FCLPC | **760** | RQFSH |
| **159** | PDTWV | **460** | MPKRV | **761** | VESWQ |
| **160** | LDEWV | **461** | GIQCD | **762** | KKTCL |
| **161** | IETWL | **462** | TERNG | **763** | VWIAV |
| **162** | YDTFV | **463** | VTDLS | **764** | LPTVG |
| **163** | FDTWV | **464** | PAVAE | **765** | KMTVE |
| **164** | FHTWV | **465** | QEDGA | **766** | LATRH |
| **165** | NSFWV | **466** | APPVP | **767** | APTLP |
| **166** | FLLWL | **467** | VLRCE | **768** | WWLGV |
| **167** | FILWL | **468** | RESKC | **769** | IALWA |
| **168** | RSTWV | **469** | RGMSI | **770** | IKDWW |
| **169** | FRLWL | **470** | RDQSI | **771** | LDDHQ |
| **170** | FRLFL | **471** | PAILE | **772** | KITWW |
| **171** | FLGWV | **472** | LVTSV | **773** | FPSWG |
| **172** | FRFWV | **473** | EFIGA | **774** | MVSWK |
| **173** | RSFWV | **474** | TAEMF | **775** | MEVWT |
| **174** | FTWWL | **475** | ANVHA | **776** | TEINV |
| **175** | TSFWV | **476** | ANPEI | **777** | MANWD |
| **176** | FLGKV | **477** | QFGIP | **778** | VEDHA |
| **177** | ILGWV | **478** | KATNE | **779** | IEQHY |
| **178** | RRSRV | **479** | NNVTQ | **780** | VAIWL |
| **179** | RVSDV | **480** | KVWTC | **781** | EELAK |
| **180** | RISDV | **481** | TIAAN | **782** | FEKWW |
| **181** | RRSDV | **482** | ITDVK | **783** | LYIFL |
| **182** | RITRV | **483** | GGEPL | **784** | SEKIM |
| **183** | RKSDV | **484** | KVSQL | **785** | QEFWS |
| **184** | RISRV | **485** | DRIRV | **786** | NEAGD |
| **185** | KRSDV | **486** | SEPPV | **787** | CEQCC |
| **186** | RCSRV | **487** | AFTDG | **788** | TEVGN |
| **187** | KISDV | **488** | ESRSE | **789** | YQRRM |
| **188** | RCSDV | **489** | WWGIH | **790** | YAVEL |
| **189** | RITDV | **490** | QDHWC | **791** | TGLQL |
| **190** | RVSRV | **491** | LPSHP | **792** | EGARL |
| **191** | RQSDV | **492** | SRSFR | **793** | NSSNC |
| **192** | RHSDV | **493** | SEDLE | **794** | WMVAL |
| **193** | KISRV | **494** | KEEHQ | **795** | ISTPV |
| **194** | WWTDV | **495** | SSITI | **796** | WSRWE |
| **195** | FSTWV | **496** | FQKFS | **797** | YSQRY |
| **196** | FWTWV | **497** | HDAII | **798** | DPLDT |
| **197** | WHTWV | **498** | CAGFP | **799** | CSIEA |
| **198** | WWTWV | **499** | WEYQI | **800** | YVCDL |
| **199** | WATWV | **500** | YDDFT | **801** | GWFQA |
| **200** | MGTWV | **501** | LILIG | **802** | QHTNV |
| **201** | WFTWV | **502** | NYQFC | **803** | RRIPQ |
| **202** | WSTWV | **503** | KQTAL | **804** | ELPDE |
| **203** | FGTWV | **504** | PAIEV | **805** | WSFPL |

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|---|---|---|---|---|---|
| **204** | WYTWV | **505** | MYDHL | **806** | HYSQI |
| **205** | RETRL | **506** | RWKFC | **807** | STLPV |
| **206** | LETDL | **507** | VQLEA | **808** | GSDDH |
| **207** | RETSM | **508** | GPVPV | **809** | HSGAV |
| **208** | RETSL | **509** | LYIYC | **810** | VKPDD |
| **209** | FETDL | **510** | FTLFK | **811** | VSTQY |
| **210** | METHL | **511** | MVSRA | **812** | RSCLK |
| **211** | CETSL | **512** | VITSH | **813** | VSCKA |
| **212** | CETDL | **513** | PHSSC | **814** | IVTWR |
| **213** | YETDL | **514** | IYYKV | **815** | YHCWR |
| **214** | KETHL | **515** | DSQTT | **816** | YDRKV |
| **215** | FETRL | **516** | KAVPV | **817** | RETPD |
| **216** | RETDI | **517** | RMVPV | **818** | YMIWS |
| **217** | SETDL | **518** | RRSSV | **819** | RLNPF |
| **218** | FETHL | **519** | DLSVV | **820** | ADKSV |
| **219** | RETHL | **520** | SSFLV | **821** | RLLNV |
| **220** | HETDL | **521** | KGFHV | **822** | AESPG |
| **221** | RETSI | **522** | KEFYA | **823** | CEKDD |
| **222** | NETHL | **523** | PFYSV | **824** | MNCMF |
| **223** | FETSL | **524** | IHQNS | **825** | PEQQS |
| **224** | SETFL | **525** | PNGLQ | **826** | PPKGT |
| **225** | LETHL | **526** | MWPLM | **827** | LHGAA |
| **226** | NETDL | **527** | PFSFY | **828** | RLDFH |
| **227** | LETNL | **528** | RTISD | **829** | NEILS |
| **228** | QWTDV | **529** | ATTMH | **830** | QSQVV |
| **229** | RQTLV | **530** | FVRLL | **831** | FLRDM |
| **230** | RQTWV | **531** | LSMFR | **832** | KLRCK |
| **231** | RQSWV | **532** | AIFHD | **833** | RLSRY |
| **232** | KETAV | **533** | VTSQL | **834** | CSRTV |
| **233** | KHTEV | **534** | ESVKI | **835** | NLTNA |
| **234** | KSTIV | **535** | IDVDD | **836** | KTERY |
| **235** | KHTWV | **536** | GCTSW | **837** | LECSN |
| **236** | RETLL | **537** | FVTMQ | **838** | TDLSI |
| **237** | RQTRV | **538** | QNVFI | **839** | EYRNV |
| **238** | YETWV | **539** | EIDRT | **840** | ILSTT |
| **239** | RSTDV | **540** | FAWRL | **841** | VIFGN |
| **240** | RSTFV | **541** | LDRIV | **842** | PDRQR |
| **241** | KETSV | **542** | FDRGK | **843** | ASVLI |
| **242** | YNTWV | **543** | SVKIF | **844** | DLTGI |
| **243** | HETLV | **544** | SESKV | **845** | FQQHT |
| **244** | RSTLV | **545** | TKGES | **846** | PNYLF |
| **245** | KHTQV | **546** | TAEEA | **847** | TTIAH |
| **246** | RNTWV | **547** | GAEVA | **848** | CRTIL |
| **247** | KTSWV | **548** | VHEDA | **849** | SRHWI |
| **248** | RNTYV | **549** | ETGST | **850** | QSTGG |
| **249** | RETIV | **550** | APRSA | **851** | EFKHL |

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|---|---|---|---|---|---|
| **250** | RETLI | **551** | ADSKQ | **852** | EEGIQ |
| **251** | RWTDV | **552** | LTEHE | **853** | EHPSD |
| **252** | KTTLV | **553** | ASKTD | **854** | TSSLR |
| **253** | RTTWV | **554** | CPSES | **855** | AQHVL |
| **254** | VWSDV | **555** | MLTDV | **856** | EARTL |
| **255** | HETWV | **556** | VGIPI | **857** | PPDEL |
| **256** | RSSDV | **557** | HPPDT | **858** | GVNIL |
| **257** | RHTIV | **558** | NPRGT | **859** | LHVCL |
| **258** | FETRV | **559** | IFGAS | **860** | EKTES |
| **259** | RWTLL | **560** | VTTDC | **861** | WITRC |
| **260** | YSTWV | **561** | LKTDC | **862** | GPLGL |
| **261** | RETSV | **562** | ISAEV | **863** | MSTNM |
| **262** | RDTPV | **563** | FSPRC | **864** | RNRPY |
| **263** | IHTWV | **564** | HKQVV | **865** | VEYRY |
| **264** | RTTDV | **565** | PYFLF | **866** | RPHPV |
| **265** | RNIWV | **566** | QSTFN | **867** | RLQDQ |
| **266** | RWTTL | **567** | YGTPP | **868** | RELVT |
| **267** | RNTLV | **568** | TTLWY | **869** | GFTLE |
| **268** | IETLV | **569** | FSDVL | **870** | LSKRL |
| **269** | KQTRV | **570** | VKRYF | **871** | PEWDL |
| **270** | RETRI | **571** | IAGVV | | |
| **271** | KSTRV | **572** | EDTDT | | |
| **272** | SETRV | **573** | KGFYV | | |
| **273** | KTTRV | **574** | RTTLV | | |
| **274** | RHTSV | **575** | IEKLM | | |
| **275** | KTTRI | **576** | HLSVL | | |
| **276** | KSTSV | **577** | EIAYK | | |
| **277** | RSTRV | **578** | PIDFS | | |
| **278** | LETPL | **579** | PIPAP | | |
| **279** | SETRL | **580** | CSTYR | | |
| **280** | HDTWV | **581** | LCCIF | | |
| **281** | LETWV | **582** | REWLF | | |
| **282** | LETDV | **583** | FHIRI | | |
| **283** | KDTWV | **584** | PMTTS | | |
| **284** | IETWV | **585** | GNTIK | | |
| **285** | DETWV | **586** | SENEL | | |
| **286** | PIYWV | **587** | LMVRV | | |
| **287** | VEYFF | **588** | DSSNC | | |
| **288** | REYFF | **589** | SWIWM | | |
| **289** | TEWFV | **590** | PSWYF | | |
| **290** | REWFV | **591** | NEVPR | | |
| **291** | HEWFV | **592** | NKQHF | | |
| **292** | KIFWV | **593** | CSCFL | | |
| **293** | RIWWV | **594** | TTGAP | | |
| **294** | EIWWV | **595** | FVGNI | | |
| **295** | RIFWV | **596** | NAYYE | | |

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|---|---|---|---|
| **296** | TEWFF | **597** | DDKFF |
| **297** | RSTSV | **598** | NQGQG |
| **298** | KQTSL | **599** | NTMGC |
| **299** | YETSV | **600** | GMVPV |
| **300** | RESSV | **601** | LFCNL |

**Table S2 Class data of PDZ domains** (PDZ domain name, Organism(M = mouse, H = human), Class Label(Class I,Class II or Class I-II))

| PDZ domain name | Organism | Class Label |
|---|---|---|
| **A1-SYNTROPHIN-1** | M | Class I |
| **CHAPSYN-110-2** | M | Class I-II |
| **CHAPSYN-110-3** | M | Class I-II |
| **CIPP-10** | M | Class II |
| **CIPP-3** | M | Class II |
| **CIPP-5** | M | Class II |
| **CIPP-8** | M | Class II |
| **CIPP-9** | M | Class I-II |
| **DVL1-1** | M | Class II |
| **DVL3-1** | M | Class II |
| **ERBIN-1** | M | Class II |
| **GRIP1-6** | M | Class II |
| **HARMONIN-2** | M | Class II |
| **LARG-1** | M | Class I |
| **LIN-7C-1** | M | Class I |
| **LRRC7-1** | M | Class I |
| **MAGI-1-6** | M | Class II |
| **MAGI-2-6** | M | Class II |
| **MAGI-3-1** | M | Class II |
| **MAGI-3-2** | M | Class II |
| **MAGI-3-5** | M | Class II |
| **MALS2-1** | M | Class I |
| **MUPP1-1** | M | Class II |
| **MUPP1-10** | M | Class II |
| **MUPP1-11** | M | Class II |
| **MUPP1-12** | M | Class II |
| **MUPP1-13** | M | Class II |
| **MUPP1-5** | M | Class II |
| **NHERF-2-2** | M | Class I-II |
| **NNOS-1** | M | Class II |

| | | |
|---|---|---|
| **OMP25-1** | M | Class I-II |
| **PSD95-2** | M | Class I-II |
| **PSD95-3** | M | Class I-II |
| **PTP-BL-2** | M | Class II |
| **SAP102-2** | M | Class I |
| **SAP102-3** | M | Class I |
| **SAP97-1** | M | Class I-II |
| **SAP97-2** | M | Class I-II |
| **SAP97-3** | M | Class I-II |
| **ZO-1-1** | M | Class I |
| **ZO-2-1** | M | Class I-II |
| **ZO-3-1** | M | Class II |
| **CASK-1** | H | Class II |
| **DLG3-2** | H | Class I-II |
| **ERBB2IP-1** | H | Class I-II |
| **MPDZ-1** | H | Class I-II |
| **MPDZ-10** | H | Class I-II |
| **MPDZ-12** | H | Class I-II |
| **SCRIB-1** | H | Class I-II |
| **DLG1-2** | H | Class II |
| **DLG4-3** | H | Class I-II |
| **SCRIB-2** | H | Class I-II |
| **INADL-2** | H | Class II |
| **DLG1-3** | H | Class I-II |
| **DLG1-1** | H | Class I-II |
| **LRRC7-1** | H | Class I-II |
| **MPP6-1** | H | Class I-II |
| **PDZK1-1** | H | Class I |
| **MAGI1-5** | H | Class II |
| **MAGI3-5** | H | Class I |
| **PSCDBP-1** | H | Class I-II |
| **DVL2-1** | H | Class II |
| **DLG2-3** | H | Class I |
| **MPDZ-3** | H | Class I-II |
| **PDLIM4-1** | H | Class I |
| **SLC9A3R2-2** | H | Class I-II |
| **SNTA1-1** | H | Class I-II |

**Table S3 Data table of 218 PDZ Domains used to scan human proteome**(In total, 61 X-ray and nine NMR structures were retrieved from the PDB and 148 homology models were created by SWISS-MODEL. Model quality is estimated using template sequence ID (percentage of the identical residues between target and template sequences) and QMEAN score (a scoring function that measures multiple geometrical aspects of protein structure, ranging from 0 to 1 with higher values indicating more reliable models))

| Uniprot | Uniprot Id | Start Index | End Index | Experiment | PDB ID | Template PDB ID | Template Seq ID | QMEAN Score |
|---|---|---|---|---|---|---|---|---|
| **AHNAK2-1** | Q8IVF2 | 122 | 195 | SWISS-MODEL | | 3SHW A | 0,39 | 0,603 |
| **APBA1-1** | Q02410 | 660 | 741 | SWISS-MODEL | | 1U3B A | 1,00 | 0,810 |
| **APBA1-2** | Q02410 | 755 | 821 | SWISS-MODEL | | 1U3B A | 1,00 | 0,581 |
| **APBA2-1** | Q99767 | 571 | 653 | SWISS-MODEL | | 1U3B A | 0,85 | 0,792 |
| **APBA2-2** | Q99767 | 666 | 733 | SWISS-MODEL | | 1U3B A | 0,93 | 0,514 |
| **APBA3-1** | O96018 | 396 | 479 | SWISS-MODEL | | 2YT7 A | 1,00 | 0,806 |
| **APBA3-2** | O96018 | 491 | 559 | XRAY | 2YT8 | | | |
| **ARHGAP21-1** | Q5T5U3 | 49 | 159 | NMR | 2YUY | | | |
| **ARHGAP23-1** | Q9P227 | 52 | 156 | SWISS-MODEL | | 2YUY A | 0,81 | 0,609 |
| **ARHGEF11-1** | O15085 | 51 | 118 | SWISS-MODEL | | 2DLS A | 1,00 | 0,921 |
| **ARHGEF12-1** | Q9NZN5 | 77 | 147 | SWISS-MODEL | | 2OMJ A | 1,00 | 0,847 |
| **CAR14-1** | Q9BXL6 | 570 | 659 | SWISS-MODEL | | 1Z87 A | 0,30 | 0,442 |
| **CASK-1** | O14936 | 489 | 573 | XRAY | 1KWA | | | |
| **CNKR1-1** | Q969H4 | 198 | 286 | SWISS-MODEL | | 2DKR A | 0,22 | 0,458 |
| **CNKSR2-1** | Q8WXI2 | 225 | 293 | SWISS-MODEL | | 2E7K A | 0,29 | 0,643 |
| **CNKSR3-1** | Q6P9H4 | 219 | 288 | SWISS-MODEL | | 2E7K A | 0,29 | 0,688 |
| **CYTIP-1** | O60759 | 76 | 163 | XRAY | 2Z17 | | | |
| **DEPTOR-1** | Q8TB45 | 330 | 408 | SWISS-MODEL | | 2D90 A | 0,31 | 0,879 |
| **DLG1-1** | Q12959 | 221 | 312 | SWISS-MODEL | | 1ZOK A | 0,99 | 0,603 |
| **DLG1-2** | Q12959 | 316 | 406 | XRAY | 2G2L | | | |
| **DLG1-3** | Q12959 | 463 | 544 | SWISS-MODEL | | 1PDR A | 1,00 | 0,938 |
| **DLG2-1** | Q15700 | 100 | 183 | SWISS-MODEL | | 2WL7 A | 0,98 | 0,997 |
| **DLG2-2** | Q15700 | 196 | 278 | SWISS-MODEL | | 2BYG A | 1,00 | 0,953 |
| **DLG2-3** | Q15700 | 418 | 518 | XRAY | 2HE2 | | | |
| **DLG3-1** | Q92796 | 134 | 216 | XRAY | 2I1N | | | |
| **DLG3-2** | Q92796 | 223 | 315 | XRAY | 2FE5 | | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **DLG3-3** | Q92796 | 389 | 464 | XRAY | 1UM7 | | | |
| **DLG4-1** | P78352 | 67 | 151 | SWISS-MODEL | | 3GSL B | 1,00 | 0,966 |
| **DLG4-2** | P78352 | 163 | 245 | SWISS-MODEL | | 3GSL A | 1,00 | 0,991 |
| **DLG4-3** | P78352 | 301 | 416 | XRAY | 1TP3 | | | |
| **DLG5-3** | Q8TDM6 | 1353 | 1426 | XRAY | 1UIT | | | |
| **DLG5-4** | Q8TDM6 | 1509 | 1580 | SWISS-MODEL | | 2QG1 A | 0,32 | 0,594 |
| **DVL1-1** | O14640 | 254 | 337 | SWISS-MODEL | | 1MC7 A | 1,00 | 0,624 |
| **DVL1L1-1** | P54792 | 260 | 340 | SWISS-MODEL | | 2KAW A | 0,99 | 0,629 |
| **DVL2-1** | O14641 | 270 | 353 | XRAY | 2REY | | | |
| **DVL3-1** | Q92997 | 252 | 335 | SWISS-MODEL | | 1L6O A | 0,96 | 0,977 |
| **ERBB2IP-1** | Q96RT1 | 1321 | 1413 | XRAY | 1MFL | | | |
| **FRMPD1-1** | Q5SYB0 | 67 | 133 | SWISS-MODEL | | 2FNE C | 0,33 | 0,791 |
| **FRMPD2-2** | Q68DX3 | 950 | 1036 | SWISS-MODEL | | 1VJ6 A | 0,61 | 0,910 |
| **FRMPD2-3** | Q68DX3 | 1080 | 1168 | SWISS-MODEL | | 1B8Q A | 0,38 | 0,518 |
| **FRMPD3-1** | Q5JV73 | 62 | 132 | SWISS-MODEL | | 1WHD A | 0,34 | 0,819 |
| **FRMPD4-1** | Q14CM0 | 79 | 156 | SWISS-MODEL | | 2EDV A | 0,36 | 0,837 |
| **GIPC1-1** | O14908 | 136 | 211 | SWISS-MODEL | | 3GGE A | 0,65 | 0,852 |
| **GIPC2-1** | Q8TF65 | 125 | 200 | XRAY | 3GGE | | | |
| **GIPC3-1** | Q8TF64 | 120 | 195 | SWISS-MODEL | | 3GGE A | 0,63 | 0,698 |
| **GOPC-1** | Q9HD26 | 293 | 369 | XRAY | 2DC2 | | | |
| **GORASP2-1** | Q9H8Y8 | 5 | 76 | SWISS-MODEL | | 3RLE A | 1,00 | 0,857 |
| **GRD2I-1** | A4D2P6 | 10 | 85 | SWISS-MODEL | | 2EDV A | 0,36 | 0,509 |
| **GRD2I-2** | A4D2P6 | 279 | 357 | SWISS-MODEL | | 2KV8 A | 0,36 | 0,686 |
| **GRIP1-1** | Q9Y3R0 | 56 | 135 | SWISS-MODEL | | 2QT5 A | 1,00 | 0,866 |
| **GRIP1-2** | Q9Y3R0 | 154 | 237 | XRAY | 2JIL | | | |
| **GRIP1-3** | Q9Y3R0 | 261 | 335 | SWISS-MODEL | | 1V62 A | 0,64 | 0,804 |
| **GRIP1-4** | Q9Y3R0 | 472 | 562 | SWISS-MODEL | | 1P1D A | 0,99 | 0,624 |
| **GRIP1-5** | Q9Y3R0 | 577 | 657 | SWISS-MODEL | | 1P1D A | 0,98 | 0,804 |
| **GRIP1-6** | Q9Y3R0 | 676 | 753 | SWISS-MODEL | | 1N7E A | 1,00 | 0,953 |
| **GRIP1-7** | Q9Y3R0 | 1008 | 1084 | SWISS-MODEL | | 1M5Z A | 0,99 | 0,902 |
| **GRIP2-1** | Q9C0E4 | 52 | 130 | SWISS-MODEL | | 2QT5 A | 0,79 | 0,889 |
| **GRIP2-2** | Q9C0E4 | 151 | 227 | SWISS-MODEL | | 2QT5 A | 0,70 | 0,962 |

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|---|---|---|---|---|---|---|---|---|
| **GRIP2-3** | Q9C0E4 | 254 | 331 | XRAY | 1V62 | | | |
| **GRIP2-4** | Q9C0E4 | 466 | 543 | SWISS-MODEL | | 1X5R A | 1,00 | 0,766 |
| **GRIP2-5** | Q9C0E4 | 561 | 640 | SWISS-MODEL | | 1P1D A | 0,88 | 0,704 |
| **GRIP2-6** | Q9C0E4 | 659 | 736 | SWISS-MODEL | | 1N7E A | 0,90 | 1,000 |
| **GRIP2-7** | Q9C0E4 | 944 | 1021 | SWISS-MODEL | | 1M5Z A | 0,70 | |
| **HTRA1-1** | Q92743 | 370 | 468 | NMR | 2YTW | | | |
| **HTRA2-1** | O43464 | 359 | 442 | SWISS-MODEL | | 2PZD B | 1,00 | 0,838 |
| **HTRA3-1** | P83110 | 350 | 441 | XRAY | 2P3W | | | |
| **IL16-1** | Q14005 | 221 | 301 | SWISS-MODEL | | 2ENO A | 0,49 | 0,778 |
| **IL16-3** | Q14005 | 1117 | 1189 | SWISS-MODEL | | 1X6D A | 1,00 | 0,866 |
| **INADL-1** | Q8NI35 | 138 | 219 | SWISS-MODEL | | 2DB5 A | 1,00 | 0,792 |
| **INADL-2** | Q8NI35 | 231 | 342 | NMR | 2DLU | | | |
| **INADL-3** | Q8NI35 | 369 | 451 | SWISS-MODEL | | 2DMZ A | 0,99 | 0,845 |
| **INADL-5** | Q8NI35 | 692 | 769 | XRAY | 2D92 | | | |
| **INADL-6** | Q8NI35 | 1073 | 1155 | XRAY | 2EHR | | | |
| **INADL-7** | Q8NI35 | 1243 | 1319 | XRAY | 2DAZ | | | |
| **INADL-8** | Q8NI35 | 1441 | 1518 | XRAY | 2DM8 | | | |
| **INADL-9** | Q8NI35 | 1537 | 1613 | SWISS-MODEL | | 2QG1 A | 0,75 | 1,000 |
| **INADL-10** | Q8NI35 | 1684 | 1760 | SWISS-MODEL | | 2IWP B | 0,66 | 0,973 |
| **LDB3-1** | O75112 | 11 | 83 | XRAY | 1RGW | | | |
| **LIMK1-1** | P53667 | 168 | 256 | SWISS-MODEL | | 2YUB A | 0,40 | 0,583 |
| **LIMK2-1** | P53671 | 155 | 238 | SWISS-MODEL | | 2YUB A | 0,95 | 0,622 |
| **LIN7A-1** | O14910 | 111 | 188 | SWISS-MODEL | | 2DKR A | 0,92 | 0,793 |
| **LIN7B-1** | Q9HAP6 | 96 | 172 | XRAY | 2DKR | | | |
| **LIN7C-1** | Q9NUP9 | 96 | 173 | SWISS-MODEL | | 2DKR A | 0,94 | 0,827 |
| **LMO7-1** | Q8WWI1 | 1042 | 1129 | XRAY | 2EAQ | | | |
| **LRRC7-1** | Q96NW7 | 1454 | 1535 | SWISS-MODEL | | 2H3L B | 0,75 | 0,856 |
| **MAGI1-2** | Q96QZ7 | 478 | 544 | XRAY | 2KPK | | | |
| **MAGI1-3** | Q96QZ7 | 646 | 722 | SWISS-MODEL | | 3BPU A | 0,95 | 0,756 |
| **MAGI1-4** | Q96QZ7 | 849 | 923 | SWISS-MODEL | | 2Q9V A | 0,97 | 0,949 |
| **MAGI1-5** | Q96QZ7 | 1001 | 1092 | SWISS-MODEL | | 1UEW A | 0,67 | 0,752 |
| **MAGI1-6** | Q96QZ7 | 1155 | 1230 | SWISS-MODEL | | 2R4H A | 0,96 | 0,901 |
| **MAGI2-1** | Q86UL8 | 26 | 98 | SWISS-MODEL | | 2HE4 A | 0,35 | 0,535 |

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|---|---|---|---|---|---|---|---|---|
| **MAGI2-2** | Q86UL8 | 429 | 497 | XRAY | 1UEQ | | | |
| **MAGI2-3** | Q86UL8 | 605 | 684 | SWISS-MODEL | | 1UJV A | 1,00 | 0,824 |
| **MAGI2-4** | Q86UL8 | 783 | 860 | XRAY | 1UEW | | | |
| **MAGI2-5** | Q86UL8 | 923 | 1008 | SWISS-MODEL | | 1UEW A | 1,00 | 0,708 |
| **MAGI2-6** | Q86UL8 | 1150 | 1227 | XRAY | 1WFV | | | |
| **MAGI3-2** | Q5TCQ9 | 440 | 504 | SWISS-MODEL | | 1UEQ A | 0,74 | 0,725 |
| **MAGI3-3** | Q5TCQ9 | 603 | 680 | SWISS-MODEL | | 3SOE A | 1,00 | 0,924 |
| **MAGI3-4** | Q5TCQ9 | 757 | 833 | SWISS-MODEL | | 1UEP A | 0,63 | 0,750 |
| **MAGI3-5** | Q5TCQ9 | 879 | 961 | SWISS-MODEL | | 1UEW A | 0,63 | 0,754 |
| **MAGI3-6** | Q5TCQ9 | 1049 | 1126 | SWISS-MODEL | | 1WFV A | 0,65 | 1,000 |
| **MAST1-1** | Q9Y2H9 | 974 | 1052 | XRAY | 3PS4 | | | |
| **MAST2-1** | Q6P0Q8 | 1104 | 1193 | SWISS-MODEL | | 2KQF A | 1,00 | 0,710 |
| **MAST3-1** | O60307 | 950 | 1039 | SWISS-MODEL | | 3KHF B | 1,00 | 0,875 |
| **MLLT4-1** | P55196 | 1014 | 1091 | SWISS-MODEL | | 1XZ9 A | 1,00 | 0,530 |
| **MPDZ-1** | O75970 | 136 | 228 | SWISS-MODEL | | 2O2T A | 0,98 | 0,855 |
| **MPDZ-2** | O75970 | 258 | 334 | SWISS-MODEL | | 2DLU A | 0,68 | 0,758 |
| **MPDZ-3** | O75970 | 373 | 464 | SWISS-MODEL | | 2IWN A | 0,95 | 0,955 |
| **MPDZ-4** | O75970 | 562 | 630 | SWISS-MODEL | | 2DAZ A | 0,38 | 0,850 |
| **MPDZ-5** | O75970 | 703 | 784 | SWISS-MODEL | | 2D92 A | 0,63 | 0,836 |
| **MPDZ-6** | O75970 | 1011 | 1077 | SWISS-MODEL | | 3B76 B | 0,39 | 0,601 |
| **MPDZ-7** | O75970 | 1151 | 1240 | XRAY | 2IWQ | | | |
| **MPDZ-8** | O75970 | 1353 | 1429 | SWISS-MODEL | | 2DAZ A | 0,76 | 0,785 |
| **MPDZ-9** | O75970 | 1487 | 1562 | SWISS-MODEL | | 2DKR A | 0,39 | 0,732 |
| **MPDZ-10** | O75970 | 1623 | 1717 | XRAY | 2OPG | | | |
| **MPDZ-11** | O75970 | 1728 | 1805 | XRAY | 2QG1 | | | |
| **MPDZ-12** | O75970 | 1862 | 1945 | SWISS-MODEL | | 2IWP B | 1,00 | 0,887 |
| **MPDZ-13** | O75970 | 1990 | 2070 | XRAY | 2FNE | | | |
| **MPP1-1** | Q00013 | 74 | 150 | XRAY | 2EV8 | | | |
| **MPP3-1** | Q13368 | 141 | 216 | SWISS-MODEL | | 3O46 A | 0,80 | 0,853 |
| **MPP4-1** | Q96JB8 | 161 | 233 | SWISS-MODEL | | 3O46 A | 0,59 | 0,912 |
| **MPP5-1** | Q8N3R9 | 260 | 333 | XRAY | 1VA8 | | | |
| **MPP6-1** | Q9NZW5 | 129 | 207 | SWISS-MODEL | | 2E7K A | 0,75 | 0,771 |

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|---|---|---|---|---|---|---|---|---|
| **MYO18A-1** | Q92614 | 225 | 310 | SWISS-MODEL | | 1G9O A | 0,29 | 0,631 |
| **NOS1-1** | P29475 | 20 | 96 | XRAY | 1QAV | | | |
| **PARD3-1** | Q8TEW0 | 282 | 349 | SWISS-MODEL | | 2DB5 A | 0,29 | 0,587 |
| **PARD3-3** | Q8TEW0 | 597 | 667 | SWISS-MODEL | | 2K1Z A | 0,97 | 0,630 |
| **PARD3B-1** | Q8TEW8 | 211 | 292 | SWISS-MODEL | | 2O2T A | 0,30 | 0,716 |
| **PARD3B-2** | Q8TEW8 | 391 | 471 | SWISS-MODEL | | 2KOJ A | 0,61 | 0,842 |
| **PARD3B-3** | Q8TEW8 | 507 | 593 | SWISS-MODEL | | 1WG6 A | 0,99 | 0,533 |
| **PARD6A-1** | Q9NPB6 | 160 | 248 | SWISS-MODEL | | 1RZX A | 0,84 | 0,779 |
| **PARD6B-1** | Q9BYG5 | 162 | 240 | XRAY | 1NF3 | | | |
| **PARD6G-1** | Q9BYG4 | 163 | 241 | SWISS-MODEL | | 1NF3 D | 0,90 | 0,682 |
| **PDLIM1-1** | O00151 | 7 | 83 | XRAY | 2PKT | | | |
| **PDLIM2-1** | Q96JY6 | 1 | 85 | XRAY | 2PA1 | | | |
| **PDLIM3-1** | Q53GG5 | 11 | 85 | SWISS-MODEL | | 1V5L A | 0,96 | 0,706 |
| **PDLIM4-1** | P50479 | 1 | 90 | XRAY | 2V1W | | | |
| **PDLIM5-1** | Q96HC4 | 12 | 84 | XRAY | 2UZC | | | |
| **PDLIM7-1** | Q9NR12 | 10 | 82 | XRAY | 2Q3G | | | |
| **PDZD11-1** | Q5EBL8 | 50 | 126 | SWISS-MODEL | | 1WI2 A | 1,00 | 0,835 |
| **PDZD2-2** | O15018 | 342 | 417 | SWISS-MODEL | | 2DM8 A | 0,47 | 0,812 |
| **PDZD2-3** | O15018 | 592 | 665 | SWISS-MODEL | | 2ENO A | 0,44 | 0,968 |
| **PDZD2-4** | O15018 | 728 | 814 | SWISS-MODEL | | 2JRE A | 0,35 | 0,533 |
| **PDZD2-5** | O15018 | 2626 | 2694 | SWISS-MODEL | | 1X6D A | 0,52 | 0,846 |
| **PDZD3-1** | Q86UT5 | 121 | 194 | SWISS-MODEL | | 1G9O A | 0,41 | 0,821 |
| **PDZD3-2** | Q86UT5 | 231 | 298 | SWISS-MODEL | | 2OCS A | 0,39 | 0,866 |
| **PDZD3-3** | Q86UT5 | 333 | 410 | SWISS-MODEL | | 2V9O E | 1,00 | 1,000 |
| **PDZD4-1** | Q76G19 | 130 | 215 | SWISS-MODEL | | 1WH1 A | 0,75 | 0,710 |
| **PDZD7-1** | Q9H5P4 | 86 | 169 | NMR | 2EEH | | | |
| **PDZK1-1** | Q5T2W1 | 1 | 108 | SWISS-MODEL | | 2EDZ A | 0,89 | 0,813 |
| **PDZK1-2** | Q5T2W1 | 142 | 210 | NMR | 2EEI | | | |
| **PDZK1-3** | Q5T2W1 | 247 | 321 | SWISS-MODEL | | 2D90 A | 0,88 | 0,855 |
| **PDZK1-4** | Q5T2W1 | 384 | 456 | SWISS-MODEL | | 2VSP D | 1,00 | 0,932 |
| **PDZRN3-1** | Q9UPQ7 | 257 | 340 | NMR | 1UHP | | | |
| **PDZRN3-2** | Q9UPQ7 | 429 | 505 | SWISS-MODEL | | 1WH1 A | 1,00 | 0,730 |
| **PDZRN4-1** | Q6ZMN7 | 232 | 315 | SWISS-MODEL | | 1UHP A | 0,70 | 0,839 |
| **PDZRN4-2** | Q6ZMN | 412 | 488 | SWISS- | | 1WH1 A | 0,79 | 0,782 |

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|---|---|---|---|---|---|---|---|---|
| | 7 | | | MODEL | | | | |
| **PICK1-1** | Q9NRD5 | 25 | 101 | XRAY | 2GZV | | | |
| **PPP1R9A-1** | Q9ULJ8 | 509 | 590 | SWISS-MODEL | | 3HVQ C | 1,00 | 0,933 |
| **PPP1R9B-1** | Q96SB3 | 498 | 578 | XRAY | 3EGG | | | |
| **PTPN13-1** | Q12923 | 1096 | 1176 | SWISS-MODEL | | 2DKR A | 0,49 | 0,788 |
| **PTPN13-2** | Q12923 | 1371 | 1445 | SWISS-MODEL | | 1Q7X A | 0,99 | 0,355 |
| **PTPN13-3** | Q12923 | 1504 | 1584 | SWISS-MODEL | | 2OGP A | 0,39 | 0,688 |
| **PTPN13-4** | Q12923 | 1793 | 1866 | SWISS-MODEL | | 2DKR A | 0,35 | 0,616 |
| **PTPN13-5** | Q12923 | 1891 | 1955 | SWISS-MODEL | | 1UEZ A | 0,39 | 0,772 |
| **PTPN3-1** | P26045 | 513 | 596 | SWISS-MODEL | | 2VPH A | 0,71 | 0,830 |
| **PTPN4-1** | P29074 | 520 | 603 | XRAY | 2CS5 | | | |
| **RADIL-1** | Q96JH8 | 976 | 1062 | NMR | 1UM1 | | | |
| **RAPGEF6-1** | Q8TEU7 | 538 | 610 | SWISS-MODEL | | 1UF1 A | 0,51 | 0,821 |
| **RGS12-1** | O14924 | 26 | 97 | XRAY | 2KV8 | | | |
| **RGS3-1** | P49796 | 302 | 374 | XRAY | 2F5Y | | | |
| **RHPN1-1** | Q8TCX5 | 542 | 611 | SWISS-MODEL | | 1VAE A | 0,43 | 0,662 |
| **RHPN2-1** | Q8IUC4 | 524 | 592 | XRAY | 2VSV | | | |
| **RIMS1-1** | Q86UR5 | 608 | 689 | SWISS-MODEL | | 2CSS A | 1,00 | 0,734 |
| **SCRIB-1** | Q14160 | 725 | 816 | XRAY | 2W4F | | | |
| **SCRIB-2** | Q14160 | 853 | 958 | NMR | 1WHA | | | |
| **SCRIB-3** | Q14160 | 1007 | 1091 | SWISS-MODEL | | 3GSL A | 0,44 | 0,745 |
| **SCRIB-4** | Q14160 | 1106 | 1190 | XRAY | 1UJU | | | |
| **SDCBP-1** | O00560 | 117 | 193 | XRAY | 1YBO | | | |
| **SDCBP-2** | O00560 | 198 | 274 | SWISS-MODEL | | 1NFE A | 1,00 | 0,865 |
| **SDCBP2-1** | Q9H190 | 111 | 186 | SWISS-MODEL | | 1W9E B | 0,69 | 0,872 |
| **SDCBP2-2** | Q9H190 | 195 | 265 | SWISS-MODEL | | 1NFE A | 0,70 | 0,869 |
| **SHANK2-1** | Q9UPX8 | 250 | 339 | SWISS-MODEL | | 1Q3O A | 0,90 | 0,832 |
| **SHANK3-1** | Q9BYB0 | 565 | 668 | SWISS-MODEL | | 1Q3O A | 0,86 | 0,719 |
| **SHROOM3-1** | Q8TF72 | 36 | 111 | SWISS-MODEL | | 2EDP A | 0,63 | 0,745 |
| **SHROOM4-1** | Q9ULL8 | 19 | 93 | NMR | 2EDP | | | |
| **SIPA1-1** | Q96FS4 | 690 | 759 | SWISS-MODEL | | 2EEH A | 0,32 | 0,723 |
| **SIPA1L1-1** | O43166 | 957 | 1026 | SWISS-MODEL | | 2YT8 A | 0,31 | 0,684 |
| **SIPA1L2-1** | Q9P2F8 | 959 | 1026 | SWISS-MODEL | | 1G9O A | 0,33 | 0,804 |
| **SIPA1L3-1** | O60292 | 975 | 1042 | SWISS-MODEL | | 2YT8 A | 0,34 | 0,671 |

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|---|---|---|---|---|---|---|---|---|
| **SLC9A3R1-1** | O14745 | 20 | 92 | XRAY | 1G9O | | | |
| **SLC9A3R1-2** | O14745 | 159 | 232 | SWISS-MODEL | | 2KRG A | 1,00 | 0,824 |
| **SLC9A3R2-2** | Q15599 | 147 | 229 | XRAY | 2HE4 | | | |
| **SNTA1-1** | Q13424 | 83 | 171 | SWISS-MODEL | | 1QAV A | 0,99 | 0,804 |
| **SNTB1-1** | Q13884 | 117 | 193 | SWISS-MODEL | | 2VRF A | 0,86 | 0,993 |
| **SNTB2-1** | Q13425 | 118 | 196 | XRAY | 2VRF | | | |
| **SNTG1-1** | Q9NSN8 | 60 | 137 | SWISS-MODEL | | 1Z87 A | 0,45 | 0,769 |
| **SNTG2-1** | Q9NY99 | 76 | 155 | SWISS-MODEL | | 1Z87 A | 0,54 | 0,639 |
| **SYNJ2BP-1** | P57105 | 16 | 99 | SWISS-MODEL | | 2JIK A | 1,00 | 0,977 |
| **SYNPO2-1** | Q9UMS6 | 7 | 89 | SWISS-MODEL | | 1WF7 A | 0,38 | 0,696 |
| **SYNPO2L-1** | Q9H987 | 7 | 89 | SWISS-MODEL | | 2EDP A | 0,43 | 0,644 |
| **TIAM1-1** | Q13009 | 856 | 920 | XRAY | 2D8I | | | |
| **TIAM2-1** | Q8IVF5 | 891 | 977 | SWISS-MODEL | | 1KY9 B | 0,36 | 0,588 |
| **TJP1-1** | Q07157 | 26 | 108 | XRAY | 2H2C | | | |
| **TJP1-2** | Q07157 | 189 | 263 | XRAY | 2RCZ | | | |
| **TJP1-3** | Q07157 | 429 | 499 | SWISS-MODEL | | 1UF1 A | 0,40 | 0,783 |
| **TJP2-1** | Q9UDY2 | 35 | 118 | XRAY | 1CSJ | | | |
| **TJP2-2** | Q9UDY2 | 307 | 386 | XRAY | 3E17 | | | |
| **TJP2-3** | Q9UDY2 | 518 | 581 | SWISS-MODEL | | 1UF1 A | 0,38 | 0,783 |
| **TJP3-1** | O95049 | 16 | 90 | SWISS-MODEL | | 2H2B A | 0,56 | 0,966 |
| **TJP3-2** | O95049 | 195 | 272 | SWISS-MODEL | | 2OSG A | 0,58 | 0,594 |
| **TJP3-3** | O95049 | 394 | 461 | SWISS-MODEL | | 1UM7 A | 0,43 | 0,792 |
| **USH1C-1** | Q9Y6N9 | 91 | 166 | SWISS-MODEL | | 3K1R A | 0,99 | 1,000 |
| **USH1C-2** | Q9Y6N9 | 220 | 289 | SWISS-MODEL | | 2KBS A | 1,00 | 0,932 |
| **USH1C-3** | Q9Y6N9 | 460 | 527 | SWISS-MODEL | | 1V6B A | 0,96 | 0,837 |
| **WHRN-1** | Q9P202 | 144 | 217 | XRAY | 1UEZ | | | |
| **WHRN-2** | Q9P202 | 288 | 358 | XRAY | 1UF1 | | | |
| **WHRN-3** | Q9P202 | 820 | 888 | SWISS-MODEL | | 1UFX A | 1,00 | 1,000 |

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