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Honors Thesis

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Abstract:

ATRT (Atypical Teratoid Rhabdoid Tumor) is an aggressive pediatric brain tumor. Scientists believe that INI-1's loss from the SWI/SNF complex is what causes the ATRT tumor to develop. However, I hypothesized that rather than the loss of INI-1 from the SWI/SNF complex, it is the loss of INI-1 from some other unidentified INI-1 associated protein complex that causes the tumor to develop. To begin to answer this question, I set out to identify proteins that associated with INI-1. Multiple techniques were used over the duration of this project. Cell culture techniques were employed to grow two HeLa cell lines, one line had a FLAG tag version of INI-1 and the other HeLa cell line was used a control. These cells were grown and then lysed. Then half of the protein sample was run on a SDS-PAGE gel and the other half of the sample was sent to mass spectrum for analysis. Protein lists were then compiled and compared for different samples to determine the significance of the proteins attached to INI-1.

Project Title:

INI-1 and All of Its Friends: The Analysis of the INI-1 Protein and Associated Proteins That Contribute to Cancer Formation.

Goal:

Identify INI-1 associated proteins and determine their role in tumor formation.

Introduction:

Cancer is a devastating, progressive disease that affects millions of people each year. One type of cancer is a pediatric atypical teratoid rhabdoid tumor (ATRT). This cancer's victims are usually less than 3 years old and undergo a variety of treatments, such as chemotherapy, radiation, and surgery, to combat the very progressive malignant tumor [2]. ATRT is very aggressive, and, unfortunately, extremely difficult to diagnosis. Some of these symptoms are early morning headaches, vomiting, and lethargy [2]. Unfortunately, these symptoms can be associated with a variety of medical issues. Consequently, this increases the difficulty of diagnosis since multiple variables need to be ruled out in order to come to the conclusion of the possibility of a tumor. Not much is known about the direct cause of the ATRT tumor, but there is a known correlation between the INI-1 protein and the tumor's development. The INI-1 protein is a very elusive protein that scientists know exists, but they do not know the function of it. Consequently, they cannot determine its precise role in the development of the pediatric tumor.

Although it is known that INI-1 is part of the SWI/SNF complex, which is comprised of about ten proteins that unravel DNA, INI-1's specific role in the SWI/SNF complex has not been found to directly correlate to tumor formation. The current theory states that it is the loss of INI-1 from the SWI/SNF complex leads to the cancer development. However, what if it is not the loss

of INI-1 from the SWI/SNF complex that is causing the cancer, but rather what if the cancer is caused by the unknown proteins that INI-1 is also occasionally attached to?

Figure 1

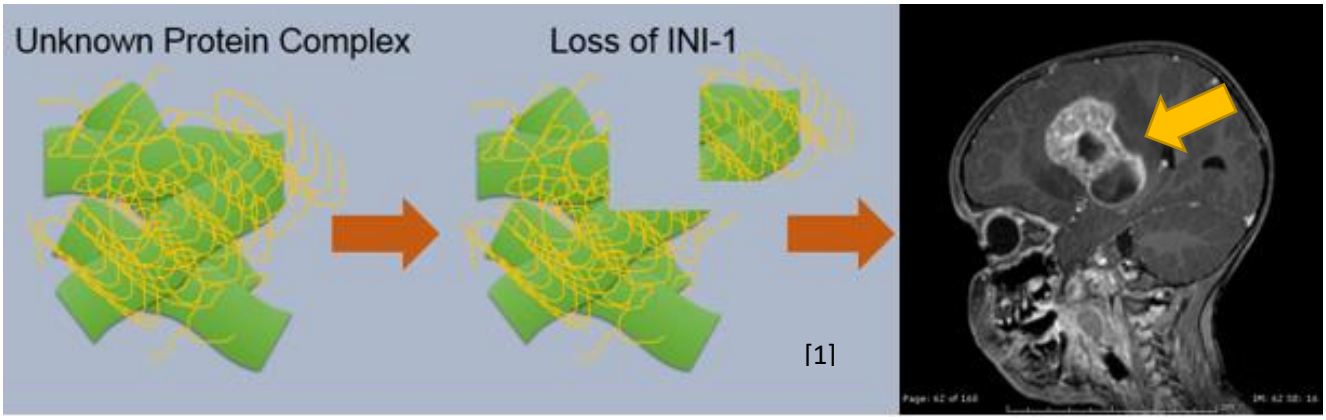

Figure 1: This is a visual that illustrates my hypothesis. The loss of the INI-1 from some unknown protein complex is what causes ATRT to develop.

Experimentation:

My hypothesis is that the loss of INI-1 leads to the malfunction of an unknown protein complex, thus leading to tumor formation. To test the hypothesis, I will identify interacting INI-1 proteins.

Cell Culture

Experimentation began with the use of sterile techniques and methods for growing a HeLa culture, which is a cell culture of a line of cancer cells. Both a control cell line of HeLa cells and a HeLa cell line containing a FLAG tagged version of INI-1 that allows INI-1 to be isolated by column chromatography were grown. HeLa cells were used because they are easily grown and are

not extremely prone to contamination. I learned a wide variety of sterile cell culture techniques in this stage of the experiment.

The cells grew quite well most of the time. The incubator did malfunction over the course of my production and carbon dioxide levels fell below that necessary for HeLa cell growth. Also, one instance of contamination did occur. This contamination was isolated to one plate. This plate was immediately disposed of and sterilized. After the incubator failed, it took a month to grow the cells back up to the confluency needed to begin to split them and save them at a rapid rate. However, by the end of the year, I had developed quite a stock of large cell plates for both the tagged and control versions of the HeLa cells. The picture below is one of a plate of HeLa cells that contained the FLAG tag version of INI-1.

Figure 2

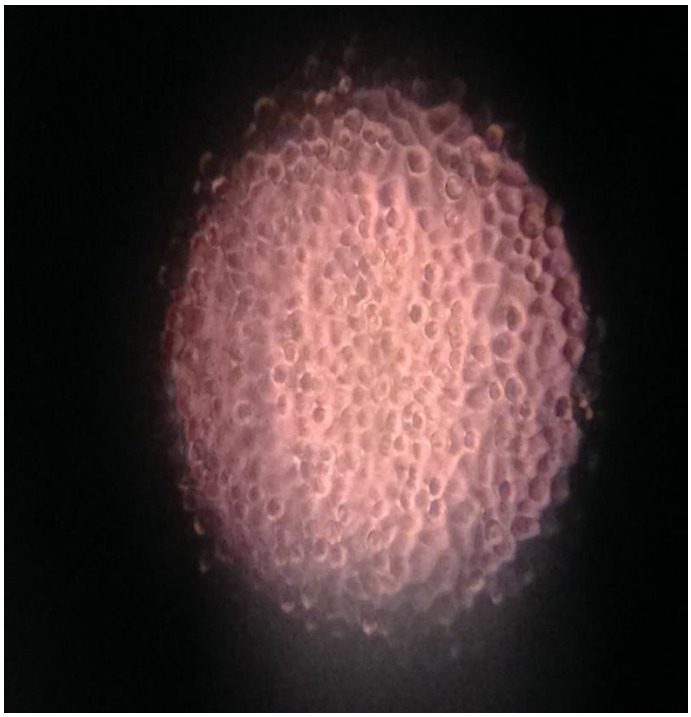

Figure 2: This is a picture of the FLAG tag INI-1 HeLa cells growing on a plate. This was viewed using a light microscope.

My original lines were grown from a cell sample that had been placed in a cryovial and frozen at -80°C. The exact date of freezing of the frozen samples was unknown; however, it is safe to conclude that they had been frozen for many years. Consequently, it was difficult to get them to grow effectively after being frozen for so long. However, eventually the cells began to grow.

In order to properly grow the cells, one must be sure to make everything as sterile as possible. All work must be done in a cell culture room in a hood with proper air circulation as well as proper UV light to sterilize the room when finished. Cellular media was made 3 days prior to attempting to grow the cells. All of the components of the media were filtered in order to prevent contamination from occurring. This media also contained Fetal Bovine Serum, which was not filtered to make sure the nutrients necessary for cellular growth did not get removed.

The pH of the media was at a physiological pH of 7.4. This was necessary because the cells used were human cells and the human body is at a pH of 7.4. Thus, this pH optimizes growth of the cells. After the media was created, it was plated and left in the incubator for 3 days, after which the plate was removed from the incubator and examined under a microscope to look for contamination. If the media was contaminated, it was not used on the cells. Fortunately, there was never a case of contaminated media.

In order to actually begin growing cells, the media needs to be room temperature. Then the cells start out growing on a small plate. Ten milliliters of media was plated and then the cryovial was warmed until the contents were completely thawed. After this, the cryovial was dumped onto the small media containing plate and the lid was put on top. A figure-eight motion was made with the plate in order to make sure that the cells spread out. Then the plate was properly labeled and placed in an incubator at a temperature of 37°C. The plates were checked every other day to make sure that growth was normal and no contamination had occurred.

After the cells had reached 85-100% confluency, the cells were removed from the small plates and placed on larger plates to grow. One can tell when the cells are ready to be split by the fact that they begin to stack up on top of each other. The stacking prevents cells from truly being able to grow to their fullest potential, because the cells on top of the stacking blob essentially smother the cells underneath. Cells were transferred from the plate by adding Trypsin. Trypsin cleaves the cells from the plates so that they can be pipetted up and placed onto a new plate. For the larger plate 30 milliliters of media was used to grow the cells. Multiple figure eights were used to make sure that the cells were evenly spread around so that they are able to grow most efficiently.

Unfortunately, my supply of INI-1 Flag tagged and control cell cryovials were limited. To combat the total loss of all stored cryovials, I froze some cryovials of the HeLa cell lines I grew for later use. I did this because it is easier to grow samples that have not been frozen for a long time rather than ones that have been frozen for years. I wanted to create a security that I could look to in case my cell plates that were growing had spontaneous death or if I wanted to resume cell culture again after stopping for any reason in the future. The cryovials that I froze are going to be used by another member of the laboratory who will continue this project.

After the cultures had grown to approximately 85-100% confluency, the cells were scraped off of the plate. This was done by first washing the cells with PBS. After the washing was completed, 1mL of PBS was added to the plate to make sure that there was enough liquid to scrap the cells off the plate. The actual scraping of the cells was done with a Rubber Policeman. When scrapping cells, it is very important to not be too rough with them. The cells could possibly burst open if they are pressed too hard. After the cells were scrapped off of the plate, the cells were centrifuged and stored in the -80°C freezer until I had enough built up pelleted cells that I could begin experimentation.

After I had an ample supply of frozen cell pellets, the cells were then lysed or broken open and the cell extract from the cells were collected. Column chromatography techniques were employed with a resin that is only capable of removing INI-1 and its associated proteins (anti-FLAG resin) to isolate the INI-1 protein from the HeLa cell extract. The resin was washed with the same buffer that was used in lysing open the cells. This was done to make sure that the resin was compatible with the proteins and able to induce protein-resin binding. A HeLa cell line that did not contain the tagged INI-1 was used as a control. The control line was grown using the same methods as the tagged version of INI-1.

Figure 3

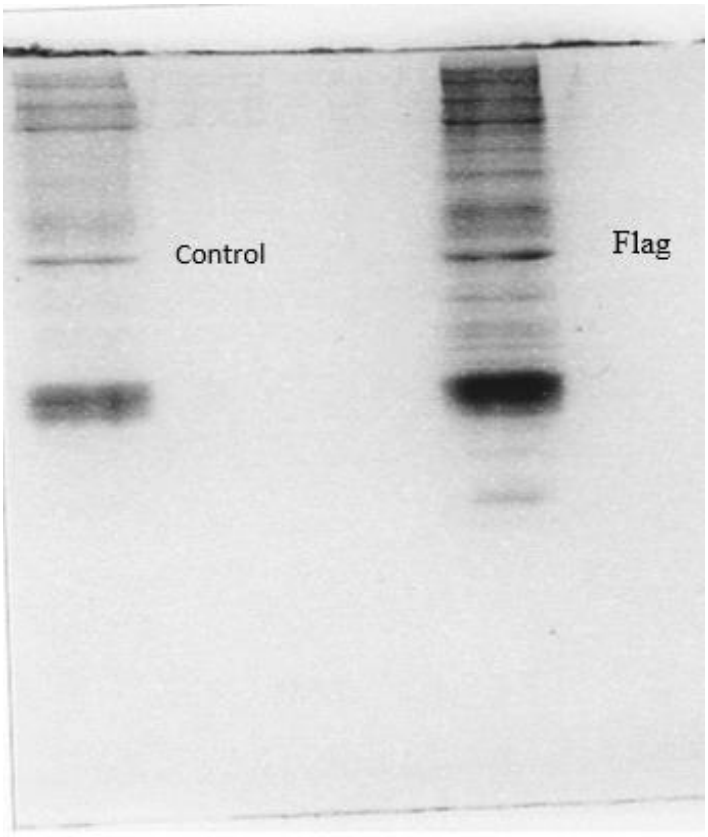

Figure 3: This is an SDS-PAGE gel that indicates the different protein banding patterns of the two lanes. The banding pattern for both the FLAG tag INI-1 Lane and the Control Lane was the same. This is a 12% gel.

An SDS-PAGE gel was used to analyze the proteins. This is because SDS-PAGE gels can separate proteins based on size. A high molecular weight ladder was chosen to be the comparison for protein weights from a high molecular ladder. When analyzing the gel above, it is evident that the protein banding pattern is the same in the control lane and the FLAG lane. This protein banding pattern was not expected to be the same for the flagged and control lines of HeLa cells. This was not expected because one of the lines has the FLAG tag version of INI-1 that would attach to the anti-FLAG resin. Therefore there should have been more proteins in the FLAG lane than the Control lane. This unexpected result was quite puzzling.

Control Tests

Consequently, different scenarios were proposed to explain the phenomenon. Were the gel techniques poor? Were the cells actually lysed open? Many more questions were asked. In order to answer these questions, control experiments were run to determine the cause of the unexpected banding patterns in the cell lines. For instance, in one control experiment, the resin was washed more than the previous gel to see if the resin was able to bind INI-1 more efficiently if the resin was immersed in the buffer prior to introduction to the cellular extracts. This method, however, only caused a slight protein binding increase. Therefore, it was concluded that the resin was not the reason why the two cell line proteins looked the same on the gels.

Another control test was conducted in order to see to see if the SDS-PAGE gel was being correctly run with good technique. (An SDS-PAGE gel is simply a gel that separate proteins to distinguish between different cell lines.) The control sample was a sample of INI-1 protein and those associated with it. This sample was from a frozen immunoprecipitation experiment

conducted by Dr. Ruhl several years before. The exact date of the creation of this nuclear extract sample was not known. The buffer was also run on the SDS-PAGE gel to determine if the protein bands on the gel were simply from the buffer being used or if they were actually from the cell extracts. The results from this control run indicated that the buffer did not contain any of the proteins that were associated with INI-1. The only proteins evidenced in the buffer lane were the antibody chains. This was expected due to the fact that resin was added to the buffer. The resin is the part of the combination of resin and sample that actually contains the antibody.

Figure 4

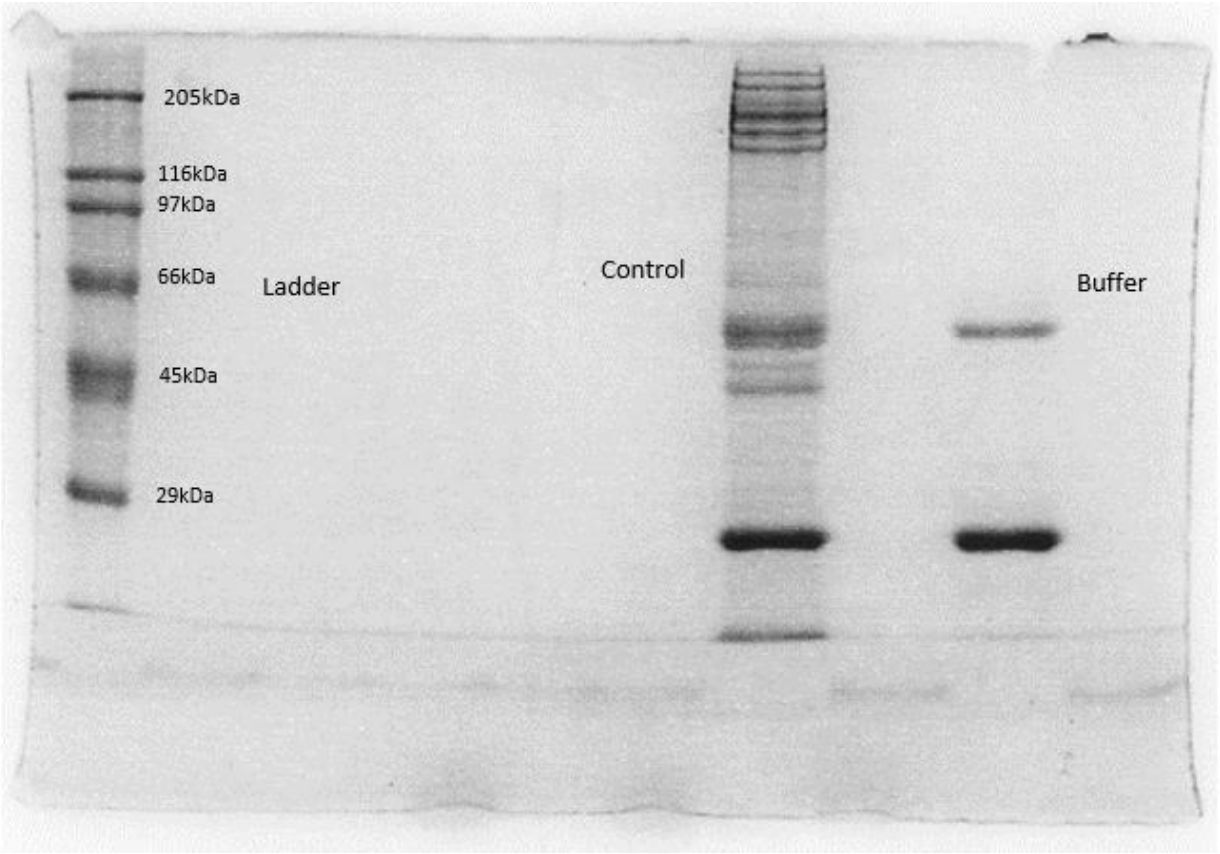

Figure 4: This is a SDS-PAGE gel that indicates that the gel techniques used were effective. This is an example of a type of control tests conducted to see if cell lysis was effective. This is an 8% gel.

This gel also proved that I did have good technique in my gel electrophoresis and that the two darker bands in the lanes were actually from the buffer not from the cell extract. This still did not answer the question of why the banding patterns were the same in the original SDS-PAGE gel. Eventually, the conclusion was made that the cell was not being lysed completely. Since INI-1 is found in the SWI/SNF complex and that is a complex that helps cells read DNA, INI-1 is expected to be inside of the nucleus of the cell. This is because DNA is actually found inside of the nucleus of the cell and is replicated inside the nucleus as well. Since INI-1 is not being removed from the cell, the conclusion was made that the nucleus of the cell was not being lysed, only the cell wall was being broken open. This explains why the gel (Figure 3) at the beginning of this page had similar protein banding patterns. The only difference between the two different cell lines is really the flagging of the INI-1 protein inside of the nucleus.

Consequently, a majority of project was trying to figure out a way to break the nucleus open without damaging the protein. This was a puzzling problem in that the proteins are quite sensitive and destroying them is very possible if too harsh of techniques are being employed. Mechanical, chemical, and freeze-thaw lysis techniques were all utilized; however, none of the techniques were very effective. Some would consider conducting a nuclear extract of the cell since a nuclear extract is only all of the proteins from inside the nucleus and nothing else. However, it is not known whether or not INI-1 interacts with proteins that are located outside of the nucleus. Consequently, this eliminates the nuclear extracts as a viable option since it could eliminate possible INI-1 to other protein interaction.

The Analytical Biochemistry Laboratory class graciously served as a method testing unit for testing different methods of breaking open the cells to extract protein. All of the cell pellets they used for their method testing were pellets previously saved over the course of my experiment.

The pellet sizes were all relatively the same. This was done to make sure that there was not a lane that had a significantly darker banding pattern for one group. The laboratory class used a mechanical lysis with a dounce. This method yielded excellent results that were able to be sent for proteomics. Each laboratory group conducted experiments on two sets of cells. One sample was the proteins from the cell with the FLAG tag version of INI-1 and the other sample was the control cells. The lanes in the graph are in pairs. The first lane is the FLAG tag and the second lane is the control. As an example, lane 2 and 3 is from one laboratory group. Lane 2 is the FLAG tag sample and lane 3 is the control sample. Lane 4 and 5 are from the next laboratory group. This pattern continues all the way to the final group with the lanes 22 and 23. Lane 1 is the High Molecular Weight Ladder.

Figure 5

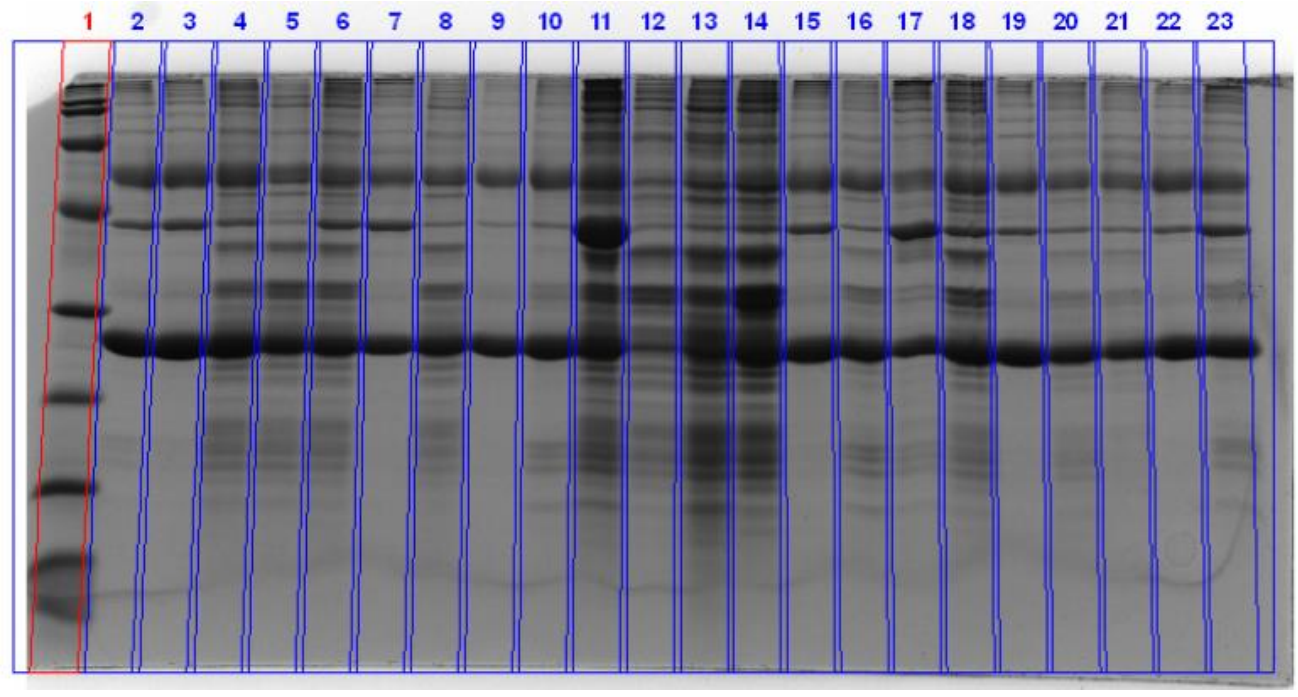

Figure 5: SDS-PAGE gel created by the Analytical Biochemistry Lab course. Lane 1 is the High Molecular Ladder. The lanes chosen to continue onward to Mass Spectrum Analysis were Lanes 2 (FLAG tag INI-1) and Lane 3(Control). Lanes 6 (FLAG tag INI-1) and Lane 7 (Control) were also chosen. This is a 12% gel.

After the chromatography was completed, both the tagged and non-tagged samples were sent off for mass spectrum analysis. The tagged and non-tagged samples were the samples from lanes 2,3 and lanes 6,7. These two groups of lanes were chosen due to the fact that they seemed to have the most expected banding pattern. By this it is meant that that the INI-1 Flag tag lane visually looks different than the Control Lane. There are different banding patterns. However, these lanes are not so different that it indicates suspicion in the group's methods.

Proteomics

This statistical analysis provided a set of other proteins associated with INI-1. This statistical analysis was completed by sending the mass spectrum samples saved from the laboratory's experiment to mass spectrum for analysis. After the analysis was complete a list of proteins was sent back. This protein list was read in the computer program Scaffold 4. Scaffold 4 can organize proteomic data and look for significance. After comparing both the tagged and non-tagged lines using the "Total Spectrum Count" setting, it was determined which proteins are only associated with INI-1. (The "Total Spectrum Count setting was used to distinguish all of the differences between the proteins when analyzing the proteomic data for significance.) This was done by evaluating the p-value of the proteins. If the p-value of the protein was less than 0.05, then the protein was deemed to significantly associate with INI-1. Since INI-1 attaches to the SWI/SNF complex, it was expected that some of the identified proteins would be members of the SWI/SNF complex. (There were 5 proteins that are identified with the SWI/SNF complex that were significantly associated with INI-1 in both the 2,3 and 6,7 trials.) It would have been interesting to see the other Analytical Biochemistry Laboratory group's proteomic data results. However,

running the mass spectrum requires money and time. The two items limited the number of samples that could sent at once.

The submission of only two trails of this experiment, however, are not enough trails for me to conclusively determine whether or not the proteins are actually associated with INI-1. More trails must be implemented to conclusively determine which proteins are associated with INI-1. This is important due to the fact that human error is always present. More experimental trials need to be conducted so that this human error would be less significant. For instance, the protein keratin was found in both cell line protein lists. This keratin is not from the cells. Rather, the keratin is from human skin cells. Granted this protein was marked off significance list due to the lack of a significant p-value. There is still the possibility for other human error like possible protein contamination. It is very unlikely that this happened; however, more Ns (trails) would really strengthen the findings of the experiment. Consequently, more trails were conducted in order to determine the significance of the experimental finding.

More Trials Conducted

More cells were broken open over the course of the semester; however, there, once again, were difficulties in breaking open the cells. This problem in the methodology was unexpected. The Analytical Biochemistry Laboratory used the protocol and it worked well. For reasons unknown, their protocol was not achieving the results desired when replicated. Multiple different steps were taken to try to replicate the results obtained by the Analytical Biochemistry Laboratory. Unfortunately, this proved to be challenging.

Figure 6

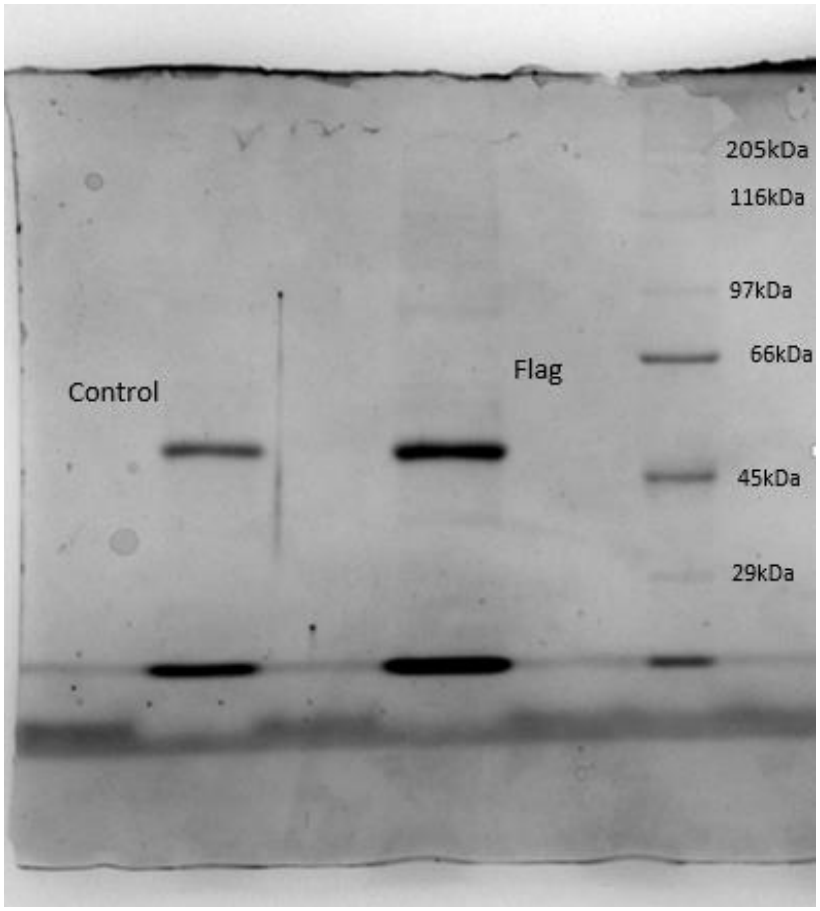

Figure 6: This is an SDS-PAGE gel Kristy Johnson and I prepared that illustrates the poor results obtained when we used the same cell lysis methods utilized by the Analytical Biochemistry Lab course. This is an 8% gel.

The previous douncing method was not as effective as it was for the laboratory. There also were more washing methods implemented in the new trails, and the addition of more washing could have possibly caused protein to become lost. This is evidenced by the gel above. The banding pattern was the same between the lane containing the Flag tag version of INI-1 and the control HeLa cells. The antibody resin does show up on the gel. The light chain is the darker band on the gel below the 29 kDa mark on the ladder. The light chain should be at about the 27 kDa mark. The heavy chain is at about the 50 kDa mark on the gel. This band, however, is about where it should be on the gel. This indicates that the lighter proteins moved through the gel faster than the ladder.

After multiple trials, it was determined that the method of breaking open cells should be the freeze/thaw method. This method was very effective and 2 more sample pairs were run on a gel.

Figure 7

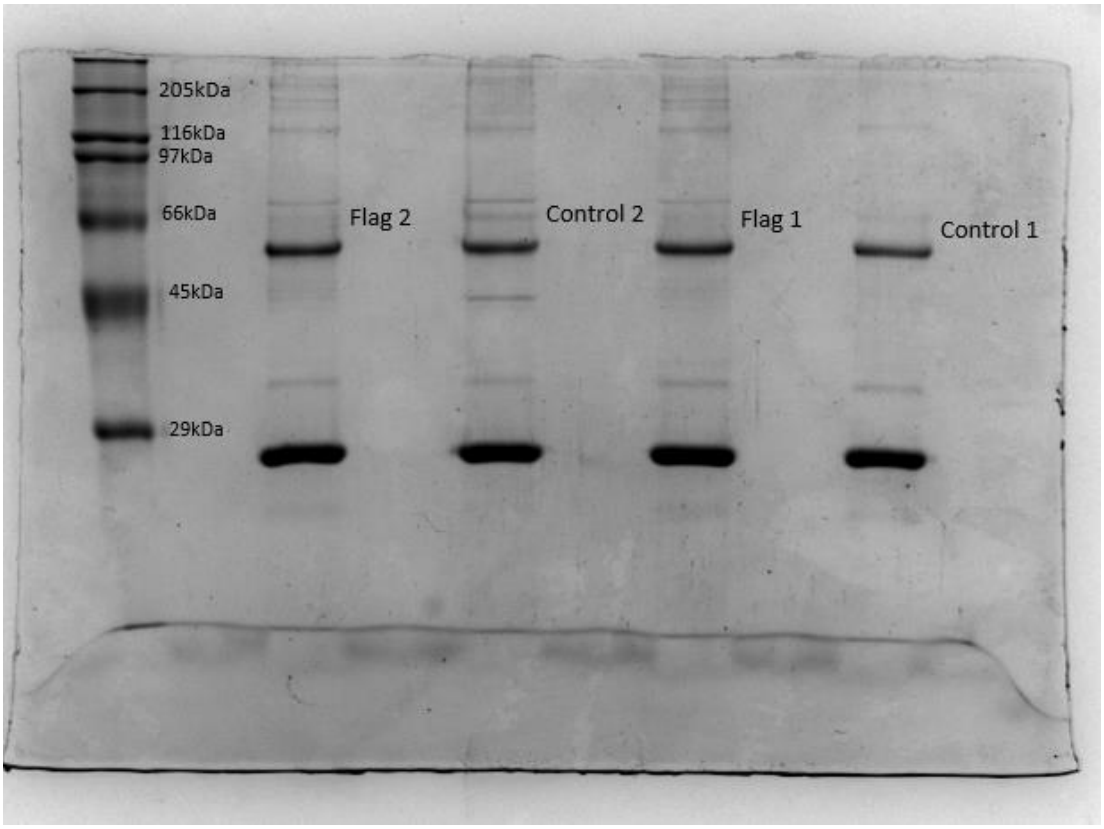

Figure 7: This SDS-PAGE gel illustrates that the cells were effectively lysed with the freeze/thaw method. This is a 12 % gel.

This gel contains all the markers expected for a good gel. Both the light chain and the heavy chain from the antibody are present on the gel. The INI-1 band is also located on the gel at about the 47kDa mark. It is very light in the picture; however, when viewing the gel directly with light, the band was much more evident. There are obvious differences between the lanes of the FLAG tag version of the INI-1 protein and the control lane. These different bands can be viewed between the flag and the control between the 116kDa mark and the 205 kDa mark. This indicates that there are differences in protein for the two samples. These samples have not been sent to mass spectrum

for analysis, yet. However, the samples are saved at -80°C with little to no buffer in the vials. They are ready to be sent off to mass spectrum for analysis whenever the laboratory is ready to send more samples.

Future Studies:

More immunoprecipitation experiments will take place to provide more quality samples to be sent off to mass spectrum for analysis. This will provide more N-values so that it can be better confirmed what proteins associate with INI-1 consistently. Also, the provision of more experimental runs will better enable a consistent experimental technique to be obtained for breaking open the HeLa cells. The mass spectrum results will then be confirmed by using coimmunoprecipitation to pull INI-1 out of the HeLa cell and using an IP-Western blot. Using this technique, specific proteins like INI-1 can be identified. This process will allow me to reconfirm the exact protein that attaches to INI-1.

Results and Conclusion:

The results from the experiment were that I identified proteins associated with INI-1 from the mass spectrum and proteomic analysis of the lanes 2,3 and 6,7 from the Analytical Biochemistry Laboratory course. (A list of proteins that associated with INI-1 protein exclusively is provided in Appendix 1. The descriptions of the proteins found significant in both 2,3 and 6,7 can be found in Appendix 2.) In results of the 6,7 lanes, 312 proteins were identified. However, only 212 of the proteins significantly associated with INI-1. Significance was determined by those proteins whose p-value was under 0.05. In the results of the 2,3 lanes, 162 proteins were identified. However, only 93 of these proteins were significantly associated with INI-1. The fact that not all proteins that were found were significant is an important reminder of why the control sample is

important. Without the control, it would be easy to assume that all the proteins that were pulled out of the cell were attached to INI-1. This is simply not the case. Sometimes non-specific proteins attach to resins. The use of the control allows for the elimination of these non-specific proteins and helps strengthen the conclusions of this experiment.

Fifty-four proteins were found to have a significant p-value in both the 2,3 lanes and the 6,7 lanes. The common theme between a lot of the proteins is that they are involved in some form with cytokinesis. This is an interesting observation that needs to be explored in more depth in order to fully understand the INI-1 proteins role in the development of ATRT. Some other proteins were found to be crucial in maintaining a proper cytoskeletal structure. This is also an interesting observation in that INI-1 may be contributing to the structural integrity of the cell, and, possibly, when that integrity falters ATRT develops. One of the significant proteins identified in both of the trials that went to mass spectrum for analysis was Myosin. This protein plays a major role in cellular development, specifically cytokinesis. Myosin is also important in maintaining a proper cellular shape and structure [3]. Another protein identified was Isoform 2 of Filamin A. This protein is also involved in cytoskeleton maintenance. It binds transmembrane protein to the cytoskeleton and is crucial to the signaling mechanisms of the cell [4]. These are just two proteins from the list of 54 proteins that were significant in both the proteomics results from the 6,7 lanes as well as the 2,3 lanes. However, these are the two proteins I am most interested in exploring their role with INI-1 in the development of ATRT.

The finding of all of these non-SWI/SNF proteins associating with INI-1 was initially expected because INI-1's role in tumor formation is not directly known to be associated with the SWI/SNF complex. It is simply the current theory. INI-1 may have a variety of different roles in the cell that are not currently known. The identification of these new proteins could help scientists

understand the correlation and causation INI-1 has with the development of the pediatric tumor ATRT. Could this newly discovered protein be the key to unlocking the cause of the devastating pediatric cancer? Could the analyses of this new protein have the potential to save lives? These are questions that must be answered, and they will be answered in future studies. More research time and money is necessary to determine the extent to which these newly associated proteins could be significant in finding a treatment or even a cure for ATRT.

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Appendix 1:

List of proteins for 6,7 and 2,3.

A significant p-value is highlighted in green.

#	Identified Proteins (312)	Accession Number	Molecular Weight	Protein Grouping Ambiguity	Lanes 6,7 P-values	Lanes 2,3 P-values
1	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	sp|P35579|MYH9_HUMAN	227 kDa	TRUE	<0.00010	<0.00010
2	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	sp|P63261|ACTG_HUMAN	42 kDa	TRUE	0.0024	0.09
3	Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA	sp|P21333-2|FLNA_HUMAN (+2)	280 kDa	TRUE	0.00014	0.02
4	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	sp|Q13813|SPTN1_HUMAN	285 kDa		0.00027	0.00012
5	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	sp|Q01082|SPTB2_HUMAN	275 kDa	TRUE	<0.00010	<0.00010
6	RecName: Full=Keratin, type II cytoskeletal 1; AltName: Full=67 kDa cytokeratin; AltName: Full=Cytokeratin-1; Short=CK-1; AltName: Full=Hair alpha protein; AltName: Full=Keratin-1; Short=K1; AltName: Full=Type-II keratin Kb1	gi|238054406|sp|P04264.6|K2C1_HUMAN (+1)	66 kDa	TRUE	0.00019	0.017
7	RecName: Full=Keratin, type II cytoskeletal 2 epidermal; AltName: Full=Cytokeratin-2e; Short=CK-2e; AltName: Full=Epithelial keratin-2e; AltName: Full=Keratin-2 epidermis; AltName: Full=Keratin-2e;	gi|239938650|sp|P35908.2|K22E_HUMAN (+1)	65 kDa	TRUE	0.00095	0.0032

	Short=K2e; AltName: Full=Type-II keratin Kb2					
8	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=2 SV=1	tr|E9PMS6|E9PMS6_HUMAN	145 kDa	TRUE	0.0013	0.00016
9	RecName: Full=Keratin, type I cytoskeletal 10; AltName: Full=Cytokeratin-10; Short=CK-10; AltName: Full=Keratin-10; Short=K10	gi|269849769|sp|P13645.6|K1C10_HUMAN (+1)	59 kDa	TRUE	0.018	0.076
10	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	sp|Q04695|K1C17_HUMAN	48 kDa	TRUE	0.058	0.34
11	Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB	sp|O75369-8|FLNB_HUMAN	282 kDa	TRUE	<0.00010	
12	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	sp|P05783|K1C18_HUMAN	48 kDa	TRUE	0.0043	0.011
13	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	sp|P16403|H12_HUMAN	21 kDa	TRUE	0.0012	0.49
14	RecName: Full=Keratin, type I cytoskeletal 9; AltName: Full=Cytokeratin-9; Short=CK-9; AltName: Full=Keratin-9; Short=K9	gi|239938886|sp|P35527.3|K1C9_HUMAN (+1)	62 kDa	TRUE	0.043	0.19
15	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2	sp|P46013|KI67_HUMAN	359 kDa		0.00044	
16	Isoform 2 of Plectin OS=Homo sapiens GN=PLEC	sp|Q15149-2|PLEC_HUMAN	518 kDa		0.069	
17	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	sp|P62701|RS4X_HUMAN	30 kDa		0.00019	0.0059
18	Uncharacterized protein C19orf21 OS=Homo sapiens GN=C19orf21 PE=1 SV=1	sp|Q8IVT2|CS021_HUMAN	75 kDa		0.0024	<0.00010

19	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	sp|P61247|RS3A_HUMAN	30 kDa		0.0014	
20	Isoform 2 of Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8	sp|P05787-2|K2C8_HUMAN (+1)	57 kDa	TRUE	<0.00010	0.12
21	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	sp|O43707|ACTN4_HUMAN	105 kDa	TRUE	<0.00010	0.0029
22	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	sp|Q9NR30|DDX21_HUMAN	87 kDa	TRUE	0.00012	
23	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	sp|Q02878|RL6_HUMAN	33 kDa		<0.00010	0.049
24	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3	sp|Q14690|RRP5_HUMAN	209 kDa		<0.00010	
25	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	sp|Q9Y2W1|TR150_HUMAN	109 kDa	TRUE	<0.00010	0.00068
26	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM	sp|P52272-2|HNRPM_HUMAN (+1)	74 kDa	TRUE	<0.00010	
27	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	sp|P18124|RL7_HUMAN	29 kDa		0.00017	0.026
28	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	sp|O14744|ANM5_HUMAN	73 kDa		0.06	0.027
29	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	sp|P06748|NPM_HUMAN	33 kDa	TRUE(6,7)	0.0026	0.44
30	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	sp|P68363|TBA1B_HUMAN	50 kDa	TRUE	0.12	
31	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	sp|P62424|RL7A_HUMAN	30 kDa		0.00024	0.0059
32	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	sp|P39023|RL3_HUMAN	46 kDa		0.00034	0.15
33	Isoform 3 of Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A	sp|Q92614-3|MY18A_HUMAN (+3)	227 kDa	TRUE (2,3)	<0.00010	0.00017

34	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	sp|P11387|TOP1_HUMAN	91 kDa		<0.00010	
35	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	sp|P62917|RL8_HUMAN	28 kDa	TRUE (2,3)	0.007	0.00094
36	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3	sp|O76021|RL1D1_HUMAN	55 kDa		<0.00010	
37	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	sp|P62807|H2B1C_HUMAN	14 kDa	TRUE	0.0034	0.0017
38	Isoform 3 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1	sp|Q9NYF8-3|BCLF1_HUMAN (+1)	100 kDa	TRUE	0.00044	
39	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	sp|P46779|RL28_HUMAN	16 kDa		0.008	
40	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	sp|Q8TAQ2|SMRC2_HUMAN	133 kDa	TRUE	<0.00010	<0.00010
41	LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	sp|Q9UHB6|LIMA1_HUMAN	85 kDa		0.0015	0.0023
42	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	sp|P19338|NUCL_HUMAN	77 kDa	TRUE	<0.00010	
43	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	sp|P26373|RL13_HUMAN	24 kDa		0.00057	0.00054
44	Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2	sp|Q86V48|LUZP1_HUMAN	120 kDa		<0.00010	0.0035
45	Unconventional myosin-Ig OS=Homo sapiens GN=MYO1G PE=1 SV=2	sp|B0I1T2|MYO1G_HUMAN	116 kDa	TRUE	0.00017	<0.00010
46	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	sp|P46778|RL21_HUMAN	19 kDa		0.001	0.15
47	Isoform Beta of Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1	sp|Q14978-2|NOLC1_HUMAN	75 kDa		0.00017	
48	H/ACA ribonucleoprotein complex subunit 4	sp|O60832|DKC1_HUMAN	58 kDa		<0.00010	

	OS=Homo sapiens GN=DKC1 PE=1 SV=3					
49	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	sp|P62753|RS6_HUMAN	29 kDa		0.00013	0.12
50	Isoform 4 of Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2	sp|P46087-4|NOP2_HUMAN (+1)	93 kDa		<0.00010	
51	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	sp|Q02543|RL18A_HUMAN	21 kDa		0.00028	
52	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	sp|P62241|RS8_HUMAN	24 kDa		<0.00010	
53	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	sp|Q07020|RL18_HUMAN	22 kDa		0.028	
54	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	sp|P15880|RS2_HUMAN	31 kDa		0.0042	
55	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	sp|P07437|TBB5_HUMAN (+4)	50 kDa	TRUE	0.0042	
56	N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2	sp|Q9H0A0|NAT10_HUMAN	116 kDa		<0.00010	
57	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	sp|P02533|K1C14_HUMAN	52 kDa	TRUE	0.0012	0.0051
58	Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	sp|P23588|IF4B_HUMAN (+1)	69 kDa		0.00086	0.69
59	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	sp|P13647|K2C5_HUMAN	62 kDa	TRUE	0.00043	0.31
60	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	sp|O00567|NOP56_HUMAN	66 kDa		<0.00010	
61	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	sp|Q08211|DHX9_HUMAN	141 kDa		0.00057	
62	Isoform 2 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	sp|O00159-2|MYO1C_HUMAN (+3)	118 kDa		0.12	0.0026

63	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	sp|P22087|FBRL_HUMAN	34 kDa		0.00022	
64	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	sp|P62805|H4_HUMAN	11 kDa		0.055	0.0059
65	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	sp|P62277|RS13_HUMAN	17 kDa		0.0091	<0.00010
66	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3	sp|Q92922|SMRC1_HUMAN	123 kDa	TRUE	0.0019	<0.00010
67	Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2	sp|P07355-2|ANXA2_HUMAN (+1)	40 kDa		0.0002	0.027
68	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	sp|P18621|RL17_HUMAN	21 kDa		0.00019	
69	Isoform 2 of Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4	sp|P51532-2|SMCA4_HUMAN (+5)	181 kDa	TRUE	0.0019	<0.0010
70	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	sp|P08729|K2C7_HUMAN	51 kDa	TRUE	0.023	0.025
71	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	sp|P61254|RL26_HUMAN (+3)	17 kDa		0.0039	
72	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	sp|P50914|RL14_HUMAN	23 kDa	TRUE	0.00096	0.0086
73	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	sp|P36578|RL4_HUMAN	48 kDa		0.002	
74	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	sp|P62280|RS11_HUMAN	18 kDa		0.0097	
75	Isoform 2 of Synaptopodin OS=Homo sapiens GN=SYNPO	sp|Q8N3V7-2|SYNPO_HUMAN	96 kDa		0.26	0.011
76	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	sp|P62249|RS16_HUMAN	16 kDa		0.00031	
77	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	sp|P62906|RL10A_HUMAN	25 kDa		0.0079	

78	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	sp|P84098|RL19_HUMAN (+2)	23 kDa		0.011	0.12
79	Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	sp|Q9NYL9|TMOD3_HUMAN	40 kDa		0.0036	0.043
80	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	sp|P62266|RS23_HUMAN	16 kDa		0.0044	0.0084
81	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	sp|P38159|RBMX_HUMAN	42 kDa		0.0015	
82	Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	sp|Q12965|MYO1E_HUMAN	127 kDa		0.06	
83	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	sp|Q92522|H1X_HUMAN	22 kDa		<0.00010	0.12
84	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	sp|P62910|RL32_HUMAN (+1)	16 kDa		0.0079	0.0051
85	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	sp|P62244|RS15A_HUMAN	15 kDa	TRUE	0.0042	
86	Isoform 3 of Myosin-10 OS=Homo sapiens GN=MYH10	sp|P35580-3|MYH10_HUMAN (+1)	231 kDa	TRUE	0.00082	
87	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	sp|P62851|RS25_HUMAN	14 kDa		0.0024	0.98
88	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	sp|P68431|H31_HUMAN (+1)	15 kDa		0.0031	
89	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	sp|P83731|RL24_HUMAN	18 kDa		<0.00010	
90	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	sp|Q5SSJ5|HP1B3_HUMAN	61 kDa		<0.00010	
91	Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB	sp|P47756-2|CAPZB_HUMAN (+2)	31 kDa		0.1	0.13
92	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	sp|P62750|RL23A_HUMAN	18 kDa		0.0092	
93	Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1	sp|P12814-2|ACTN1_HUMAN (+3)	103 kDa	TRUE	0.15	0.055

94	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	sp|P11142|HSP7C_HUMAN	71 kDa	TRUE	0.013	
95	RecName: Full=Gelsolin; AltName: Full=AGEL; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor	gi|121116|sp|P06396.1|GELS_HUMAN (+4)	86 kDa		<0.00010	0.00013
96	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	sp|O43143|DHX15_HUMAN	91 kDa		0.0015	
97	CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3	sp|Q03701|CEBPZ_HUMAN	121 kDa		0.00019	
98	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	sp|P52907|CAZA1_HUMAN	33 kDa	TRUE	0.023	0.087
99	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	sp|P05388|RLA0_HUMAN (+2)	34 kDa		0.00031	
100	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	sp|P62263|RS14_HUMAN	16 kDa		0.0022	0.14
101	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	sp|P49207|RL34_HUMAN	13 kDa		0.0024	0.079
102	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	sp|P17844|DDX5_HUMAN (+1)	69 kDa	TRUE	0.00056	
103	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	sp|P23396|RS3_HUMAN (+2)	27 kDa		0.00028	
104	Isoform 2 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6	sp|Q9H6R4-2|NOL6_HUMAN (+2)	112 kDa		0.00084	
105	AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3	sp|O14497|ARI1A_HUMAN	242 kDa	True (2,3)	<0.00010	0.00018
106	Nucleolar complex protein 2 homolog	sp|Q9Y3T9|NOC2L_HUMAN	85 kDa		<0.00010	

	OS=Homo sapiens GN=NOC2L PE=1 SV=4					
107	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	sp|P61353|RL27_HUMAN	16 kDa		0.0039	0.47
108	Isoform 2 of 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24	sp|P62847-2|RS24_HUMAN (+4)	15 kDa		<0.00010	
109	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	sp|P46776|RL27A_HUMAN	17 kDa		0.00073	
110	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	sp|Q6S8J3|POTEE_HUMAN	121 kDa	TRUE	0.37	0.37
111	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	sp|P62269|RS18_HUMAN	18 kDa		0.00072	0.035
112	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	sp|P39019|RS19_HUMAN	16 kDa		0.00017	
113	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	sp|P47914|RL29_HUMAN	18 kDa		0.03	
114	Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	sp|Q16643|DREB_HUMAN (+1)	71 kDa		0.013	0.0058
115	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	sp|Q9Y3U8|RL36_HUMAN	12 kDa	TRUE	0.0054	
116	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	sp|Q9BQA1|MEP50_HUMAN	37 kDa		0.025	0.65
117	Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	sp|Q9Y2X3|NOP58_HUMAN	60 kDa		<0.00010	
118	Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B	sp|Q14684-2|RRP1B_HUMAN (+1)	82 kDa		<0.00010	
119	RecName: Full=Trypsin; Flags: Precursor	gi|136429|sp|P00761.1|TRYP_PIG	24 kDa		0.33	0.18
120	ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1	sp|Q9GZR7|DDX24_HUMAN (+1)	96 kDa		0.0025	
121	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	sp|P84090|ERH_HUMAN	12 kDa		1	0.091

122	60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	sp|P18077|RL35A_HUMAN	13 kDa	TRUE (6,7)	0.038	0.24
123	RecName: Full=Serum albumin; Flags: Precursor	gi|113576|sp|P02768.2|ALBU_HUMAN (+1)	69 kDa	True (2,3)	0.00017	0.37
124	Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1	sp|Q969G3-2|SMCE1_HUMAN (+2)	42 kDa		0.0023	0.0003
125	RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3	sp|Q9NW13|RBM28_HUMAN	86 kDa	TRUE	<0.00010	
126	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	sp|P07305|H10_HUMAN	21 kDa		0.034	0.13
127	Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1	sp|P51114-2|FXR1_HUMAN (+1)	61 kDa	TRUE	0.0031	
128	Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA	sp|P62136-2|PP1A_HUMAN (+1)	39 kDa	TRUE	0.48	0.0034
129	Isoform 2 of RNA-binding protein 10 OS=Homo sapiens GN=RBM10	sp|P98175-2|RBM10_HUMAN (+3)	103 kDa		0.023	0.0078
130	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	sp|P16401|H15_HUMAN	23 kDa	TRUE	0.00014	
131	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	sp|P62899|RL31_HUMAN	14 kDa		0.027	0.073
132	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	sp|P62829|RL23_HUMAN	15 kDa		0.16	0.35
133	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	sp|P68032|ACTC_HUMAN (+1)	42 kDa	TRUE	0.37	0.45
134	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	sp|P62888|RL30_HUMAN	13 kDa		<0.00010	
135	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp|P10412|H14_HUMAN	22 kDa	TRUE	<0.00010	0.1

136	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	sp|P62913|RL11_HUMAN	20 kDa		0.0062	
137	Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3	sp|P06753-2|TPM3_HUMAN (+2)	29 kDa	TRUE	0.0014	
138	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	sp|P46940|IQGA1_HUMAN	189 kDa		<0.00010	
139	Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2	sp|Q92925-2|SMRD2_HUMAN (+3)	57 kDa	TRUE	0.0034	
140	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	sp|Q96PK6|RBM14_HUMAN	69 kDa		0.0025	
141	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	sp|Q96C19|EFHD2_HUMAN	27 kDa		0.00018	0.0048
142	Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54	sp|Q8TDD1-2|DDX54_HUMAN (+1)	99 kDa		0.00046	
143	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	sp|Q07955|SRSF1_HUMAN (+1)	28 kDa		0.0075	
144	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	sp|P42766|RL35_HUMAN	15 kDa		0.0078	0.12
145	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2	sp|P61927|RL37_HUMAN	11 kDa		0.0011	
146	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	sp|P08779|K1C16_HUMAN	51 kDa	TRUE	0.057	0.041
147	Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2	sp|Q96SB3|NEB2_HUMAN	89 kDa	TRUE	0.0059	0.013
148	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2	sp|Q14254|FLOT2_HUMAN (+2)	47 kDa		0.00028	0.001
149	Isoform 2 of Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A	sp|Q9BQG0-2|MBB1A_HUMAN (+1)	149 kDa		<0.00010	

150	Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6	sp|P60660-2|MYL6_HUMAN (+8)	17 kDa		0.0012	
151	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	sp|P02538|K2C6A_HUMAN	60 kDa	TRUE	0.023	0.026
152	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2	sp|Q96GQ7|DDX27_HUMAN	90 kDa		0.00039	
153	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	sp|P30050|RL12_HUMAN	18 kDa		0.00039	
154	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	sp|Q00839|HNRPU_HUMAN	91 kDa		<0.00010	
155	Isoform UBF2 of Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF	sp|P17480-2|UBF1_HUMAN (+2)	85 kDa		0.01	
156	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	sp|P35268|RL22_HUMAN	15 kDa	TRUE	0.012	
157	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	sp|P46777|RL5_HUMAN	34 kDa		0.002	
158	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GN=BRIX1 PE=1 SV=2	sp|Q8TDN6|BRX1_HUMAN	41 kDa		0.00068	
159	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	sp|P13010|XRCC5_HUMAN	83 kDa		0.00027	<0.00010
160	Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2	sp|Q99848|EBP2_HUMAN (+1)	35 kDa		0.00089	
161	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	sp|P68104|EF1A1_HUMAN (+1)	50 kDa		0.026	
162	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	sp|P46781|RS9_HUMAN	23 kDa		0.00043	
163	Isoform 2 of Unconventional myosin-	sp|O43795-2|MYO1B_HUMAN (+2)	125 kDa		0.00056	0.18

	Ib OS=Homo sapiens GN=MYO1B					
164	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	sp|P12956|XRCC6_HUMAN (+1)	70 kDa		0.00013	0.0005
165	Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1	sp|Q12824-2|SNF5_HUMAN (+2)	43 kDa		0.00039	0.00011
166	Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3	sp|Q9BVP2-2|GNL3_HUMAN (+1)	61 kDa		<0.00010	
167	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens GN=DDX47 PE=1 SV=1	sp|Q9H0S4|DDX47_HUMAN	51 kDa		1	
168	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3	sp|Q9BZE4|NOG1_HUMAN	74 kDa		0.011	
169	Isoform 2 of Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2	sp|Q86SQ0-2|PHLB2_HUMAN (+2)	137 kDa		0.067	
170	Isoform 3 of Neurabin-1 OS=Homo sapiens GN=PPP1R9A	sp|Q9ULJ8-3|NEB1_HUMAN (+3)	154 kDa	TRUE	<0.00010	
171	Nucleolar protein 10 OS=Homo sapiens GN=NOL10 PE=1 SV=1	sp|Q9BSC4|NOL10_HUMAN (+1)	80 kDa		0.00013	
172	Isoform 2 of RRP12-like protein OS=Homo sapiens GN=RRP12	sp|Q5JTH9-2|RRP12_HUMAN (+2)	133 kDa		0.00015	
173	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	sp|P62841|RS15_HUMAN (+1)	17 kDa		0.051	0.14
174	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	sp|Q86YZ3|HORN_HUMAN	282 kDa		0.0037	0.21
175	pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2	sp|Q8IY81|SPB1_HUMAN	97 kDa		0.00084	
176	Isoform 2 of Probable ATP-dependent RNA	sp|Q92841-1|DDX17_HUMAN (+3)	72 kDa	TRUE	0.00026	

	helicase DDX17 OS=Homo sapiens GN=DDX17					
	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1					
177	SV=2	sp|P0C0S8|H2A1_HUMAN (+3)	14 kDa	True (2,3)	0.87	0.61
	Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo					
178	sapiens GN=NUMA1	sp|Q14980-2|NUMA1_HUMAN (+1)	237 kDa		<0.00010	
	40S ribosomal protein S17 OS=Homo sapiens					
179	GN=RPS17 PE=1 SV=2	sp|P08708|RS17_HUMAN (+3)	16 kDa		0.052	
	Ig alpha-1 chain C region OS=Homo sapiens					
180	GN=IGHA1 PE=1 SV=2	sp|P01876|IGHA1_HUMAN	38 kDa		0.00033	
	Isoform 2 of Actin-related protein 2 OS=Homo sapiens					
181	GN=ACTR2	sp|P61160-2|ARP2_HUMAN (+1)	45 kDa		0.052	
	RRP15-like protein OS=Homo sapiens					
182	GN=RRP15 PE=1 SV=2	sp|Q9Y3B9|RRP15_HUMAN	31 kDa		0.01	
	Isoform 2 of Probable ATP-dependent RNA helicase DDX31 OS=Homo sapiens					
183	GN=DDX31	sp|Q9H8H2-2|DDX31_HUMAN (+2)	86 kDa		0.00027	
	78 kDa glucose-regulated protein OS=Homo sapiens					
184	GN=HSPA5 PE=1 SV=2	sp|P11021|GRP78_HUMAN	72 kDa	TRUE	0.58	
	Folate receptor alpha OS=Homo sapiens					
185	GN=FOLR1 PE=1 SV=3	sp|P15328|FOLR1_HUMAN	30 kDa		0.37	
	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B					
186	PE=1 SV=2	sp|O14950|ML12B_HUMAN (+2)	20 kDa		0.003	0.0011
	Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens					
187	GN=HSPA1A	sp|P08107-2|HSP71_HUMAN (+1)	64 kDa	TRUE	0.64	
	Beta-actin-like protein 2 OS=Homo sapiens					
188	GN=ACTBL2 PE=1 SV=2	sp|Q562R1|ACTBL_HUMAN	42 kDa	TRUE	0.33	0.12
	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens					
189	GN=FXR2 PE=1 SV=2	sp|P51116|FXR2_HUMAN	74 kDa	TRUE	<0.00010	

190	Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=1 SV=2	sp|Q92785|REQU_HUMAN	44 kDa	0.00027	
191	Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens GN=RRP7A PE=1 SV=2	sp|Q9Y3A4|RRP7A_HUMAN	32 kDa	0.00027	
192	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	sp|P61513|RL37A_HUMAN	10 kDa	0.079	
193	Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1	sp|P09651-2|ROA1_HUMAN (+5)	34 kDa	0.0039	
194	Isoform 2 of Actin-like protein 6A OS=Homo sapiens GN=ACTL6A	sp|O96019-2|ACL6A_HUMAN (+1)	43 kDa	0.023	<0.00010
195	Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2	sp|Q9NX58|LYAR_HUMAN	44 kDa	0.00069	
196	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	sp|P02786|TFR1_HUMAN	85 kDa	0.0039	
197	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3	sp|Q86V81|THOC4_HUMAN	27 kDa	0.002	
198	Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1	sp|Q6NYC8|PPR18_HUMAN (+1)	68 kDa	0.009	0.12
199	Isoform Short of TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15	sp|Q92804-2|RBP56_HUMAN (+1)	62 kDa	0.00069	
200	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	sp|P62854|RS26_HUMAN (+1)	13 kDa	0.012	
201	p21-activated protein kinase-interacting protein 1 OS=Homo sapiens GN=PAK1IP1 PE=1 SV=2	sp|Q9NWT1|PK1IP_HUMAN	44 kDa	0.00048	
202	Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1	sp|Q8WTT2|NOC3L_HUMAN (+1)	93 kDa	1	
203	Isoform 2 of Probable ATP-dependent RNA helicase DDX56	sp|Q9NY93-2|DDX56_HUMAN (+1)	57 kDa	0.0039	

	OS=Homo sapiens GN=DDX56					
204	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	sp|P60709|ACTB_HUMAN	42 kDa	TRUE	0.37	0.37
205	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	sp|P62979|RS27A_HUMAN	18 kDa		0.3	0.37
206	Protein KRI1 homolog OS=Homo sapiens GN=KRI1 PE=1 SV=2	sp|Q8N9T8|KRI1_HUMAN	83 kDa		0.0011	
207	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1	sp|P62861|RS30_HUMAN	7 kDa		0.12	
208	Isoform 2 of ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X	sp|O00571-2|DDX3X_HUMAN (+1)	71 kDa		0.033	
209	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=2 SV=2	sp|P62891|RL39_HUMAN	6 kDa		0.37	
210	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	sp|P08727|K1C19_HUMAN	44 kDa	TRUE	0.021	
211	Isoform 1 of Complement decay-accelerating factor OS=Homo sapiens GN=CD55	sp|P08174-2|DAF_HUMAN (+7)	49 kDa		0.025	
212	Isoform 2 of Supervillin OS=Homo sapiens GN=SVIL	sp|O95425-2|SVIL_HUMAN (+1)	201 kDa		0.0038	0.022
213	NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=1 SV=3	sp|P55769|NH2L1_HUMAN	14 kDa		0.011	
214	Transformer-2 protein homolog beta (Fragment) OS=Homo sapiens GN=TRA2B PE=4 SV=1	tr|H7C2L4|H7C2L4_HUMAN	13 kDa	TRUE	<0.00010	
215	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2	sp|P83881|RL36A_HUMAN (+1)	12 kDa		<0.00010	
216	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	sp|P62081|RS7_HUMAN (+1)	22 kDa		0.12	
217	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2	sp|P62273|RS29_HUMAN	7 kDa		0.091	0.00099

218	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	sp|Q14247|SRC8_HUMAN	62 kDa		1	
219	Unhealthy ribosome biogenesis protein 2 homolog OS=Homo sapiens GN=URB2 PE=1 SV=2	sp|Q14146|URB2_HUMAN	171 kDa		0.021	
220	Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2	sp|Q15269|PWP2_HUMAN	102 kDa		0.00098	
221	H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens GN=NOP10 PE=1 SV=1	sp|Q9NPE3|NOP10_HUMAN	8 kDa		0.00098	
222	Isoform 2 of Protein polybromo-1 OS=Homo sapiens GN=PBRM1	sp|Q86U86-2|PB1_HUMAN (+6)	187 kDa		0.12	
223	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	sp|P62140|PP1B_HUMAN	37 kDa	TRUE	0.12	
224	Isoform 2 of Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A	sp|O14974-2|MYPT1_HUMAN (+5)	111 kDa		0.016	0.29
225	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	sp|P61313|RL15_HUMAN	24 kDa		0.031	
226	Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2	sp|Q12788|TBL3_HUMAN (+1)	89 kDa		0.0022	
227	RNA-binding protein 34 OS=Homo sapiens GN=RBM34 PE=1 SV=2	sp|P42696|RBM34_HUMAN	49 kDa		0.0061	
228	Isoform 3 of G patch domain-containing protein 4 OS=Homo sapiens GN=GPATCH4	sp|Q5T3I0-3|GPTC4_HUMAN (+2)	51 kDa		0.0061	
229	Isoform 2 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR	sp|P55265-2|DSRAD_HUMAN (+6)	133 kDa		0.0061	
230	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	sp|P62158|CALM_HUMAN (+3)	17 kDa		0.12	0.37

231	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	sp|P47755|CAZA2_HUMAN	33 kDa	TRUE	0.00028	0.12
232	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	sp|Q15293|RCN1_HUMAN	39 kDa		0.0023	
233	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens GN=DDX10 PE=1 SV=2	sp|Q13206|DDX10_HUMAN (+1)	101 kDa		0.0023	
234	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	sp|P80723|BASP1_HUMAN	23 kDa		0.0002	
235	Isoform SRP55-3 of Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6	sp|Q13247-3|SRSF6_HUMAN (+1)	38 kDa		0.008	
236	mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2	sp|Q9UKD2|MRT4_HUMAN	28 kDa		0.008	
237	Isoform 3 of Death-associated protein kinase 1 OS=Homo sapiens GN=DAPK1	sp|P53355-3|DAPK1_HUMAN (+3)	161 kDa		0.0029	
238	ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1	sp|Q9BQ39|DDX50_HUMAN	83 kDa	TRUE	0.002	
239	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	sp|O75955|FLOT1_HUMAN (+1)	47 kDa		0.0002	
240	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3	sp|Q16778|H2B2E_HUMAN	14 kDa	TRUE	0.58	0.0081
241	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	sp|P52597|HNRPF_HUMAN	46 kDa		0.00039	
242	WD repeat-containing protein 5 OS=Homo sapiens GN=WDR5 PE=1 SV=1	sp|P61964|WDR5_HUMAN	37 kDa		0.026	
243	Isoform Short of Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2	sp|P51531-2|SMCA2_HUMAN (+1)	179 kDa	TRUE	0.00022	<0.00010

244	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	sp|Q13242|SRSF9_HUMAN	26 kDa		0.0053	
245	WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1	sp|Q8NI36|WDR36_HUMAN (+1)	105 kDa		0.0053	
246	Isoform 2 of RNA-binding protein 39 OS=Homo sapiens GN=RBM39	sp|Q14498-2|RBM39_HUMAN (+4)	59 kDa		0.0053	
247	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC	sp|P07910-2|HNRPC_HUMAN (+14)	32 kDa		0.038	
248	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2	sp|Q9NVP1|DDX18_HUMAN	75 kDa		0.00039	
249	Isoform 1 of Fragile X mental retardation protein 1 OS=Homo sapiens GN=FMR1	sp|Q06787-2|FMR1_HUMAN (+2)	67 kDa	TRUE	0.16	
250	Isoform 2 of KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1	sp|Q13601-2|KRR1_HUMAN (+1)	37 kDa		0.16	
251	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	sp|P68371|TBB4B_HUMAN	50 kDa	TRUE	0.12	
252	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	sp|O15143|ARC1B_HUMAN	41 kDa		0.37	
253	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	sp|Q8WXX5|DNJC9_HUMAN	30 kDa		0.0075	
254	Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	sp|Q15208|STK38_HUMAN	54 kDa		0.00056	0.37
255	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3	sp|Q9Y2R4|DDX52_HUMAN	68 kDa		0.0075	
256	PIN2/TERF1-interacting telomerase inhibitor 1	sp|Q96BK5|PINX1_HUMAN	37 kDa		0.12	

	OS=Homo sapiens GN=PINX1 PE=1 SV=2					
257	Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4	sp|O60287|NPA1P_HUMAN	254 kDa		0.14	
258	Isoform 2 of Basigin OS=Homo sapiens GN=BSG	sp|P35613-2|BASI_HUMAN (+3)	29 kDa		0.12	
259	Isoform 4 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7	sp|Q16629-4|SRSF7_HUMAN (+1)	26 kDa		0.13	
260	Isoform 2 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4	sp|P59998-2|ARPC4_HUMAN (+3)	72 kDa		0.37	0.0016
261	Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	sp|Q13045|FLII_HUMAN	145 kDa		0.0065	
262	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	sp|P62318|SMD3_HUMAN (+1)	14 kDa		0.00039	0.37
263	Isoform 5 of Putative oxidoreductase GLYR1 OS=Homo sapiens GN=GLYR1	sp|Q49A26-5|GLYR1_HUMAN	52 kDa		1	
264	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	sp|P49458|SRP09_HUMAN	10 kDa		1	
265	RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3	sp|Q9Y2P8|RCL1_HUMAN	41 kDa		0.12	
266	Isoform 2 of Protein SSXT OS=Homo sapiens GN=SS18	sp|Q15532-2|SSXT_HUMAN (+7)	42 kDa		0.12	0.16
267	Isoform 2 of Signal-induced proliferation-associated 1-like protein 1 OS=Homo sapiens GN=SIPA1L1	sp|O43166-2|SI1L1_HUMAN (+2)	197 kDa		0.12	0.0025
268	Keratin, type II cytoskeletal 73	sp|Q86Y46|K2C73_HUMAN	59 kDa	TRUE	0.12	

	OS=Homo sapiens GN=KRT73 PE=1 SV=1					
269	Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 OS=Homo sapiens GN=SMARCD1	sp|Q96GM5-2|SMRD1_HUMAN (+1)	53 kDa	TRUE	0.019	0.00049
270	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	sp|Q15393|SF3B3_HUMAN	136 kDa		0.016	
271	Protein C16orf88 OS=Homo sapiens GN=C16orf88 PE=1 SV=1	sp|Q1ED39|CP088_HUMAN	52 kDa		0.16	
272	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	sp|P43243|MATR3_HUMAN (+3)	95 kDa		0.12	
273	Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1	sp|Q9NY61|AATF_HUMAN	63 kDa		0.12	
274	Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1	sp|Q01082-3|SPTB2_HUMAN	251 kDa	TRUE	0.37	
275	Isoform 2 of Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2	sp|O15020-2|SPTN2_HUMAN (+1)	268 kDa	TRUE	0.37	
276	Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=1 SV=1	sp|Q13610|PWP1_HUMAN (+1)	56 kDa		0.12	
277	Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A	sp|P11388-2|TOP2A_HUMAN (+3)	178 kDa	TRUE	0.12	
278	Isoform 2 of Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN	sp|Q9NQ55-2|SSF1_HUMAN (+2)	52 kDa	TRUE	0.12	
279	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	sp|P67936|TPM4_HUMAN	29 kDa	TRUE	0.12	
280	Isoform 2 of Neuroguidin OS=Homo sapiens GN=NGDN	sp|Q8NEJ9-2|NGDN_HUMAN (+2)	35 kDa		0.16	
281	Q8TD57|DYH3_HUMAN-DECOY	Q8TD57|DYH3_HUMAN-DECOY	?		0.37	

282	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	sp|P27635|RL10_HUMAN (+1)	25 kDa		0.37
283	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	sp|P05023|AT1A1_HUMAN	113 kDa		0.13
284	H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1	sp|Q9NX24|NHP2_HUMAN	17 kDa		0.37
285	Isoform 6 of Cyclin-dependent kinase inhibitor 2A, isoform 4 OS=Homo sapiens GN=CDKN2A	sp|Q8N726-2|CD2A2_HUMAN (+1)	9 kDa		0.13
286	Isoform 2 of Nucleolar protein 8 OS=Homo sapiens GN=NOL8	sp|Q76FK4-2|NOL8_HUMAN (+5)	124 kDa		0.37
287	Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20	sp|P60866-2|RS20_HUMAN (+1)	16 kDa		0.37
288	ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=1 SV=3	sp|Q8N8A6|DDX51_HUMAN	72 kDa		0.37
289	Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK	sp|P61978-2|HNRPK_HUMAN (+4)	51 kDa		0.12
290	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	sp|P32969|RL9_HUMAN (+1)	22 kDa		0.12
291	SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2	sp|Q9NWH9|SLTM_HUMAN	117 kDa		0.37
292	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1	sp|O95478|NSA2_HUMAN	30 kDa	TRUE	0.12
293	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3	sp|Q9Y5J1|UTP18_HUMAN	62 kDa		0.37
294	Isoform 2 of Protein ELYS OS=Homo sapiens GN=AHCTF1	sp|Q8WYP5-2|ELYS_HUMAN (+2)	256 kDa		0.37

295	Isoform 2 of DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC	sp|P78527-2|PRKDC_HUMAN (+2)	466 kDa	0.37	
296	Q9C0G0-2|ZN407_HUMAN-DECOY	Q9C0G0-2|ZN407_HUMAN-DECOY	?	0.37	
297	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	sp|P08238|HS90B_HUMAN	83 kDa	0.37	
298	Isoform 2 of Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP	sp|Q6WCQ1-2|MPRIP_HUMAN (+3)	118 kDa	0.37	
299	U3 small nucleolar ribonucleoprotein protein IMP4 OS=Homo sapiens GN=IMP4 PE=1 SV=1	sp|Q96G21|IMP4_HUMAN (+3)	34 kDa	0.37	
300	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	sp|Q9Y5B9|SP16H_HUMAN	120 kDa	0.37	
301	Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1	sp|P22626-2|ROA2_HUMAN (+1)	36 kDa	0.37	
302	Isoform 2 of AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2	sp|Q68CP9-3|ARID2_HUMAN (+1)	191 kDa	0.37	0.0057
303	Zinc finger protein 234 OS=Homo sapiens GN=ZNF234 PE=2 SV=3	sp|Q14588|ZN234_HUMAN	81 kDa	0.37	
304	Putative ATP-dependent RNA helicase DHX33 OS=Homo sapiens GN=DHX33 PE=1 SV=2	sp|Q9H6R0|DHX33_HUMAN	79 kDa	0.37	
305	Isoform 2 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3	sp|Q12906-2|ILF3_HUMAN (+6)	76 kDa	0.37	
306	NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2	sp|O15226|NKRF_HUMAN (+1)	78 kDa	0.37	
307	Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus	sp|Q9UKV3-5|ACINU_HUMAN (+2)	151 kDa	0.37	

	OS=Homo sapiens GN=ACIN1				
308	RecName: Full=Lactotransferrin; Short=Lactoferrin; AltName: Full=Talalactoferrin; Contains: RecName: Full=Kaliocin-1; Contains: RecName: Full=Lactoferroxin-A; Contains: RecName: Full=Lactoferroxin-B; Contains: RecName: Full=Lactoferroxin-C; Flags: Precursor	gi|85700158|sp|P02788.6|TRFL_HUMAN (+3)	78 kDa		0.37
309	Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2	sp|Q15366-2|PCBP2_HUMAN (+9)	39 kDa	TRUE	0.37
310	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	sp|Q14692|BMS1_HUMAN	146 kDa		0.37
311	Interferon-stimulated 20 kDa exonuclease-like 2 OS=Homo sapiens GN=ISG20L2 PE=1 SV=1	sp|Q9H9L3|I20L2_HUMAN	39 kDa		0.37
312	Q7Z7A1-5|CNTRL_HUMAN-DECOY	Q7Z7A1-5|CNTRL_HUMAN-DECOY	?		0.37

List of Proteins Only in Lanes 2,3

#	Identified Proteins (162)	Accession Number	Molecular Weight	Protein Grouping Ambiguity	Lanes 2,3 P-values	What protein from 6,7 is it similar to?
16	RecName: Full=Serum albumin; AltName: Full=BSA; AltName: Allergen=Bos d 6; Flags: Precursor	gi|1351907|sp|P02769.4|ALBU_BOVIN	69 kDa	TRUE	<0.00010	Similar to 123
19	Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB	sp|O75369-2|FLNB_HUMAN (+3)	276 kDa	TRUE	0.0011	
22	Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6	sp|P11217|PYGM_HUMAN	97 kDa		<0.00010	
32	RecName: Full=Carbonic anhydrase 2; AltName: Full=Carbonate dehydratase II; AltName: Full=Carbonic anhydrase II; Short=CA-II	gi|41019480|sp|P00921.3|CAH2_BOVIN	29 kDa		<0.00010	
33	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	sp|P68431|H31_HUMAN (+2)	15 kDa		0.00053	Extremely similar to 88
34	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	sp|P68363|TBA1B_HUMAN (+5)	50 kDa		0.11	Extremely similar to 30
39	Isoform 2 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1	sp|Q9NYF8-2|BCLF1_HUMAN (+1)	106 kDa	TRUE	0.0011	
40	RecName: Full=Beta-galactosidase; Short=Beta-gal; AltName: Full=Lactase	gi|114939|sp|P00722.2|BGAL_ECOLI	116 kDa		0.00031	
42	RecName: Full=Ovalbumin; AltName: Full=Allergen Gal d II; AltName: Full=Egg albumin; AltName: Full=Plakalbumin; AltName: Allergen=Gal d 2	gi|129293|sp|P01012.2|OVAL_CHICK	43 kDa		0.00067	

44	Isoform 2 of Plectin OS=Homo sapiens GN=PLEC	sp|Q15149-2|PLEC_HUMAN (+7)	518 kDa		0.016	Extremely similar to 16
47	Isoform 8 of Protein polybromo-1 OS=Homo sapiens GN=PBRM1	sp|Q86U86-8|PB1_HUMAN (+1)	190 kDa		<0.00010	
48	Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2	sp|Q92925-3|SMRD2_HUMAN (+2)	55 kDa	TRUE	<0.00010	
62	Isoform 2 of AT-rich interactive domain-containing protein 1B OS=Homo sapiens GN=ARID1B	sp|Q8NFD5-2|ARI1B_HUMAN (+2)	238 kDa	TRUE	<0.00010	
66	Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6	sp|P60660-2|MYL6_HUMAN (+1)	17 kDa		0.028	Extremely similar to 150
70	Isoform 3 of Neurabin-1 OS=Homo sapiens GN=PPP1R9A	sp|Q9ULJ8-3|NEB1_HUMAN (+2)	154 kDa	TRUE	0.18	Extremely similar to 170
72	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	sp|P62280|RS11_HUMAN (+1)	18 kDa		0.045	Extremely similar to 74
75	Isoform 2 of 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28	sp|P46779-2|RL28_HUMAN (+3)	18 kDa		0.00051	
78	Isoform 2 of Myosin-10 OS=Homo sapiens GN=MYH10	sp|P35580-2|MYH10_HUMAN (+4)	231 kDa	TRUE	<0.00010	
79	Isoform 2 of Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2	sp|Q86SQ0-2|PHLB2_HUMAN (+3)	137 kDa		0.00067	Extremely similar to 169
85	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	sp|P62249|RS16_HUMAN (+1)	16 kDa		0.037	Extremely similar to 76
86	RecName: Full=Lysozyme C; AltName: Full=1,4-beta-N-acetylmuramidase C; AltName: Full=Allergen Gal d IV; AltName:	gi|126608|sp|P00698.1|LYSC_CHICK	16 kDa		0.0099	

	Allergen=Gal d 4; Flags: Precursor					
96	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	sp|P15880|RS2_HUMAN (+1)	31 kDa		0.018	Extremely similar to 54
100	Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=1 SV=2	sp|Q92785|REQU_HUMAN (+2)	44 kDa		0.00084	Extremely similar to 190
101	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	sp|P68104|EF1A1_HUMAN (+2)	50 kDa		0.45	Extremely similar to 161
104	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	sp|P62241|RS8_HUMAN (+1)	24 kDa		0.0011	Extremely similar to 52
109	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	sp|P61247|RS3A_HUMAN (+1)	30 kDa		0.1	Extremely similar to 19
110	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	sp|P11142|HSP7C_HUMAN (+1)	71 kDa	TRUE	0.76	Extremely similar to 94
114	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	sp|P62244|RS15A_HUMAN (+1)	15 kDa		0.0091	Extremely similar to 85
117	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	sp|P61254|RL26_HUMAN (+5)	17 kDa		0.11	Extremely similar to 71
118	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	sp|P35268|RL22_HUMAN (+3)	15 kDa		0.00055	Extremely similar to 156
119	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	sp|P46776|RL27A_HUMAN (+1)	17 kDa		0.14	Extremely similar to 109
120	OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=3	sp|Q01804|OTUD4_HUMAN (+1)	124 kDa		0.31	
127	Isoform 3 of Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13	sp|P13646-3|K1C13_HUMAN (+2)	46 kDa	TRUE	0.13	
128	60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	sp|P61513|RL37A_HUMAN (+3)	10 kDa		0.0034	Extremely similar to 192

136	Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC	sp|P36873-2|PP1G_HUMAN (+2)	39 kDa	TRUE	0.37	
137	40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	sp|P08708|RS17_HUMAN (+5)	16 kDa		0.37	Extremely similar to 179
138	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	sp|P62750|RL23A_HUMAN (+4)	18 kDa		<0.00010	Extremely similar to 92
140	Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2	sp|P61160-2|ARP2_HUMAN (+2)	45 kDa		0.37	Extremely similar to 181
141	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2	sp|P63173|RL38_HUMAN	8 kDa		0.36	
147	60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1	tr|Q5VVC8|Q5VVC8_HUMAN	20 kDa		0.37	
148	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	sp|P39019|RS19_HUMAN (+4)	16 kDa		0.00039	Extremely similar to 112
149	Isoform 3 of B-cell CLL/lymphoma 7 protein family member B OS=Homo sapiens GN=BCL7B	sp|Q9BQE9-3|BCL7B_HUMAN (+4)	18 kDa		0.37	
152	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	sp|O60814|H2B1K_HUMAN	14 kDa	TRUE	0.37	
154	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	sp|Q02543|RL18A_HUMAN (+3)	21 kDa		0.37	Extremely similar to 51
155	Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3	sp|P12882|MYH1_HUMAN	223 kDa	TRUE	0.13	
156	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	sp|O15144|ARPC2_HUMAN	34 kDa		0.12	
157	60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=3 SV=1	tr|H0YHA7|H0YHA7_HUMAN	19 kDa		0.37	

158	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	sp|P83731|RL24_HUMAN (+2)	18 kDa	0.37	Extremely similar to 89
159	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	sp|P46940|IQGA1_HUMAN (+1)	189 kDa	0.12	Extremely similar to 138
160	Isoform 2 of PHD finger protein 10 OS=Homo sapiens GN=PHF10	sp|Q8WUB8-2|PHF10_HUMAN (+2)	56 kDa	0.37	
161	Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN	sp|Q14247-2|SRC8_HUMAN (+2)	71 kDa	0.37	
162	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	sp|P18621|RL17_HUMAN (+5)	21 kDa	0.37	Extremely similar to 68

Appendix 2: List of Protein Descriptions for Proteins with a Significant P-value in both the 6,7 and 2,3 Proteomics Results

(Some of the description were unable to be determined.)

References 5,6, and 7 from the Bibliography were used to find the protein descriptions.

Protein Name	Description
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	Cellular myosin that appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. During cell spreading, plays an important role in cytoskeleton reorganization, focal contacts formation (in the margins but not the central part of spreading cells), and lamellipodial retraction; this function is mechanically antagonized by MYH10. http://www.uniprot.org/uniprot/P35579
Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA	Promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. Interaction with FLNA may allow neuroblast migration from the ventricular zone into the cortical plate. Tethers cell surface-localized furin, modulates its rate of internalization and directs its intracellular trafficking (By similarity). Involved in ciliogenesis. http://www.uniprot.org/uniprot/P21333
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	Fodrin, which seems to be involved in secretion, interacts with calmodulin in a calcium-dependent manner and is thus candidate for the calcium-dependent movement of the cytoskeleton at the membrane. http://www.uniprot.org/uniprot/Q13813
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	Fodrin, which seems to be involved in secretion, interacts with calmodulin in a calcium-dependent manner and is thus candidate for the calcium-dependent movement of the cytoskeleton at the membrane. http://www.uniprot.org/uniprot/Q01082
LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=2 SV=1	• ubiquitin-protein transferase activity • zinc ion binding • protein ubiquitination • regulation of cell adhesion • regulation of signaling http://www.uniprot.org/uniprot/Q8WWI1
RecName: Full=Keratin, type II cytoskeletal 1; AltName: Full=67 kDa cytokeratin; AltName:	• May regulate the activity of kinases such as PKC and SRC via binding to integrin beta-1 (ITB1) and the receptor of activated protein C kinase 1

Full=Cytokeratin-1; Short=CK-1; AltName: Full=Hair alpha protein; AltName: Full=Keratin-1; Short=K1; AltName: Full=Type-II keratin Kb1	(RACK1). In complex with C1QBP is a high affinity receptor for kininogen-1/HMWK. • Carbohydrate binding • Receptor activity • Structural molecule activity http://www.uniprot.org/uniprot/P04264
RecName: Full=Keratin, type II cytoskeletal 2 epidermal; AltName: Full=Cytokeratin-2e; Short=CK-2e; AltName: Full=Epithelial keratin-2e; AltName: Full=Keratin-2 epidermis; AltName: Full=Keratin-2e; Short=K2e; AltName: Full=Type-II keratin Kb2	• Probably contributes to terminal cornification. Associated with keratinocyte activation, proliferation and keratinization • Structural constituent of cytoskeleton http://www.uniprot.org/uniprot/P35908
RecName: Full=Keratin, type I cytoskeletal 9; AltName: Full=Cytokeratin-9; Short=CK-9; AltName: Full=Keratin-9; Short=K9	• May serve an important special function either in the mature palmar and plantar skin tissue or in the morphogenetic program of the formation of these tissues. Plays a role in keratin filament assembly. • Structural constituent of cytoskeleton http://www.uniprot.org/uniprot/P35527
Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	• Involved in the uptake of thrombin-antithrombin complexes by hepatic cells (By similarity). When phosphorylated, plays a role in filament reorganization. Involved in the delivery of mutated CFTR to the plasma membrane. Together with KRT8, is involved in interleukin-6 (IL-6)-mediated barrier protection. • poly(A) RNA binding • scaffold protein • structural molecule activity http://www.uniprot.org/uniprot/P05783
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	• poly(A) RNA binding • rRNA binding • structural constituent of ribosome • cellular protein metabolic process • gene expression • multicellular organismal development • nuclear-transcribed mRNA catabolic process, nonsense-mediated decay • positive regulation of cell proliferation • positive regulation of translation

	• SRP-dependent cotranslational protein targeting to membrane • translation • translational elongation • translational initiation • translational termination • viral life cycle • viral process • viral transcription http://www.uniprot.org/uniprot/P62701
Uncharacterized protein C19orf21 OS=Homo sapiens GN=C19orf21 PE=1 SV=1	Could not find a lot of info about this protein.
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	• F-actin cross-linking protein which is thought to anchor actin to a variety of intracellular structures. This is a bundling protein (Probable). Probably involved in vesicular trafficking via its association with the CART complex. The CART complex is necessary for efficient transferrin receptor recycling but not for EGFR degradation (PubMed:15772161). Involved in tight junction assembly in epithelial cells probably through interaction with MICALL2. Links MICALL2 to the actin cytoskeleton and recruits it to the tight junctions (By similarity). May also function as a transcriptional coactivator, stimulating transcription mediated by the nuclear hormone receptors PPARG and RARA • actin binding • actin filament binding • calcium ion binding • chromatin DNA binding • integrin binding • ion channel binding • ligand-dependent nuclear receptor transcription coactivator activity • nuclear hormone receptor binding • nucleoside binding • poly(A) RNA binding • protein homodimerization activity • retinoic acid receptor binding • RNA polymerase II regulatory region sequence-specific DNA binding http://www.uniprot.org/uniprot/O43707

60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	• Specifically binds to domain C of the Tax-responsive enhancer element in the long terminal repeat of HTLV-I. • DNA binding • poly(A) RNA binding • RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/Q02878
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	Involved in pre-mRNA splicing. Remains associated with spliced mRNA after splicing which probably involves interactions with the exon junction complex (EJC). Can trigger mRNA decay which seems to be independent of nonsense-mediated decay involving premature stop codons (PTC) recognition. May be involved in nuclear mRNA decay. Involved in regulation of signal-induced alternative splicing. During splicing of PTPRC/CD45 is proposed to sequester phosphorylated SFPQ from PTPRC/CD45 pre-mRNA in resting T-cells. Involved in cyclin-D1/CCND1 mRNA stability probably by acting as component of the SNARP complex which associates with both the 3'end of the CCND1 gene and its mRNA. Involved in response to DNA damage. Is excluced from DNA damage sites in a manner that parallels transcription inhibition; the function may involve the SNARP complex. Initially thought to play a role in transcriptional coactivation through its association with the TRAP complex; however, it is not regarded as a stable Mediator complex subunit. Cooperatively with HELZ2, enhances the transcriptional activation mediated by PPARG, maybe through the stabilization of the PPARG binding to DNA in presence of ligand. May play a role in the terminal stage of adipocyte differentiation. Plays a role in the positive regulation of the circadian clock. Acts as a coactivator of the CLOCK-ARNTL/BMAL1 heterodimer and promotes its transcriptional activator activity and binding to circadian target genes. http://www.uniprot.org/uniprot/Q9Y2W1
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	Part of Ribosome. Can't really find anything
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	• poly(A) RNA binding • RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62424

Isoform 3 of Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A	May link Golgi membranes to the cytoskeleton and participate in the tensile force required for vesicle budding from the Golgi. Thereby, may play a role in Golgi membrane trafficking and could indirectly give its flattened shape to the Golgi apparatus. Alternatively, in concert with LURAP1 and CDC42BPA/CDC42BPB, has been involved in modulating lamellar actomyosin retrograde flow that is crucial to cell protrusion and migration. May be involved in the maintenance of the stromal cell architectures required for cell to cell contact. http://www.uniprot.org/uniprot/Q92614 **Couldn't really find anything on Isoform 3 specifically**
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	• poly(A) RNA binding • RNA binding • rRNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62917
Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling. Has broad antibacterial activity. May contribute to the formation of the functional antimicrobial barrier of the colonic epithelium, and to the bactericidal activity of amniotic fluid. http://www.uniprot.org/uniprot/P62807
SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	SWI/SNF
LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	• Binds to actin monomers and filaments. Increases the number and size of actin stress fibers and inhibits membrane ruffling. Inhibits actin filament depolymerization. Bundles actin filaments, delays filament nucleation and reduces formation of branched filaments.1 Publication • actin filament binding • actin monomer binding • zinc ion binding http://www.uniprot.org/uniprot/Q9UHB6

60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	• poly(A) RNA binding • RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P26373#P26373-1
Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2	• artery development • neural fold bending • ventricular septum development http://www.uniprot.org/uniprot/Q86V48 • This gene encodes a protein that contains a leucine zipper motif. The exact function of the encoded protein is not known. In mice this gene affects neural tube closure. Alternative splicing results in multiple transcript variants. http://www.ncbi.nlm.nih.gov/gene/7798
Unconventional myosin-Ig OS=Homo sapiens GN=MYO1G PE=1 SV=2	• Unconventional myosin required during immune response for detection of rare antigen-presenting cells by regulating T-cell migration. Unconventional myosins are actin-based motor molecules with ATPase activity and serve in intracellular movements. Acts as a regulator of T-cell migration by generating membrane tension, enforcing cell-intrinsic meandering search, thereby enhancing detection of rare antigens during lymph-node surveillance, enabling pathogen eradication. Also required in B-cells, where it regulates different membrane/cytoskeleton-dependent processes. Involved in Fc-gamma receptor (Fc-gamma-R) phagocytosis. • Minor histocompatibility antigen HA-2: Constitutes the minor histocompatibility antigen HA-2. More generally, minor histocompatibility antigens (mHags) refer to immunogenic peptide which, when complexed with MHC, can generate an immune response after recognition by specific T-cells. The peptides are derived from polymorphic intracellular proteins, which are cleaved by normal pathways of antigen processing. The binding of these peptides to MHC class I or class II molecules and their expression on the cell surface can stimulate T-cell responses and thereby trigger graft rejection or graft-versus-host disease (GVHD) after

	hematopoietic stem cell transplantation from HLA-identical sibling donor. GVHD is a frequent complication after bone marrow transplantation (BMT), due to mismatch of minor histocompatibility antigen in HLA-matched sibling marrow transplants. HA-2 is restricted to MHC class I HLA-A*0201 • ATP Binding • Motor Activity • phosphatidylinositol-3,4,5-trisphosphate binding • phosphatidylinositol-3,4-bisphosphate binding • phosphatidylinositol-4,5-bisphosphate binding http://www.uniprot.org/uniprot/B0I1T2
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	• poly(A) RNA binding • RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P46778
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	• keratin filament bindingSource: UniProtKB • structural constituent of cytoskeleton • The nonhelical tail domain is involved in promoting KRT5-KRT14 filaments to self-organize into large bundles and enhances the mechanical properties involved in resilience of keratin intermediate filaments in vitro. http://www.uniprot.org/uniprot/P02533
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	• mRNA binding • poly(A) RNA binding • small ribosomal subunit rRNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62277
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	• scaffold protein binding • structural constituent of cytoskeleton http://www.uniprot.org/uniprot/P13647
SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3	SWI/SNF
Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2	• calcium-dependent phospholipid binding • calcium-dependent protein binding • calcium ion binding • phosphatidylinositol-4,5-bisphosphate binding • phospholipase A2 inhibitor activity • poly(A) RNA binding • protease binding • S100 protein binding

	http://www.uniprot.org/uniprot/P07355
Isoform 2 of Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4	• Transcriptional coactivator cooperating with nuclear hormone receptors to potentiate transcriptional activation. • Component of the CREST-BRG1 complex, a multiprotein complex that regulates promoter activation by orchestrating a calcium-dependent release of a repressor complex and a recruitment of an activator complex. http://www.uniprot.org/uniprot/P51532#P51532-2
Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	• Blocks interferon-dependent interphase and stimulates DNA synthesis in cells. Involved in the translational regulation of the human papillomavirus type 16 E7 mRNA (HPV16 E7). • Structural Molecule Activity http://www.uniprot.org/uniprot/P08729
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	• poly(A) RNA binding • RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P50914
Isoform 2 of Synaptopodin OS=Homo sapiens GN=SYNPO	Actin-associated protein that may play a role in modulating actin-based shape and motility of dendritic spines and renal podocyte foot processes. Seems to be essential for the formation of spine apparatuses in spines of telencephalic neurons, which is involved in synaptic plasticity (By similarity). http://www.uniprot.org/uniprot/Q8N3V7
Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	• Blocks the elongation and depolymerization of the actin filaments at the pointed end. The Tmod/TM complex contributes to the formation of the short actin protofilament, which in turn defines the geometry of the membrane skeleton (By similarity). • tropomyosin binding http://www.uniprot.org/uniprot/Q9NYL9
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	• poly(A) RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62266
60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	• poly(A) RNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62910
AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3	• DNA binding • ligand-dependent nuclear receptor binding • transcription coactivator activity http://www.uniprot.org/uniprot/O14497

40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	• poly(A) RNA binding • rRNA binding • structural constituent of ribosome http://www.uniprot.org/uniprot/P62269
Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	Drebrins might play some role in cell migration, extension of neuronal processes and plasticity of dendrites. Required for actin polymerization at immunological synapses (IS) and for CXCR4 recruitment to IS. http://www.uniprot.org/uniprot/Q16643
RecName: Full=Gelsolin; AltName: Full=AGEL; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor	Calcium-regulated, actin-modulating protein that binds to the plus (or barbed) ends of actin monomers or filaments, preventing monomer exchange (end-blocking or capping). It can promote the assembly of monomers into filaments (nucleation) as well as sever filaments already formed. http://moma.ki.au.dk/genome-mirror//cgi-bin/hgGene?org=Human&hgg_gene=uc004blf.1&hgg_chrom=none&db=hg19
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1	SWI/SNF
EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	• Calcium ion binding http://www.uniprot.org/uniprot/Q96C19
Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2	• Scaffold Protein in Multiple Signaling Pathways • actin filament binding • protein phosphatase 1 binding • protein phosphatase inhibitor activity http://www.uniprot.org/uniprot/Q96SB3
Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2	• May act as a scaffolding protein within caveolar membranes, functionally participating in formation of caveolae or caveolae-like vesicles. May be involved in epidermal cell adhesion and epidermal structure and function. • protein heterodimerization activity http://www.uniprot.org/uniprot/Q14254
Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	• Epidermis-specific type I keratin involved in wound healing. Involved in the activation of follicular keratinocytes after wounding, while it does not play a major role in keratinocyte proliferation or migration. Participates in the regulation of epithelial migration by inhibiting the activity of SRC during wound repair.

	• Structural Constituent of Cytoskeleton http://www.uniprot.org/uniprot/P02538
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	• ATP binding • ATP-dependent DNA helicase activity • damaged DNA binding • DNA binding • double-stranded DNA binding • poly(A) RNA binding • protein C-terminus binding • telomeric DNA binding • transcription regulatory region DNA binding • ubiquitin protein ligase binding http://www.uniprot.org/uniprot/P13010
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	• 5'-deoxyribose-5-phosphate lyase activity • ATP binding • ATP-dependent DNA helicase activity • damaged DNA binding • DNA binding • double-stranded DNA binding • poly(A) RNA binding • protein C-terminus binding • telomeric DNA binding • transcription regulatory region DNA binding http://www.uniprot.org/uniprot/P12956
Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1	SWI/SNF
Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	• Myosin regulatory subunit that plays an important role in regulation of both smooth muscle and nonmuscle cell contractile activity via its phosphorylation. Phosphorylation triggers actin polymerization in vascular smooth muscle. Implicated in cytokinesis, receptor cap ping, and cell locomotion (By similarity). • Calcium Ion Binding http://www.uniprot.org/uniprot/O14950
Isoform 2 of Actin-like protein 6A OS=Homo sapiens GN=ACTL6A	• chromatin binding • transcription coactivator activity http://www.uniprot.org/uniprot/O96019
Isoform 2 of Supervillin OS=Homo sapiens GN=SVIL	Forms a high-affinity link between the actin cytoskeleton and the membrane. Isoform 2 may be involved in modulation of focal adhesions. Supervillin-mediated down-regulation of focal adhesions involves binding to

	TRIP6. Plays a role in cytokinesis through KIF14 interaction (By similarity). http://www.uniprot.org/uniprot/O95425
Isoform Short of Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2	• ATP binding • chromatin binding • DNA-dependent ATPase activity • helicase activity • RNA polymerase II transcription coactivator activity • transcription coactivator activity • transcription regulatory region DNA binding http://www.uniprot.org/uniprot/P51531
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 OS=Homo sapiens GN=SMARCD1	Chromatin Remodeling http://www.uniprot.org/uniprot/Q96GM5