

Supplementary Data Summary

A Targeted Quantitative Proteomic Approach for Examining the Reprogramming of Small GTPases during Melanoma Metastasis

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Supplementary Figures

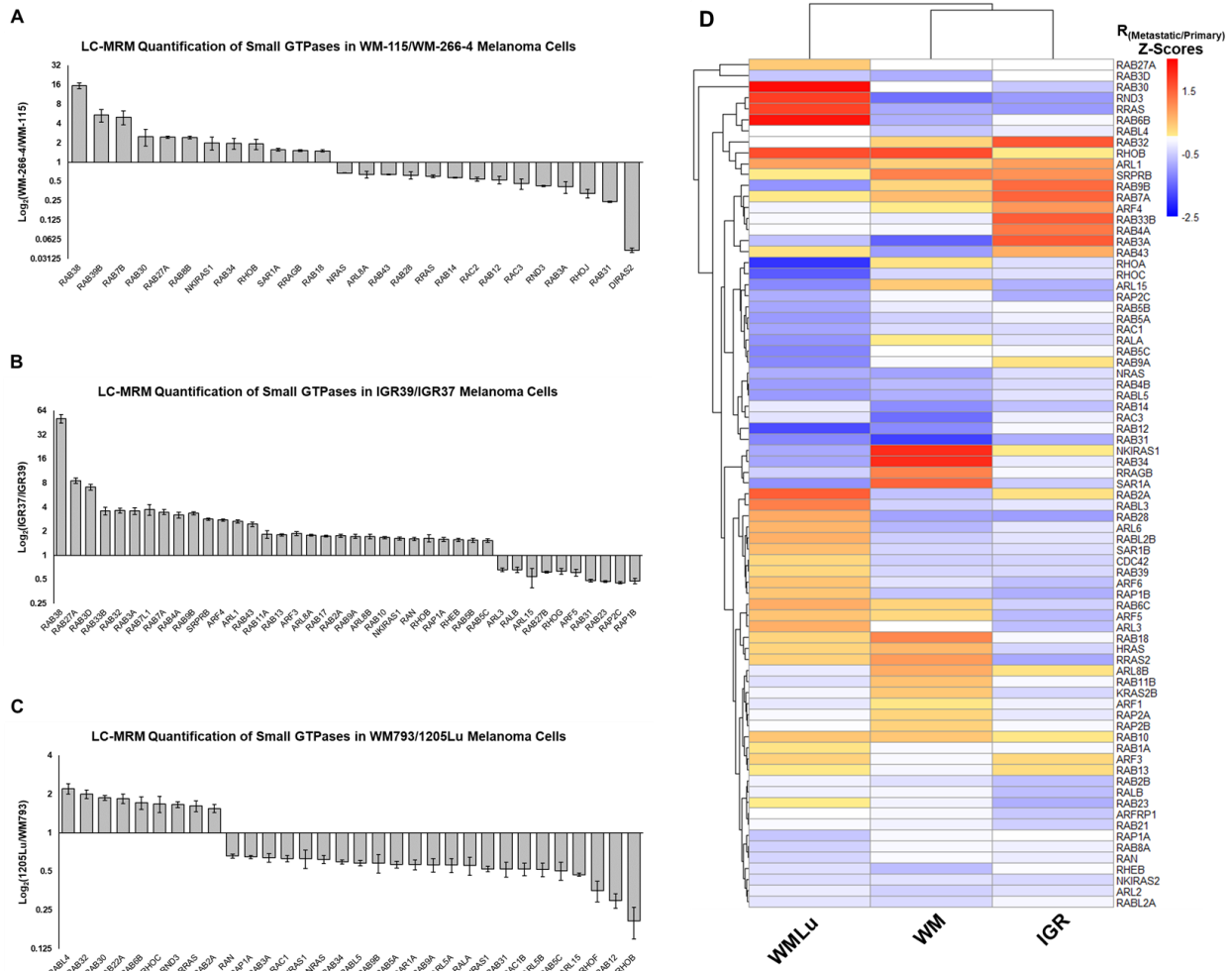


Fig. S1. LC-MRM-based targeted quantitative proteomic assay revealed differential expression of small GTPases during melanoma metastasis.

(A–C) Bar graphs showing substantially up-regulated (> 1.5-fold) and down-regulated (> 1.5-fold) small GTPases quantified from LC-MRM experiments for: (A) WM-115/WM-266-4 paired melanoma cell lines; (B) IGR39/IGR37 paired melanoma cell lines; and (C) WM793/1205Lu paired melanoma cell lines; Error bars in (A)–(C) represent mean \pm standard deviation of results from three independent SILAC labeling experiments (2 forward and 1 reverse SILAC labelings);

(D) Hierarchical clustering of commonly quantified small GTPases among the WM, IGR and WMLu paired melanoma cell lines using the Z-score values for $R_{(metastatic/primary)}$ for individual proteins.

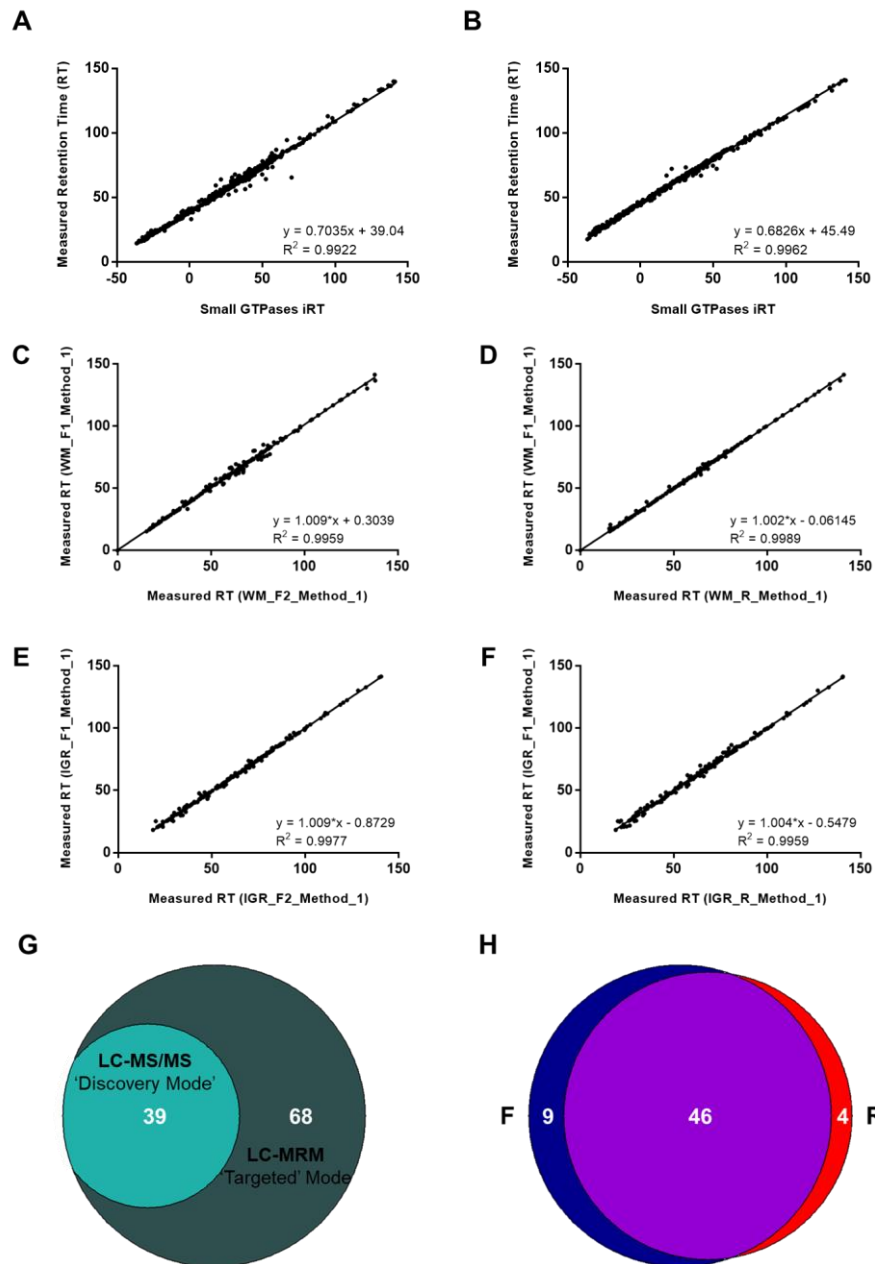


Fig. S2. The scheduled LC-MRM platform provides accurate retention time (RT) prediction of targeted peptides, high sensitivity and excellent reproducibility.

(A) The correlation between iRT and measured RT values in LC-MRM experiments using WM-115 and WM-266-4 SILAC cell lysates on a TSQ Vantage triple-quadrupole mass spectrometer (157-min linear gradient) with a very high correlation coefficient ($R^2 = 0.992$);

(B) The correlation between iRT and measured RT values in LC-MRM experiments using IGR39 and IGR37 SILAC cell lysates on the same instrument with the same gradient as in (A) with a very high correlation coefficient ($R^2 = 0.996$);

(C) The measured RT obtained in two forward labeling reactions (F1 vs. F2) for WM samples with a very high correlation coefficient ($R^2 = 0.9997$);

- (D)** The measured RT obtained in one forward and one reverse labeling reactions (F1 vs. R) for WM samples with a very high correlation coefficient ($R^2 = 0.9998$);
- (E)** The measured RT obtained in two forward labeling reactions (F1 vs. F2) for IGR samples with a very high correlation coefficient ($R^2 = 0.9997$);
- (F)** The measured RT obtained in one forward and one reverse labeling reactions (F1 vs. R) for IGR samples with a very high correlation coefficient ($R^2 = 0.9996$);
- (G)** A Venn diagram showing the overlap of quantified small GTPases from WM-115 and WM-266-4 SILAC cell lysates obtained from LC-MRM analysis and shotgun proteomics experiments;
- (H)** A Venn diagram depicting the overlap of quantified small GTPases from WM-115 and WM-266-4 SILAC cell lysates the forward (F) and the reverse (R) labeling experiments obtained from shotgun proteomics experiments.

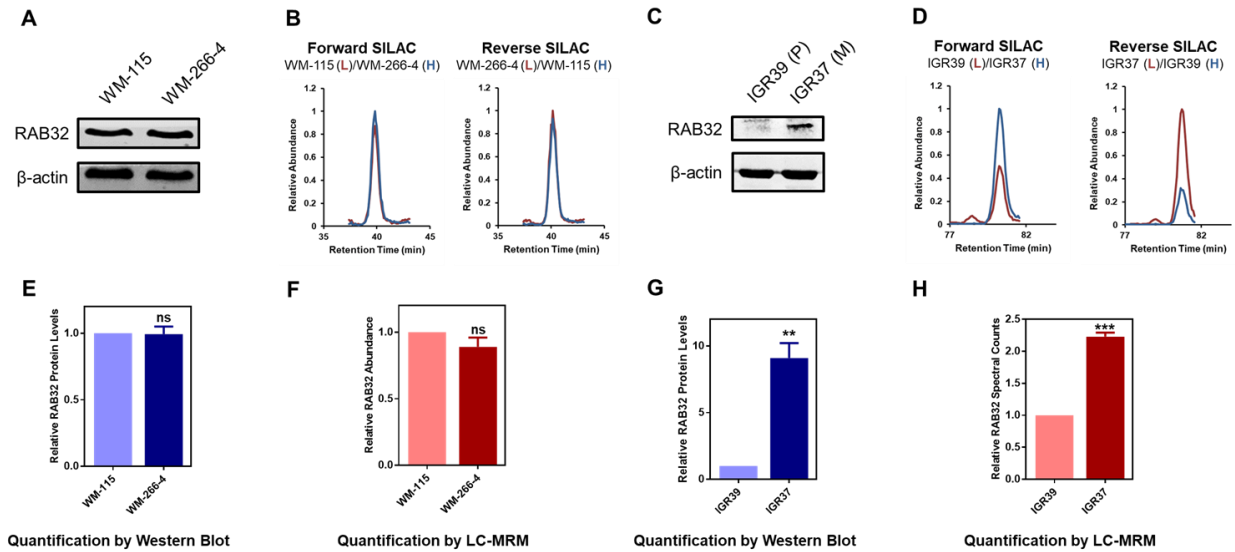


Fig. S3. Validation of RAB32 expression in WM-115/WM-266-4 and IGR39/IGR37 paired melanoma cell lines.

(A, C) Immunoblots of RAB32 in whole cell lysates from (A) WM-115/WM-266-4 and (C) IGR39/IGR37 cells, respectively, where β -actin served as a loading control;

(B, D) Representative LC-MRM traces for the quantification of peptide VLVIGELGVGK from RAB32 in forward and reverse SILAC labeling experiments for (B) WM-115/WM-266-4 and (D) IGR39/IGR37 cells, respectively;

(E, G) Quantification results for RAB32 based on Western blots analyses in panels (A) and (C);

(F, H) Quantification results for RAB32 based on LC-MRM analyses in panels (B) and (D). Error bars in (C) and (D) represent mean \pm standard deviation ($n = 3$). The p values were calculated by using a paired two-tailed Student's t test: “ns”, not significant; “**”, $0.001 < p < 0.01$; “***”, $p < 0.001$.

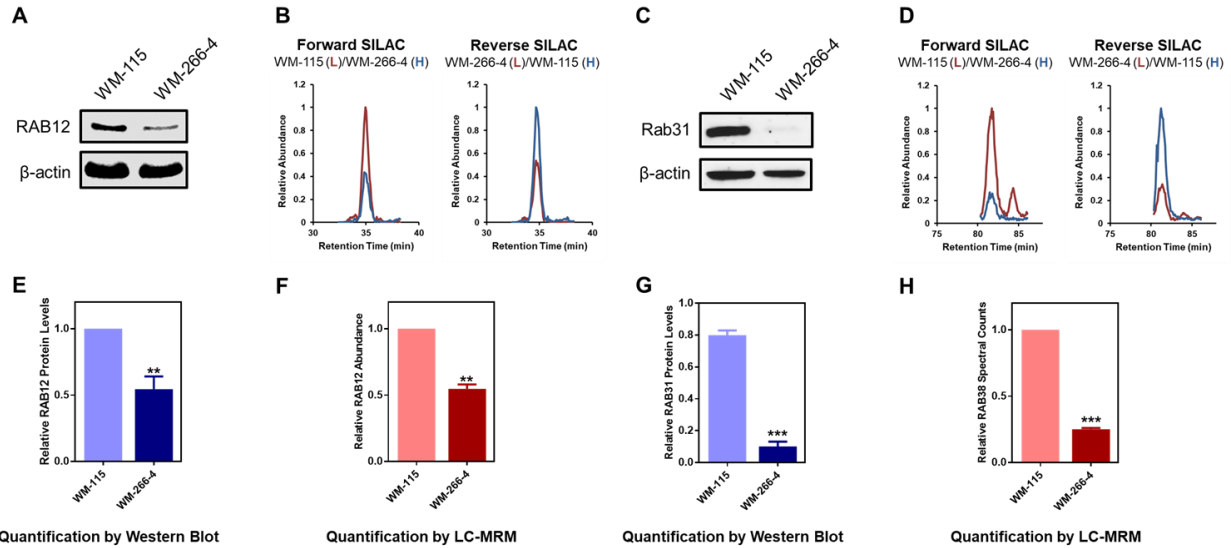


Fig. S4. RAB12 and RAB31 were differentially expressed in WM-115 and WM-266-4 cells.

(A) Immunoblots of RAB12 in whole cell lysates from WM-115 and WM-266-4 cells, where β -actin served as a loading control;

(B) Representative LC-MRM traces for the quantification of peptide AGGGGGLGAGSPALSGGQGR from RAB12 in forward and reverse SILAC labeling experiments;

(C) Quantification results for RAB12 based on Western blots analyses;

(D) Quantification results for RAB12 based on LC-MRM analyses. Error bars in (C) and (D) represent standard deviation ($n = 3$);

(E) Immunoblots of whole cell lysates from WM-115 and WM-266-4 cells, where β -actin served as a loading control;

(F) Representative LC-MRM traces for the quantification of peptide GSAAAVIVYDITK from RAB31 in forward and reverse SILAC labeling experiments;

(G) Quantification results for RAB31 based on Western blots analyses;

(H) Quantification results for RAB31 based on LC-MRM analyses. Error bars represent mean \pm standard deviation ($n = 3$). The p values were calculated by using a paired two-tailed Student's t test: “**”, $0.001 < p < 0.01$; “***”, $p < 0.001$.

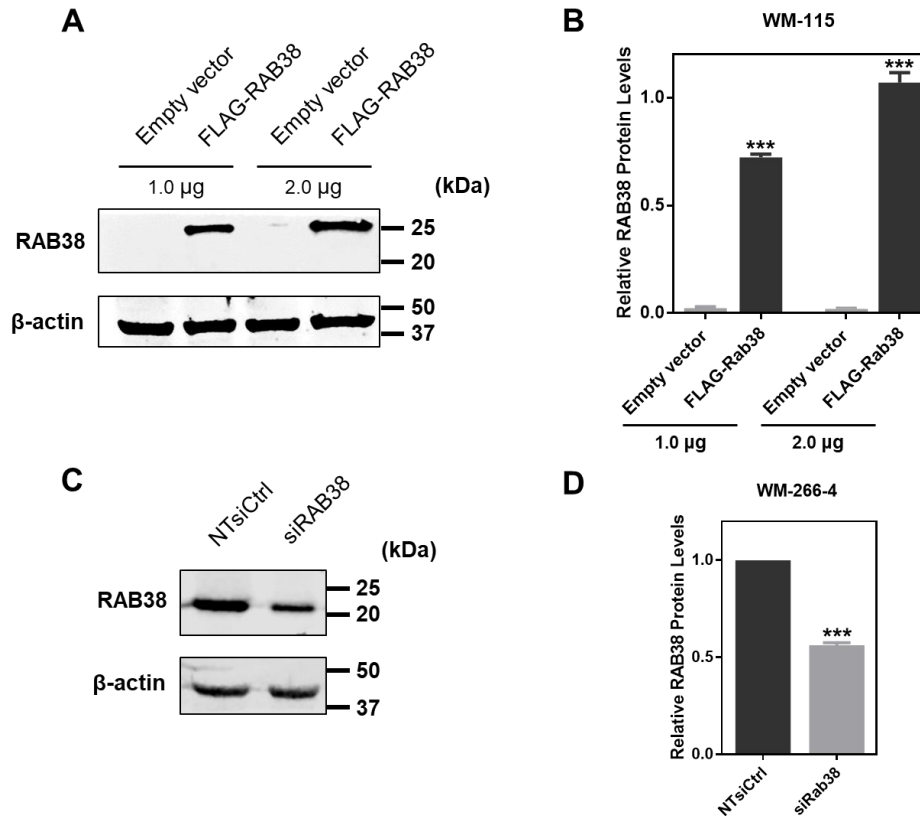


Fig. S5. Western blots confirmed the overexpression and knockdown of RAB38 in WM-115 and WM-266-4 cells, respectively.

(A) Representative immunoblots showing the ectopic expression of RAB38 in WM-115 cells, where β -actin served as a loading control;

(B) Quantification results for Western blot analyses;

(C) Representative immunoblots showing siRNA-mediated knockdown of RAB38 in WM-266-4 cells, where β -actin served as a loading control;

(D) Quantification results for Western blot analyses. Error bars in panels (B) and (D) represent standard deviation ($n = 3$). The p values were calculated by using an unpaired two-tailed Student's t test: “***”, $p < 0.001$.

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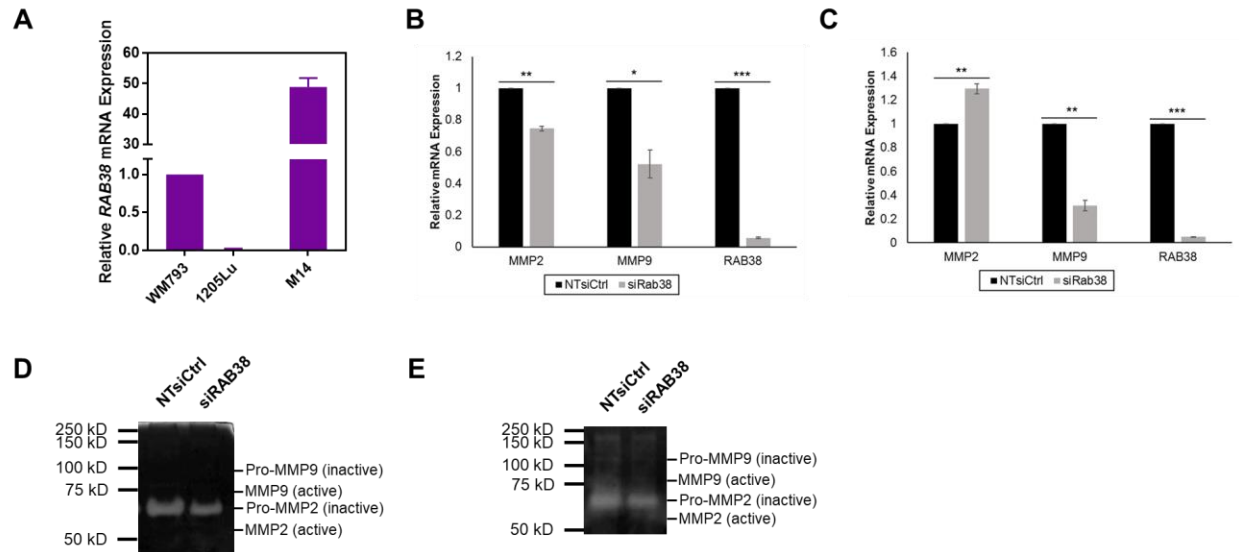


Fig. S6. RAB38 mediates both the expression levels and activities of MMP2 and MMP9 in metastatic M14 and IGR37 cells.

(A) RT-qPCR analysis showed pronouncedly higher expression levels of *RAB38* in M14 cells as compared to WM793 and 1205Lu cells. Error bars represent mean \pm SEM (n = 3);

(B) RT-qPCR analysis showed decreased expression levels of *MMP2* and *MMP9* in M14 cells with siRAB38 knockdown as compared to non-targeting siRNA control. Error bars represent mean \pm SEM (n = 3);

(C) RT-qPCR analysis showed decreased expression level of *MMP9*, but not *MMP2*, in IGR37 cells with siRAB38 knockdown as compared to non-targeting siRNA control. Error bars represent mean \pm SEM (n = 3); The *p* values in (A) and (B) were calculated by using unpaired two-tailed Student's *t* test: “*”, 0.01 < *p* < 0.05; “**”, 0.001 < *p* < 0.01; “***”, *p* < 0.001;

(D) Gelatin zymography assays revealed diminished enzymatic activities of MMP2 and MMP9 in M14 cells with siRAB38 knockdown as compared to non-targeting siRNA control;

(E) Gelatin zymography assays revealed diminished enzymatic activities of MMP2 and MMP9 in IGR37 cells with siRAB38 knockdown as compared to non-targeting siRNA control.

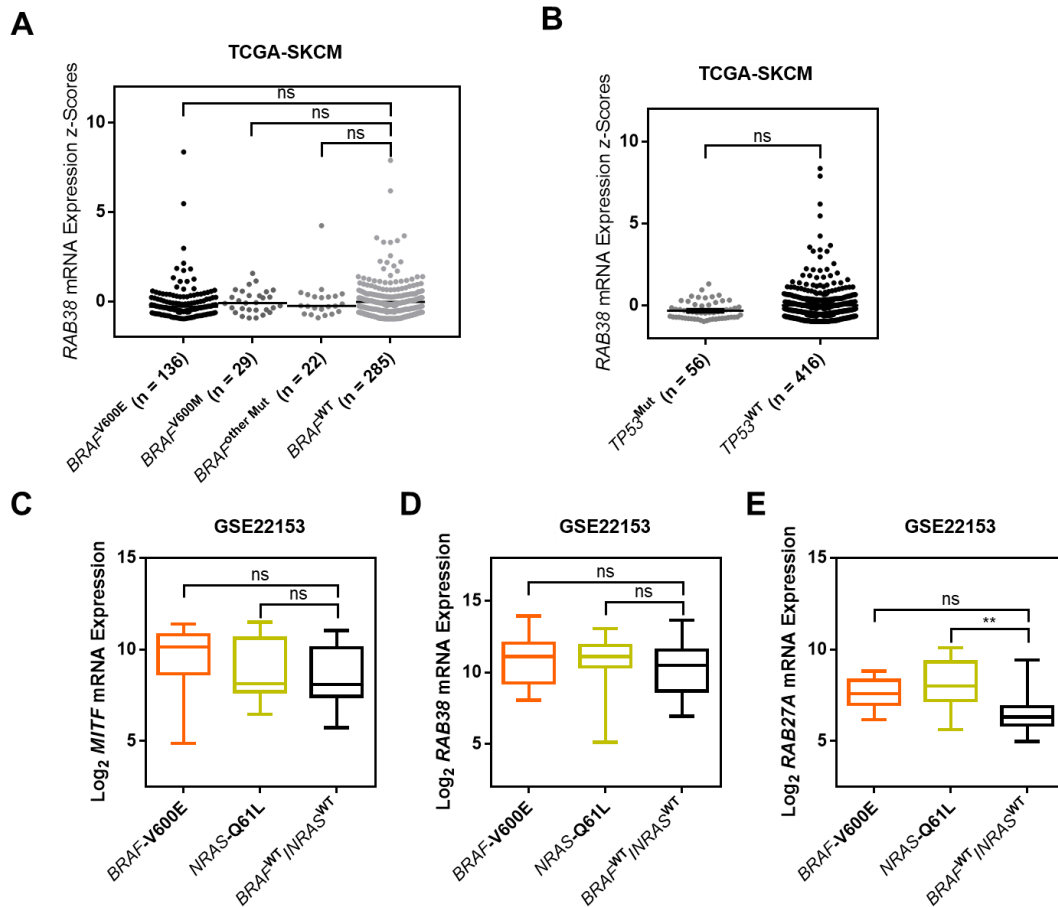


Fig. S7. Correlations of mRNA expressions of *MITF*, *RAB38* and *RAB27A* with different genetic backgrounds of melanoma patients.

(A) Scatter plot showing the lack of correlations of *RAB38* mRNA expressions with wild-type/mutant *BRAF* in the TCGA-SKCM melanoma patient cohort;

(B) Scatter plot showing the lack of correlations of *RAB38* mRNA expressions with wild-type/mutant *TP53* in the TCGA-SKCM melanoma patient cohort;

(C–E) Box plots showing the correlations of (C) *MITF* mRNA expressions, (D) *RAB38* mRNA expressions and (E) *RAB27A* mRNA expressions with wild-type/mutant *BRAF* and *NRAS* oncogenes in melanoma patient cohort GSE22153.

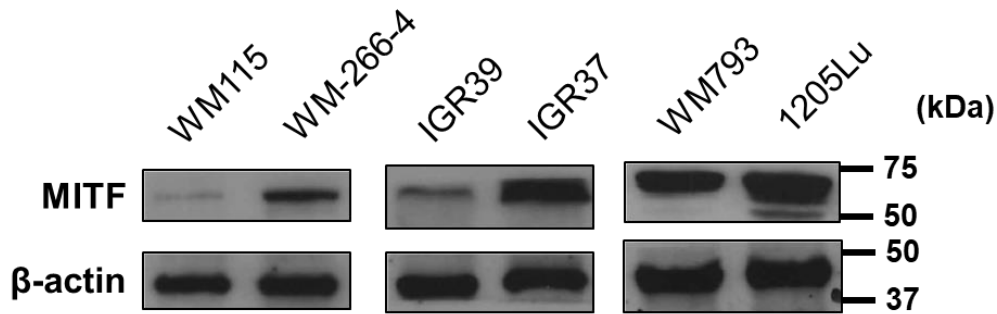
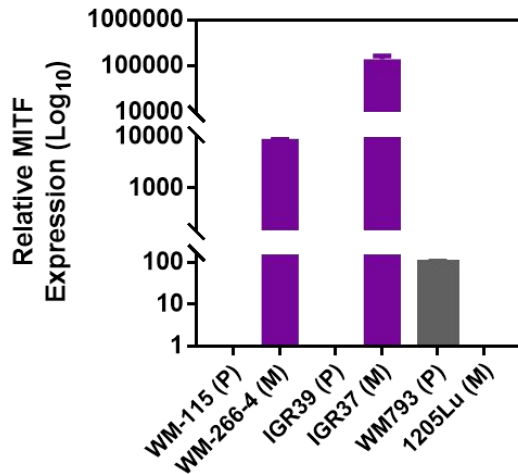
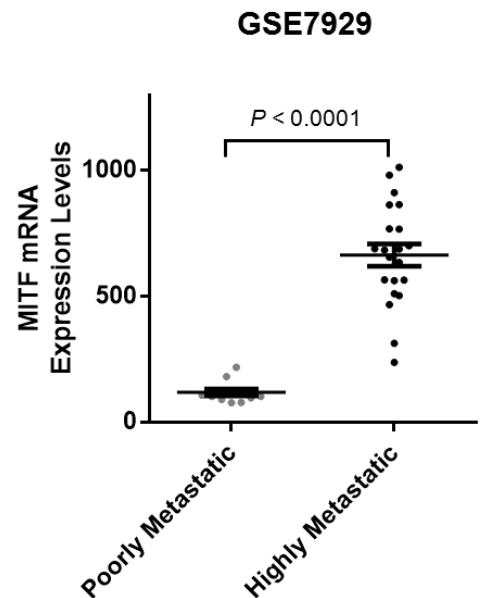
A**B****C**

Fig. S8. Up-regulation of *MITF* in metastatic melanoma cells.

(A) Immunoblots of MITF in the whole cell lysates from WM-115/WM-266-4, IGR39/IGR37 and WM793/1205Lu melanoma cells, where β -actin served as a loading control;

(B) RT-qPCR measurements of relative *MITF* mRNA expression levels in WM-115/WM-266-4, IGR39/IGR37 and WM793/1205Lu melanoma cells (n = 3);

(C) *RAB38* and *MITF* mRNA levels were significantly up-regulated in the highly metastatic derivatives of A375 cells cell lines compared to the poorly metastatic A375 parental cells (GEO data series: GSE7929). The *p* values were calculated by using an unpaired two-tailed Student's *t* test.

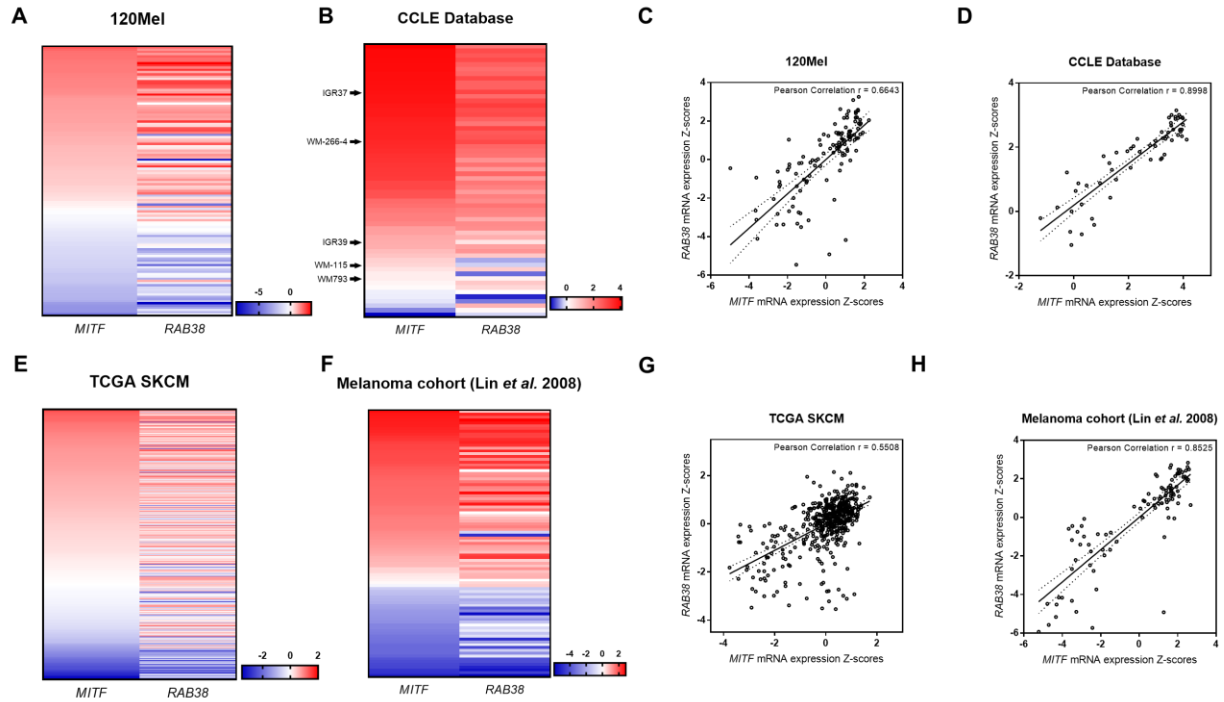


Fig. S9. *RAB38* expressions were highly correlated with *MITF* in melanoma cell lines and melanoma patient cohorts. Shown are heatmaps displaying the correlations between *RAB38* and *MITF* mRNA expressions in the:

(A) 120Mel melanoma cell line cohort; (B) CCLE melanoma cell line cohort; (C–D) A scatter plot showing the Pearson correlation analysis of data shown in (A) and (B);

(E) TCGA-SKCM patient cohort; (F) another melanoma patient cohort provided by Lin *et al.* (2008); (G–H) A scatter plot showing the Pearson correlation analysis of data shown in (E) and (F).

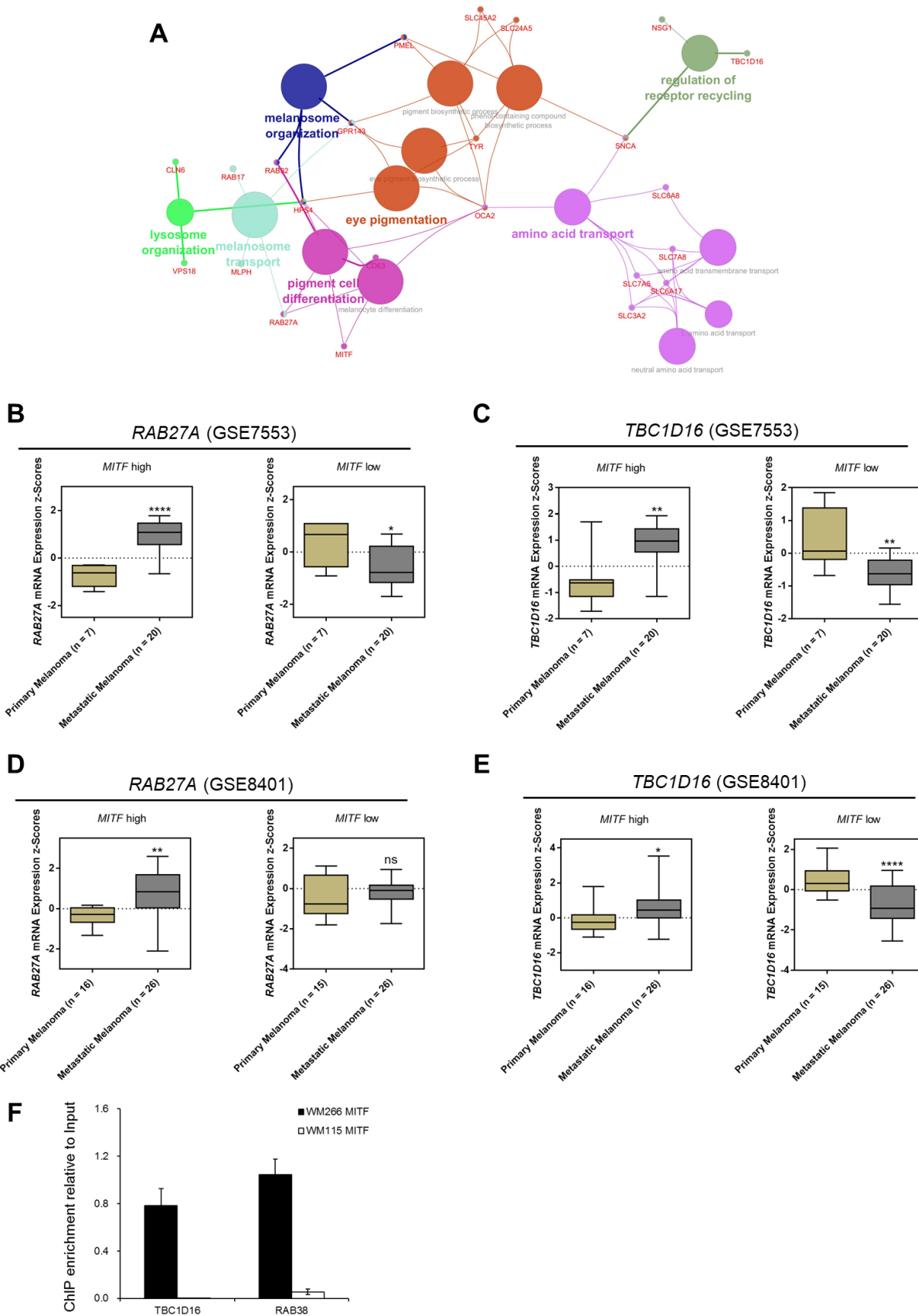


Fig. S10. Higher levels of expression of *RAB38* in metastatic melanoma compared to primary melanoma were observed in melanoma patient with *MITF* high signature.

(A) Pathway analysis showed enrichment of *MITF*, *TBC1D16* and *RAB27A* in the *RAB38* co-expression signature;

(B) Box plot showed *RAB27A* mRNA expressions in the metastatic patient tissues carrying *MITF*-high or *MITF*-low signature in the GSE7553 cohort;

(C) Box plot showed *TBC1D16* mRNA expressions in the metastatic patient tissues carrying *MITF*-high or *MITF*-low signature in the GSE7553 cohort;

(D) Box plot showed *RAB27A* mRNA expressions in the metastatic patient tissues carrying *MITF*-high or *MITF*-low signature in the GSE8401 cohort;

(E) Box plot showed *TBC1D16* mRNA expressions in the metastatic patient tissues carrying *MITF*-high or *MITF*-low signature in the GSE8401 cohort;

(F) ChIP-PCR assays showed enrichment of the association of *MITF* with the promoters of *TBC1D16* and *RAB38* genes in WM-266-4 cells relative to WM-115 cells. Data were normalized to control IgG ChIP. Error bars represent mean \pm standard deviation (n = 3).

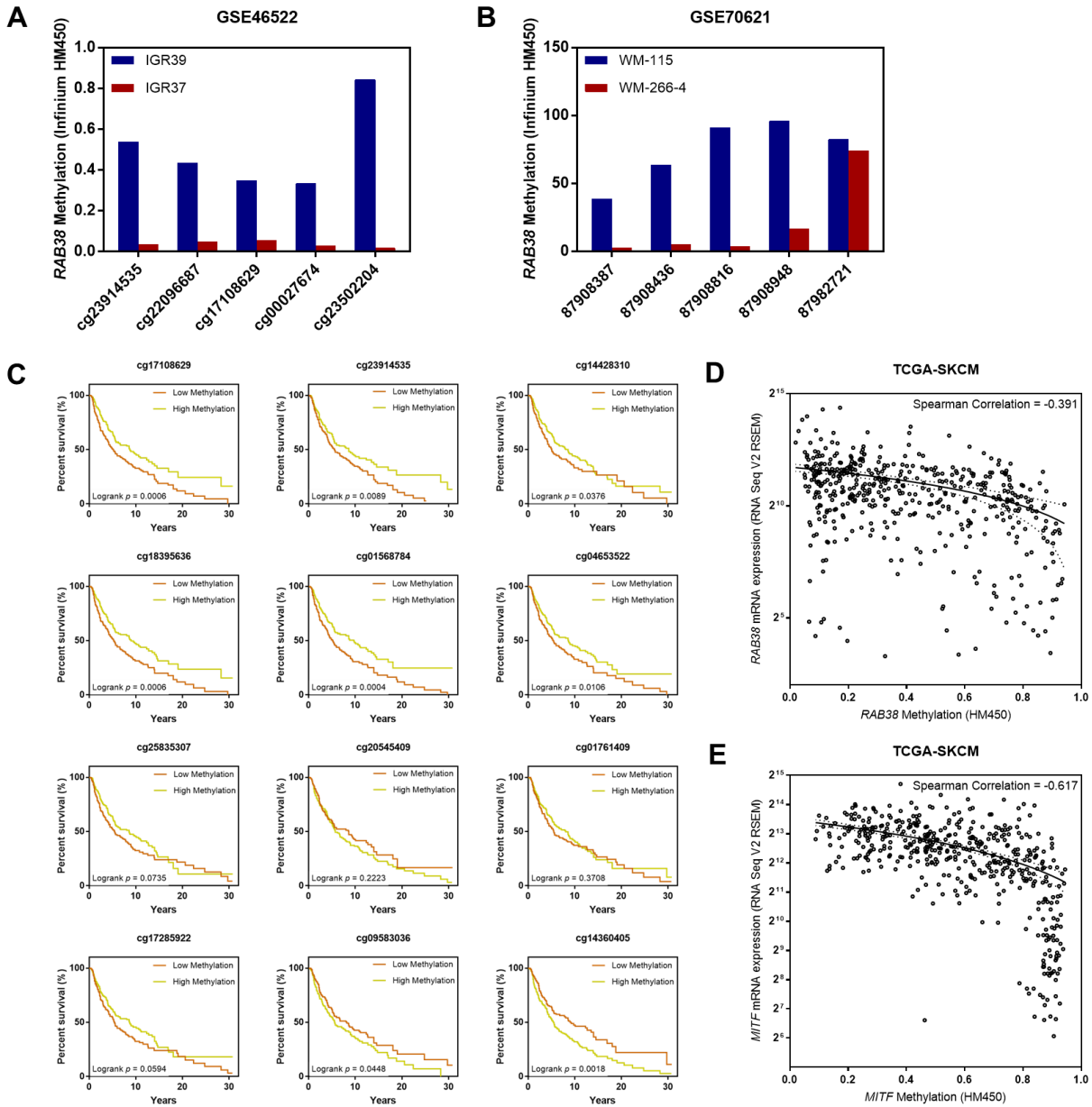


Fig. S11. Occurrence and prognostic values of *RAB38* promoter hypomethylation.

(A) Methylation microarray data showed lower methylation levels at multiple CpG sites of the *RAB38* promoter region in IGR37 cell line relative to IGR39 cell line in the GSE46522 cohort;

(B) Methylation microarray data showed lower methylation levels at multiple CpG sites of the *RAB38* promoter region in WM-266-4 cell line relative to WM-115 cell line in the GSE70621 cohort;

(C) Kaplan-Meier curves showing that the presence of *RAB38* hypomethylation at multiple CpG sites in melanoma patients (n = 464) is significantly associated with shorter overall survival in the TCGA-SKCM cohort;

(D) Scatter plot showing the correlations of *RAB38* mRNA expressions with *RAB38* promoter CpG methylation in the TCGA-SKCM cohort;

(E) Scatter plot showing the correlations of *MITF* mRNA expressions with *MITF* promoter CpG methylation in the TCGA-SKCM cohort.

Supplementary Materials and Methods

Sample Preparation and LC-MS/MS for Shotgun Proteomic Analysis. For acquiring shotgun proteomic data to establish an MRM library for small GTPases, the individually collected cell pellets from 9 human cell lines were lysed, and the resulting cell lysates were collected by centrifugation and separated by electrophoresis using a 16% SDS-PAGE gel. The gel bands in the molecular weight range of 15–37 kDa were cut into 7 pieces, reduced with dithiothreitol, alkylated with iodoacetamide, and in-gel digested with trypsin at an enzyme/protein ratio of 1:100.

In shotgun proteomic experiments, peptide samples were subjected to LC-MS/MS analysis on either an LTQ Orbitrap Velos mass spectrometer or a Q Exactive Plus mass spectrometer that was equipped with a nanoelectrospray ionization source and coupled to an EASY-nLC II (Thermo, San Jose, CA), as described previously.⁶³ A homemade trapping column (150 μm \times 50 mm), packed with ReproSil-Pur C18-AQ resin, and an analytical column (75 μm \times 120 mm), packed with ReproSil-Pur C18-AQ resin (Dr. Maisch HPLC GmbH, Germany) with particle sizes of 5 μm and 3 μm , respectively, were used for peptide separation. Peptide samples were initially loaded onto the trapping column with a solvent mixture of 0.1% formic acid in $\text{CH}_3\text{CN}/\text{H}_2\text{O}$ (2:98, v/v) at a flow rate of 3.0 $\mu\text{L}/\text{min}$. The peptides were then separated using a 150-min linear gradient of 8–35% acetonitrile in 0.1% formic acid at a flow rate of 300 nL/min. The mass spectrometer was operated in data-dependent acquisition (DDA) mode, where one full MS scan (resolution = 60,000) at an automatic gain control (AGC) target of 10^6 was followed with up to 20 MS/MS scans for the most abundant ions observed in MS. The selected ions were excluded from further analysis for 90 s. Ions with singly or unassigned charge states were not fragmented. The maximum ion accumulation time was 1000 ms for each full MS scan, and 50 ms for each MS/MS scan. The raw data were searched against the IPI human database (version 3.68, 87,061 entries). For database

search, up to one trypsin missed cleavage per peptide was allowed, and MS/MS spectral assignment was performed with less than 1% false discovery rate (FDR).

Retention time (RT) Prediction for Small GTPase Peptides. To facilitate automated and multiplexed MRM analyses, we generated an interactive MRM spectral library file containing the tandem mass spectra of peptides derived from small GTPases, which were acquired from the above-described shotgun proteomic experiments, using Skyline (version 3.5). Precursor and fragment ions for targeted GTPase peptides were selected and further refined to avoid spectral interference. If applicable, three unique peptides were selected for subsequent targeted analysis in the MRM mode.(1) In addition, we employed the aforementioned iRT algorithm to develop the scheduled MRM method.(2) To calculate the iRT score for each targeted peptide from small GTPases in the MRM spectral library, we selected 10 peptides from the tryptic digestion mixture of bovine serum albumin (BSA) as reference peptides to set up an iRT scale. By manually setting the iRT values of the BSA peptides AEFVEVTK and DAFLGSFLYEYSR as 0 and 100, respectively, a linear regression equation was obtained by plotting the iRT scores against their empirically measured retention times (RTs) derived from the LC-MS/MS analyses. Subsequently, the iRT values for the other eight standard BSA peptides were determined using the above-mentioned linear equation along with their empirically measured RTs in the shotgun proteomic experiments.

The BSA peptide mixture was then spiked into the small GTPase peptide mixtures for the LC-MS/MS analyses on an LTQ Orbitrap Velos mass spectrometer equipped with an Easy-nLC II system with a 150-min linear gradient of 8–35% acetonitrile in 0.1% formic acid, or a Q Exactive Plus mass spectrometer equipped with an Easy-nLC 1000 system with a 172-min linear gradient of 8–35% acetonitrile in 0.1% formic acid. RTs were extracted for all BSA standard peptides as

well as targeted peptides using the Skyline MS1 filtering workflow. The iRT values for all small GTPase peptides were calculated based on linear regression of iRT and experimentally measured RT of peptides with previously determined iRT scores.

Sample Preparation and Scheduled LC-MRM Analysis. To rigorously examine the differential expression of small GTPases in paired primary/metastatic melanoma cells, we conducted forward and reverse SILAC experiments, where the light and heavy lysates of paired primary melanoma cells (WM-115, IGR39 or WM793) were mixed with the heavy and light lysates from metastatic melanoma cells (WM-266-4, IGR37 or 1205Lu), respectively, at a 1:1 ratio (by mass). The mixed cell lysates were then loaded onto a 10% SDS-PAGE gel and separated by electrophoresis. The gel bands corresponding to the molecular weight range of 15–37 kDa were cut, reduced with 20 mM dithiothreitol, alkylated with 55 mM iodoacetamide, and in-gel digested with trypsin at an enzyme/protein ratio of 1:100.

All LC-MRM analyses were performed on a TSQ Vantage triple-quadrupole mass spectrometer equipped with an Easy-nLC II system. The peptide mixtures were separated with a 157-min linear gradient of 2–35% acetonitrile in 0.1% formic acid and at a flow rate of 230 nL/min. The spray voltage was 1.8 kV, Q1 and Q3 resolutions were 0.7 Da, and the cycle time was 5 s. The optimal collisional energy (CE) set for each targeted peptide was calculated using a linear equation specific to the TSQ Vantage instrument and the precursor mass-to-charge ratio (m/z) according to the default setting in Skyline.

The tryptic peptide mixture of BSA was subjected to unscheduled LC-MRM analyses prior to the analyses of targeted peptides of small GTPases in order to calibrate for possible retention time shifts due to changes in chromatographic conditions. The prediction of empirical RT based on the individual iRT scores of the targeted small GTPase peptides was then determined by the linear

regression of RTs of BSA standard peptides obtained under the same chromatography conditions. This iRT-based predictor was examined between every six MRM runs by injecting another BSA reference peptide mixture to ensure precise RT prediction.

A total of 432 peptides representing 113 non-redundant or 131 isoform-specific small GTPases were monitored in each scheduled LC-MRM run. For SILAC labeling experiments, the LC-MRM method was further expanded into two runs for monitoring the precursor and fragment ions of peptides harboring the light and heavy forms of lysine and/or arginine. In this regard, three transitions were monitored for each light-/heavy-isotope-coded peptide for LC-MRM quantification. A complete list of all the transitions monitored in the SILAC labeling experiments is provided in **Supplementary Table S2A**. These targeted transitions were monitored in the scheduled MRM mode with a 6-min retention time duration.

All raw files were processed using Skyline (version 3.5) for the generation of extracted-ion chromatograms and peak integration. The targeted peptides were first manually checked to ensure the overlaid chromatographic profiles of multiple fragment ions derived from the light and heavy forms of the same peptide. The data were then processed to ensure that the distribution of the relative intensities of multiple transitions associated with the same precursor ion correlates with the theoretical distribution derived from the tandem mass spectra in the library. The sum of peak area from all transitions of light- or heavy-labeled peptides was used for the quantification. A complete list of all quantification data for the SILAC labeling experiments is available in **Supplementary Table S2B**.

Construction and Transfection of FLAG-tagged Fusion Protein Expression Plasmid. To generate expression plasmid for 3×FLAG-tagged RAB38, the full-length coding sequence of human *RAB38* gene was amplified by PCR using Phusion High-Fidelity DNA Polymerase (NEB).

The PCR product was digested with HindIII and EcoRI, and the resulting DNA fragment was inserted into p3×FLAG-CMV-10 (Sigma) to construct the plasmid. The sequence of the constructed plasmid was validated by Sanger sequencing.

For plasmid transfection, WM-115 cells were cultured in six-well plates and transfected at 70% confluency with either the p3×FLAG-CMV-10 empty vector or the FLAG-RAB38 plasmid using TransIT-2020 transfection reagent (Mirus Bio LLC) following the manufacturer's recommended protocol. Transfected cells were incubated for an additional 24 h and analyzed for gene expression of the relative targeted protein using immunoblotting with specific antibodies.

siRNA Transfection. siGENOME non-targeting (NT) siRNA control (D-001210-02-05) and RAB38 SMARTpool (L-010059-00-0005) siRNA were purchased from Dharmacon (Lafayette, CO). The non-targeting siRNA control was designed not to target any known genes in human, mouse or rat, as described by the manufacturer. Briefly, WM-266-4, IGR37 and M14 melanoma cells were cultured in six-well plates and transfected at 50% confluency with 100 nM non-targeting siRNA or RAB38-targeting siRNA using TransIT-X2 transfection reagent (Mirus Bio LLC) following the manufacturer's protocol. Transfected cells were incubated for an additional 48–72 h and analyzed for the expression level of the RAB38 protein using immunoblotting with specific antibodies.

Real-time Quantitative PCR (RT-qPCR). At 24-72 h following transfection, total RNA was extracted from the cells using the Total RNA Kit I (Omega Bio-Tech), and 1 µg of total RNA was reverse-transcribed to generate cDNA by using M-MLV reverse transcriptase (Promega) and an oligo(dT)₁₆ primer. Gene expression levels were evaluated by real-time quantitative PCR (RT-qPCR) using iQ SYBR Green Supermix kit (Bio-Rad) with 100 ng cDNA input in a 20-µL total reaction volume. The expression level of glyceraldehyde 3-phosphate dehydrogenase (*GAPDH*)

gene was used as an internal control for normalization. Oligonucleotide sequences of primer pairs used in the RT-qPCR experiments are listed in **Supplementary Table S1**. All primers were used at a final concentration of 500 nM. The relative gene expression was analyzed by the comparative cycle threshold ($2^{-\Delta\Delta C_t}$) method.

1. Yocum AK, Chinnaiyan AM. Current affairs in quantitative targeted proteomics: multiple reaction monitoring-mass spectrometry. *Brief Funct Genomic Proteomic* **2009**;8:145-57
2. Escher C, Reiter L, MacLean B, Ossola R, Herzog F, Chilton J, *et al.* Using iRT, a normalized retention time for more targeted measurement of peptides. *Proteomics* **2012**;12:1111-21

Table S1. A complete list of primers used for real-time quantitative PCR (RT-qPCR) in this study.

Primers		Sequences		RefSeq accession numbers
GAPDH forward	5'-	TTAGCACCCCTGGCCAAGG	-3'	NM_002046.5
GAPDH reverse		CTTACTCCTTGGAGGCCATG		NM_002046.5
RAB38 forward		CATGAACAATGGCCTCAAGATG		NM_022337
RAB38 reverse		CCATTAGGTCACACTCATTTC		NM_022337
MMP2 forward		ACCCATTTACACCTACACCAAG		NM_004530.5
MMP2 reverse		TGTTTGCAGATCTCAGGAGTG		NM_004530.5
MMP9 forward		CGAACTTTGACAGCGACAAG		NM_004994.2
MMP9 reverse		CACTGAGGAATGATCTAAGCCC		NM_004994.2
TBC1D16-47KDa forward		CGATTTTAAGATGAAGGTCG		NM_001271846.1
TBC1D16-47KDa reverse		TCAGGTGGTTGAGCCAG		NM_001271846.1
MITF-M forward		CATTGTTATGCTGGAAATGCTAGAA		NM_000248.3
MITF-M reverse		GGCTTGCTGTATGTGGTACTTGG		NM_000248.3

Table S2. A complete list of small GTPases of the Ras superfamily in the human proteome.

IPI ID	Subfamily	Full name	Uniprot	MW	gene name	other name	
IPI00930413, IPI00215914, IPI00930	Sar1/Arf	ADP-ribosylation factor 1	P84077	20,697	ARF1		*Arf (27)
IPI00797941, IPI00215917	Sar1/Arf	ADP-ribosylation factor 3	P61204	20,601	ARF3		*Arf (27)
IPI00792330, IPI00215918, IPI00946	Sar1/Arf	ADP-ribosylation factor 4	P18085	20,511	ARF4	ARF2	*Arf (27)
IPI00215919, IPI00853337	Sar1/Arf	ADP-ribosylation factor 5	P84085	20,530	ARF5		*Arf (27)
IPI00215920	Sar1/Arf	ADP-ribosylation factor 6	P62330	20,082	ARF6		*Arf (27)
IPI00028549, IPI00028547, IPI00914	Sar1/Arf	ADP-ribosylation factor related protein 1	Q13795	22,614	ARFRP1		*Arf (27)
IPI00791961, IPI00219518	Sar1/Arf	ADP-ribosylation factor-like 1	P84077	20,697	ARL1		*Arf (27)
IPI00167501	Sar1/Arf	ADP-ribosylation factor-like 10	Q8N8L6	27,459	ARL10	ARL10A	*Arf (27)
IPI00056495	Sar1/Arf	ADP-ribosylation factor-like 11	Q969Q4	21,391	ARL11		*Arf (27)
IPI00472207, IPI00797369, IPI00945	Sar1/Arf	ADP-ribosylation factor-like 13B	Q3SXY8	48,643	ARL13B	ARL2L1	*Arf (27)
IPI00296664	Sar1/Arf	ADP-ribosylation factor-like 14 (FLJ22595)	Q8N4G2	21,588	ARL14	ARF7, FLJ22595	*Arf (27)
IPI00005163	Sar1/Arf	ADP-ribosylation factor-like protein 15	Q9NXU5	22,876	ARL15	ARFRP2	*Arf (27)
IPI00793250, IPI00242972, IPI00792	Sar1/Arf	ADP-ribosylation factor-like 16 (LOC339231)	Q0P5N6	20,936	ARL16	LOC339231	*Arf (27)
IPI00847722, IPI00003326	Sar1/Arf	ADP-ribosylation factor-like 2	P36404	20,878	ARL2		*Arf (27)
IPI00003327	Sar1/Arf	ADP-ribosylation factor-like 3	P36405	20,456	ARL3		*Arf (27)
IPI00029596, IPI00893142, IPI00893	Sar1/Arf	ADP-ribosylation factor-like 4A	P40617	22,615	ARL4A	ARL4	*Arf (27)
IPI00936024, IPI00010149	Sar1/Arf	ADP-ribosylation factor-like 4C	P56559	21,487	ARL4C	ARL7	*Arf (27)
IPI00027971	Sar1/Arf	ADP-ribosylation factor-like 4D	P49703	22,156	ARL4D	ARF4L	*Arf (27)
IPI00001923, IPI00924699, IPI00412	Sar1/Arf	ADP-ribosylation factor-like 5A	Q9Y689	20,728	ARL5A	ARL5	*Arf (27)
IPI00102036	Sar1/Arf	ADP-ribosylation factor-like 5B	Q96KC2	20,375	ARL5B	ARL8	*Arf (27)
IPI00789499, IPI00946662, IPI00021	Sar1/Arf	ADP-ribosylation factor-like 6	Q9H0F7	21,097	ARL6		*Arf (27)
IPI00060031	Sar1/Arf	ADP-ribosylation factor-like 8A	Q96BM9	21,416	ARL8A	ARL10B	*Arf (27)
IPI00793455, IPI00788984, IPI00789	Sar1/Arf	ADP-ribosylation factor-like 8B	Q9NVJ2	21,539	ARL8B	ARL10C	*Arf (27)
IPI00419109	Sar1/Arf	ADP-ribosylation factor-like 9	Q6T311	20,755	ARL9		*Arf (27)
IPI00002919	Ras	DIRAS family, GTP-binding RAS-like 1	Q95057	22,329	DIRAS1		*Ras (36)
IPI00063302	Ras	DIRAS family, GTP-binding RAS-like 2	Q96HU8	22,485	DIRAS2		*Ras (36)
IPI00032112	Ras	DIRAS family, GTP-binding RAS-like 3	O95661	25,861	DIRAS3	NOEY2, RHOF	*Ras (36)
IPI00018593, IPI00220244, IPI00003	Sar1/Arf	Tripartite motif-containing 23; E3 ubiquitin-protein ligase TRIM23	P36406	64,067	TRIM23	ARD1, RNF46	*Arf (27)
IPI00375882	Ras	ES cell expressed Ras	Q7Z444	25,287	ERAS	HRAS2	*Ras (36)
IPI00022710	Ras	GTP binding protein overexpressed in skeletal muscle; GTP-binding protein	P55040	33,949	GEM	KIR	*Ras (36)
IPI00289912	Ras	RAS (RAD and GEM)-like GTP-binding 1; GTP-binding protein REM 1	O75628	32,947	REM1		*Ras (36)
IPI00793200	Ras	RAS (RAD and GEM)-like GTP-binding 2; GTP-binding protein REM 2	Q81YK8	37,139	REM2		*Ras (36)
IPI00922845, IPI00925921, IPI00011	Others	RAB, member RAS oncogene family-like 5	Q9H7X7	20,835	RABL5	IFT22	*Others (9)
IPI00916134, IPI00916779, IPI00221	Others	RAB, member of RAS oncogene family-like 2A	Q9UBK7	26,115	RABL2A		*Others (9)
IPI00916134, IPI00916779, IPI00924	Others	RAB, member of RAS oncogene family-like 2B	Q9UNT1	26,101	RABL2B		*Others (9)
IPI00946728, IPI00946067, IPI00946	Others	RAB, member of RAS oncogene family-like 3	Q5HYI8	26,423	RABL3		*Others (9)
IPI00878639, IPI00879146, IPI00878	Rab	RAB, member of RAS oncogene family-like 4	Q9BW83	20,480	RABL4	IFT27	*Rab (61)
IPI00016513	Rab	RAB10, member RAS oncogene family	P61026	22,541	RAB10		*Rab (61)
IPI00795676, IPI00911020, IPI00941	Rab	RAB11A, member RAS oncogene family	P62491	24,394	RAB11A	RAB11	*Rab (61)
IPI00930720, IPI00020436	Rab	RAB11B, member RAS oncogene family	Q15907	24,489	RAB11B		*Rab (61)
IPI00419932	Rab	RAB12, member RAS oncogene family	Q6IQ22	27,248	RAB12		*Rab (61)
IPI00016373, IPI00877662	Rab	RAB13, member RAS oncogene family; similar to hCG24991	P51153	22,774	RAB13		*Rab (61)
IPI00291928, IPI00646415	Rab	RAB14, member RAS oncogene family	P61106	23,897	RAB14		*Rab (61)
IPI00383449, IPI00394882	Rab	RAB15, member RAS oncogene family	P59190	24,391	RAB15		*Rab (61)
IPI00916806, IPI00007866, IPI00917	Rab	RAB17, member RAS oncogene family	Q9H0T7	23,491	RAB17		*Rab (61)
IPI00479988, IPI00478787, IPI00844	Rab	RAB18, member RAS oncogene family	Q9NP72	22,977	RAB18		*Rab (61)
IPI00478209, IPI00923598, IPI00946	Rab	RAB19, member RAS oncogene family	A4D1S5	24,400	RAB19	RAB19B	*Rab (61)
IPI00185217, IPI00005719, IPI00917	Rab	RAB1A, member RAS oncogene family	P62820	22,678	RAB1A		*Rab (61)
IPI00008964, IPI00022134, IPI00896	Rab	RAB1B, member RAS oncogene family	Q9H0U4	22,171	RAB1B		*Rab (61)
IPI00015839	Others	RAB20, member RAS oncogene family	Q9NX57	26,277	RAB20		*Others (9)
IPI00790578, IPI00007755	Rab	RAB21, member RAS oncogene family	Q9UL25	24,348	RAB21		*Rab (61)
IPI00007756	Rab	RAB22A, member RAS oncogene family	Q9UL26	21,855	RAB22A	RAB22	*Rab (61)
IPI00080834	Rab	RAB23, member RAS oncogene family	Q9ULC3	26,659	RAB23		*Rab (61)
IPI00383176, IPI00792833, IPI00396	Rab	RAB24, member RAS oncogene family	Q969Q5	23,124	RAB24		*Rab (61)
IPI00027993	Rab	RAB25, member RAS oncogene family	P57735	23,496	RAB25		*Rab (61)
IPI00419883	Rab	RAB26, member RAS oncogene family	Q9ULW5	27,900	RAB26		*Rab (61)
IPI00219858, IPI00016381	Rab	RAB27A, member RAS oncogene family	P51159	24,868	RAB27A	RAB27	*Rab (61)
IPI00010491, IPI00643312	Rab	RAB27B, member RAS oncogene family	O00194	24,608	RAB27B		*Rab (61)
IPI00016377, IPI00929378, IPI00219	Rab	RAB28, member RAS oncogene family	P51157	24,841	RAB28		*Rab (61)
IPI00794027, IPI00790570, IPI00794	Rab	RAB2A, member RAS oncogene family	P61019	23,546	RAB2A		*Rab (61)
IPI00879279, IPI00064352, IPI00102	Rab	RAB2B, member RAS oncogene family	Q8WUD1	24,214	RAB2B		*Rab (61)
IPI00302030, IPI00425916	Rab	RAB30, member RAS oncogene family	Q15771	23,058	RAB30		*Rab (61)
IPI00646692, IPI00014376	Rab	RAB31, member RAS oncogene family	Q13636	21,569	RAB31	RAB22B	*Rab (61)
IPI00014377	Rab	RAB32, member RAS oncogene family	Q13637	24,997	RAB32		*Rab (61)
IPI00028517	Rab	RAB33A, member RAS oncogene family	Q14088	26,541	RAB33A		*Rab (61)
IPI00021475	Rab	RAB33B, member RAS oncogene family	Q9H082	25,718	RAB33B		*Rab (61)
IPI00795399, IPI00796900, IPI00790	Rab	RAB34, member RAS oncogene family	Q9BZG1	29,044	RAB34	RAB39	*Rab (61)
IPI00032916, IPI00909855, IPI00879	Rab	RAB36, member RAS oncogene family	O95755	36,322	RAB36		*Rab (61)
IPI00332970, IPI00789993, IPI00788	Rab	RAB37, member RAS oncogene family	Q96AX2	24,815	RAB37		*Rab (61)
IPI00027981, IPI00939888	Rab	RAB38, member RAS oncogene family	P57729	23,712	RAB38		*Rab (61)
IPI00001618	Rab	RAB39, member RAS oncogene family	Q14964	25,007	RAB39	RAB39A	*Rab (61)
IPI00060801	Rab	RAB39B, member RAS oncogene family	Q96DA2	24,622	RAB39B		*Rab (61)
IPI00023504	Rab	RAB3A, member RAS oncogene family	P20336	24,984	RAB3A		*Rab (61)
IPI00300562	Rab	RAB3B, member RAS oncogene family	P20337	24,758	RAB3B		*Rab (61)
IPI00061114, IPI00871276	Rab	RAB3C, member RAS oncogene family	Q96E17	25,952	RAB3C		*Rab (61)
IPI00032808	Rab	RAB3D, member RAS oncogene family	O95716	24,267	RAB3D		*Rab (61)
IPI00514509	Rab	RAB40A, member RAS oncogene family	Q8WXH6	31,076	RAB40A		*Rab (61)
IPI00009953, IPI00790429	Rab	RAB40B, member RAS oncogene family	Q12829	30,956	RAB40B		*Rab (61)
IPI00045478	Rab	RAB40C, member RAS oncogene family	Q96S21	31,304	RAB40C		*Rab (61)

IP100929731, IP100232898	Rab	RAB41, member RAS oncogene family	Q5JT25	25,038	RAB41			*Rab (61)
IP100843865	Rab	RAB42, member RAS oncogene family	Q8N4Z0	11,364	RAB42			*Rab (61)
IP100329441, IP100789395, IP100744	Rab	RAB43, member RAS oncogene family; hypothetical LOC100131426	Q86YS6	23,339	RAB43	RAB41		*Rab (61)
IP100480056, IP100939242	Rab	RAB4A, member RAS oncogene family	P20338	24,390	RAB4A			*Rab (61)
IP100448725, IP100477489, IP100187	Rab	RAB4B, member RAS oncogene family	P61018	23,587	RAB4B			*Rab (61)
IP100924852, IP100797838, IP100927	Rab	RAB5A, member RAS oncogene family	P20339	23,659	RAB5A			*Rab (61)
IP100017344, IP100908835	Rab	RAB5B, member RAS oncogene family	P61020	23,707	RAB5B			*Rab (61)
IP100789439, IP100016339	Rab	RAB5C, member RAS oncogene family	P51148	23,483	RAB5C			*Rab (61)
IP100023526	Rab	Ras-related protein Rab-6A	P20340	23,593	RAB6A	RAB6		*Rab (61)
IP100945534, IP100016891, IP100946	Rab	RAB6B, member RAS oncogene family	Q9NRW1	23,462	RAB6B			*Rab (61)
IP100023526, IP100748927, IP100030	Rab	RAB6C, member RAS oncogene family; RAB6A, member RAS oncogene	Q9H0N0	28,355	RAB6C			*Rab (61)
IP100913930, IP100909756, IP100024	Rab	RAB7, member RAS oncogene family-like 1	O14966	23,155	RAB7L1	RAB29		*Rab (61)
IP100946776, IP100016342, IP100945	Rab	RAB7A, member RAS oncogene family	P51149	23,490	RAB7A			*Rab (61)
IP100556414, IP100028481	Rab	RAB8A, member RAS oncogene family	P61006	23,668	RAB8A	RAB8		*Rab (61)
IP100024282, IP100903040	Rab	RAB8B, member RAS oncogene family	Q92930	23,584	RAB8B			*Rab (61)
IP100016372	Rab	RAB9A, member RAS oncogene family	P51151	22,838	RAB9A			*Rab (61)
IP100014603	Rab	RAB9B, member RAS oncogene family	Q9NP90	22,719	RAB9B			*Rab (61)
IP100795671, IP100044779, IP100795	Ran	RAN, member RAS oncogene family	P62826	24,423	RAN			*Ran (1)
IP100019345, IP100877120	Ras	RAP1A, member of RAS oncogene family	P62834	20,987	RAP1A			*Ras (36)
IP100796349, IP100908754, IP100816	Ras	RAP1B, member of RAS oncogene family	P61224	20,825	RAP1B			*Ras (36)
IP100019346	Ras	RAP2A, member of RAS oncogene family	P10114	20,615	RAP2A			*Ras (36)
IP100018364	Ras	RAP2B, member of RAS oncogene family	P61225	20,504	RAP2B			*Ras (36)
IP100009607	Ras	RAP2C, member of RAS oncogene family	Q9Y3L5	20,745	RAP2C			*Ras (36)
IP100412443, IP100043268	Ras	RAS and EF-hand domain containing	Q8IZ41	82,879	RASEF	RAB45		*Rab (61)
IP100007111	Ras	RAS, dexamethasone-induced 1	Q9Y272	31,642	RASD1	DexRas		*Ras (36)
IP100059267	Ras	RAS-like, estrogen-regulated, growth inhibitor	Q9H628	22,608	RERG			*Ras (36)
IP100478878, IP100023219	Ras	RAS-like, family 10, member A	Q92737	22,541	RASL10A	RRRP22		*Ras (36)
IP100045517	Ras	RAS-like, family 10, member B	Q96579	23,229	RASL10B			*Ras (36)
IP100156120	Ras	RAS-like, family 11, member A	Q6T310	27,006	RASL11A			*Ras (36)
IP100386910	Ras	RAS-like, family 11, member B	Q9BPW5	27,508	RASL11B			*Ras (36)
IP100789503, IP100009813, IP100909	Ras	RAS-like, family 12	Q9NYN1	29,662	RASL12	RIS		*Ras (36)
IP100304150	Ras	RASD family, member 2	Q96D21	30,366	RASD2	RHES		*Ras (36)
IP100015447	Ras	RERG/RAS-like (FLJ22655)	Q9H628	23,855	RERGL	FLJ22655		*Ras (36)
IP100016669, IP100945356, IP100947	Ras	Ras homolog enriched in brain	Q15382	20,497	RHEB	RHEB1		*Ras (36)
IP100942159, IP100152059, IP100556	Ras	Ras homolog enriched in brain like 1	Q8TAI7	20,682	RHEBL1	RHEB2		*Ras (36)
IP100639824, IP100144289	Ras	Ras-like without CAAX 1	Q92963	25,145	RIT1	ROC1		*Ras (36)
IP100163763, IP100289566	Ras	Ras-like without CAAX 2	Q99578	24,668	RIT2	ROC2		*Ras (36)
IP100375333	Ras	Ras-related associated with diabetes	A0A024R	33,245	RRAD	RAD, REM3		*Ras (36)
IP100023211	Rho/Rac/Cdc42	Rho family GTPase 1	Q92730	26,056	RND1	RHO7		*Rho (20)
IP100001436	Rho/Rac/Cdc42	Rho family GTPase 2	P52198	25,369	RND2	RHO6, RHON		*Rho (20)
IP100917768, IP100916668, IP100908	Rho/Rac/Cdc42	Rho family GTPase 3	P61587	27,368	RND3	ROHE		*Rho (20)
IP100001317	Rho/Rac/Cdc42	Rho-related BTB domain containing 1	O94844	79,417	RHOBTB1			*Rho (20)
IP100794883, IP100930055, IP100816	Rho/Rac/Cdc42	Rho-related BTB domain containing 2	Q9BYZ6	82,626	RHOBTB2			*Rho (20)
IP100513941, IP100015954, IP100644	Sar1/Arf	SAR1 homolog A (S. cerevisiae)	Q9NR31	22,367	SAR1A			*Arf (27)
IP100002149	Sar1/Arf	SAR1 homolog B (S. cerevisiae)	Q9Y6B6	22,410	SAR1B			*Arf (27)
IP100016786, IP100007189, IP100642	Rho/Rac/Cdc42	cell division cycle 42 (GTP binding protein, 25kDa); cell division cycle 42 ps	P60953	21,259	CDC42			*Rho (20)
IP100792754, IP100791074, IP100024	Ras	muscle RAS oncogene homolog	O14807	23,846	MRAS	RRAS3		*Ras (36)
IP100000005	Ras	neuroblastoma RAS viral (v-ras) oncogene homolog	P01111	21,229	NRAS			*Ras (36)
IP100925690, IP100926151, IP100410	Ras	NFKB inhibitor interacting Ras-like 1	Q9NYS0	21,643	NKIRAS1			*Ras (36)
IP100791151, IP100789320, IP100021	Ras	NFKB inhibitor interacting Ras-like 2	Q9NYR9	21,508	NKIRAS2			*Ras (36)
IP100926881, IP100478231, IP100926	Rho/Rac/Cdc42	ras homolog gene family, member A	P61586	21,768	RHOA			*Rho (20)
IP100893313, IP100000041	Rho/Rac/Cdc42	ras homolog gene family, member B	P62745	22,123	RHOB			*Rho (20)
IP100647268, IP100644425, IP100643	Rho/Rac/Cdc42	ras homolog gene family, member C	P08134	22,006	RHOC			*Rho (20)
IP100010841	Rho/Rac/Cdc42	ras homolog gene family, member D	O00212	23,413	RHOD			*Rho (20)
IP100382965, IP100307458	Rho/Rac/Cdc42	ras homolog gene family, member F (in filopodia)	Q9HBH0	23,625	RHOF	RIF		*Rho (20)
IP100017342	Rho/Rac/Cdc42	ras homolog gene family, member G (rho G)	P84095	21,309	RHOG			*Rho (20)
IP100018882	Rho/Rac/Cdc42	ras homolog gene family, member H	Q15669	21,331	RHOH			*Rho (20)
IP100249526, IP100027952	Rho/Rac/Cdc42	ras homolog gene family, member J	Q9H4E5	23,821	RHOJ	TCL, RHOT, R		*Rho (20)
IP100880127, IP100012511	Rho/Rac/Cdc42	ras homolog gene family, member Q; similar to small GTP binding protein 1	P17081	22,659	RHOQ	TC10, RASL7A		*Rho (20)
IP100759627, IP100217536, IP100759	Others	ras homolog gene family, member T1	Q8IXI2	70,784	RHOT1	Miro-1		*Others (9)
IP100465059, IP100647917	Others	ras homolog gene family, member T2	Q8IXI1	68,118	RHOT2	Miro-2		*Others (9)
IP100889079, IP100009644	Rho/Rac/Cdc42	ras homolog gene family, member U	Q7L0Q8	28,218	RHOV	WRCH1		*Rho (20)
IP100154827, IP100844512	Rho/Rac/Cdc42	ras homolog gene family, member V	Q96L33	26,217	RHOV	WRCH2		*Rho (20)
IP100394837, IP100219675, IP100555	Rho/Rac/Cdc42	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding p	P63000	21,450	RAC1			*Rho (20)
IP100877816, IP100877663, IP100010	Rho/Rac/Cdc42	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding p	P15153	21,429	RAC2			*Rho (20)
IP100023138	Rho/Rac/Cdc42	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding p	P60763	21,379	RAC3			*Rho (20)
IP100020418	Ras	related RAS viral (v-ras) oncogene homolog	P10301	23,480	RRAS			*Ras (36)
IP100012512, IP100856004	Ras	related RAS viral (v-ras) oncogene homolog 2; similar to related RAS viral	P62070	23,400	RRAS2	TC21		*Ras (36)
IP100797747, IP100947333, IP100295	Others	signal recognition particle receptor, B subunit	Q9Y5M8	29,702	SRPRB			*Others (9)
IP100791123, IP100300096, IP100910	Rab	similar to hCG1778032; RAB35, member RAS oncogene family	Q15286	23,025	RAB35	RAB1C		*Rab (61)
IP100741763, IP100000006, IP100796	Ras	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	X5D945	21,298	HRAS			*Ras (36)
IP100423568, IP100791238, IP100423	Ras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	P01116	21,656	KRAS			*Ras (36)
IP100927712, IP100217519, IP100927	Ras	v-ral simian leukemia viral oncogene homolog A (ras related)	P11233	23,567	RALA			*Ras (36)
IP100925885, IP100004397, IP100927	Ras	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding	P11234	23,409	RALB			*Ras (36)

Table S3A. A complete list of small GTPases in the Skyline MRM library with their gene names, IPI numbers, and targeted peptides and transitions.

Gene Name	Detailed description of targeted proteins, peptides and transitions used for Skyline library and LC-MRM analysis		
NRAS	IPI: IPI00000005.1 SWISS-PROT: P01111 NRAS GTPase NRas		
	R.TGEGFLC V FAINNS K .S [73, 87]	K.SFADINLY R .E [88, 96]	R.QGVEDAFYTL V R.E [149, 160]
	828.9061++	549.7826++	699.3566++
	C [y9] - 1052.5193+ (rank 2)	A [y7] - 864.4574+ (rank 1)	A [y7] - 869.4880+ (rank 3)
	F [y7] - 793.4203+ (rank 1)	D [y6] - 793.4203+ (rank 2)	F [y6] - 798.4509+ (rank 1)
	A [y6] - 646.3519+ (rank 3)	N [y4] - 565.3093+ (rank 3)	Y [y5] - 651.3824+ (rank 2)
	832.9132++ (heavy)	552.7926++ (heavy)	702.3667++ (heavy)
	C [y9] - 1060.5335+ (rank 2)	A [y7] - 870.4775+ (rank 1)	A [y7] - 875.5081+ (rank 3)
	F [y7] - 801.4345+ (rank 1)	D [y6] - 799.4404+ (rank 2)	F [y6] - 804.4710+ (rank 1)
	A [y6] - 654.3661+ (rank 3)	N [y4] - 571.3294+ (rank 3)	Y [y5] - 657.4026+ (rank 2)
HRAS	IPI: IPI00000006.1 SWISS-PROT: P01112 HRAS GTPase HRas		
	R.TGEGFLC V FAINNT K .S [73, 87]	K.SFEDIHQY R .E [88, 96]	R.SYGIPYIETSA K .T [135, 146]
	835.9140++	597.7805++	664.8403++
	C [y9] - 1066.5350+ (rank 1)	E [y7] - 960.4534+ (rank 1)	G [y10] - 1078.5779+ (rank 2)
	F [y7] - 807.4359+ (rank 2)	I [y5] - 716.3838+ (rank 3)	P [y8] - 908.4724+ (rank 1)
	A [y6] - 660.3675+ (rank 3)	H [y4] - 603.2998+ (rank 2)	I [y6] - 648.3563+ (rank 3)
	839.9211++ (heavy)	600.7906++ (heavy)	668.8474++ (heavy)
	C [y9] - 1074.5492+ (rank 1)	E [y7] - 966.4735+ (rank 1)	G [y10] - 1086.5921+ (rank 2)
	F [y7] - 815.4501+ (rank 2)	I [y5] - 722.4040+ (rank 3)	P [y8] - 916.4866+ (rank 1)
	A [y6] - 668.3817+ (rank 3)	H [y4] - 609.3199+ (rank 2)	I [y6] - 656.3705+ (rank 3)
		398.8561+++	
		I [y5] - 716.3838+ (rank 3)	
		H [y4] - 603.2998+ (rank 1)	
		Q [y3] - 466.2409+ (rank 2)	
		400.8628+++ (heavy)	
	I [y5] - 722.4040+ (rank 3)		
	H [y4] - 609.3199+ (rank 1)		
	Q [y3] - 472.2610+ (rank 2)		
RHOB	IPI: IPI00000041.1 SWISS-PROT: P62745 RHOB Rho-related GTP-binding protein RhoB		
	K.LVVVGDGAC G K.T [7, 17]	K.DEFPEVYVPTVFENYVADIEVD G K.Q [25, 35]	R.IQAYDYLE C SA K .T [150, 161]
	537.7842++	925.4410+++	730.8399++
	V [y9] - 862.4087+ (rank 4)	V [y9] - 945.4888+ (rank 1)	Y [y9] - 1148.4929+ (rank 3)
	V [y8] - 763.3403+ (rank 3)	A [y8] - 846.4203+ (rank 2)	D [y8] - 985.4295+ (rank 2)
	G [y7] - 664.2719+ (rank 1)	D [y7] - 775.3832+ (rank 3)	Y [y7] - 870.4026+ (rank 4)
	541.7913++ (heavy)	928.1124+++ (heavy)	734.8470++ (heavy)
	V [y9] - 870.4229+ (rank 4)	V [y9] - 953.5030+ (rank 1)	Y [y9] - 1156.5071+ (rank 3)
	V [y8] - 771.3545+ (rank 3)	A [y8] - 854.4345+ (rank 2)	D [y8] - 993.4437+ (rank 2)
	G [y7] - 672.2861+ (rank 1)	D [y7] - 783.3974+ (rank 3)	Y [y7] - 878.4168+ (rank 4)
	R.EVFETAT R .A [168, 175]		
	476.7404++		
	F [y6] - 724.3624+ (rank 1)		
	E [y5] - 577.2940+ (rank 3)		
	T [y4] - 448.2514+ (rank 2)		
479.7504++ (heavy)			
F [y6] - 730.3826+ (rank 1)			
E [y5] - 583.3141+ (rank 3)			
T [y4] - 454.2716+ (rank 2)			
RND3	IPI: IPI00001437.3 SWISS-PROT: P61587 RND3 Rho-related GTP-binding protein RhoE		
	K.IVVVGD S Q C G K .T [25, 35]	K.TALLHV F A K .D [36, 44]	K.GEIQEF C P N T K .M [118, 128]
	581.3003++	500.3029++	661.8059++
	V [y9] - 949.4408+ (rank 2)	L [y7] - 827.5138+ (rank 3)	I [y9] - 1136.5405+ (rank 1)
	V [y8] - 850.3723+ (rank 3)	L [y6] - 714.4297+ (rank 2)	E [y7] - 895.3978+ (rank 4)
	G [y7] - 751.3039+ (rank 1)	H [y5] - 601.3457+ (rank 1)	P [y4] - 459.2562+ (rank 3)
	585.3074++ (heavy)	504.3100++ (heavy)	665.8130++ (heavy)
	V [y9] - 957.4550+ (rank 2)	L [y7] - 835.5280+ (rank 3)	I [y9] - 1144.5547+ (rank 1)
	V [y8] - 858.3865+ (rank 3)	L [y6] - 722.4439+ (rank 2)	E [y7] - 903.4120+ (rank 4)
	G [y7] - 759.3181+ (rank 1)	H [y5] - 609.3599+ (rank 1)	P [y4] - 467.2704+ (rank 3)
	R.TDVSTLVELSN H R.Q [140, 152]	R.DIFHVATL A C V N K .T [187, 199]	
	735.8810++	744.3874++	
	L [y8] - 967.5320+ (rank 3)	V [y9] - 975.5292+ (rank 2)	
	V [y7] - 854.4479+ (rank 1)	A [y8] - 876.4608+ (rank 1)	
	E [y6] - 755.3795+ (rank 2)	T [y7] - 805.4236+ (rank 3)	
738.8911++ (heavy)	748.3945++ (heavy)		
L [y8] - 973.5521+ (rank 3)	V [y9] - 983.5434+ (rank 2)		
V [y7] - 860.4680+ (rank 1)	A [y8] - 884.4750+ (rank 1)		
E [y6] - 761.3996+ (rank 2)	T [y7] - 813.4378+ (rank 3)		
RAB39	IPI: IPI00001618.2 SWISS-PROT: Q14964 RAB39 Ras-related protein Rab-39A		
	R.LIVIGDSTV G K.S [10, 20]	R. I K L Q L W D T A G Q R F .F [61, 73] (missed)	K.LQLWDTAG Q R F .F [63, 73]
551.3293++	779.4228++	658.8333++	

	V [y9] - 875.4833+ (rank 1)		L [y9] - 1075.5167+ (rank 3)		L [y9] - 1075.5167+ (rank 1)
	I [y8] - 776.4149+ (rank 3)		W [y8] - 962.4326+ (rank 1)		W [y8] - 962.4326+ (rank 2)
	G [y7] - 663.3308+ (rank 2)		T [y6] - 661.3264+ (rank 2)		D [y7] - 776.3533+ (rank 3)
	555.3364++ (heavy)		786.4400++ (heavy)		661.8434++ (heavy)
	V [y9] - 883.4975+ (rank 1)		L [y9] - 1081.5368+ (rank 3)		L [y9] - 1081.5368+ (rank 1)
	I [y8] - 784.4291+ (rank 3)		W [y8] - 968.4528+ (rank 1)		W [y8] - 968.4528+ (rank 2)
	G [y7] - 671.3450+ (rank 2)		T [y6] - 667.3465+ (rank 2)		D [y7] - 782.3735+ (rank 3)
			519.9510+++		
			D [y7] - 776.3533+ (rank 3)		
			G [y4] - 489.2416+ (rank 1)		
			E [y2] - 304.1615+ (rank 5)		
			524.6291+++ (heavy)		
			D [y7] - 782.3735+ (rank 3)		
			G [y4] - 495.2617+ (rank 1)		
			E [y2] - 310.1817+ (rank 5)		
ARL5A	IPI:IP100001923.5 REFSEQ:NP_001032251;NP_817114 ARL5A ADP-ribosylation factor-like protein 5A isoform 2				
	R.FLMWDIGGQESLR.S [24, 36]		K.MLAHEDLR.K [71, 78]		K.AGLLIFANK.Q [80, 88]
	776.3849++		492.7502++		473.7897++
	D [y9] - 974.4901+ (rank 3)		L [y7] - 853.4526+ (rank 5)		I [y5] - 592.3453+ (rank 2)
	I [y8] - 859.4632+ (rank 2)		A [y6] - 740.3686+ (rank 2)		F [y4] - 479.2613+ (rank 1)
	G [y7] - 746.3791+ (rank 1)		H [y5] - 669.3315+ (rank 3)		A [y3] - 332.1928+ (rank 4)
	779.3949++ (heavy)		495.7603++ (heavy)		477.7968++ (heavy)
	D [y9] - 980.5103+ (rank 3)		L [y7] - 859.4728+ (rank 5)		I [y5] - 600.3595+ (rank 2)
	I [y8] - 865.4833+ (rank 2)		A [y6] - 746.3887+ (rank 2)		F [y4] - 487.2755+ (rank 1)
	G [y7] - 752.3993+ (rank 1)		H [y5] - 675.3516+ (rank 3)		A [y3] - 340.2070+ (rank 4)
SAR1B	IPI:IP100002149.1 SWISS-PROT:Q9Y6B6 SAR1B GTP-binding protein SAR1b				
	K.IDRPEAISEER.L [135, 145]		R.EMFGLYGQTTGK.G [148, 159]		K.ELNARPLEVFMCSVLK.R [166, 181]
	657.8360++		666.3186++		953.4999++
	P [y8] - 930.4527+ (rank 1)		G [y9] - 924.4785+ (rank 3)		M [y6] - 737.3684+ (rank 3)
	A [y6] - 704.3573+ (rank 3)		Y [y7] - 754.3730+ (rank 1)		C [y5] - 606.3280+ (rank 2)
	S [y4] - 520.2362+ (rank 4)		G [y6] - 591.3097+ (rank 2)		S [y4] - 446.2973+ (rank 5)
	663.8562++ (heavy)		670.3257++ (heavy)		960.5171++ (heavy)
	P [y8] - 936.4728+ (rank 1)		G [y9] - 932.4927+ (rank 3)		M [y6] - 745.3826+ (rank 3)
	A [y6] - 710.3775+ (rank 3)		Y [y7] - 762.3872+ (rank 1)		C [y5] - 614.3422+ (rank 2)
	S [y4] - 526.2563+ (rank 4)		G [y6] - 599.3239+ (rank 2)		S [y4] - 454.3115+ (rank 5)
	438.8931+++				
	I [y5] - 633.3202+ (rank 4)				
	S [y4] - 520.2362+ (rank 1)				
	E [y3] - 433.2041+ (rank 2)				
	442.9065+++ (heavy)				
	I [y5] - 639.3404+ (rank 4)				
	S [y4] - 526.2563+ (rank 1)				
	E [y3] - 439.2243+ (rank 2)				
RABL2A	IPI:IP100002644.1 SWISS-PROT:Q9UBK7-1 RABL2A Isoform 1 of Rab-like protein 2A				
	K.TKPSELDDQGGK.Y [5, 14]		K.IICLGDSAVGK.S [23, 33]		R.NLSTWYTELR.E [110, 119]
	368.1961+++		566.8052++		641.8250++
	L [y5] - 560.3039+ (rank 4)		C [y9] - 906.4349+ (rank 1)		S [y8] - 1055.5156+ (rank 1)
	D [y4] - 447.2198+ (rank 1)		L [y8] - 746.4043+ (rank 3)		T [y7] - 968.4836+ (rank 2)
	Q [y3] - 332.1928+ (rank 3)		G [y7] - 633.3202+ (rank 2)		W [y6] - 867.4359+ (rank 3)
	373.5389+++ (heavy)		570.8123++ (heavy)		644.8350++ (heavy)
	L [y5] - 568.3181+ (rank 4)		C [y9] - 914.4491+ (rank 1)		S [y8] - 1061.5358+ (rank 1)
	D [y4] - 455.2340+ (rank 1)		L [y8] - 754.4185+ (rank 3)		T [y7] - 974.5037+ (rank 2)
	Q [y3] - 340.2070+ (rank 3)		G [y7] - 641.3344+ (rank 2)		W [y6] - 873.4561+ (rank 3)
	R.EFRPEIPCIVVANK.I [120, 133]				
	836.4480++				
	E [y10] - 1142.6238+ (rank 1)				
	V [y4] - 431.2613+ (rank 4)				
	A [y3] - 332.1928+ (rank 2)				
	843.4651++ (heavy)				
	E [y10] - 1150.6380+ (rank 1)				
	V [y4] - 439.2755+ (rank 4)				
	A [y3] - 340.2070+ (rank 2)				
DIRAS1	IPI:IP100002919.2 SWISS-PROT:O95057 DIRAS1 GTP-binding protein Di-Ras1				
	R.VVVFAGGGVVGK.S [9, 19]		R.DTYIPTIEDTYR.Q [33, 44]		K.GSVEDIPVMLVGNK.C [108, 121]
	495.2926++		743.8566++		729.3871++
	V [y9] - 791.4410+ (rank 2)		I [y9] - 1107.5681+ (rank 3)		P [y8] - 857.4913+ (rank 1)
	F [y8] - 692.3726+ (rank 1)		P [y8] - 994.4840+ (rank 1)		M [y6] - 661.3702+ (rank 4)
	G [y7] - 545.3042+ (rank 3)		E [y5] - 683.2995+ (rank 2)		V [y4] - 417.2456+ (rank 2)
	499.2997++ (heavy)		746.8667++ (heavy)		733.3942++ (heavy)
	V [y9] - 799.4552+ (rank 2)		I [y9] - 1113.5882+ (rank 3)		P [y8] - 865.5055+ (rank 1)
	F [y8] - 700.3868+ (rank 1)		P [y8] - 1000.5041+ (rank 1)		M [y6] - 669.3844+ (rank 4)
	G [y7] - 553.3184+ (rank 3)		E [y5] - 689.3196+ (rank 2)		V [y4] - 425.2598+ (rank 2)
	R.EAQAVAQEWK.C [133, 142]				
	580.2907++				
	A [y7] - 831.4359+ (rank 2)				
	V [y6] - 760.3988+ (rank 3)				
	A [y5] - 661.3304+ (rank 1)				

	I [y7] - 826.4305+ (rank 2)		T [y6] - 779.3617+ (rank 3)		V [y8] - 901.5102+ (rank 2)
	S [y6] - 713.3464+ (rank 1)		H [y4] - 541.2551+ (rank 2)		G [y7] - 802.4417+ (rank 1)
	661.3492++ (heavy)		706.3552++ (heavy)		739.9373++ (heavy)
	L [y9] - 1060.6128+ (rank 3)		P [y9] - 1126.5553+ (rank 1)		L [y9] - 1020.6143+ (rank 3)
	I [y7] - 834.4447+ (rank 2)		T [y6] - 787.3759+ (rank 3)		V [y8] - 907.5303+ (rank 2)
	S [y6] - 721.3606+ (rank 1)		H [y4] - 549.2693+ (rank 2)		G [y7] - 808.4619+ (rank 1)
RAB21	IPI: IPI00007755.3 SWISS-PROT: Q9UL25 RAB21 Ras-related protein Rab-21				
	K.VVLLGEGCVGK.T [21, 31]		R.VNLAIWDTAGQER.F [67, 79]		R.HVSIQEAESYAESVGAH.H [140, 156]
	565.8155++		736.8782++		902.9392++
	L [y9] - 932.4870+ (rank 2)		W [y8] - 962.4326+ (rank 1)		Q [y13] - 1368.6278+ (rank 3)
	L [y8] - 819.4029+ (rank 3)		D [y7] - 776.3533+ (rank 2)		E [y12] - 1240.5692+ (rank 2)
	G [y7] - 706.3189+ (rank 1)		G [y4] - 489.2416+ (rank 3)		A [y11] - 1111.5266+ (rank 1)
	569.8226++ (heavy)		739.8883++ (heavy)		906.9463++ (heavy)
	L [y9] - 940.5012+ (rank 2)		W [y8] - 968.4528+ (rank 1)		Q [y13] - 1376.6420+ (rank 3)
	L [y8] - 827.4171+ (rank 3)		D [y7] - 782.3735+ (rank 2)		E [y12] - 1248.5834+ (rank 2)
	G [y7] - 714.3330+ (rank 1)		G [y4] - 495.2617+ (rank 3)		A [y11] - 1119.5408+ (rank 1)
RAB22A	IPI: IPI00007756.1 SWISS-PROT: Q9UL26 RAB22A Ras-related protein Rab-22A				
	K.TVQYQNELHK.F [45, 54]		K.EETFSTLKN.N [89, 96]		K.DYADSIHAIFVETSAK.N [134, 149]
	630.3226++		477.7426++		883.9334++
	Q [y8] - 1059.5218+ (rank 3)		T [y6] - 696.3927+ (rank 4)		H [y10] - 1102.5891+ (rank 1)
	Y [y7] - 931.4632+ (rank 1)		F [y5] - 595.3450+ (rank 3)		A [y9] - 965.5302+ (rank 2)
	N [y5] - 640.3413+ (rank 4)		S [y4] - 448.2766+ (rank 1)		F [y7] - 781.4090+ (rank 3)
	634.3297++ (heavy)		481.7497++ (heavy)		887.9405++ (heavy)
	Q [y8] - 1067.5360+ (rank 3)		T [y6] - 704.4069+ (rank 4)		H [y10] - 1110.6033+ (rank 1)
	Y [y7] - 939.4774+ (rank 1)		F [y5] - 603.3592+ (rank 3)		A [y9] - 973.5444+ (rank 2)
	N [y5] - 648.3555+ (rank 4)		S [y4] - 456.2908+ (rank 1)		F [y7] - 789.4232+ (rank 3)
	R.IPSTDANLPSSGGK.G [165, 177]				
	628.8277++				
	S [y11] - 1046.5113+ (rank 2)				
	A [y8] - 743.4046+ (rank 3)				
	P [y5] - 445.2405+ (rank 1)				
	632.8348++ (heavy)				
	S [y11] - 1054.5255+ (rank 2)				
	A [y8] - 751.4188+ (rank 3)				
	P [y5] - 453.2547+ (rank 1)				
RAB17	IPI: IPI00007866.1 SWISS-PROT: Q9H0T7 RAB17 Ras-related protein Rab-17				
	K.SILPTVGCFFTK.V [45, 57]		K.LEIWDTAGQEK.Y [68, 78]		K.YHSVCHLYFR.G [79, 88]
	720.8814++		645.3222++		461.2205+++
	P [y10] - 1127.5554+ (rank 1)		W [y8] - 934.4265+ (rank 1)		C [y6] - 895.4243+ (rank 4)
	G [y7] - 830.3865+ (rank 2)		D [y7] - 748.3472+ (rank 2)		L [y4] - 598.3348+ (rank 2)
	F [y3] - 395.2289+ (rank 3)		T [y6] - 633.3202+ (rank 4)		Y [y3] - 485.2507+ (rank 1)
	724.8885++ (heavy)		649.3293++ (heavy)		463.2272+++ (heavy)
	P [y10] - 1135.5696+ (rank 1)		W [y8] - 942.4407+ (rank 1)		C [y6] - 901.4444+ (rank 4)
	G [y7] - 838.4007+ (rank 2)		D [y7] - 756.3614+ (rank 2)		L [y4] - 604.3549+ (rank 2)
	F [y3] - 403.2431+ (rank 3)		T [y6] - 641.3344+ (rank 4)		Y [y3] - 491.2708+ (rank 1)
	R.SDEEGQALR.G [183, 191]				
	502.7358++				
	E [y7] - 802.4054+ (rank 3)				
	E [y6] - 673.3628+ (rank 2)				
	G [y5] - 544.3202+ (rank 1)				
	505.7459++ (heavy)				
	E [y7] - 808.4255+ (rank 3)				
	E [y6] - 679.3829+ (rank 2)				
	G [y5] - 550.3403+ (rank 1)				
RAB23	IPI: IPI00008034.1 SWISS-PROT: Q9ULC3 RAB23 Ras-related protein Rab-23				
	K.TIGVDFLER.Q [40, 48]		R.QIQVNDEDVRL.L [49, 58]		K.EDLNVNEVFK.Y [153, 162]
	525.2849++		608.3018++		603.8037++
	G [y7] - 835.4308+ (rank 1)		Q [y8] - 974.4538+ (rank 3)		N [y7] - 849.4465+ (rank 3)
	D [y5] - 679.3410+ (rank 2)		V [y7] - 846.3952+ (rank 2)		V [y6] - 735.4036+ (rank 2)
	F [y4] - 564.3140+ (rank 3)		N [y6] - 747.3268+ (rank 1)		N [y5] - 636.3352+ (rank 1)
	528.2950++ (heavy)		611.3119++ (heavy)		607.8108++ (heavy)
	G [y7] - 841.4510+ (rank 1)		Q [y8] - 980.4739+ (rank 3)		N [y7] - 857.4607+ (rank 3)
	D [y5] - 685.3611+ (rank 2)		V [y7] - 852.4153+ (rank 2)		V [y6] - 743.4178+ (rank 2)
	F [y4] - 570.3342+ (rank 3)		N [y6] - 753.3469+ (rank 1)		N [y5] - 644.3494+ (rank 1)
RAB1B	IPI: IPI00008964.3 SWISS-PROT: Q9H0U4 RAB1B Ras-related protein Rab-1B				
	-.MNPEYDYLFK.L [0, 9]		K.NATNVEQAFMTMAAEIK.K [153, 169]		R.MGPGAASGGERPNIK.I [172, 186]
	660.3025++		934.9477++		721.3644++
	P [y8] - 1074.5142+ (rank 1)		A [y10] - 1112.5479+ (rank 3)		A [y10] - 1028.5483+ (rank 3)
	E [y7] - 977.4615+ (rank 5)		F [y9] - 1041.5108+ (rank 1)		S [y9] - 957.5112+ (rank 2)
	Y [y6] - 848.4189+ (rank 2)		M [y8] - 894.4423+ (rank 4)		728.3816++ (heavy)
	664.3096++ (heavy)		938.9548++ (heavy)		A [y10] - 1042.5827+ (rank 3)
	P [y8] - 1082.5284+ (rank 1)		A [y10] - 1120.5621+ (rank 3)		S [y9] - 971.5455+ (rank 2)
	E [y7] - 985.4757+ (rank 5)		F [y9] - 1049.5249+ (rank 1)		K.IDSTPVKPAAGGGCC.- [187, 200]
	Y [y6] - 856.4331+ (rank 2)		M [y8] - 902.4565+ (rank 4)		709.8238++
			623.6342+++		P [y10] - 1002.4495+ (rank 1)
			M [y8] - 894.4423+ (rank 3)		K [y8] - 806.3284+ (rank 3)
			A [y5] - 531.3137+ (rank 2)		P [y7] - 678.2334+ (rank 2)

			A [y4] - 460.2766+ (rank 1)		713.8309++ (heavy)
			626.3056+++ (heavy)		P [y10] - 1010.4637+ (rank 1)
			M [y8] - 902.4565+ (rank 3)		K [y8] - 814.3426+ (rank 3)
			A [y5] - 539.3279+ (rank 2)		P [y7] - 678.2334+ (rank 2)
			A [y4] - 468.2908+ (rank 1)		
RABL2B	IPI: IPI00009415.1 SWISS-PROT: Q9UNT1-1 RABL2B Isoform 1 of Rab-like protein 2B				
	K.AHACIMVFDVQR.K [93, 104]				
	723.8527++				
	A [y10] - 1238.6020+ (rank 1)				
	C [y9] - 1167.5649+ (rank 2)				
	M [y7] - 894.4502+ (rank 3)				
	726.8627++ (heavy)				
	A [y10] - 1244.6222+ (rank 1)				
	C [y9] - 1173.5850+ (rank 2)				
	M [y7] - 900.4703+ (rank 3)				
	482.9042+++				
	F [y5] - 664.3413+ (rank 1)				
	D [y4] - 517.2729+ (rank 3)				
	V [y3] - 402.2459+ (rank 2)				
	484.9109+++ (heavy)				
	F [y5] - 670.3614+ (rank 1)				
	D [y4] - 523.2930+ (rank 3)				
	V [y3] - 408.2661+ (rank 2)				
RAP2C	IPI: IPI00009607.1 RAP2C Ras-related protein Rap-2c				
	K.VPLILVGNK.V [108, 116]		K.VDLEPER.E [117, 123]		R.EVMSSEGR.A [124, 131]
	476.8131++		429.2218++		447.7029++
	L [y7] - 756.4978+ (rank 1)		D [y6] - 758.3679+ (rank 3)		M [y6] - 666.2876+ (rank 2)
	I [y6] - 643.4137+ (rank 3)		L [y5] - 643.3410+ (rank 2)		S [y5] - 535.2471+ (rank 1)
	L [y5] - 530.3297+ (rank 2)		P [y3] - 401.2143+ (rank 1)		S [y4] - 448.2150+ (rank 3)
	480.8202++ (heavy)		432.2319++ (heavy)		450.7130++ (heavy)
	L [y7] - 764.5120+ (rank 1)		D [y6] - 764.3880+ (rank 3)		M [y6] - 672.3077+ (rank 2)
	I [y6] - 651.4279+ (rank 3)		L [y5] - 649.3611+ (rank 2)		S [y5] - 541.2672+ (rank 1)
	L [y5] - 538.3439+ (rank 2)		P [y3] - 407.2344+ (rank 1)		S [y4] - 454.2352+ (rank 3)
	R.ALAQEWGCPFMETSAK.S [132, 147]		R.QMNYSSLPEK.Q [162, 171]		
	913.4160++		598.7844++		
	G [y10] - 1127.4860+ (rank 1)		S [y6] - 660.3563+ (rank 2)		
	C [y9] - 1070.4645+ (rank 3)		S [y5] - 573.3243+ (rank 3)		
	E [y5] - 535.2722+ (rank 5)		P [y3] - 373.2082+ (rank 1)		
	917.4231++ (heavy)		602.7915++ (heavy)		
	G [y10] - 1135.5002+ (rank 1)		S [y6] - 668.3705+ (rank 2)		
	C [y9] - 1078.4787+ (rank 3)		S [y5] - 581.3385+ (rank 3)		
	E [y5] - 543.2864+ (rank 5)		P [y3] - 381.2224+ (rank 1)		
RHO	IPI: IPI00009644.1 SWISS-PROT: Q7L0Q8-1 RHO Isoform 1 of Rho-related GTP-binding protein RhoU				
	K.CVLVGDGAVGK.T [51, 61]				
	537.7842++				
	V [y8] - 702.3781+ (rank 1)				
	G [y7] - 603.3097+ (rank 2)				
	A [y4] - 374.2398+ (rank 3)				
	541.7913++ (heavy)				
	V [y8] - 710.3923+ (rank 1)				
	G [y7] - 611.3239+ (rank 2)				
	A [y4] - 382.2540+ (rank 3)				
RABL5	IPI: IPI00009700.4 SWISS-PROT: Q9H7X7-1 RABL5 Isoform 1 of Rab-like protein 5				
	K.ILFVGPCESGK.T [5, 15]		R.ILEFENPHVTSNNK.G [39, 52]		K.FESCWPALMK.D [69, 78]
	603.8130++		821.4152++		634.7938++
	F [y9] - 980.4506+ (rank 2)		N [y9] - 1010.5014+ (rank 3)		S [y8] - 992.4692+ (rank 1)
	G [y7] - 734.3138+ (rank 1)		P [y8] - 896.4585+ (rank 1)		W [y6] - 745.4065+ (rank 3)
	P [y6] - 677.2923+ (rank 3)		T [y5] - 563.2784+ (rank 2)		P [y5] - 559.3272+ (rank 2)
	607.8201++ (heavy)		825.4223++ (heavy)		638.8009++ (heavy)
	F [y9] - 988.4648+ (rank 2)		N [y9] - 1018.5156+ (rank 3)		S [y8] - 1000.4834+ (rank 1)
	G [y7] - 742.3280+ (rank 1)		P [y8] - 904.4727+ (rank 1)		W [y6] - 753.4207+ (rank 3)
	P [y6] - 685.3065+ (rank 3)		T [y5] - 571.2926+ (rank 2)		P [y5] - 567.3414+ (rank 2)
	K.SIINSMSER.D [166, 175]				
	562.2742++				
	I [y8] - 923.4251+ (rank 2)				
	N [y7] - 810.3410+ (rank 1)				
	S [y6] - 696.2981+ (rank 3)				
	565.2843++ (heavy)				
	I [y8] - 929.4452+ (rank 2)				
	N [y7] - 816.3612+ (rank 1)				
	S [y6] - 702.3182+ (rank 3)				
RRAGD	IPI: IPI00009737.1 SWISS-PROT: Q9NQL2-1 RRAGD Isoform 1 of Ras-related GTP-binding protein D				
	K.MSPNETLFLESTNK.I [85, 98]		K.LNNTTVLYLK.E [320, 329]		
	805.8902++		589.8426++		
	F [y7] - 838.4305+ (rank 1)		N [y8] - 951.5510+ (rank 1)		
	L [y6] - 691.3621+ (rank 2)		T [y7] - 837.5080+ (rank 3)		
	S [y4] - 449.2354+ (rank 3)		T [y6] - 736.4604+ (rank 2)		

	809.8973++ (heavy)		593.8497++ (heavy)				
	F [y7] - 846.4447+ (rank 1)		N [y8] - 959.5652+ (rank 1)				
	L [y6] - 699.3763+ (rank 2)		T [y7] - 845.5222+ (rank 3)				
	S [y4] - 457.2496+ (rank 3)		T [y6] - 744.4746+ (rank 2)				
ARL4C	IPI:IP100010149.2 TREMBL:Q4A519 ARL4C ADP ribosylation factor-like protein 7						
	K.GISCHFWDVGGQEK.L [60, 73]		K.FAENQGTPLLVIANK.Q [113, 127]			K.LYEMILK.R [174, 180]	
	540.5806+++		807.9461++			455.2593++	
	W [y8] - 918.4316+ (rank 3)		G [y10] - 1025.6354+ (rank 2)			Y [y6] - 796.4273+ (rank 2)	
	V [y6] - 617.3253+ (rank 2)		P [y8] - 867.5662+ (rank 1)			E [y5] - 633.3640+ (rank 3)	
	G [y5] - 518.2569+ (rank 1)		I [y4] - 445.2769+ (rank 3)			M [y4] - 504.3214+ (rank 5)	
	543.2520+++ (heavy)		811.9532++ (heavy)			459.2664++ (heavy)	
	W [y8] - 926.4458+ (rank 3)		G [y10] - 1033.6496+ (rank 2)			Y [y6] - 804.4415+ (rank 2)	
	V [y6] - 625.3395+ (rank 2)		P [y8] - 875.5804+ (rank 1)			E [y5] - 641.3782+ (rank 3)	
	G [y5] - 526.2711+ (rank 1)		I [y4] - 453.2911+ (rank 3)			M [y4] - 512.3356+ (rank 5)	
RAC2	IPI:IP100010270.1 SWISS-PROT:P15153 RAC2 Ras-related C3 botulinum toxin substrate 2						
	R.HHCPTPIILVGTK.L [102, 115]		K.LAPITYPQGLALAK.E [133, 146]			R.AVLCPQPTR.Q [174, 182]	
	780.4218++		728.4321++			1041.5510+	
	P [y11] - 1125.6878+ (rank 1)		T [y10] - 1061.5990+ (rank 2)			P [y5] - 598.3307+ (rank 1)	
	P [y8] - 840.5553+ (rank 3)		Y [y9] - 960.5513+ (rank 3)			P [y3] - 373.2194+ (rank 2)	
	L [y5] - 517.3344+ (rank 4)		P [y8] - 797.4880+ (rank 1)			1047.5711+ (heavy)	
	784.4289++ (heavy)		732.4392++ (heavy)			P [y5] - 604.3509+ (rank 1)	
	P [y11] - 1133.7020+ (rank 1)		T [y10] - 1069.6132+ (rank 2)			P [y3] - 379.2395+ (rank 2)	
	P [y8] - 848.5695+ (rank 3)		Y [y9] - 968.5655+ (rank 3)			521.2791++	
	L [y5] - 525.3486+ (rank 4)		P [y8] - 805.5022+ (rank 1)			L [y7] - 871.4454+ (rank 3)	
			485.9572+++			C [y6] - 758.3614+ (rank 2)	
			P [y8] - 797.4880+ (rank 3)			P [y5] - 598.3307+ (rank 1)	
			Q [y7] - 700.4352+ (rank 2)			524.2892++ (heavy)	
			G [y6] - 572.3766+ (rank 1)			L [y7] - 877.4656+ (rank 3)	
			488.6286+++ (heavy)			C [y6] - 764.3815+ (rank 2)	
			P [y8] - 805.5022+ (rank 3)			P [y5] - 604.3509+ (rank 1)	
			Q [y7] - 708.4494+ (rank 2)				
			G [y6] - 580.3908+ (rank 1)				
RAC1	IPI:IP100010271.3 SWISS-PROT:P63000-1 RAC1 Isoform A of Ras-related C3 botulinum toxin substrate 1						
	R.HHCPTPIILVGTK.L [102, 115]		K.LTPITYPQGLAMAK.E [133, 146]			K.LTPITYPQGLAMAK.E [133, 146]	
	793.9272++		752.4156++			760.4131++	
	P [y11] - 1152.6987+ (rank 1)		T [y10] - 1079.5554+ (rank 3)			T [y10] - 1095.5503+ (rank 2)	
	L [y5] - 517.3344+ (rank 3)		Y [y9] - 978.5077+ (rank 2)			Y [y9] - 994.5026+ (rank 3)	
	V [y4] - 404.2504+ (rank 5)		P [y8] - 815.4444+ (rank 1)			P [y8] - 831.4393+ (rank 1)	
	797.9343++ (heavy)		756.4227++ (heavy)			764.4202++ (heavy)	
	P [y11] - 1160.7129+ (rank 1)		T [y10] - 1087.5696+ (rank 3)			T [y10] - 1103.5645+ (rank 2)	
	L [y5] - 525.3486+ (rank 3)		Y [y9] - 986.5219+ (rank 2)			Y [y9] - 1002.5168+ (rank 3)	
	V [y4] - 412.2646+ (rank 5)		P [y8] - 823.4586+ (rank 1)			P [y8] - 839.4535+ (rank 1)	
RRAGB	IPI:IP100010317.4 SWISS-PROT:Q5VZM2-1 RRAGB Isoform 1 of Ras-related GTP-binding protein B						
	R.SIIFANYIAR.D [57, 66]		R.NFAEIIIEADEVLLFER.A [253, 268]			K.LAASFQSMEVR.N [305, 315]	
	584.3297++		954.4911++			619.8135++	
	I [y8] - 967.5360+ (rank 2)		E [y10] - 1220.6157+ (rank 2)			A [y9] - 1054.4986+ (rank 3)	
	F [y7] - 854.4519+ (rank 1)		A [y9] - 1091.5732+ (rank 4)			S [y8] - 983.4615+ (rank 2)	
	A [y6] - 707.3835+ (rank 3)		D [y8] - 1020.5360+ (rank 5)			Q [y6] - 749.3610+ (rank 1)	
	587.3397++ (heavy)		957.5012++ (heavy)			622.8236++ (heavy)	
	I [y8] - 973.5561+ (rank 2)		E [y10] - 1226.6359+ (rank 2)			A [y9] - 1060.5187+ (rank 3)	
	F [y7] - 860.4720+ (rank 1)		A [y9] - 1097.5933+ (rank 4)			S [y8] - 989.4816+ (rank 2)	
	A [y6] - 713.4036+ (rank 3)		D [y8] - 1026.5562+ (rank 5)			Q [y6] - 755.3812+ (rank 1)	
RAB27B	IPI:IP100010491.3 SWISS-PROT:O00194 RAB27B Ras-related protein Rab-27B						
	K.LLALGDSGVGK.T [11, 21]		R.VVYNAQGPNGSSGK.A [50, 63]			K.VHLQLWDTAGQER.F [67, 79]	
	515.3006++		689.3415++			776.8970++	
	A [y9] - 803.4258+ (rank 1)		Y [y12] - 1179.5389+ (rank 3)			W [y8] - 962.4326+ (rank 4)	
	L [y8] - 732.3886+ (rank 3)		A [y10] - 902.4326+ (rank 2)			D [y7] - 776.3533+ (rank 1)	
	G [y7] - 619.3046+ (rank 2)		G [y8] - 703.3369+ (rank 1)			T [y6] - 661.3264+ (rank 2)	
	519.3077++ (heavy)		693.3486++ (heavy)			779.9070++ (heavy)	
	A [y9] - 811.4400+ (rank 1)		Y [y12] - 1187.5531+ (rank 3)			W [y8] - 968.4528+ (rank 4)	
	L [y8] - 740.4028+ (rank 3)		A [y10] - 910.4468+ (rank 2)			D [y7] - 782.3735+ (rank 1)	
	G [y7] - 627.3188+ (rank 2)		G [y8] - 711.3511+ (rank 1)			T [y6] - 667.3465+ (rank 2)	
	K.YGIPYFETSAATGQNVEK.A [154, 171]		K.AVETLLDLIMK.R [172, 182]			518.2671+++	
	987.9758++		623.3598++			T [y6] - 661.3264+ (rank 2)	
	T [y11] - 1105.5484+ (rank 2)		E [y9] - 1075.6068+ (rank 4)			A [y5] - 560.2787+ (rank 3)	
	S [y10] - 1004.5007+ (rank 1)		L [y6] - 732.4324+ (rank 1)			G [y4] - 489.2416+ (rank 1)	
	A [y8] - 846.4316+ (rank 3)		D [y5] - 619.3484+ (rank 2)			520.2738+++ (heavy)	
	991.9829++ (heavy)		627.3669++ (heavy)			T [y6] - 667.3465+ (rank 2)	
	T [y11] - 1113.5626+ (rank 2)		E [y9] - 1083.6210+ (rank 4)			A [y5] - 566.2988+ (rank 3)	
	S [y10] - 1012.5149+ (rank 1)		L [y6] - 740.4466+ (rank 1)			G [y4] - 495.2617+ (rank 1)	
	A [y8] - 854.4458+ (rank 3)		D [y5] - 627.3626+ (rank 2)				
RHOD	IPI:IP100010841.2 SWISS-PROT:O00212 RHOD Rho-related GTP-binding protein RhoD						
	K.GKPVHLHIWDTAGQDDYDR.L [61, 79]		R.WYPEVNHFK.K [110, 119]			R.SVGAVAYLECSAR.L [161, 173]	
	741.6908+++		460.5449+++			691.8403++	
	A [y8] - 939.3803+ (rank 2)		P [y8] - 1030.4775+ (rank 1)			V [y9] - 1068.5143+ (rank 3)	
	G [y7] - 868.3432+ (rank 1)		E [y7] - 933.4247+ (rank 3)			A [y8] - 969.4458+ (rank 1)	
	D [y4] - 568.2362+ (rank 3)		V [y6] - 804.3821+ (rank 4)			Y [y7] - 898.4087+ (rank 2)	

	746.3689+++ (heavy)		463.2163+++ (heavy)		694.8503++ (heavy)
	A [y8] - 945.4004+ (rank 2)		P [y8] - 1038.4917+ (rank 1)		V [y9] - 1074.5344+ (rank 3)
	G [y7] - 874.3633+ (rank 1)		E [y7] - 941.4389+ (rank 3)		A [y8] - 975.4660+ (rank 1)
	D [y4] - 574.2563+ (rank 3)		V [y6] - 812.3963+ (rank 4)		Y [y7] - 904.4289+ (rank 2)
RHOQ	IPI:IP100012511.6 SWISS-PROT:P17081 RHOQ Rho-related GTP-binding protein RhoQ				
	K.EEWVPELK.E [100, 107]		K.EIGACCYVECSALTQK.G [153, 168]		K.TVFDEAIIAILTPK.K [172, 185]
	515.2662++		944.9155++		765.9425++
	W [y6] - 771.4400+ (rank 5)		V [y9] - 1035.5139+ (rank 3)		I [y7] - 755.5026+ (rank 3)
	V [y5] - 585.3606+ (rank 3)		E [y8] - 936.4455+ (rank 1)		A [y6] - 642.4185+ (rank 4)
	P [y4] - 486.2922+ (rank 1)		C [y7] - 807.4029+ (rank 2)		T [y3] - 345.2132+ (rank 2)
	519.2733++ (heavy)		948.9226++ (heavy)		769.9496++ (heavy)
	W [y6] - 779.4542+ (rank 5)		V [y9] - 1043.5281+ (rank 3)		I [y7] - 763.5168+ (rank 3)
	V [y5] - 593.3748+ (rank 3)		E [y8] - 944.4597+ (rank 1)		A [y6] - 650.4327+ (rank 4)
	P [y4] - 494.3064+ (rank 1)		C [y7] - 815.4171+ (rank 2)		T [y3] - 353.2274+ (rank 2)
RRAS2	IPI:IP100012512.2 SWISS-PROT:P62070 RRAS2 cDNA FLJ61162, highly similar to Ras-related protein R-Ras2				
	R.LVVVGGGGVVGK.S [16, 26]		R.LDILDTAGQEEFGAMR.E [69, 84]		R.TGEGFLLVFSVTD.R.G [90, 103]
	471.2926++		883.4249++		770.9039++
	V [y9] - 729.4254+ (rank 1)		A [y10] - 1095.4888+ (rank 2)		L [y8] - 936.5149+ (rank 1)
	V [y8] - 630.3570+ (rank 3)		G [y9] - 1024.4517+ (rank 1)		V [y7] - 823.4308+ (rank 2)
	G [y7] - 531.2885+ (rank 2)		E [y7] - 839.3716+ (rank 3)		F [y6] - 724.3624+ (rank 3)
	475.2997++ (heavy)		886.4350++ (heavy)		773.9140++ (heavy)
	V [y9] - 737.4396+ (rank 1)		A [y10] - 1101.5089+ (rank 2)		L [y8] - 942.5350+ (rank 1)
	V [y8] - 638.3711+ (rank 3)		G [y9] - 1030.4718+ (rank 1)		V [y7] - 829.4510+ (rank 2)
	G [y7] - 539.3027+ (rank 2)		E [y7] - 845.3917+ (rank 3)		F [y6] - 730.3826+ (rank 3)
	R.QVTQEEGQQLAR.Q [141, 152]				
	693.8522++				
	T [y10] - 1159.5702+ (rank 2)				
	E [y7] - 801.4213+ (rank 3)				
	G [y6] - 672.3787+ (rank 1)				
	696.8623++ (heavy)				
	T [y10] - 1165.5903+ (rank 2)				
	E [y7] - 807.4415+ (rank 3)				
	G [y6] - 678.3989+ (rank 1)				
RAB31	IPI:IP100014376.5 SWISS-PROT:Q13636 RAB31 ras-related protein Rab-31				
	R.FHSLAPMYR.G [67, 76]		R.GSAAVIVYDITK.Q [77, 89]		K.QDSFYTLK.K [90, 97]
	642.8133++		654.3639++		501.2506++
	S [y8] - 1000.4921+ (rank 1)		I [y7] - 851.4873+ (rank 1)		S [y6] - 758.4083+ (rank 3)
	A [y6] - 800.3760+ (rank 3)		V [y6] - 738.4032+ (rank 2)		Y [y4] - 524.3079+ (rank 1)
	P [y5] - 729.3389+ (rank 2)		Y [y5] - 639.3348+ (rank 3)		T [y3] - 361.2445+ (rank 2)
	645.8234++ (heavy)		658.3710++ (heavy)		505.2577++ (heavy)
	S [y8] - 1006.5122+ (rank 1)		I [y7] - 859.5015+ (rank 1)		S [y6] - 766.4225+ (rank 3)
	A [y6] - 806.3961+ (rank 3)		V [y6] - 746.4174+ (rank 2)		Y [y4] - 532.3221+ (rank 1)
	P [y5] - 735.3590+ (rank 2)		Y [y5] - 647.3490+ (rank 3)		T [y3] - 369.2587+ (rank 2)
RAB32	IPI:IP100014377.3 SWISS-PROT:Q13637 RAB32 Ras-related protein Rab-32				
	K.VLVIGELGVGK.T [27, 37]		R.SSTFEAVLK.W [110, 118]		K.DNINIEEAAR.F [176, 185]
	542.3422++		491.2662++		572.7833++
	V [y9] - 871.5247+ (rank 1)		T [y7] - 807.4611+ (rank 2)		N [y7] - 802.4054+ (rank 1)
	I [y8] - 772.4563+ (rank 3)		F [y6] - 706.4134+ (rank 1)		I [y6] - 688.3624+ (rank 2)
	G [y7] - 659.3723+ (rank 2)		E [y5] - 559.3450+ (rank 3)		E [y4] - 446.2358+ (rank 3)
	546.3493++ (heavy)		495.2733++ (heavy)		575.7933++ (heavy)
	V [y9] - 879.5389+ (rank 1)		T [y7] - 815.4753+ (rank 2)		N [y7] - 808.4255+ (rank 1)
	I [y8] - 780.4705+ (rank 3)		F [y6] - 714.4276+ (rank 1)		I [y6] - 694.3826+ (rank 2)
	G [y7] - 667.3865+ (rank 2)		E [y5] - 567.3592+ (rank 3)		E [y4] - 452.2559+ (rank 3)
RAB18	IPI:IP100014577.1 SWISS-PROT:Q9NP72 RAB18 Ras-related protein Rab-18				
	K.IIIGESGVGK.S [10, 20]		K.LAIWDTAGQER.F [58, 68]		R.TLTPSYR.G [71, 78]
	543.3319++		630.3226++		500.7585++
	I [y9] - 859.4884+ (rank 2)		W [y8] - 962.4326+ (rank 1)		T [y6] - 786.3781+ (rank 2)
	I [y8] - 746.4043+ (rank 3)		D [y7] - 776.3533+ (rank 2)		P [y5] - 685.3304+ (rank 1)
	G [y7] - 633.3202+ (rank 1)		G [y4] - 489.2416+ (rank 3)		S [y4] - 588.2776+ (rank 3)
	547.3390++ (heavy)		633.3326++ (heavy)		503.7686++ (heavy)
	I [y9] - 867.5026+ (rank 2)		W [y8] - 968.4528+ (rank 1)		T [y6] - 792.3982+ (rank 2)
	I [y8] - 754.4185+ (rank 3)		D [y7] - 782.3735+ (rank 2)		P [y5] - 691.3505+ (rank 1)
	G [y7] - 641.3344+ (rank 1)		G [y4] - 495.2617+ (rank 3)		S [y4] - 594.2978+ (rank 3)
	R.NDIVNMLVGNK.I [112, 122]				
	608.8214++				
	I [y9] - 987.5656+ (rank 3)				
	V [y8] - 874.4815+ (rank 1)				
	N [y7] - 775.4131+ (rank 2)				
	612.8285++ (heavy)				
	I [y9] - 995.5798+ (rank 3)				
	V [y8] - 882.4957+ (rank 1)				
	N [y7] - 783.4273+ (rank 2)				
RAB9B	IPI:IP100014603.1 SWISS-PROT:Q9NP90 RAB9B Ras-related protein Rab-9B				
	K.VILLGDGGVVGK.S [9, 19]		R.QSFENLGNWQK.E [92, 102]		K.EFIYYADV.K.D [103, 111]
	514.3109++		675.8255++		574.2871++
	L [y9] - 815.4621+ (rank 1)		G [y5] - 632.3151+ (rank 1)		Y [y6] - 758.3719+ (rank 1)
	L [y8] - 702.3781+ (rank 3)		N [y4] - 575.2936+ (rank 3)		Y [y5] - 595.3086+ (rank 2)

	G [y7] - 589.2940+ (rank 2)	W [y3] - 461.2507+ (rank 4)	A [y4] - 432.2453+ (rank 3)
	518.3180++ (heavy)	679.8326++ (heavy)	578.2942++ (heavy)
	L [y9] - 823.4763+ (rank 1)	G [y5] - 640.3293+ (rank 1)	Y [y6] - 766.3861+ (rank 1)
	L [y8] - 710.3923+ (rank 3)	N [y4] - 583.3078+ (rank 3)	Y [y5] - 603.3228+ (rank 2)
	G [y7] - 597.3082+ (rank 2)	W [y3] - 469.2649+ (rank 4)	A [y4] - 440.2595+ (rank 3)
RAP1B	IPI:IP100015148.3 SWISS-PROT:P61224 RAP1B Ras-related protein Rap-1b		
	K.DTDDVPMILVGNK.C [104, 116]	K.DTDDVPMILVGNK.C [104, 116]	R.QWNNCAFLESSAK.S [136, 148]
	708.8556++	716.8530++	777.8539++
	P [y8] - 871.5070+ (rank 1)	P [y8] - 887.5019+ (rank 1)	A [y8] - 852.4462+ (rank 2)
	L [y5] - 530.3297+ (rank 2)	L [y5] - 530.3297+ (rank 4)	L [y6] - 634.3406+ (rank 1)
	V [y4] - 417.2456+ (rank 3)	V [y4] - 417.2456+ (rank 3)	E [y5] - 521.2566+ (rank 3)
	712.8627++ (heavy)	720.8601++ (heavy)	781.8610++ (heavy)
	P [y8] - 879.5212+ (rank 1)	P [y8] - 895.5161+ (rank 1)	A [y8] - 860.4604+ (rank 2)
	L [y5] - 538.3439+ (rank 2)	L [y5] - 538.3439+ (rank 4)	L [y6] - 642.3548+ (rank 1)
	V [y4] - 425.2598+ (rank 3)	V [y4] - 425.2598+ (rank 3)	E [y5] - 529.2708+ (rank 3)
ARFRP1	IPI:IP100015178.1 SWISS-PROT:Q13795 ARFRP1 ADP-ribosylation factor-related protein 1		
	K.TTFLEQSK.T [30, 37]	K.ITTTVGLNIGTVDVGK.A [52, 67]	K.QDVETCLSLIPDIK.T [135, 147]
	477.2506++	794.4512++	759.3794++
	F [y6] - 751.3985+ (rank 1)	G [y11] - 1072.5997+ (rank 1)	E [y10] - 1175.5977+ (rank 5)
	L [y5] - 604.3301+ (rank 2)	N [y9] - 902.4942+ (rank 3)	S [y6] - 672.3927+ (rank 4)
	E [y4] - 491.2460+ (rank 3)	G [y7] - 675.3672+ (rank 2)	P [y4] - 472.2766+ (rank 1)
	481.2577++ (heavy)	798.4583++ (heavy)	763.3865++ (heavy)
	F [y6] - 759.4127+ (rank 1)	G [y11] - 1080.6139+ (rank 1)	E [y10] - 1183.6119+ (rank 5)
	L [y5] - 612.3443+ (rank 2)	N [y9] - 910.5084+ (rank 3)	S [y6] - 680.4069+ (rank 4)
	E [y4] - 499.2602+ (rank 3)	G [y7] - 683.3814+ (rank 2)	P [y4] - 480.2908+ (rank 1)
	K.TAFSDCTSK.I [148, 156]	R.DCLTQACSAITGK.G [161, 173]	R.EGIEWMVK.C [177, 184]
	508.7213++	712.8291++	496.2495++
	F [y7] - 844.3505+ (rank 1)	T [y10] - 1036.5092+ (rank 1)	E [y5] - 692.3436+ (rank 2)
	S [y6] - 697.2821+ (rank 2)	Q [y9] - 935.4615+ (rank 3)	W [y4] - 563.3010+ (rank 3)
	C [y4] - 495.2232+ (rank 3)	A [y8] - 807.4029+ (rank 2)	M [y3] - 377.2217+ (rank 5)
	512.7284++ (heavy)	716.8362++ (heavy)	500.2566++ (heavy)
	F [y7] - 852.3647+ (rank 1)	T [y10] - 1044.5234+ (rank 1)	E [y5] - 700.3578+ (rank 2)
	S [y6] - 705.2963+ (rank 2)	Q [y9] - 943.4757+ (rank 3)	W [y4] - 571.3152+ (rank 3)
	C [y4] - 503.2374+ (rank 3)	A [y8] - 815.4171+ (rank 2)	M [y3] - 385.2359+ (rank 5)
RAB20	IPI:IP100015839.1 SWISS-PROT:Q9NX57 RAB20 Ras-related protein Rab-20		
	K.IVLLGDMNVGK.T [7, 17]	R.GAAAILTYDVNHR.Q [71, 84]	R.FLGLTDTASK.D [94, 103]
	579.8312++	505.2756+++	526.7848++
	L [y9] - 946.5026+ (rank 2)	L [y8] - 1017.5112+ (rank 3)	G [y8] - 792.4098+ (rank 1)
	L [y8] - 833.4186+ (rank 3)	T [y7] - 904.4272+ (rank 1)	T [y6] - 622.3042+ (rank 2)
	G [y7] - 720.3345+ (rank 1)	V [y4] - 525.2892+ (rank 4)	T [y4] - 406.2296+ (rank 4)
	583.8383++ (heavy)	507.2823+++ (heavy)	530.7919++ (heavy)
	L [y9] - 954.5168+ (rank 2)	L [y8] - 1023.5313+ (rank 3)	G [y8] - 800.4240+ (rank 1)
	L [y8] - 841.4328+ (rank 3)	T [y7] - 910.4473+ (rank 1)	T [y6] - 630.3184+ (rank 2)
	G [y7] - 728.3487+ (rank 1)	V [y4] - 531.3093+ (rank 4)	T [y4] - 414.2438+ (rank 4)
	K.QVQLEDAVALYK.K [147, 158]		
	688.8746++		
	L [y9] - 1021.5564+ (rank 5)		
	E [y8] - 908.4724+ (rank 2)		
	A [y4] - 494.2973+ (rank 3)		
	692.8817++ (heavy)		
	L [y9] - 1029.5706+ (rank 5)		
	E [y8] - 916.4866+ (rank 2)		
	A [y4] - 502.3115+ (rank 3)		
SAR1A	IPI:IP100015954.1 SWISS-PROT:Q9NR31 SAR1A GTP-binding protein SAR1a		
	K.NYLPAINGIVFLVDCADHSR.L [87, 106]	R.TDAISEEK.L [138, 145]	R.EIFGLYGQTTGK.G [148, 159]
	1137.5704++	446.7165++	657.3404++
	L [y9] - 1072.4840+ (rank 1)	A [y6] - 676.3512+ (rank 1)	G [y9] - 924.4785+ (rank 3)
	V [y8] - 959.4000+ (rank 4)	I [y5] - 605.3141+ (rank 3)	Y [y7] - 754.3730+ (rank 1)
	C [y6] - 745.3046+ (rank 2)	S [y4] - 492.2300+ (rank 2)	G [y6] - 591.3097+ (rank 2)
	1140.5805++ (heavy)	450.7236++ (heavy)	661.3475++ (heavy)
	L [y9] - 1078.5041+ (rank 1)	A [y6] - 684.3654+ (rank 1)	G [y9] - 932.4927+ (rank 3)
	V [y8] - 965.4201+ (rank 4)	I [y5] - 613.3283+ (rank 3)	Y [y7] - 762.3872+ (rank 1)
	C [y6] - 751.3247+ (rank 2)	S [y4] - 500.2442+ (rank 2)	G [y6] - 599.3239+ (rank 2)
RAB5C	IPI:IP100016339.4 SWISS-PROT:P51148 RAB5C Ras-related protein Rab-5C		
	R.QASPNIVIALAGNK.A [121, 134]	K.NEPQNATGAPGR.N [184, 195]	R.GVDLQENNPASR.S [198, 209]
	698.4014++	606.2918++	650.3180++
	V [y8] - 785.4880+ (rank 1)	P [y10] - 968.4908+ (rank 1)	Q [y8] - 915.4279+ (rank 3)
	I [y7] - 686.4196+ (rank 2)	T [y6] - 558.2994+ (rank 3)	E [y7] - 787.3693+ (rank 2)
	A [y6] - 573.3355+ (rank 3)	P [y3] - 329.1932+ (rank 2)	P [y4] - 430.2409+ (rank 1)
	702.4085++ (heavy)	609.3019++ (heavy)	653.3281++ (heavy)
	V [y8] - 793.5022+ (rank 1)	P [y10] - 974.5109+ (rank 1)	Q [y8] - 921.4480+ (rank 3)
	I [y7] - 694.4337+ (rank 2)	T [y6] - 564.3196+ (rank 3)	E [y7] - 793.3894+ (rank 2)
	A [y6] - 581.3497+ (rank 3)	P [y3] - 335.2133+ (rank 2)	P [y4] - 436.2610+ (rank 1)
RAB7A	IPI:IP100016342.1 SWISS-PROT:P51149 RAB7A Ras-related protein Rab-7a		
	R.FQSLGVAFYR.G [69, 78]	R.DEFLIQASPR.D [103, 112]	R.AQAWCYSK.N [138, 145]
	594.3140++	588.3064++	507.2291++
	S [y8] - 912.4938+ (rank 1)	I [y6] - 671.3835+ (rank 4)	A [y6] - 814.3552+ (rank 1)

	G [y6] - 712.3777+ (rank 2)		Q [y5] - 558.2994+ (rank 3)		C [y4] - 557.2388+ (rank 2)
	A [y4] - 556.2878+ (rank 3)		S [y3] - 359.2037+ (rank 2)		Y [y3] - 397.2082+ (rank 3)
	597.3241++ (heavy)		591.3165++ (heavy)		511.2362++ (heavy)
	S [y8] - 918.5139+ (rank 1)		I [y6] - 677.4036+ (rank 4)		A [y6] - 822.3694+ (rank 1)
	G [y6] - 718.3978+ (rank 2)		Q [y5] - 564.3196+ (rank 3)		C [y4] - 565.2530+ (rank 2)
	A [y4] - 562.3079+ (rank 3)		S [y3] - 365.2239+ (rank 2)		Y [y3] - 405.2224+ (rank 3)
	K.NNIPYFETSAK.E [146, 156]		K.EAINVEQAFQTIAR.N [157, 170]		
	642.3170++		795.4177++		
	I [y9] - 1055.5408+ (rank 2)		E [y9] - 1063.5531+ (rank 1)		
	P [y8] - 942.4567+ (rank 1)		Q [y8] - 934.5105+ (rank 3)		
	Y [y7] - 845.4040+ (rank 3)		F [y6] - 735.4148+ (rank 2)		
	646.3241++ (heavy)		798.4278++ (heavy)		
	I [y9] - 1063.5550+ (rank 2)		E [y9] - 1069.5732+ (rank 1)		
	P [y8] - 950.4709+ (rank 1)		Q [y8] - 940.5306+ (rank 3)		
	Y [y7] - 853.4182+ (rank 3)		F [y6] - 741.4349+ (rank 2)		
RAB9A	IPI:IP100016372.1 SWISS-PROT:P51151 RAB9A Ras-related protein Rab-9A				
	R.QVSTEEAQAWCR.D [131, 142]		K.DATNVAAAFEEAVR.R [156, 169]		R.SDHLIQTDTVNLHR.K [178, 191]
	732.8304++		732.3599++		824.9237++
	A [y6] - 791.3617+ (rank 4)		A [y9] - 963.4894+ (rank 1)		I [y10] - 1196.6382+ (rank 3)
	A [y4] - 592.2660+ (rank 2)		A [y7] - 821.4152+ (rank 2)		Q [y9] - 1083.5541+ (rank 1)
	W [y3] - 521.2289+ (rank 1)		F [y6] - 750.3781+ (rank 3)		T [y8] - 955.4956+ (rank 2)
	735.8405++ (heavy)		735.3700++ (heavy)		827.9338++ (heavy)
	A [y6] - 797.3818+ (rank 4)		A [y9] - 969.5096+ (rank 1)		I [y10] - 1202.6583+ (rank 3)
	A [y4] - 598.2862+ (rank 2)		A [y7] - 827.4353+ (rank 2)		Q [y9] - 1089.5743+ (rank 1)
	W [y3] - 527.2490+ (rank 1)		F [y6] - 756.3982+ (rank 3)		T [y8] - 961.5157+ (rank 2)
			488.5757+++		
			F [y6] - 750.3781+ (rank 3)		
			E [y5] - 603.3097+ (rank 1)		
			E [y4] - 474.2671+ (rank 2)		
			490.5824+++ (heavy)		
			F [y6] - 756.3982+ (rank 3)		
			E [y5] - 609.3298+ (rank 1)		
			E [y4] - 480.2872+ (rank 2)		
RAB13	IPI:IP100016373.3 SWISS-PROT:P51153 RAB13 Ras-related protein Rab-13				
	K.LQVWDTAGQER.F [58, 68]		K.SFENIQNWMK.S [94, 103]		K.ENASAGVER.L [107, 115]
	651.8255++		648.8057++		466.7252++
	V [y9] - 1061.5010+ (rank 1)		E [y8] - 1062.5037+ (rank 3)		S [y6] - 618.3206+ (rank 3)
	W [y8] - 962.4326+ (rank 2)		Q [y5] - 706.3341+ (rank 1)		A [y5] - 531.2885+ (rank 2)
	G [y4] - 489.2416+ (rank 3)		N [y4] - 578.2755+ (rank 2)		G [y4] - 460.2514+ (rank 1)
	654.8355++ (heavy)		652.8128++ (heavy)		469.7353++ (heavy)
	V [y9] - 1067.5212+ (rank 1)		E [y8] - 1070.5179+ (rank 3)		S [y6] - 624.3407+ (rank 3)
	W [y8] - 968.4528+ (rank 2)		Q [y5] - 714.3483+ (rank 1)		A [y5] - 537.3087+ (rank 2)
	G [y4] - 495.2617+ (rank 3)		N [y4] - 586.2897+ (rank 2)		G [y4] - 466.2716+ (rank 1)
RAB28	IPI:IP100016377.2 SWISS-PROT:P51157-1 RAB28 Isoform S of Ras-related protein Rab-28				
	K.IVVLGDGASGK.T [14, 24]		K.TSLTTCFAQETFGK.Q [25, 38]		K.VSEESQPLVALVGNK.I [113, 129]
	508.2928++		795.8771++		900.4729++
	V [y9] - 803.4258+ (rank 1)		T [y10] - 1188.5354+ (rank 2)		T [y11] - 1139.6783+ (rank 3)
	L [y8] - 704.3573+ (rank 3)		C [y9] - 1087.4877+ (rank 1)		P [y9] - 910.5720+ (rank 1)
	G [y7] - 591.2733+ (rank 2)		A [y7] - 780.3886+ (rank 3)		A [y6] - 601.3668+ (rank 2)
	512.2999++ (heavy)		799.8842++ (heavy)		904.4800++ (heavy)
	V [y9] - 811.4400+ (rank 1)		T [y10] - 1196.5496+ (rank 2)		T [y11] - 1147.6925+ (rank 3)
	L [y8] - 712.3715+ (rank 3)		C [y9] - 1095.5019+ (rank 1)		P [y9] - 918.5862+ (rank 1)
	G [y7] - 599.2875+ (rank 2)		A [y7] - 788.4028+ (rank 3)		A [y6] - 609.3810+ (rank 2)
	K.VAAEILGIK.L [172, 180]		K.AEIEQSQR.V [184, 191]		K.ADIVNYNQEPMSR.T [195, 207]
	457.2895++		480.7409++		768.8592++
	A [y8] - 814.5033+ (rank 2)		I [y6] - 760.3948+ (rank 2)		N [y9] - 1138.4946+ (rank 3)
	A [y7] - 743.4662+ (rank 1)		E [y5] - 647.3107+ (rank 1)		E [y5] - 619.2868+ (rank 2)
	E [y6] - 672.4291+ (rank 3)		Q [y4] - 518.2681+ (rank 3)		P [y4] - 490.2442+ (rank 1)
	461.2966++ (heavy)		483.7510++ (heavy)		771.8693++ (heavy)
	A [y8] - 822.5175+ (rank 2)		I [y6] - 766.4149+ (rank 2)		N [y9] - 1144.5147+ (rank 3)
	A [y7] - 751.4804+ (rank 1)		E [y5] - 653.3309+ (rank 1)		E [y5] - 625.3070+ (rank 2)
	E [y6] - 680.4433+ (rank 3)		Q [y4] - 524.2883+ (rank 3)		P [y4] - 496.2644+ (rank 1)
RAB27A	IPI:IP100016381.2 SWISS-PROT:P51159-1 RAB27A Isoform Long of Ras-related protein Rab-27A				
	K.FLALGDSGVGK.T [11, 21]		K.TSVLYQYTDGK.F [22, 32]		R.IHLQLWDTAGQER.F [67, 79]
	532.2928++		637.8168++		783.9048++
	A [y9] - 803.4258+ (rank 1)		L [y8] - 987.4782+ (rank 2)		L [y9] - 1075.5167+ (rank 4)
	L [y8] - 732.3886+ (rank 3)		Y [y7] - 874.3941+ (rank 1)		W [y8] - 962.4326+ (rank 1)
	G [y7] - 619.3046+ (rank 2)		Q [y6] - 711.3308+ (rank 3)		D [y7] - 776.3533+ (rank 3)
	536.2999++ (heavy)		641.8239++ (heavy)		786.9149++ (heavy)
	A [y9] - 811.4400+ (rank 1)		L [y8] - 995.4924+ (rank 2)		L [y9] - 1081.5368+ (rank 4)
	L [y8] - 740.4028+ (rank 3)		Y [y7] - 882.4083+ (rank 1)		W [y8] - 968.4528+ (rank 1)
	G [y7] - 627.3188+ (rank 2)		Q [y6] - 719.3450+ (rank 3)		D [y7] - 782.3735+ (rank 3)
	K.SDLEDQR.V [134, 140]		K.SWIPEGVVR.S [191, 199]		
	431.6987++		521.7876++		
	L [y5] - 660.3311+ (rank 3)		I [y7] - 769.4567+ (rank 5)		
	E [y4] - 547.2471+ (rank 2)		P [y6] - 656.3726+ (rank 2)		
	D [y3] - 418.2045+ (rank 4)		G [y4] - 430.2772+ (rank 3)		

	434.7088++ (heavy)		524.7977++ (heavy)		
	L [y5] - 666.3513+ (rank 3)		I [y7] - 775.4768+ (rank 5)		
	E [y4] - 553.2672+ (rank 2)		P [y6] - 662.3927+ (rank 2)		
	D [y3] - 424.2246+ (rank 4)		G [y4] - 436.2974+ (rank 3)		
RAB10	IPI:IP100016513.5 SWISS-PROT:P61026 RAB10 Ras-related protein Rab-10				
	K.TYDLLFK.L [4, 10]		R.FHTITTSYYR.G [70, 79]		R.NIDEHANEDVER.M [105, 116]
	450.2473++		644.8197++		720.8211++
	Y [y6] - 798.4396+ (rank 3)		T [y8] - 1004.5047+ (rank 1)		H [y8] - 969.4384+ (rank 1)
	D [y5] - 635.3763+ (rank 1)		I [y7] - 903.4571+ (rank 3)		A [y7] - 832.3795+ (rank 3)
	L [y4] - 520.3493+ (rank 4)		T [y6] - 790.3730+ (rank 2)		N [y6] - 761.3424+ (rank 4)
	454.2544++ (heavy)		647.8297++ (heavy)		723.8312++ (heavy)
	Y [y6] - 806.4538+ (rank 3)		T [y8] - 1010.5249+ (rank 1)		H [y8] - 975.4586+ (rank 1)
	D [y5] - 643.3905+ (rank 1)		I [y7] - 909.4772+ (rank 3)		A [y7] - 838.3997+ (rank 3)
	L [y4] - 528.3635+ (rank 4)		T [y6] - 796.3931+ (rank 2)		N [y6] - 767.3626+ (rank 4)
RHEB	IPI:IP100016669.1 SWISS-PROT:Q15382 RHEB GTP-binding protein Rheb				
	K.IAILGYR.S [8, 14]		K.VQIPIMLVGNK.K [109, 119]		K.ALAESWNAAFLESSAK.E [135, 150]
	403.2502++		606.3627++		847.9229++
	A [y6] - 692.4090+ (rank 4)		I [y9] - 984.5910+ (rank 2)		N [y10] - 1037.5262+ (rank 1)
	I [y5] - 621.3719+ (rank 1)		P [y8] - 871.5070+ (rank 1)		A [y9] - 923.4833+ (rank 2)
	L [y4] - 508.2878+ (rank 3)		V [y4] - 417.2456+ (rank 3)		F [y7] - 781.4090+ (rank 4)
	406.2602++ (heavy)		610.3698++ (heavy)		851.9300++ (heavy)
	A [y6] - 698.4291+ (rank 4)		I [y9] - 992.6052+ (rank 2)		N [y10] - 1045.5404+ (rank 1)
	I [y5] - 627.3920+ (rank 1)		P [y8] - 879.5212+ (rank 1)		A [y9] - 931.4975+ (rank 2)
	L [y4] - 514.3079+ (rank 3)		V [y4] - 425.2598+ (rank 3)		F [y7] - 789.4232+ (rank 4)
	K.ENQTAVDVF.R [151, 160]				
	589.7937++				
	A [y6] - 706.3883+ (rank 3)				
	V [y5] - 635.3511+ (rank 2)				
	D [y4] - 536.2827+ (rank 1)				
	592.8037++ (heavy)				
	A [y6] - 712.4084+ (rank 3)				
	V [y5] - 641.3713+ (rank 2)				
	D [y4] - 542.3029+ (rank 1)				
CDC42	IPI:IP100016786.1 SWISS-PROT:P60953-2 CDC42 Isoform 2 of Cell division control protein 42 homolog				
	K.YVECSALTQK.G [153, 162]		K.NVFDEAILAALEPPEPK.K [166, 182]		
	599.7923++		926.9882++		
	E [y8] - 936.4455+ (rank 1)		A [y8] - 880.4775+ (rank 3)		
	C [y7] - 807.4029+ (rank 2)		E [y6] - 696.3563+ (rank 2)		
	T [y3] - 376.2191+ (rank 3)		P [y5] - 567.3137+ (rank 1)		
	603.7994++ (heavy)		930.9953++ (heavy)		
	E [y8] - 944.4597+ (rank 1)		A [y8] - 888.4917+ (rank 3)		
	C [y7] - 815.4171+ (rank 2)		E [y6] - 704.3705+ (rank 2)		
	T [y3] - 384.2333+ (rank 3)		P [y5] - 575.3279+ (rank 1)		
			618.3279+++		
			L [y7] - 809.4403+ (rank 3)		
			E [y6] - 696.3563+ (rank 2)		
			P [y5] - 567.3137+ (rank 1)		
			620.9993+++ (heavy)		
			L [y7] - 817.4545+ (rank 3)		
			E [y6] - 704.3705+ (rank 2)		
			P [y5] - 575.3279+ (rank 1)		
RAB6B	IPI:IP100016891.1 SWISS-PROT:Q9NRW1 RAB6B Ras-related protein Rab-6B				
	R.QITIEEGEQR.A [134, 143]		K.ELSMFIETSAK.T [146, 157]		R.VASALPGMENVQEK.S [169, 182]
	601.8042++		677.8498++		736.8743++
	T [y8] - 961.4585+ (rank 1)		M [y8] - 926.4652+ (rank 1)		L [y10] - 1144.5667+ (rank 2)
	E [y6] - 747.3268+ (rank 2)		F [y7] - 795.4247+ (rank 2)		P [y9] - 1031.4826+ (rank 1)
	E [y5] - 618.2842+ (rank 3)		I [y6] - 648.3563+ (rank 3)		G [y8] - 934.4299+ (rank 3)
	604.8143++ (heavy)		681.8569++ (heavy)		740.8814++ (heavy)
	T [y8] - 967.4786+ (rank 1)		M [y8] - 934.4794+ (rank 1)		L [y10] - 1152.5809+ (rank 2)
	E [y6] - 753.3469+ (rank 2)		F [y7] - 803.4389+ (rank 2)		P [y9] - 1039.4968+ (rank 1)
	E [y5] - 624.3043+ (rank 3)		I [y6] - 656.3705+ (rank 3)		G [y8] - 942.4441+ (rank 3)
	R.VASALPGMENVQEK.S [169, 182]				
	744.8718++				
	P [y9] - 1047.4775+ (rank 1)				
	G [y8] - 950.4248+ (rank 2)				
	V [y4] - 503.2824+ (rank 3)				
	748.8789++ (heavy)				
	P [y9] - 1055.4917+ (rank 1)				
	G [y8] - 958.4390+ (rank 2)				
	V [y4] - 511.2966+ (rank 3)				
RHOG	IPI:IP100017342.1 SWISS-PROT:P84095 RHOG Rho-related GTP-binding protein RhoG				
	R.TVNLNLWDTAGQEEYDR.L [49, 65]		K.EQGQAPITPQQGQALAK.Q [130, 146]		R.YLECSALQQDGVK.E [153, 165]
	1012.4714++		882.9656++		755.8639++
	D [y10] - 1183.4862+ (rank 2)		P [y12] - 1251.7056+ (rank 1)		C [y10] - 1105.5306+ (rank 3)
	T [y9] - 1068.4592+ (rank 4)		T [y10] - 1041.5687+ (rank 2)		L [y7] - 787.4308+ (rank 2)
	G [y7] - 896.3745+ (rank 1)		P [y9] - 940.5211+ (rank 3)		Q [y6] - 674.3468+ (rank 1)
	1015.4815++ (heavy)		886.9727++ (heavy)		759.8710++ (heavy)

	D [y10] - 1189.5063+ (rank 2)	P [y12] - 1259.7198+ (rank 1)	C [y10] - 1113.5448+ (rank 3)
	T [y9] - 1074.4794+ (rank 4)	T [y10] - 1049.5829+ (rank 2)	L [y7] - 795.4450+ (rank 2)
	G [y7] - 902.3946+ (rank 1)	P [y9] - 948.5353+ (rank 3)	Q [y6] - 682.3610+ (rank 1)
RAB5B	IPI:IP100017344.3 SWISS-PROT:P61020 RAB5B Ras-related protein Rab-5B		
	R.QASPSVIALAGN K .A [120, 133]	K.TAMNVNDLFLAIA K .K [165, 178]	K.SEPQNLGGAAG R .S [183, 194]
	684.8959++	760.9107++	578.7889++
	P [y11] - 1082.6568+ (rank 2)	N [y11] - 1217.6888+ (rank 2)	P [y10] - 940.4959+ (rank 2)
	V [y8] - 785.4880+ (rank 1)	V [y10] - 1103.6459+ (rank 3)	L [y7] - 601.3416+ (rank 3)
	A [y6] - 573.3355+ (rank 3)	N [y9] - 1004.5775+ (rank 1)	G [y6] - 488.2576+ (rank 1)
	688.9030++ (heavy)	764.9178++ (heavy)	581.7990++ (heavy)
	P [y11] - 1090.6710+ (rank 2)	N [y11] - 1225.7030+ (rank 2)	P [y10] - 946.5160+ (rank 2)
	V [y8] - 793.5022+ (rank 1)	V [y10] - 1111.6601+ (rank 3)	L [y7] - 607.3618+ (rank 3)
	A [y6] - 581.3497+ (rank 3)	N [y9] - 1012.5917+ (rank 1)	G [y6] - 494.2777+ (rank 1)
	R.GVDLHEQSQQN K .S [197, 208]		
	691.8366++		
	H [y8] - 998.4650+ (rank 2)		
	E [y7] - 861.4061+ (rank 1)		
	S [y5] - 604.3049+ (rank 3)		
	695.8437++ (heavy)		
	H [y8] - 1006.4792+ (rank 2)		
	E [y7] - 869.4203+ (rank 1)		
	S [y5] - 612.3191+ (rank 3)		
RAP2B	IPI:IP100018364.2 SWISS-PROT:P61225 RAP2B Ras-related protein Rap-2b		
	R.VPMILVGN K .V [108, 116]	R.VPMILVGN K .V [108, 116]	K.VDLEGER E .E [117, 123]
	485.7913++	493.7888++	409.2061++
	M [y7] - 774.4542+ (rank 1)	P [y8] - 887.5019+ (rank 1)	D [y6] - 718.3366+ (rank 1)
	I [y6] - 643.4137+ (rank 2)	I [y6] - 643.4137+ (rank 2)	L [y5] - 603.3097+ (rank 2)
	L [y5] - 530.3297+ (rank 3)	L [y5] - 530.3297+ (rank 3)	G [y3] - 361.1830+ (rank 3)
	489.7984++ (heavy)	497.7959++ (heavy)	412.2162++ (heavy)
	M [y7] - 782.4684+ (rank 1)	P [y8] - 895.5161+ (rank 1)	D [y6] - 724.3567+ (rank 1)
	I [y6] - 651.4279+ (rank 2)	I [y6] - 651.4279+ (rank 2)	L [y5] - 609.3298+ (rank 2)
	L [y5] - 538.3439+ (rank 3)	L [y5] - 538.3439+ (rank 3)	G [y3] - 367.2031+ (rank 3)
	K.ASVDELFAEIV R .Q [150, 161]		
	674.8590++		
	F [y6] - 734.4196+ (rank 1)		
	A [y5] - 587.3511+ (rank 2)		
	E [y4] - 516.3140+ (rank 3)		
	677.8691++ (heavy)		
	F [y6] - 740.4397+ (rank 1)		
	A [y5] - 593.3713+ (rank 2)		
	E [y4] - 522.3342+ (rank 3)		
ARL8B	IPI:IP100018871.2 TREMBL:B4E1J8 ARL8B cDNA FLJ56285, highly similar to ADP-ribosylation factor-like protein 8B		
	R.DLPNALDE K .Q [184, 192]	K.MNLSAIQD R .E [198, 206]	R.EI CC YSIS CK .E [207, 216]
	507.7587++	524.2662++	660.2751++
	P [y7] - 786.3992+ (rank 1)	L [y7] - 802.4417+ (rank 2)	C [y7] - 917.3856+ (rank 3)
	N [y6] - 689.3464+ (rank 2)	S [y6] - 689.3577+ (rank 1)	S [y5] - 594.2916+ (rank 2)
	E [y2] - 276.1554+ (rank 3)	A [y5] - 602.3257+ (rank 3)	S [y3] - 394.1755+ (rank 1)
	511.7658++ (heavy)	527.2763++ (heavy)	664.2822++ (heavy)
	P [y7] - 794.4134+ (rank 1)	L [y7] - 808.4619+ (rank 2)	C [y7] - 925.3997+ (rank 3)
	N [y6] - 697.3606+ (rank 2)	S [y6] - 695.3778+ (rank 1)	S [y5] - 602.3058+ (rank 2)
	E [y2] - 284.1696+ (rank 3)	A [y5] - 608.3458+ (rank 3)	S [y3] - 402.1897+ (rank 1)
RHOH	IPI:IP100018882.1 SWISS-PROT:Q15669 RHOH Rho-related GTP-binding protein RhoH		
	R.SNLP C TPVLVATQTDQ R .E [103, 120]	R.A SC VNAMEG K .K [127, 136]	K.GYLE CS ALS NR .G [146, 156]
	1000.0175++	533.7364++	635.2982++
	P [y12] - 1326.7376+ (rank 1)	V [y7] - 748.3658+ (rank 2)	E [y8] - 936.4204+ (rank 2)
	V [y9] - 1017.5323+ (rank 4)	N [y6] - 649.2974+ (rank 1)	C [y7] - 807.3778+ (rank 1)
	V [y8] - 918.4639+ (rank 2)	E [y3] - 333.1769+ (rank 5)	S [y6] - 647.3471+ (rank 3)
	1003.0276++ (heavy)	537.7435++ (heavy)	638.3083++ (heavy)
	P [y12] - 1332.7577+ (rank 1)	V [y7] - 756.3800+ (rank 2)	E [y8] - 942.4405+ (rank 2)
	V [y9] - 1023.5525+ (rank 4)	N [y6] - 657.3116+ (rank 1)	C [y7] - 813.3979+ (rank 1)
	V [y8] - 924.4841+ (rank 2)	E [y3] - 341.1911+ (rank 5)	S [y6] - 653.3672+ (rank 3)
	R.GVQQVFEC A V R .T [157, 167]		
	646.8244++		
	Q [y8] - 1008.4931+ (rank 3)		
	F [y6] - 781.3661+ (rank 1)		
	E [y5] - 634.2977+ (rank 2)		
	649.8345++ (heavy)		
	Q [y8] - 1014.5133+ (rank 3)		
	F [y6] - 787.3863+ (rank 1)		
	E [y5] - 640.3179+ (rank 2)		
RAP1A	IPI:IP100019345.1 SWISS-PROT:P62834 RAP1A Ras-related protein Rap-1A		
	R.V K DTEDVPMILVGN K .C [102, 116] (mis)	R.V K DTEDVPMILVGN K .C [102, 116] (mis)	K.DTEDVPMILVGN K .C [104, 116]
	829.4451++	837.4426++	715.8634++
	D [y10] - 1085.6023+ (rank 4)	P [y8] - 887.5019+ (rank 1)	V [y9] - 970.5754+ (rank 4)
	V [y9] - 970.5754+ (rank 3)	V [y4] - 417.2456+ (rank 3)	P [y8] - 871.5070+ (rank 1)
	P [y8] - 871.5070+ (rank 1)	G [y3] - 318.1772+ (rank 2)	L [y5] - 530.3297+ (rank 2)
	837.4593++ (heavy)	845.4568++ (heavy)	719.8705++ (heavy)

	D [y10] - 1093.6165+ (rank 4)	P [y8] - 895.5161+ (rank 1)	V [y9] - 978.5896+ (rank 4)
	V [y9] - 978.5896+ (rank 3)	V [y4] - 425.2598+ (rank 3)	P [y8] - 879.5212+ (rank 1)
	P [y8] - 879.5212+ (rank 1)	G [y3] - 326.1914+ (rank 2)	L [y5] - 538.3439+ (rank 2)
	R.QWCNCAFLESSAK.S [136, 148]		
	800.8478++		
	A [y8] - 852.4462+ (rank 3)		
	F [y7] - 781.4090+ (rank 2)		
	L [y6] - 634.3406+ (rank 1)		
	804.8549++ (heavy)		
	A [y8] - 860.4604+ (rank 3)		
	F [y7] - 789.4232+ (rank 2)		
	L [y6] - 642.3548+ (rank 1)		
RAP2A	IPI: IPI00019346.1 SWISS-PROT: P10114 RAP2A Ras-related protein Rap-2a		
	K.VPVILVGNK.V [108, 116]	R.ALAEEWGCPFMETSAK.S [132, 147]	K.TMVDELFAEIVR.Q [150, 161]
	469.8053++	913.9080++	711.8685++
	V [y7] - 742.4822+ (rank 1)	W [y11] - 1313.5653+ (rank 2)	V [y10] - 1190.6416+ (rank 3)
	I [y6] - 643.4137+ (rank 2)	G [y10] - 1127.4860+ (rank 1)	F [y6] - 734.4196+ (rank 1)
	L [y5] - 530.3297+ (rank 3)	C [y9] - 1070.4645+ (rank 3)	A [y5] - 587.3511+ (rank 2)
	473.8124++ (heavy)	917.9151++ (heavy)	714.8786++ (heavy)
	V [y7] - 750.4963+ (rank 1)	W [y11] - 1321.5795+ (rank 2)	V [y10] - 1196.6617+ (rank 3)
	I [y6] - 651.4279+ (rank 2)	G [y10] - 1135.5002+ (rank 1)	F [y6] - 740.4397+ (rank 1)
	L [y5] - 538.3439+ (rank 3)	C [y9] - 1078.4787+ (rank 3)	A [y5] - 593.3713+ (rank 2)
RRAS	IPI: IPI00020418.1 SWISS-PROT: P10301 RRAS Ras-related protein R-Ras		
	K.ICSVDIGIPAR.L [68, 77]	R.QSFNEVGK.L [113, 120]	K.LFTQILR.V [121, 127]
	544.2819++	454.7272++	445.7765++
	S [y8] - 814.4417+ (rank 1)	F [y6] - 693.3566+ (rank 5)	T [y5] - 630.3933+ (rank 1)
	V [y7] - 727.4097+ (rank 3)	N [y5] - 546.2882+ (rank 3)	Q [y4] - 529.3457+ (rank 2)
	P [y3] - 343.2088+ (rank 2)	E [y4] - 432.2453+ (rank 6)	I [y3] - 401.2871+ (rank 4)
	547.2919++ (heavy)	458.7343++ (heavy)	448.7866++ (heavy)
	S [y8] - 820.4619+ (rank 1)	F [y6] - 701.3708+ (rank 5)	T [y5] - 636.4135+ (rank 1)
	V [y7] - 733.4298+ (rank 3)	N [y5] - 554.3024+ (rank 3)	Q [y4] - 535.3658+ (rank 2)
	P [y3] - 349.2290+ (rank 2)	E [y4] - 440.2595+ (rank 6)	I [y3] - 407.3072+ (rank 4)
	K.ADLESQR.Q [143, 149]		
	409.7038++		
	L [y5] - 632.3362+ (rank 3)		
	E [y4] - 519.2522+ (rank 1)		
	S [y3] - 390.2096+ (rank 2)		
	412.7138++ (heavy)		
	L [y5] - 638.3563+ (rank 3)		
	E [y4] - 525.2723+ (rank 1)		
	S [y3] - 396.2297+ (rank 2)		
RAB11B	IPI: IPI00020436.4 SWISS-PROT: Q15907 RAB11B Ras-related protein Rab-11B		
	K.AQIWDTAGQER.Y [61, 71]	R.GAVGALLVYDIAK.H [82, 94]	K.NILTEIYR.I [166, 173]
	637.8098++	645.3768++	511.2875++
	I [y9] - 1075.5167+ (rank 2)	L [y7] - 821.4767+ (rank 1)	L [y6] - 794.4407+ (rank 1)
	W [y8] - 962.4326+ (rank 1)	V [y6] - 708.3927+ (rank 2)	T [y5] - 681.3566+ (rank 2)
	D [y7] - 776.3533+ (rank 3)	Y [y5] - 609.3243+ (rank 3)	E [y4] - 580.3089+ (rank 3)
	640.8199++ (heavy)	649.3839++ (heavy)	514.2975++ (heavy)
	I [y9] - 1081.5368+ (rank 2)	L [y7] - 829.4909+ (rank 1)	L [y6] - 800.4608+ (rank 1)
	W [y8] - 968.4528+ (rank 1)	V [y6] - 716.4069+ (rank 2)	T [y5] - 687.3767+ (rank 2)
	D [y7] - 782.3735+ (rank 3)	Y [y5] - 617.3385+ (rank 3)	E [y4] - 586.3291+ (rank 3)
NKIRAS2	IPI: IPI00021124.3 SWISS-PROT: Q9NYR9-1 NKIRAS2 Isoform 1 of NF-kappa-B inhibitor-interacting Ras-like protein 2		
	K.VVVCQGASVGK.T [6, 16]	K.EVTIVVLGNK.C [111, 120]	R.VDPDVAQHWAK.S [129, 139]
	552.2975++	536.3241++	633.3173++
	V [y9] - 905.4509+ (rank 1)	V [y6] - 629.3981+ (rank 1)	P [y9] - 1051.5320+ (rank 1)
	C [y8] - 806.3825+ (rank 2)	V [y5] - 530.3297+ (rank 2)	D [y8] - 954.4792+ (rank 4)
	G [y7] - 646.3519+ (rank 3)	L [y4] - 431.2613+ (rank 3)	A [y6] - 740.3838+ (rank 3)
	556.3046++ (heavy)	540.3312++ (heavy)	637.3244++ (heavy)
	V [y9] - 913.4651+ (rank 1)	V [y6] - 637.4123+ (rank 1)	P [y9] - 1059.5462+ (rank 1)
	C [y8] - 814.3967+ (rank 2)	V [y5] - 538.3439+ (rank 2)	D [y8] - 962.4934+ (rank 4)
	G [y7] - 654.3661+ (rank 3)	L [y4] - 439.2755+ (rank 3)	A [y6] - 748.3980+ (rank 3)
	R.SLLEPFVYLASK.M [155, 166]		
	683.8845++		
	L [y10] - 1166.6456+ (rank 3)		
	E [y9] - 1053.5615+ (rank 2)		
	P [y8] - 924.5189+ (rank 1)		
	687.8916++ (heavy)		
	L [y10] - 1174.6598+ (rank 3)		
	E [y9] - 1061.5757+ (rank 2)		
	P [y8] - 932.5331+ (rank 1)		
RAB33B	IPI: IPI00021475.1 SWISS-PROT: Q9H082 RAB33B Ras-related protein Rab-33B		
	K.IIVIGDSNVGK.T [35, 45]	R.AVEIDGER.I [73, 80]	R.SAIQVPTDLAQK.F [153, 164]
	557.8270++	444.7247++	635.8537++
	V [y9] - 888.4785+ (rank 1)	E [y6] - 718.3366+ (rank 1)	Q [y9] - 999.5469+ (rank 3)
	I [y8] - 789.4101+ (rank 3)	I [y5] - 589.2940+ (rank 3)	V [y8] - 871.4884+ (rank 2)
	G [y7] - 676.3260+ (rank 2)	D [y4] - 476.2100+ (rank 4)	P [y7] - 772.4199+ (rank 1)
	561.8341++ (heavy)	447.7348++ (heavy)	639.8608++ (heavy)

	V [y9] - 896.4927+ (rank 1)	E [y6] - 724.3567+ (rank 1)	Q [y9] - 1007.5611+ (rank 3)
	I [y8] - 797.4243+ (rank 3)	I [y5] - 595.3141+ (rank 3)	V [y8] - 879.5026+ (rank 2)
	G [y7] - 684.3402+ (rank 2)	D [y4] - 482.2301+ (rank 4)	P [y7] - 780.4341+ (rank 1)
ARL6	IPI:IP100021685.1 SWISS-PROT:Q9H0F7 ARL6 ADP-ribosylation factor-like protein 6		
	R.NLWEHYK.E [77, 84]	K.EELDTLLNHPDIK.H [106, 118]	R.IPILFFANK.M [122, 130]
	576.7773++	768.8988++	531.8210++
	W [y6] - 925.4203+ (rank 1)	L [y7] - 836.4625+ (rank 1)	I [y7] - 852.4978+ (rank 2)
	E [y5] - 739.3410+ (rank 2)	N [y6] - 723.3784+ (rank 4)	L [y6] - 739.4137+ (rank 1)
	H [y4] - 610.2984+ (rank 3)	P [y4] - 472.2766+ (rank 2)	F [y5] - 626.3297+ (rank 3)
	580.7844++ (heavy)	772.9059++ (heavy)	535.8281++ (heavy)
	W [y6] - 933.4345+ (rank 1)	L [y7] - 844.4767+ (rank 1)	I [y7] - 860.5120+ (rank 2)
	E [y5] - 747.3552+ (rank 2)	N [y6] - 731.3926+ (rank 4)	L [y6] - 747.4279+ (rank 1)
	H [y4] - 618.3126+ (rank 3)	P [y4] - 480.2908+ (rank 2)	F [y5] - 634.3439+ (rank 3)
	K.VSQLLLENIK.D [142, 152]		
	658.8658++		
	L [y7] - 889.4812+ (rank 2)		
	C [y6] - 776.3971+ (rank 1)		
	E [y4] - 503.2824+ (rank 3)		
	662.8729++ (heavy)		
	L [y7] - 897.4954+ (rank 2)		
	C [y6] - 784.4113+ (rank 1)		
	E [y4] - 511.2966+ (rank 3)		
RAC3	IPI:IP100023138.1 SWISS-PROT:P60763 RAC3 Ras-related C3 botulinum toxin substrate 3		
	K.LAPITYPQGLAMAR.E [133, 146]	K.LAPITYPQGLAMAR.E [133, 146]	R.AVLCPPPVK.K [174, 182]
	751.4134++	759.4109++	490.7835++
	T [y10] - 1107.5615+ (rank 2)	T [y10] - 1123.5565+ (rank 2)	L [y7] - 810.4542+ (rank 3)
	Y [y9] - 1006.5139+ (rank 3)	Y [y9] - 1022.5088+ (rank 3)	C [y6] - 697.3702+ (rank 2)
	P [y8] - 843.4505+ (rank 1)	P [y8] - 859.4454+ (rank 1)	P [y5] - 537.3395+ (rank 1)
	754.4235++ (heavy)	762.4209++ (heavy)	494.7906++ (heavy)
	T [y10] - 1113.5817+ (rank 2)	T [y10] - 1129.5766+ (rank 2)	L [y7] - 818.4684+ (rank 3)
	Y [y9] - 1012.5340+ (rank 3)	Y [y9] - 1028.5289+ (rank 3)	C [y6] - 705.3844+ (rank 2)
	P [y8] - 849.4707+ (rank 1)	P [y8] - 865.4656+ (rank 1)	P [y5] - 545.3537+ (rank 1)
RAB3A	IPI:IP100023504.1 SWISS-PROT:P20336 RAB3A Ras-related protein Rab-3A		
	K.ESSDQNFDFYMFK.I [12, 23]	K.TYSWDNAQVLLVGNK.C [121, 135]	R.LVDVICEK.M [178, 185]
	755.8114++	854.4387++	488.2626++
	N [y7] - 964.4233+ (rank 1)	D [y11] - 1170.6477+ (rank 2)	D [y6] - 763.3655+ (rank 1)
	D [y5] - 703.3120+ (rank 2)	L [y6] - 643.4137+ (rank 3)	I [y4] - 549.2701+ (rank 3)
	Y [y4] - 588.2850+ (rank 3)	L [y5] - 530.3297+ (rank 1)	C [y3] - 436.1860+ (rank 2)
	759.8185++ (heavy)	858.4458++ (heavy)	492.2697++ (heavy)
	N [y7] - 972.4375+ (rank 1)	D [y11] - 1178.6619+ (rank 2)	D [y6] - 771.3797+ (rank 1)
	D [y5] - 711.3262+ (rank 2)	L [y6] - 651.4279+ (rank 3)	I [y4] - 557.2843+ (rank 3)
	Y [y4] - 596.2992+ (rank 3)	L [y5] - 538.3439+ (rank 1)	C [y3] - 444.2002+ (rank 2)
	K.MSESLDTADPAVTGAK.Q [186, 201]		
	796.8773++		
	D [y11] - 1045.5160+ (rank 2)		
	D [y8] - 758.4043+ (rank 1)		
	P [y7] - 643.3774+ (rank 3)		
	800.8844++ (heavy)		
	D [y11] - 1053.5302+ (rank 2)		
	D [y8] - 766.4185+ (rank 1)		
	P [y7] - 651.3916+ (rank 3)		
RAB5A	IPI:IP100023510.1 SWISS-PROT:P20339 RAB5A Ras-related protein Rab-5A		
	R.QASPNIVIALSGNK.A [120, 133]	K.NEPQNPGANSAR.G [183, 194]	R.GVDLTEPTQPTR.N [197, 208]
	706.3988++	627.7947++	657.3384++
	P [y11] - 1125.6626+ (rank 3)	P [y10] - 1011.4966+ (rank 2)	E [y7] - 828.4210+ (rank 2)
	V [y8] - 801.4829+ (rank 1)	Q [y9] - 914.4439+ (rank 3)	P [y6] - 699.3784+ (rank 1)
	A [y6] - 589.3304+ (rank 2)	P [y7] - 672.3424+ (rank 1)	P [y3] - 373.2194+ (rank 3)
	710.4059++ (heavy)	630.8048++ (heavy)	660.3485++ (heavy)
	P [y11] - 1133.6768+ (rank 3)	P [y10] - 1017.5168+ (rank 2)	E [y7] - 834.4411+ (rank 2)
	V [y8] - 809.4971+ (rank 1)	Q [y9] - 920.4640+ (rank 3)	P [y6] - 705.3985+ (rank 1)
	A [y6] - 597.3446+ (rank 2)	P [y7] - 678.3625+ (rank 1)	P [y3] - 379.2395+ (rank 3)
RAB6C	IPI:IP100023526.4 SWISS-PROT:P20340-1 RAB6A Isoform 1 of Ras-related protein Rab-6A		
	R.QVSIEEGER.K [134, 142]	K.ELNVMFIETSAK.A [146, 157]	R.VAAALPGMESTQDR.S [169, 182]
	523.7593++	691.3552++	723.3563++
	S [y7] - 819.3843+ (rank 2)	M [y8] - 926.4652+ (rank 1)	L [y10] - 1133.5255+ (rank 2)
	E [y5] - 619.2682+ (rank 1)	F [y7] - 795.4247+ (rank 2)	P [y9] - 1020.4415+ (rank 1)
	E [y4] - 490.2256+ (rank 3)	I [y6] - 648.3563+ (rank 3)	G [y8] - 923.3887+ (rank 3)
	526.7693++ (heavy)	695.3623++ (heavy)	726.3664++ (heavy)
	S [y7] - 825.4044+ (rank 2)	M [y8] - 934.4794+ (rank 1)	L [y10] - 1139.5457+ (rank 2)
	E [y5] - 625.2883+ (rank 1)	F [y7] - 803.4389+ (rank 2)	P [y9] - 1026.4616+ (rank 1)
	E [y4] - 496.2457+ (rank 3)	I [y6] - 656.3705+ (rank 3)	G [y8] - 929.4088+ (rank 3)
MRAS	IPI:IP100024166.3 SWISS-PROT:O14807 MRAS Ras-related protein M-Ras		
	K.IFVDPDYDPTIEDSYLK.H [36, 51]		
	957.9722++		
	D [y10] - 1180.5732+ (rank 2)		
	P [y9] - 1065.5463+ (rank 1)		
	E [y6] - 754.3618+ (rank 3)		

	961.9793++ (heavy)										
	D [y10] - 1188.5874+ (rank 2)										
	P [y9] - 1073.5605+ (rank 1)										
	E [y6] - 762.3760+ (rank 3)										
RAB8B	IPI: IPI00024282.1 SWISS-PROT: Q92930 RAB8B Ras-related protein Rab-8B										
	R.NIEEHASSDVER.M [104, 115]			K.SSANVEEAFFTLAR.D [153, 166]				K.MNDSNSAGAGGPVK.I [176, 189]			
	693.3182++			771.3834++				652.7986++			
	E [y10] - 1158.5022+ (rank 3)			E [y9] - 1083.5469+ (rank 1)				S [y9] - 743.4046+ (rank 2)			
	H [y8] - 900.4170+ (rank 2)			E [y8] - 954.5043+ (rank 3)				A [y8] - 656.3726+ (rank 3)			
	A [y7] - 763.3581+ (rank 1)			F [y6] - 754.4246+ (rank 2)				G [y7] - 585.3355+ (rank 1)			
	696.3283++ (heavy)			774.3934++ (heavy)				656.8057++ (heavy)			
	E [y10] - 1164.5223+ (rank 3)			E [y9] - 1089.5671+ (rank 1)				S [y9] - 751.4188+ (rank 2)			
	H [y8] - 906.4371+ (rank 2)			E [y8] - 960.5245+ (rank 3)				A [y8] - 664.3868+ (rank 3)			
	A [y7] - 769.3782+ (rank 1)			F [y6] - 760.4448+ (rank 2)				G [y7] - 593.3497+ (rank 1)			
	K.MNDSNSAGAGGPVK.I [176, 189]										
	660.7961++										
	S [y11] - 944.4796+ (rank 2)										
	S [y9] - 743.4046+ (rank 3)										
	G [y7] - 585.3355+ (rank 1)										
	664.8032++ (heavy)										
	S [y11] - 952.4938+ (rank 2)										
	S [y9] - 751.4188+ (rank 3)										
	G [y7] - 593.3497+ (rank 1)										
RAB7L1	IPI: IPI00024775.1 SWISS-PROT: O14966 RAB7L1 Ras-related protein Rab-7L1										
	K.VLQWSDYEIVR.L [47, 57]			K.CDLSPWAVSR.D [126, 135]				K.ENGFTGWTETSVK.E [144, 156]			
	704.3670++			595.7848++				728.3412++			
	W [y8] - 1067.5156+ (rank 1)			L [y8] - 915.5047+ (rank 3)				T [y9] - 1008.4997+ (rank 1)			
	S [y7] - 881.4363+ (rank 2)			S [y7] - 802.4206+ (rank 2)				G [y8] - 907.4520+ (rank 2)			
	Y [y5] - 679.3774+ (rank 3)			P [y6] - 715.3886+ (rank 1)				T [y6] - 664.3512+ (rank 3)			
	707.3770++ (heavy)			598.7948++ (heavy)				732.3483++ (heavy)			
	W [y8] - 1073.5358+ (rank 1)			L [y8] - 921.5248+ (rank 3)				T [y9] - 1016.5139+ (rank 1)			
	S [y7] - 887.4565+ (rank 2)			S [y7] - 808.4407+ (rank 2)				G [y8] - 915.4662+ (rank 2)			
	Y [y5] - 685.3975+ (rank 3)			P [y6] - 721.4087+ (rank 1)				T [y6] - 672.3654+ (rank 3)			
RHOC	IPI: IPI00027434.1 SWISS-PROT: P08134 RHOC Rho-related GTP-binding protein RhoC										
	K.HFCPNVPIILVGNK.K [104, 117]			K.HFCPNVPIILVGNKK.D [104, 118] (miss)				R.ISAFGYLECSAK.T [150, 161]			
	804.4400++			868.4874++				673.3265++			
	P [y11] - 1163.7147+ (rank 1)			P [y9] - 981.6455+ (rank 3)				F [y9] - 1074.4925+ (rank 2)			
	P [y8] - 853.5506+ (rank 3)			L [y6] - 658.4246+ (rank 5)				G [y8] - 927.4240+ (rank 1)			
	I [y7] - 756.4978+ (rank 4)			G [y4] - 446.2722+ (rank 4)				L [y6] - 707.3393+ (rank 3)			
	808.4471++ (heavy)			876.5016++ (heavy)				677.3336++ (heavy)			
	P [y11] - 1171.7289+ (rank 1)			P [y9] - 997.6739+ (rank 3)				F [y9] - 1082.5067+ (rank 2)			
	P [y8] - 861.5648+ (rank 3)			L [y6] - 674.4530+ (rank 5)				G [y8] - 935.4382+ (rank 1)			
	I [y7] - 764.5120+ (rank 4)			G [y4] - 462.3006+ (rank 4)				L [y6] - 715.3535+ (rank 3)			
	536.6291+++			579.3274+++							
	P [y8] - 853.5506+ (rank 1)			P [y9] - 981.6455+ (rank 1)							
	I [y7] - 756.4978+ (rank 2)			I [y7] - 771.5087+ (rank 3)							
	L [y5] - 530.3297+ (rank 3)			L [y6] - 658.4246+ (rank 2)							
	539.3005+++ (heavy)			584.6702+++ (heavy)							
	P [y8] - 861.5648+ (rank 1)			P [y9] - 997.6739+ (rank 1)							
	I [y7] - 764.5120+ (rank 2)			I [y7] - 787.5371+ (rank 3)							
	L [y5] - 538.3439+ (rank 3)			L [y6] - 674.4530+ (rank 2)							
RHOJ	IPI: IPI00027952.1 SWISS-PROT: Q9H4E5-1 RHOJ Isoform 1 of Rho-related GTP-binding protein RhoJ										
	K.AIGAQCYLECSALTQK.G [165, 180]			K.AVFDEAILTIFHPK.K [184, 197]							
	906.9346++			800.9403++							
	L [y9] - 1049.5296+ (rank 4)			L [y7] - 855.5087+ (rank 1)							
	E [y8] - 936.4455+ (rank 1)			T [y6] - 742.4246+ (rank 2)							
	C [y7] - 807.4029+ (rank 2)			I [y5] - 641.3770+ (rank 3)							
	910.9417++ (heavy)			804.9474++ (heavy)							
	L [y9] - 1057.5438+ (rank 4)			L [y7] - 863.5229+ (rank 1)							
	E [y8] - 944.4597+ (rank 1)			T [y6] - 750.4388+ (rank 2)							
	C [y7] - 815.4171+ (rank 2)			I [y5] - 649.3912+ (rank 3)							
RAB38	IPI: IPI00027981.10 SWISS-PROT: P57729 RAB38 Rab-related GTP-binding protein										
	K.LLVIGDLGVGK.T [11, 21]			K.VLHWDPETVVR.L [49, 59]				K.LSLPNGKPVSVVLLANK.C [111, 127]			
	542.3422++			675.8619++				583.6926+++			
	V [y9] - 857.5091+ (rank 1)			H [y9] - 1138.5640+ (rank 2)				V [y6] - 657.4294+ (rank 3)			
	I [y8] - 758.4407+ (rank 3)			W [y8] - 1001.5051+ (rank 3)				L [y5] - 558.3610+ (rank 1)			
	G [y7] - 645.3566+ (rank 2)			P [y6] - 700.3988+ (rank 1)				L [y4] - 445.2769+ (rank 2)			
	546.3493++ (heavy)			678.8719++ (heavy)				589.0354+++ (heavy)			
	V [y9] - 865.5233+ (rank 1)			H [y9] - 1144.5841+ (rank 2)				V [y6] - 665.4436+ (rank 3)			
	I [y8] - 766.4549+ (rank 3)			W [y8] - 1007.5252+ (rank 3)				L [y5] - 566.3752+ (rank 1)			
	G [y7] - 653.3708+ (rank 2)			P [y6] - 706.4189+ (rank 1)				L [y4] - 453.2911+ (rank 2)			
	K.ENINIDEASR.C [161, 170]										
	580.7807++										
	N [y7] - 804.3846+ (rank 2)										
	I [y6] - 690.3417+ (rank 3)										
	D [y5] - 577.2576+ (rank 1)										
	583.7908++ (heavy)										

	N [y7] - 810.4048+ (rank 2)								
	I [y6] - 696.3618+ (rank 3)								
	D [y5] - 583.2778+ (rank 1)								
RAB25	IPI:IP100027993.2 SWISS-PROT:P57735 RAB25 Ras-related protein Rab-25								
	K.VVLIGESGVGK.T [14, 24]			R.TTIGVEFSTR.T [42, 51]				K.AQIWDTAGLER.Y [62, 72]	
	529.3162++			555.7931++				630.3226++	
	L [y9] - 859.4884+ (rank 2)			I [y8] - 908.4836+ (rank 3)				I [y9] - 1060.5422+ (rank 2)	
	I [y8] - 746.4043+ (rank 3)			G [y7] - 795.3995+ (rank 1)				W [y8] - 947.4581+ (rank 1)	
	G [y7] - 633.3202+ (rank 1)			E [y5] - 639.3097+ (rank 2)				D [y7] - 761.3788+ (rank 3)	
	533.3233++ (heavy)			558.8032++ (heavy)				633.3326++ (heavy)	
	L [y9] - 867.5026+ (rank 2)			I [y8] - 914.5037+ (rank 3)				I [y9] - 1066.5623+ (rank 2)	
	I [y8] - 754.4185+ (rank 3)			G [y7] - 801.4197+ (rank 1)				W [y8] - 953.4782+ (rank 1)	
	G [y7] - 641.3344+ (rank 1)			E [y5] - 645.3298+ (rank 2)				D [y7] - 767.3989+ (rank 3)	
	R.EVPTEEAR.M [133, 140]								
	465.7300++								
	P [y6] - 702.3417+ (rank 1)								
	T [y5] - 605.2889+ (rank 2)								
	E [y4] - 504.2413+ (rank 3)								
	468.7401++ (heavy)								
	P [y6] - 708.3618+ (rank 1)								
	T [y5] - 611.3091+ (rank 2)								
	E [y4] - 510.2614+ (rank 3)								
RAB8A	IPI:IP100028481.1 SWISS-PROT:P61006 RAB8A Ras-related protein Rab-8A								
	R.NIEEHASADVEK.M [104, 115]			K.LALDYGIK.F [138, 145]				K.LEGNPQGSNQGVI [176, 189]	
	671.3177++			446.7606++				707.8497++	
	E [y10] - 1114.5011+ (rank 2)			A [y7] - 779.4298+ (rank 3)				S [y10] - 1001.5010+ (rank 3)	
	E [y9] - 985.4585+ (rank 3)			L [y6] - 708.3927+ (rank 1)				P [y9] - 914.4690+ (rank 1)	
	H [y8] - 856.4159+ (rank 1)			D [y5] - 595.3086+ (rank 2)				G [y7] - 689.3577+ (rank 2)	
	675.3248++ (heavy)			450.7677++ (heavy)				711.8568++ (heavy)	
	E [y10] - 1122.5153+ (rank 2)			A [y7] - 787.4440+ (rank 3)				S [y10] - 1009.5152+ (rank 3)	
	E [y9] - 993.4727+ (rank 3)			L [y6] - 716.4069+ (rank 1)				P [y9] - 922.4832+ (rank 1)	
	H [y8] - 864.4301+ (rank 1)			D [y5] - 603.3228+ (rank 2)				G [y7] - 697.3719+ (rank 2)	
ARL4A	IPI:IP100029596.1 SWISS-PROT:P40617 ARL4A ADP-ribosylation factor-like protein 4A								
	K.TVTFHFWDVGGQEK.L [67, 80]			R.ISENQGVPLIVANK.Q [120, 134]				R.NLSLSLSEIEK.L [139, 148]	
	550.9352+++			790.9540++				560.2982++	
	F [y9] - 1065.5000+ (rank 3)			P [y8] - 853.5506+ (rank 1)				L [y8] - 918.5142+ (rank 3)	
	W [y8] - 918.4316+ (rank 2)			V [y4] - 431.2613+ (rank 2)				S [y7] - 805.4302+ (rank 1)	
	G [y5] - 518.2569+ (rank 1)			A [y3] - 332.1928+ (rank 3)				S [y5] - 605.3141+ (rank 2)	
	553.6066+++ (heavy)			794.9611++ (heavy)				564.3053++ (heavy)	
	F [y9] - 1073.5142+ (rank 3)			P [y8] - 861.5648+ (rank 1)				L [y8] - 926.5284+ (rank 3)	
	W [y8] - 926.4458+ (rank 2)			V [y4] - 439.2755+ (rank 2)				S [y7] - 813.4444+ (rank 1)	
	G [y5] - 526.2711+ (rank 1)			A [y3] - 340.2070+ (rank 3)				S [y5] - 613.3283+ (rank 2)	
RAB6A	IPI:IP100030304.2 SWISS-PROT:Q9H0N0 RAB6C;LOC150786 Ras-related protein Rab-6C								
	R.DSAAAVVYDITNVNSFQQTTK.W [84]			K.WIDDVTER.G [106, 114] (missed 1)				R.TDLADKR.Q [127, 133] (missed 1)	
	791.0640+++			595.3016++				409.7220++	
	N [y8] - 953.4687+ (rank 1)			D [y7] - 890.4326+ (rank 4)				D [y6] - 717.3890+ (rank 5)	
	S [y7] - 839.4258+ (rank 3)			D [y6] - 775.4057+ (rank 3)				L [y5] - 602.3620+ (rank 3)	
	Q [y4] - 477.2667+ (rank 2)			V [y5] - 660.3787+ (rank 1)				A [y4] - 489.2780+ (rank 2)	
	793.7354+++ (heavy)			601.3218++ (heavy)				416.7391++ (heavy)	
	N [y8] - 961.4829+ (rank 1)			D [y7] - 902.4729+ (rank 4)				D [y6] - 731.4233+ (rank 5)	
	S [y7] - 847.4400+ (rank 3)			D [y6] - 787.4459+ (rank 3)				L [y5] - 616.3964+ (rank 3)	
	Q [y4] - 485.2809+ (rank 2)			V [y5] - 672.4190+ (rank 1)				A [y4] - 503.3123+ (rank 2)	
RAB2A	IPI:IP100031169.1 SWISS-PROT:P61019 RAB2A Ras-related protein Rab-2A								
	R.MITIDGK.Q [46, 52]			K.KEEGEAFAR.E [130, 138] (missed 1)				K.TASNVEEAFINTAK.E [151, 164]	
	389.2124++			518.7565++				747.8754++	
	I [y6] - 646.3770+ (rank 4)			E [y8] - 908.4108+ (rank 1)				E [y9] - 1022.5153+ (rank 1)	
	T [y5] - 533.2930+ (rank 1)			E [y7] - 779.3682+ (rank 2)				E [y8] - 893.4727+ (rank 3)	
	I [y4] - 432.2453+ (rank 5)			G [y6] - 650.3257+ (rank 3)				F [y6] - 693.3930+ (rank 2)	
	393.2195++ (heavy)			525.7737++ (heavy)				751.8825++ (heavy)	
	I [y6] - 654.3912+ (rank 4)			E [y8] - 914.4310+ (rank 1)				E [y9] - 1030.5295+ (rank 1)	
	T [y5] - 541.3072+ (rank 1)			E [y7] - 785.3884+ (rank 2)				E [y8] - 901.4869+ (rank 3)	
	I [y4] - 440.2595+ (rank 5)			G [y6] - 656.3458+ (rank 3)				F [y6] - 701.4072+ (rank 2)	
	K.IQEGVFDINNEANGIK.I [170, 185]								
	880.9443++								
	F [y11] - 1234.6062+ (rank 1)								
	D [y10] - 1087.5378+ (rank 3)								
	N [y8] - 859.4268+ (rank 2)								
	884.9514++ (heavy)								
	F [y11] - 1242.6204+ (rank 1)								
	D [y10] - 1095.5520+ (rank 3)								
	N [y8] - 867.4410+ (rank 2)								
RAB3D	IPI:IP100032808.1 SWISS-PROT:O95716 RAB3D Ras-related protein Rab-3D								
	R.DAADQNFDYMFK.L [12, 23]			K.LLLIGNSSVVGK.T [24, 34]				R.LADDLGFEEFEASAK.E [152, 166]	
	732.8086++			550.8373++				830.3987++	
	N [y7] - 964.4233+ (rank 1)			L [y9] - 874.4993+ (rank 2)				G [y10] - 1132.5310+ (rank 1)	
	F [y6] - 850.3804+ (rank 3)			I [y8] - 761.4152+ (rank 3)				F [y9] - 1075.5095+ (rank 2)	
	D [y5] - 703.3120+ (rank 2)			G [y7] - 648.3311+ (rank 1)				E [y8] - 928.4411+ (rank 3)	

	736.8157++ (heavy)		554.8444++ (heavy)		834.4058++ (heavy)
	N [y7] - 972.4375+ (rank 1)		L [y9] - 882.5135+ (rank 2)		G [y10] - 1140.5452+ (rank 1)
	F [y6] - 858.3946+ (rank 3)		I [y8] - 769.4294+ (rank 3)		F [y9] - 1083.5237+ (rank 2)
	D [y5] - 711.3262+ (rank 2)		G [y7] - 656.3453+ (rank 1)		E [y8] - 936.4553+ (rank 3)
RAB36	IPI:IP100032916.4 SWISS-PROT:O95755-1 RAB36 Isoform 1 of Ras-related protein Rab-36				
	R.EHFHGQVSAACQR.R [100, 112]		R.FEAGIPYSLQIWDTAGQEK.F [164, 18		R.VAALAFEQSVLQDLER.Q [282, 297]
	509.5688+++		1133.5732++		894.9782++
	S [y6] - 692.3144+ (rank 2)		L [y11] - 1288.6532+ (rank 4)		L [y6] - 773.4152+ (rank 1)
	A [y5] - 605.2824+ (rank 3)		Q [y10] - 1175.5691+ (rank 3)		Q [y5] - 660.3311+ (rank 2)
	A [y4] - 534.2453+ (rank 1)		W [y8] - 934.4265+ (rank 1)		D [y4] - 532.2726+ (rank 3)
	511.5755+++ (heavy)		1137.5803+++ (heavy)		897.9882+++ (heavy)
	S [y6] - 698.3346+ (rank 2)		L [y11] - 1296.6674+ (rank 4)		L [y6] - 779.4353+ (rank 1)
	A [y5] - 611.3025+ (rank 3)		Q [y10] - 1183.5833+ (rank 3)		Q [y5] - 666.3513+ (rank 2)
	A [y4] - 540.2654+ (rank 1)		W [y8] - 942.4407+ (rank 1)		D [y4] - 538.2927+ (rank 3)
RAN	IPI:IP100044779.2 TREMBL:Q0EFC9;Q96QB7 RANP1;RAN TC4 protein				
	K.LVLVGDGGTGK.T [12, 22]		K.YVATLGVEVHPLVFHTNR.G [38, 55]		K.NVPNWHR.D [99, 105]
	508.2928++		1026.5549++		461.7357++
	L [y9] - 803.4258+ (rank 1)		E [y11] - 1348.7120+ (rank 3)		P [y5] - 709.3529+ (rank 1)
	V [y8] - 690.3417+ (rank 3)		H [y9] - 1120.6010+ (rank 2)		N [y4] - 612.3001+ (rank 5)
	G [y7] - 591.2733+ (rank 2)		P [y8] - 983.5421+ (rank 1)		W [y3] - 498.2572+ (rank 2)
	512.2999+++ (heavy)		1029.5650+++ (heavy)		464.7458+++ (heavy)
	L [y9] - 811.4400+ (rank 1)		E [y11] - 1354.7322+ (rank 3)		P [y5] - 715.3730+ (rank 1)
	V [y8] - 698.3559+ (rank 3)		H [y9] - 1126.6212+ (rank 2)		N [y4] - 618.3202+ (rank 5)
	G [y7] - 599.2875+ (rank 2)		P [y8] - 989.5623+ (rank 1)		W [y3] - 504.2773+ (rank 2)
RAB40C	IPI:IP100045478.1 SWISS-PROT:Q96S21 RAB40C Ras-related protein Rab-40C				
	R.VFSLQDLCCR.A [188, 197]		R.SYSLASGAGGGGSK.G [239, 252]		
	649.3050++		599.7886++		
	S [y8] - 1051.4659+ (rank 1)		S [y12] - 948.4745+ (rank 3)		
	Q [y6] - 851.3498+ (rank 2)		A [y10] - 748.3584+ (rank 1)		
	D [y5] - 723.2913+ (rank 3)		S [y9] - 677.3213+ (rank 2)		
	652.3151+++ (heavy)		603.7957+++ (heavy)		
	S [y8] - 1057.4861+ (rank 1)		S [y12] - 956.4887+ (rank 3)		
	Q [y6] - 857.3700+ (rank 2)		A [y10] - 756.3726+ (rank 1)		
	D [y5] - 729.3114+ (rank 3)		S [y9] - 685.3355+ (rank 2)		
ARL11	IPI:IP100056495.3 SWISS-PROT:Q969Q4 ARL11 ADP-ribosylation factor-like protein 11				
	R.GCSALTGEGALPEALQSLWSLLK.S [152, 173]				
	1165.6067++				
	P [y12] - 1384.7835+ (rank 1)				
	Q [y8] - 974.5669+ (rank 2)				
	S [y7] - 846.5084+ (rank 4)				
	1169.6138+++ (heavy)				
	P [y12] - 1392.7977+ (rank 1)				
	Q [y8] - 982.5811+ (rank 2)				
	S [y7] - 854.5226+ (rank 4)				
RAB24	IPI:IP100056496.1 SWISS-PROT:Q969Q5 RAB24 Ras-related protein Rab-24				
	R.SLEEGCQIYLCGTSK.S [107, 120]		R.VDFHDVQDYADNIKA.A [133, 146]		K.AQLFETSSK.T [147, 155]
	829.3816++		839.8890++		505.7613++
	Y [y6] - 741.3600+ (rank 1)		D [y10] - 1180.5481+ (rank 2)		L [y7] - 811.4196+ (rank 1)
	L [y5] - 578.2967+ (rank 3)		Y [y6] - 723.3672+ (rank 4)		F [y6] - 698.3355+ (rank 2)
	C [y4] - 465.2126+ (rank 4)		N [y3] - 374.2398+ (rank 3)		E [y5] - 551.2671+ (rank 3)
	833.3887+++ (heavy)		843.8961+++ (heavy)		509.7684+++ (heavy)
	Y [y6] - 749.3742+ (rank 1)		D [y10] - 1188.5623+ (rank 2)		L [y7] - 819.4338+ (rank 1)
	L [y5] - 586.3109+ (rank 3)		Y [y6] - 731.3814+ (rank 4)		F [y6] - 706.3497+ (rank 2)
	C [y4] - 473.2268+ (rank 4)		N [y3] - 382.2540+ (rank 3)		E [y5] - 559.2813+ (rank 3)
	K.TGQSVDELQK.V [156, 166]				
	626.3144++				
	S [y8] - 965.4938+ (rank 2)				
	D [y6] - 779.3934+ (rank 1)				
	F [y3] - 422.2398+ (rank 3)				
	630.3215+++ (heavy)				
	S [y8] - 973.5080+ (rank 2)				
	D [y6] - 787.4076+ (rank 1)				
	F [y3] - 430.2540+ (rank 3)				
RAB7B	IPI:IP100059444.1 SWISS-PROT:Q96AH8 RAB7B;CEP63 Ras-related protein Rab-7b				
	K.IIILGDTTLK.L [48, 57]		K.LQIWDGQGER.F [58, 68]		R.YQSILENHLTESIK.L [174, 187]
	362.8971+++		651.8255+++		558.9614+++
	D [y5] - 577.3192+ (rank 3)		I [y9] - 1061.5010+ (rank 2)		L [y10] - 1183.6317+ (rank 3)
	L [y2] - 260.1969+ (rank 1)		W [y8] - 948.4170+ (rank 1)		N [y8] - 941.5051+ (rank 2)
	K [y1] - 147.1128+ (rank 2)		D [y7] - 762.3377+ (rank 3)		T [y5] - 577.3192+ (rank 5)
	365.5685+++ (heavy)		654.8355+++ (heavy)		561.6328+++ (heavy)
	D [y5] - 585.3334+ (rank 3)		I [y9] - 1067.5212+ (rank 2)		L [y10] - 1191.6459+ (rank 3)
	L [y2] - 268.2111+ (rank 1)		W [y8] - 954.4371+ (rank 1)		N [y8] - 949.5193+ (rank 2)
	K [y1] - 155.1270+ (rank 2)		D [y7] - 768.3578+ (rank 3)		T [y5] - 585.3334+ (rank 5)
ARL8A	IPI:IP100060031.3 SWISS-PROT:Q96BM9 ARL8A ADP-ribosylation factor-like protein 8A				
	K.LWDIGGQPR.F [68, 76]		R.GVSAIVYMVDAADQEK.I [87, 102]		R.DLPGALDEKELIEK.M [132, 145] (missed 1
	521.2774++		848.4165++		785.4222++
	D [y7] - 742.3842+ (rank 1)		Y [y10] - 1169.5143+ (rank 1)		L [y9] - 1116.6147+ (rank 2)

	I [y6] - 627.3573+ (rank 4)		D [y7] - 776.3421+ (rank 2)		D [y8] - 1003.5306+ (rank 1)
	G [y5] - 514.2732+ (rank 2)		D [y4] - 519.2409+ (rank 4)		E [y7] - 888.5037+ (rank 3)
	524.2875++ (heavy)		852.4236++ (heavy)		793.4364++ (heavy)
	D [y7] - 748.4044+ (rank 1)		Y [y10] - 1177.5285+ (rank 1)		L [y9] - 1132.6431+ (rank 2)
	I [y6] - 633.3774+ (rank 4)		D [y7] - 784.3563+ (rank 2)		D [y8] - 1019.5590+ (rank 1)
	G [y5] - 520.2933+ (rank 2)		D [y4] - 527.2551+ (rank 4)		E [y7] - 904.5321+ (rank 3)
			565.9468+++		
			D [y7] - 776.3421+ (rank 1)		
			A [y6] - 661.3151+ (rank 4)		
			A [y5] - 590.2780+ (rank 3)		
			568.6182+++ (heavy)		
			D [y7] - 784.3563+ (rank 1)		
			A [y6] - 669.3293+ (rank 4)		
			A [y5] - 598.2922+ (rank 3)		
RAB39B	IPI:IP100060801.1 SWISS-PROT:Q96DA2 RAB39B Ras-related protein Rab-39B				
	R.SFQNVHEWLEETK.V [95, 107]		K.CDLDTQR.Q [124, 130]		K.LAAAYGMK.Y [140, 147]
	549.5985+++		454.2005++		412.7204++
	H [y8] - 1071.5106+ (rank 2)		L [y5] - 632.3362+ (rank 1)		A [y7] - 711.3494+ (rank 3)
	E [y7] - 934.4516+ (rank 5)		D [y4] - 519.2522+ (rank 3)		A [y6] - 640.3123+ (rank 1)
	W [y6] - 805.4090+ (rank 4)		T [y3] - 404.2252+ (rank 2)		Y [y4] - 498.2381+ (rank 4)
	552.2699+++ (heavy)		457.2106++ (heavy)		416.7275++ (heavy)
	H [y8] - 1079.5247+ (rank 2)		L [y5] - 638.3563+ (rank 1)		A [y7] - 719.3636+ (rank 3)
	E [y7] - 942.4658+ (rank 5)		D [y4] - 525.2723+ (rank 3)		A [y6] - 648.3265+ (rank 1)
	W [y6] - 813.4232+ (rank 4)		T [y3] - 410.2453+ (rank 2)		Y [y4] - 506.2523+ (rank 4)
	K.YIETSAR.D [148, 154]		K.SGFVPPNVVHSSEEVV.K.S [190, 205]		
	420.2165++		571.9651+++		
	I [y6] - 676.3624+ (rank 3)		V [y9] - 1013.5262+ (rank 4)		
	E [y5] - 563.2784+ (rank 1)		H [y8] - 914.4578+ (rank 1)		
	T [y4] - 434.2358+ (rank 2)		S [y7] - 777.3989+ (rank 5)		
	423.2266++ (heavy)		574.6365+++ (heavy)		
	I [y6] - 682.3826+ (rank 3)		V [y9] - 1021.5404+ (rank 4)		
	E [y5] - 569.2985+ (rank 1)		H [y8] - 922.4720+ (rank 1)		
	T [y4] - 440.2559+ (rank 2)		S [y7] - 785.4131+ (rank 5)		
DIRAS2	IPI:IP100063302.1 SWISS-PROT:Q96HU8 DIRAS2 GTP-binding protein Di-Ras2				
	R.VAVFGAGGVGK.S [9, 19]		K.SICTLQITDTTGSHPQFPAMQR.L [52, 72]		
	481.2769++		798.0510+++		
	A [y10] - 862.4781+ (rank 3)		Q [y7] - 877.4349+ (rank 4)		
	F [y8] - 692.3726+ (rank 2)		F [y6] - 749.3763+ (rank 2)		
	G [y7] - 545.3042+ (rank 1)		P [y5] - 602.3079+ (rank 1)		
	485.2840++ (heavy)		800.0577+++ (heavy)		
	A [y10] - 870.4923+ (rank 3)		Q [y7] - 883.4550+ (rank 4)		
	F [y8] - 700.3868+ (rank 2)		F [y6] - 755.3964+ (rank 2)		
	G [y7] - 553.3184+ (rank 1)		P [y5] - 608.3280+ (rank 1)		
RAB2B	IPI:IP100064352.5 TRMBL:Q96K32 RAB2B cDNA FLJ14824 fis, clone OVARC1000771, moderately similar to RAS-RELATED PROTEIN				
	R.ETFNHLTSWLEDAR.Q [26, 39]		K.REEGEAFAR.E [65, 73] (missed 1)		K.TACNVVEAFINTAK.E [86, 99]
	859.9103+++		532.7596++		784.3747++
	L [y9] - 1090.5527+ (rank 2)		E [y8] - 908.4108+ (rank 2)		E [y9] - 1022.5153+ (rank 1)
	T [y8] - 977.4687+ (rank 1)		E [y7] - 779.3682+ (rank 4)		I [y5] - 546.3246+ (rank 2)
	S [y7] - 876.4210+ (rank 3)		A [y4] - 464.2616+ (rank 3)		N [y4] - 433.2405+ (rank 3)
	862.9203++ (heavy)		538.7797++ (heavy)		788.3818++ (heavy)
	L [y9] - 1096.5729+ (rank 2)		E [y8] - 914.4310+ (rank 2)		E [y9] - 1030.5295+ (rank 1)
	T [y8] - 983.4888+ (rank 1)		E [y7] - 785.3884+ (rank 4)		I [y5] - 554.3388+ (rank 2)
	S [y7] - 882.4411+ (rank 3)		A [y4] - 470.2817+ (rank 3)		N [y4] - 441.2547+ (rank 3)
RAB37	IPI:IP100073180.8 SWISS-PROT:Q96AX2 RAB37 Ras-related protein Rab-37				
	R.SPPECSPSYDLTGK.V [18, 30]		K.VMLLGDTGVGK.T [31, 41]		K.TCFLIQFK.D [42, 49]
	704.8243+++		545.3023+++		528.7810++
	P [y11] - 1224.5565+ (rank 1)		L [y9] - 859.4884+ (rank 3)		F [y6] - 795.4763+ (rank 1)
	S [y9] - 967.4731+ (rank 5)		L [y8] - 746.4043+ (rank 2)		L [y5] - 648.4079+ (rank 4)
	P [y8] - 880.4411+ (rank 3)		G [y7] - 633.3202+ (rank 1)		I [y4] - 535.3239+ (rank 3)
	708.8314++ (heavy)		549.3094++ (heavy)		532.7881++ (heavy)
	P [y11] - 1232.5707+ (rank 1)		L [y9] - 867.5026+ (rank 3)		F [y6] - 803.4905+ (rank 1)
	S [y9] - 975.4873+ (rank 5)		L [y8] - 754.4185+ (rank 2)		L [y5] - 656.4221+ (rank 4)
	P [y8] - 888.4553+ (rank 3)		G [y7] - 641.3344+ (rank 1)		I [y4] - 543.3381+ (rank 3)
	R.AGHQADEPSFQIR.D [194, 206]				
	485.9040+++				
	P [y6] - 747.4148+ (rank 2)				
	S [y5] - 650.3620+ (rank 1)				
	F [y4] - 563.3300+ (rank 3)				
	487.9107+++ (heavy)				
	P [y6] - 753.4349+ (rank 2)				
	S [y5] - 656.3822+ (rank 1)				
	F [y4] - 569.3501+ (rank 3)				
ARL5B	IPI:IP100102036.1 SWISS-PROT:Q96KC2 ARL5B ADP-ribosylation factor-like protein 5B				
	K.LWSLFCNQEHK.V [7, 17]		K.NTHFLMWDIGGQESLR.S [58, 73]		K.AAVLIFANK.Q [117, 125]
	487.9030+++		635.3088+++		473.7897++
	F [y7] - 962.4149+ (rank 1)		G [y7] - 746.3791+ (rank 1)		L [y6] - 705.4294+ (rank 3)
	C [y6] - 815.3465+ (rank 2)		G [y6] - 689.3577+ (rank 2)		I [y5] - 592.3453+ (rank 2)

	N [y5] - 655.3158+ (rank 5)		E [y4] - 504.2776+ (rank 3)		F [y4] - 479.2613+ (rank 1)
	490.5744+++ (heavy)		637.3155+++ (heavy)		477.7968++ (heavy)
	F [y7] - 970.4291+ (rank 1)		G [y7] - 752.3993+ (rank 1)		L [y6] - 713.4436+ (rank 3)
	C [y6] - 823.3607+ (rank 2)		G [y6] - 695.3778+ (rank 2)		I [y5] - 600.3595+ (rank 2)
	N [y5] - 663.3300+ (rank 5)		E [y4] - 510.2978+ (rank 3)		F [y4] - 487.2755+ (rank 1)
	K.GCMTAAEISK.Y [130, 139]				
	534.2466++				
	M [y8] - 850.4339+ (rank 2)				
	T [y7] - 719.3934+ (rank 1)				
	A [y6] - 618.3457+ (rank 3)				
	538.2537++ (heavy)				
	M [y8] - 858.4481+ (rank 2)				
	T [y7] - 727.4076+ (rank 1)				
	A [y6] - 626.3599+ (rank 3)				
RAB2B	IPI:IP100102896.1 SWISS-PROT:Q8WUD1 RAB2B Ras-related protein Rab-2B				
	R.MVNIDGK.Q [46, 52]		K.IQQGLFDVHNEANGIK.I [170, 185]		K.IGPQQSISTSVGPSASQR.N [186, 203]
	388.7022++		891.9603++		900.4659++
	V [y6] - 645.3566+ (rank 5)		F [y11] - 1243.6066+ (rank 3)		S [y11] - 1076.5331+ (rank 2)
	N [y5] - 546.2882+ (rank 3)		N [y7] - 745.3839+ (rank 2)		S [y9] - 888.4534+ (rank 3)
	D [y3] - 319.1612+ (rank 1)		G [y3] - 317.2183+ (rank 1)		G [y7] - 702.3529+ (rank 1)
	392.7093++ (heavy)		895.9674++ (heavy)		903.4760++ (heavy)
	V [y6] - 653.3708+ (rank 5)		F [y11] - 1251.6208+ (rank 3)		S [y11] - 1082.5532+ (rank 2)
	N [y5] - 554.3024+ (rank 3)		N [y7] - 753.3981+ (rank 2)		S [y9] - 894.4735+ (rank 3)
	D [y3] - 327.1754+ (rank 1)		G [y3] - 325.2325+ (rank 1)		G [y7] - 708.3731+ (rank 1)
RABL3	IPI:IP100102897.4 SWISS-PROT:Q5HYI8 RABL3 Rab-like protein 3				
	R.WSLEALNR.D [108, 115]		R.YLAAGSSNAVK.L [184, 194]		R.EGNQIPGFDPDR.K [211, 221]
	494.7642++		540.7878++		615.2991++
	L [y6] - 715.4097+ (rank 1)		A [y9] - 804.4210+ (rank 1)		I [y7] - 801.4254+ (rank 3)
	E [y5] - 602.3257+ (rank 2)		A [y8] - 733.3839+ (rank 3)		P [y6] - 688.3413+ (rank 1)
	A [y4] - 473.2831+ (rank 3)		G [y7] - 662.3468+ (rank 2)		P [y3] - 387.1987+ (rank 2)
	497.7742++ (heavy)		544.7949++ (heavy)		618.3092++ (heavy)
	L [y6] - 721.4298+ (rank 1)		A [y9] - 812.4352+ (rank 1)		I [y7] - 807.4455+ (rank 3)
	E [y5] - 608.3458+ (rank 2)		A [y8] - 741.3981+ (rank 3)		P [y6] - 694.3614+ (rank 1)
	A [y4] - 479.3032+ (rank 3)		G [y7] - 670.3610+ (rank 2)		P [y3] - 393.2188+ (rank 2)
RRAGA	IPI:IP100105620.2 SWISS-PROT:Q7L523 RRAGA Ras-related GTP-binding protein A				
	R.LGATIDVEHSHVR.F [38, 50]		R.NFAQIIEADEVLLFER.A [192, 207]		
	478.5880+++		953.9991++		
	E [y6] - 764.3798+		A [y9] - 1091.5732+ (rank 5)		
	H [y5] - 635.3372+		D [y8] - 1020.5360+ (rank 3)		
	S [y4] - 498.2783+		L [y4] - 564.3140+ (rank 2)		
	480.5947+++ (heavy)		957.0092++ (heavy)		
	E [y6] - 770.3999+		A [y9] - 1097.5933+ (rank 5)		
	H [y5] - 641.3573+		D [y8] - 1026.5562+ (rank 3)		
	S [y4] - 504.2984+		L [y4] - 570.3342+ (rank 2)		
			636.3352+++		
			L [y5] - 677.3981+ (rank 3)		
			L [y4] - 564.3140+ (rank 2)		
			F [y3] - 451.2300+ (rank 1)		
			638.3419+++ (heavy)		
			L [y5] - 683.4182+ (rank 3)		
			L [y4] - 570.3342+ (rank 2)		
			F [y3] - 457.2501+ (rank 1)		
RABL6	IPI:IP100186586.10 TREMBL:C9JJY3 C9orf86 Putative uncharacterized protein C9orf86				
	K.LVGSDQAPGR.D [7, 16]		K.NIPAGLQSMNQALQR.R [19, 33]		K.FFNIPFLQLQR.E [226, 236]
	500.2645++		820.9305++		711.8983++
	G [y8] - 787.3693+ (rank 1)		Q [y9] - 1075.5313+ (rank 2)		I [y8] - 1014.6095+ (rank 3)
	A [y4] - 400.2303+ (rank 3)		S [y8] - 947.4727+ (rank 3)		P [y7] - 901.5254+ (rank 1)
	P [y3] - 329.1932+ (rank 2)		N [y6] - 729.4002+ (rank 4)		Q [y4] - 544.3202+ (rank 2)
	503.2746++ (heavy)		823.9406++ (heavy)		714.9083++ (heavy)
	G [y8] - 793.3894+ (rank 1)		Q [y9] - 1081.5514+ (rank 2)		I [y8] - 1020.6296+ (rank 3)
	A [y4] - 406.2504+ (rank 3)		S [y8] - 953.4929+ (rank 3)		P [y7] - 907.5455+ (rank 1)
	P [y3] - 335.2133+ (rank 2)		N [y6] - 735.4203+ (rank 4)		Q [y4] - 550.3403+ (rank 2)
RAB4B	IPI:IP100187143.1 SWISS-PROT:P61018-2 RAB4B Isoform 2 of Ras-related protein Rab-4B				
	K.FLVIGSAGTGK.S [45, 55]		K.SCLLHQFIENK.F [56, 66]		K.IDSGELDPER.M [207, 216]
	525.3031++		694.8532++		565.7698++
	V [y9] - 789.4465+ (rank 2)		H [y7] - 915.4683+ (rank 1)		S [y8] - 902.4214+ (rank 3)
	I [y8] - 690.3781+ (rank 1)		Q [y6] - 778.4094+ (rank 3)		L [y5] - 629.3253+ (rank 2)
	G [y7] - 577.2940+ (rank 3)		F [y5] - 650.3508+ (rank 2)		D [y4] - 516.2413+ (rank 1)
	529.3102++ (heavy)		698.8603++ (heavy)		568.7799++ (heavy)
	V [y9] - 797.4607+ (rank 2)		H [y7] - 923.4825+ (rank 1)		S [y8] - 908.4415+ (rank 3)
	I [y8] - 698.3923+ (rank 1)		Q [y6] - 786.4236+ (rank 3)		L [y5] - 635.3454+ (rank 2)
	G [y7] - 585.3082+ (rank 3)		F [y5] - 658.3650+ (rank 2)		D [y4] - 522.2614+ (rank 1)
	R.MGSGIQYGDASLR.Q [217, 229]				
	677.8246++				
	Q [y8] - 909.4425+ (rank 1)				
	Y [y7] - 781.3839+ (rank 2)				
	G [y6] - 618.3206+ (rank 3)				

	680.8347++ (heavy)								
	Q [y8] - 915.4626+ (rank 1)								
	Y [y7] - 787.4040+ (rank 2)								
	G [y6] - 624.3407+ (rank 3)								
ARF1	IPI:IP100215914.5 SWISS-PROT:P84077 ARF1 ADP-ribosylation factor 1								
	K.NISFTVWDVGGQDK.I [59, 72]		K.QDLPNAMNAAEITDK.L [127, 141]				K.QDLPNAMNAAEITDK.L [127, 141]		
	783.3834++		815.8907++				823.8882++		
	W [y8] - 904.4159+ (rank 1)		M [y9] - 992.4717+ (rank 3)				M [y9] - 1008.4666+ (rank 2)		
	D [y7] - 718.3366+ (rank 3)		N [y8] - 861.4312+ (rank 2)				N [y8] - 861.4312+ (rank 3)		
	G [y5] - 504.2413+ (rank 4)		A [y6] - 676.3512+ (rank 4)				I [y4] - 476.2715+ (rank 4)		
	787.3905++ (heavy)		819.8978++ (heavy)				827.8953++ (heavy)		
	W [y8] - 912.4301+ (rank 1)		M [y9] - 1000.4859+ (rank 3)				M [y9] - 1016.4808+ (rank 2)		
	D [y7] - 726.3508+ (rank 3)		N [y8] - 869.4454+ (rank 2)				N [y8] - 869.4454+ (rank 3)		
	G [y5] - 512.2555+ (rank 4)		A [y6] - 684.3654+ (rank 4)				I [y4] - 484.2857+ (rank 4)		
ARF3	IPI:IP100215917.3 SWISS-PROT:P61204 ARF3 ADP-ribosylation factor 3								
	R.VNEAREELMR.M [99, 108] (missed 1)		R.VNEAREELMR.M [99, 108] (missed 1)				K.LGLHSLR.H [142, 148]		
	623.8141++		631.8115++				398.2454++		
	E [y5] - 677.3287+ (rank 3)		N [y9] - 1163.5473+ (rank 3)				G [y6] - 682.3995+ (rank 3)		
	E [y4] - 548.2861+ (rank 2)		A [y7] - 920.4618+ (rank 2)				H [y4] - 512.2940+ (rank 1)		
	L [y3] - 419.2435+ (rank 1)		L [y3] - 435.2384+ (rank 4)				S [y3] - 375.2350+ (rank 2)		
	629.8342++ (heavy)		637.8316++ (heavy)				401.2555++ (heavy)		
	E [y5] - 683.3488+ (rank 3)		N [y9] - 1175.5876+ (rank 3)				G [y6] - 688.4196+ (rank 3)		
	E [y4] - 554.3062+ (rank 2)		A [y7] - 932.5021+ (rank 2)				H [y4] - 518.3141+ (rank 1)		
	L [y3] - 425.2636+ (rank 1)		L [y3] - 441.2585+ (rank 4)				S [y3] - 381.2552+ (rank 2)		
ARF4	IPI:IP100215918.3 SWISS-PROT:P18085 ARF4 ADP-ribosylation factor 4								
	K.NICFTVWDVGGQDR.I [59, 72]		R.IQEVADQLK.M [99, 108]				R.DAVLLLFANK.Q [117, 126]		
	833.8857++		586.8115++				552.3266++		
	W [y8] - 932.4221+ (rank 1)		E [y8] - 931.4731+ (rank 1)				L [y7] - 818.5135+ (rank 2)		
	D [y7] - 746.3428+ (rank 3)		V [y7] - 802.4305+ (rank 3)				L [y6] - 705.4294+ (rank 3)		
	G [y5] - 532.2474+ (rank 2)		A [y6] - 703.3621+ (rank 2)				F [y4] - 479.2613+ (rank 1)		
	836.8958++ (heavy)		590.8186++ (heavy)				556.3337++ (heavy)		
	W [y8] - 938.4422+ (rank 1)		E [y8] - 939.4873+ (rank 1)				L [y7] - 826.5277+ (rank 2)		
	D [y7] - 752.3629+ (rank 3)		V [y7] - 810.4447+ (rank 3)				L [y6] - 713.4436+ (rank 3)		
	G [y5] - 538.2675+ (rank 2)		A [y6] - 711.3763+ (rank 2)				F [y4] - 487.2755+ (rank 1)		
	K.LGLQSLR.N [142, 148]								
	393.7452++								
	G [y6] - 673.3991+ (rank 3)								
	Q [y4] - 503.2936+ (rank 1)								
	S [y3] - 375.2350+ (rank 2)								
	396.7553++ (heavy)								
	G [y6] - 679.4193+ (rank 3)								
	Q [y4] - 509.3138+ (rank 1)								
	S [y3] - 381.2552+ (rank 2)								
ARF5	IPI:IP100215919.5 SWISS-PROT:P84085 ARF5 ADP-ribosylation factor 5								
	K.NICFTVWDVGGQDK.I [59, 72]		R.VQESADELQK.M [99, 108]				K.LGLQHLSR.S [142, 148]		
	819.8827++		573.7855++				418.7587++		
	T [y10] - 1104.5320+ (rank 3)		E [y8] - 919.4367+ (rank 1)				G [y6] - 723.4260+ (rank 5)		
	W [y8] - 904.4159+ (rank 1)		S [y7] - 790.3941+ (rank 2)				Q [y4] - 553.3205+ (rank 1)		
	D [y7] - 718.3366+ (rank 2)		D [y5] - 632.3250+ (rank 3)				H [y3] - 425.2619+ (rank 2)		
	823.8898++ (heavy)		577.7926++ (heavy)				421.7688++ (heavy)		
	T [y10] - 1112.5462+ (rank 3)		E [y8] - 927.4509+ (rank 1)				G [y6] - 729.4462+ (rank 5)		
	W [y8] - 912.4301+ (rank 1)		S [y7] - 798.4083+ (rank 2)				Q [y4] - 559.3406+ (rank 1)		
	D [y7] - 726.3508+ (rank 2)		D [y5] - 640.3392+ (rank 3)				H [y3] - 431.2821+ (rank 2)		
ARF6	IPI:IP100215920.8 SWISS-PROT:P62330 ARF6 ADP-ribosylation factor 6								
	R.ILMLGLDAAGK.T [15, 25]		R.ILMLGLDAAGK.T [15, 25]				K.LGQSVTTIPTVGFNVETVTK.N [34, 54]		
	551.3205++		559.3179++				1127.6019++		
	M [y9] - 875.4655+ (rank 1)		M [y9] - 891.4604+ (rank 2)				G [y10] - 1157.5837+ (rank 2)		
	L [y8] - 744.4250+ (rank 3)		L [y8] - 744.4250+ (rank 3)				N [y8] - 953.4938+ (rank 3)		
	G [y7] - 631.3410+ (rank 2)		G [y7] - 631.3410+ (rank 1)				E [y6] - 740.3825+ (rank 4)		
	555.3276++ (heavy)		563.3250++ (heavy)				1131.6090++ (heavy)		
	M [y9] - 883.4797+ (rank 1)		M [y9] - 899.4746+ (rank 2)				G [y10] - 1165.5979+ (rank 2)		
	L [y8] - 752.4392+ (rank 3)		L [y8] - 752.4392+ (rank 3)				N [y8] - 961.5080+ (rank 3)		
	G [y7] - 639.3552+ (rank 2)		G [y7] - 639.3552+ (rank 1)				E [y6] - 748.3967+ (rank 4)		
	K.FNVWDVGGQDK.I [58, 68]								
	632.8015++								
	V [y9] - 1003.4843+ (rank 2)								
	W [y8] - 904.4159+ (rank 1)								
	D [y7] - 718.3366+ (rank 4)								
	636.8086++ (heavy)								
	V [y9] - 1011.4985+ (rank 2)								
	W [y8] - 912.4301+ (rank 1)								
	D [y7] - 726.3508+ (rank 4)								
RALA	IPI:IP100217519.3 SWISS-PROT:P11233 RALA Ras-related protein Ral-A								
	K.GQNSLALHK.V [7, 15]		K.EDENVPFLLVGNK.S [115, 127]				R.QVSVEEAK.N [135, 142]		
	484.2696++		737.3828++				445.2349++		
	N [y7] - 782.4519+ (rank 1)		P [y8] - 887.5349+ (rank 1)				S [y6] - 662.3355+ (rank 1)		
	S [y6] - 668.4090+ (rank 4)		V [y4] - 417.2456+ (rank 2)				V [y5] - 575.3035+ (rank 5)		

	A [y4] - 468.2929+ (rank 5)		G [y3] - 318.1772+ (rank 4)		E [y4] - 476.2351+ (rank 2)
	488.2767++ (heavy)		741.3899++ (heavy)		449.2420++ (heavy)
	N [y7] - 790.4661+ (rank 1)		P [y8] - 895.5491+ (rank 1)		S [y6] - 670.3497+ (rank 1)
	S [y6] - 676.4232+ (rank 4)		V [y4] - 425.2598+ (rank 2)		V [y5] - 583.3177+ (rank 5)
	A [y4] - 476.3071+ (rank 5)		G [y3] - 326.1914+ (rank 4)		E [y4] - 484.2493+ (rank 2)
	R.AEQWNVNYVETSAK.T [145, 158]				
	819.8916++				
	N [y10] - 1124.5582+ (rank 2)				
	V [y9] - 1010.5153+ (rank 4)				
	N [y8] - 911.4469+ (rank 1)				
	823.8987++ (heavy)				
	N [y10] - 1132.5724+ (rank 2)				
	V [y9] - 1018.5295+ (rank 4)				
	N [y8] - 919.4611+ (rank 1)				
RHOT1	IPI:IP00217536.3 SWISS-PROT:Q8IXI2-3 RHOT1 Isoform 3 of Mitochondrial Rho GTPase 1				
	R.LPLILVGNK.S [110, 118]		K.AVLHPTGPLYCPEEK.E [164, 178]		R.ICFNTPLAPQALVDK.N [214, 229]
	483.8210++		570.9555+++		908.4691++
	L [y7] - 756.4978+ (rank 2)		Y [y6] - 825.3447+ (rank 2)		P [y11] - 1180.6572+ (rank 2)
	I [y6] - 643.4137+ (rank 3)		C [y5] - 662.2814+ (rank 1)		A [y9] - 970.5204+ (rank 3)
	L [y5] - 530.3297+ (rank 1)		P [y4] - 502.2508+ (rank 3)		P [y8] - 899.4833+ (rank 1)
	487.8281++ (heavy)		573.6269+++ (heavy)		912.4762++ (heavy)
	L [y7] - 764.5120+ (rank 2)		Y [y6] - 833.3589+ (rank 2)		P [y11] - 1188.6714+ (rank 2)
	I [y6] - 651.4279+ (rank 3)		C [y5] - 670.2956+ (rank 1)		A [y9] - 978.5346+ (rank 3)
	L [y5] - 538.3439+ (rank 1)		P [y4] - 510.2650+ (rank 3)		P [y8] - 907.4975+ (rank 1)
ARL1	IPI:IP00219518.7 SWISS-PROT:P40616 ARL1 ADP-ribosylation factor-like protein 1				
	R.IILGLDGGAGK.T [19, 29]		K.FQVWDLGGQTSIRPYWR.C [62, 78]		K.AILVVFANK.Q [118, 126]
	535.3344++		1055.0369++		487.8053++
	I [y9] - 843.4934+ (rank 1)		I [y6] - 890.4995+ (rank 3)		L [y7] - 790.4822+ (rank 2)
	L [y8] - 730.4094+ (rank 3)		P [y4] - 621.3144+ (rank 1)		V [y5] - 578.3297+ (rank 3)
	G [y7] - 617.3253+ (rank 2)		W [y2] - 361.1983+ (rank 5)		F [y4] - 479.2613+ (rank 1)
	539.3415++ (heavy)		1061.0570++ (heavy)		491.8124++ (heavy)
	I [y9] - 851.5076+ (rank 1)		I [y6] - 902.5398+ (rank 3)		L [y7] - 798.4963+ (rank 2)
	L [y8] - 738.4236+ (rank 3)		P [y4] - 627.3345+ (rank 1)		V [y5] - 586.3439+ (rank 3)
	G [y7] - 625.3395+ (rank 2)		W [y2] - 367.2184+ (rank 5)		F [y4] - 487.2755+ (rank 1)
RAC1	IPI:IP00219675.1 SWISS-PROT:P63000-2 RAC1 Isoform B of Ras-related C3 botulinum toxin substrate 1				
	R.LRPLSYPQTVGETYQK.D [66, 81]				
	904.9807++				
	P [y10] - 1079.5368+ (rank 1)				
	T [y8] - 854.4254+ (rank 4)				
	G [y6] - 654.3093+ (rank 2)				
	911.9979++ (heavy)				
	P [y10] - 1087.5510+ (rank 1)				
	T [y8] - 862.4396+ (rank 4)				
	G [y6] - 662.3235+ (rank 2)				
	603.6562+++				
	T [y8] - 854.4254+ (rank 3)				
	V [y7] - 753.3777+ (rank 2)				
	G [y6] - 654.3093+ (rank 1)				
	608.3343+++ (heavy)				
	T [y8] - 862.4396+ (rank 3)				
	V [y7] - 761.3919+ (rank 2)				
	G [y6] - 662.3235+ (rank 1)				
RABL2B	IPI:IP00220774.1 SWISS-PROT:Q9UNT1-2 RABL2B Isoform 2 of Rab-like protein 2B				
	K.IDADINVTQK.S [134, 143]				
	558.7984++				
	A [y8] - 888.4785+ (rank 1)				
	D [y7] - 817.4414+ (rank 3)				
	N [y5] - 589.3304+ (rank 2)				
	562.8055++ (heavy)				
	A [y8] - 896.4927+ (rank 1)				
	D [y7] - 825.4556+ (rank 3)				
	N [y5] - 597.3446+ (rank 2)				
ARL16	IPI:IP00242972.2 SWISS-PROT:Q0P5N6 ARL16 ADP-ribosylation factor-like protein 16				
	K.GDLGEPPTPTVGTNLTDIVAQR.K [4		K.QNITTAESAR.E [166, 176]		R.EGTGLAGVLAWLQATHR.A [177, 193]
	835.4416+++		602.3200++		593.9882+++
	T [y7] - 802.4417+ (rank 1)		T [y8] - 848.4472+ (rank 1)		A [y8] - 982.5217+ (rank 2)
	I [y5] - 586.3671+ (rank 3)		T [y7] - 747.3995+ (rank 2)		W [y7] - 911.4846+ (rank 1)
	V [y4] - 473.2831+ (rank 2)		A [y6] - 646.3519+ (rank 3)		L [y6] - 725.4053+ (rank 3)
	839.4551+++ (heavy)		605.3301++ (heavy)		595.9949+++ (heavy)
	T [y7] - 808.4619+ (rank 1)		T [y8] - 854.4674+ (rank 1)		A [y8] - 988.5419+ (rank 2)
	I [y5] - 592.3873+ (rank 3)		T [y7] - 753.4197+ (rank 2)		W [y7] - 917.5047+ (rank 1)
	V [y4] - 479.3032+ (rank 2)		A [y6] - 652.3720+ (rank 3)		L [y6] - 731.4254+ (rank 3)
REM1	IPI:IP00289912.2 SWISS-PROT:O75628 REM1 GTP-binding protein REM 1				
	R.LSTVPSTQSQHPR.L [32, 44]		K.TSLASLFAQK.Q [93, 102]		R.DLHEQLGEDVYER.T [106, 118]
	479.9197+++		497.7820++		801.8734++
	P [y9] - 1037.5123+ (rank 1)		A [y7] - 693.3930+ (rank 1)		E [y10] - 1237.5695+ (rank 3)
	S [y8] - 940.4595+ (rank 5)		S [y6] - 622.3559+ (rank 3)		L [y8] - 980.4684+ (rank 2)

	T [y7] - 853.4275+ (rank 4)		F [y4] - 422.2398+ (rank 5)		G [y7] - 867.3843+ (rank 1)
	481.9264+++ (heavy)		501.7891++ (heavy)		804.8834++ (heavy)
	P [y9] - 1043.5324+ (rank 1)		A [y7] - 701.4072+ (rank 1)		E [y10] - 1243.5897+ (rank 3)
	S [y8] - 946.4796+ (rank 5)		S [y6] - 630.3701+ (rank 3)		L [y8] - 986.4885+ (rank 2)
	T [y7] - 859.4476+ (rank 4)		F [y4] - 430.2540+ (rank 5)		G [y7] - 873.4044+ (rank 1)
	R.GSFESASELR.I [166, 175]				534.9180+++
	541.7593++				D [y5] - 681.3202+ (rank 2)
	S [y6] - 662.3468+ (rank 1)				V [y4] - 566.2933+ (rank 3)
	A [y5] - 575.3148+ (rank 3)				Y [y3] - 467.2249+ (rank 1)
	S [y4] - 504.2776+ (rank 2)				536.9247+++ (heavy)
	544.7693++ (heavy)				D [y5] - 687.3404+ (rank 2)
	S [y6] - 668.3669+ (rank 1)				V [y4] - 572.3134+ (rank 3)
	A [y5] - 581.3349+ (rank 3)				Y [y3] - 473.2450+ (rank 1)
	S [y4] - 510.2978+ (rank 2)				
RAB14	IPI:IP00291928.8 SWISS-PROT:P61106 RAB14 Ras-related protein Rab-14				
	K.YIIIGDMGVGK.S [13, 23]		R.STYNHLSSWLTDAR.N [96, 109]		K.TGENVEDAFLEAAK.K [156, 169]
	583.3179++		825.8972++		747.3596++
	I [y9] - 889.4812+ (rank 1)		L [y9] - 1048.5422+ (rank 2)		E [y9] - 993.4888+ (rank 1)
	I [y8] - 776.3971+ (rank 3)		S [y8] - 935.4581+ (rank 1)		D [y8] - 864.4462+ (rank 2)
	G [y7] - 663.3130+ (rank 2)		S [y7] - 848.4261+ (rank 3)		F [y6] - 678.3821+ (rank 3)
	587.3250++ (heavy)		828.9072++ (heavy)		751.3667++ (heavy)
	I [y9] - 897.4954+ (rank 1)		L [y9] - 1054.5623+ (rank 2)		E [y9] - 1001.5030+ (rank 1)
	I [y8] - 784.4113+ (rank 3)		S [y8] - 941.4782+ (rank 1)		D [y8] - 872.4604+ (rank 2)
	G [y7] - 671.3272+ (rank 2)		S [y7] - 854.4462+ (rank 3)		F [y6] - 686.3963+ (rank 3)
SRPRB	IPI:IP00295098.3 SWISS-PROT:Q9Y5M8 SRPRB Signal recognition particle receptor subunit beta				
	R.AVLLVGLCDGSK.T [65, 76]		R.DTQTSITDSCAVYR.V [90, 103]		K.LIQQQLEK.E [191, 198]
	616.3394++		808.8647++		500.2953++
	V [y8] - 835.3978+ (rank 2)		I [y9] - 1084.5092+ (rank 2)		Q [y6] - 773.4152+ (rank 1)
	G [y7] - 736.3294+ (rank 1)		T [y8] - 971.4251+ (rank 1)		Q [y5] - 645.3566+ (rank 2)
	C [y5] - 566.2239+ (rank 3)		D [y7] - 870.3774+ (rank 3)		L [y3] - 389.2395+ (rank 4)
	620.3465++ (heavy)		811.8747++ (heavy)		504.3024++ (heavy)
	V [y8] - 843.4120+ (rank 2)		I [y9] - 1090.5293+ (rank 2)		Q [y6] - 781.4294+ (rank 1)
	G [y7] - 744.3436+ (rank 1)		T [y8] - 977.4452+ (rank 1)		Q [y5] - 653.3708+ (rank 2)
	C [y5] - 574.2381+ (rank 3)		D [y7] - 876.3976+ (rank 3)		L [y3] - 397.2537+ (rank 4)
RAB35	IPI:IP00300096.4 SWISS-PROT:Q15286 RAB35 Ras-related protein Rab-35				
	R.TITSTYYR.G [71, 78]		R.WLHEINQNCDDVCR.I [101, 114]		K.VVETEDAYK.F [128, 136]
	502.7560++		620.2702+++		527.2586++
	T [y6] - 790.3730+ (rank 1)		C [y6] - 824.3025+ (rank 2)		E [y7] - 855.3731+ (rank 1)
	S [y5] - 689.3253+ (rank 2)		D [y5] - 664.2719+ (rank 1)		T [y6] - 726.3305+ (rank 3)
	T [y4] - 602.2933+ (rank 4)		D [y4] - 549.2450+ (rank 3)		E [y5] - 625.2828+ (rank 2)
	505.7661++ (heavy)		622.2769+++ (heavy)		531.2657++ (heavy)
	T [y6] - 796.3931+ (rank 1)		C [y6] - 830.3227+ (rank 2)		E [y7] - 863.3873+ (rank 1)
	S [y5] - 695.3454+ (rank 2)		D [y5] - 670.2920+ (rank 1)		T [y6] - 734.3447+ (rank 3)
	T [y4] - 608.3134+ (rank 4)		D [y4] - 555.2651+ (rank 3)		E [y5] - 633.2970+ (rank 2)
	K.FAGQMGIQLFETSAK.E [137, 151]		K.FAGQMGIQLFETSAK.E [137, 151]		K.QQQQQNDVVK.L [178, 188]
	814.4111++		822.4085++		671.8391++
	G [y10] - 1093.5888+ (rank 1)		G [y10] - 1093.5888+ (rank 2)		Q [y7] - 830.4367+ (rank 2)
	Q [y8] - 923.4833+ (rank 3)		Q [y8] - 923.4833+ (rank 1)		Q [y6] - 702.3781+ (rank 1)
	F [y6] - 682.3406+ (rank 2)		L [y7] - 795.4247+ (rank 3)		N [y5] - 574.3195+ (rank 3)
	818.4182++ (heavy)		826.4156++ (heavy)		675.8462++ (heavy)
	G [y10] - 1101.6030+ (rank 1)		G [y10] - 1101.6030+ (rank 2)		Q [y7] - 838.4509+ (rank 2)
	Q [y8] - 931.4975+ (rank 3)		Q [y8] - 931.4975+ (rank 1)		Q [y6] - 710.3923+ (rank 1)
	F [y6] - 690.3548+ (rank 2)		L [y7] - 803.4389+ (rank 3)		N [y5] - 582.3337+ (rank 3)
RAB3B	IPI:IP00300562.2 SWISS-PROT:P20337 RAB3B Ras-related protein Rab-3B				
	K.DASDQNFDFYMFK.L [12, 23]		K.GQLLAEQLGFDFFEASAK.E [149, 166]		K.MSDSLDTPSMLGSSK.N [186, 201]
	740.8061++		985.9965++		835.8660++
	N [y7] - 964.4233+ (rank 1)		L [y11] - 1231.5994+ (rank 2)		D [y11] - 1137.5092+ (rank 2)
	F [y6] - 850.3804+ (rank 3)		G [y10] - 1118.5153+ (rank 1)		T [y10] - 1022.4823+ (rank 3)
	D [y5] - 703.3120+ (rank 2)		F [y9] - 1061.4938+ (rank 3)		P [y8] - 806.4077+ (rank 1)
	744.8132++ (heavy)		990.0036++ (heavy)		839.8731++ (heavy)
	N [y7] - 972.4375+ (rank 1)		L [y11] - 1239.6136+ (rank 2)		D [y11] - 1145.5234+ (rank 2)
	F [y6] - 858.3946+ (rank 3)		G [y10] - 1126.5295+ (rank 1)		T [y10] - 1030.4965+ (rank 3)
	D [y5] - 711.3262+ (rank 2)		F [y9] - 1069.5080+ (rank 3)		P [y8] - 814.4219+ (rank 1)
RAB30	IPI:IP00302030.2 SWISS-PROT:Q15771 RAB30 Ras-related protein Rab-30				
	K.IVLIGNAGVGK.T [11, 21]		R.EIEQYASNK.V [105, 113]		K.VITVLVGNK.I [114, 122]
	520.8268++		541.2617++		471.8028++
	L [y9] - 828.4938+ (rank 3)		Y [y5] - 582.2882+ (rank 2)		T [y7] - 730.4458+ (rank 1)
	I [y8] - 715.4097+ (rank 4)		A [y4] - 419.2249+ (rank 1)		L [y5] - 530.3297+ (rank 3)
	G [y7] - 602.3257+ (rank 1)		S [y3] - 348.1878+ (rank 3)		V [y4] - 417.2456+ (rank 4)
	524.8339++ (heavy)		545.2688++ (heavy)		475.8099++ (heavy)
	L [y9] - 836.5080+ (rank 3)		Y [y5] - 590.3024+ (rank 2)		T [y7] - 738.4600+ (rank 1)
	I [y8] - 723.4239+ (rank 4)		A [y4] - 427.2391+ (rank 1)		L [y5] - 538.3439+ (rank 3)
	G [y7] - 610.3398+ (rank 1)		S [y3] - 356.2020+ (rank 3)		V [y4] - 425.2598+ (rank 4)
	K.LFLDLACR.L [161, 168]		R.QNTLVNNSVSSPLPGEK.S [175, 191]		
	504.2708++		877.4576++		
	L [y6] - 747.3818+ (rank 1)		S [y9] - 871.4520+ (rank 3)		
	D [y5] - 634.2977+ (rank 2)		P [y7] - 697.3879+ (rank 2)		

	L [y4] - 519.2708+ (rank 3)		P [y5] - 487.2511+ (rank 1)				
	507.2808++ (heavy)		881.4647++ (heavy)				
	L [y6] - 753.4019+ (rank 1)		S [y9] - 879.4662+ (rank 3)				
	D [y5] - 640.3179+ (rank 2)		P [y7] - 705.4021+ (rank 2)				
	L [y4] - 525.2909+ (rank 3)		P [y5] - 495.2653+ (rank 1)				
RHOF	IPI: IPI00307458.3 SWISS-PROT: Q9HBH0-1 RHOF Isoform 1 of Rho-related GTP-binding protein RhoF						
	K.IVIVGDGGCGK.T [21, 31]		K.YTASVTVGSK.E [55, 64]			K.EVTLNLYDTAGQEDYDR.L [65, 81]	
	537.7842++		506.7691++			1001.4554++	
	I [y9] - 862.4087+ (rank 4)		A [y8] - 748.4199+ (rank 1)			Y [y11] - 1332.5339+ (rank 2)	
	V [y8] - 749.3247+ (rank 3)		S [y7] - 677.3828+ (rank 2)			D [y10] - 1169.4705+ (rank 3)	
	G [y7] - 650.2563+ (rank 2)		T [y5] - 491.2824+ (rank 3)			G [y7] - 882.3588+ (rank 1)	
	541.7913++ (heavy)		510.7762++ (heavy)			1004.4655++ (heavy)	
	I [y9] - 870.4229+ (rank 4)		A [y8] - 756.4341+ (rank 1)			Y [y11] - 1338.5540+ (rank 2)	
	V [y8] - 757.3389+ (rank 3)		S [y7] - 685.3970+ (rank 2)			D [y10] - 1175.4907+ (rank 3)	
	G [y7] - 658.2704+ (rank 2)		T [y5] - 499.2966+ (rank 3)			G [y7] - 888.3789+ (rank 1)	
	K.WFPEVTHFCR.G [112, 121]		R.AALYLECSAK.F [166, 175]				
	689.8217++		563.2841++				
	P [y8] - 1045.4884+ (rank 1)		Y [y7] - 870.4026+ (rank 2)				
	V [y6] - 819.3930+ (rank 2)		L [y6] - 707.3393+ (rank 1)				
	T [y5] - 720.3246+ (rank 3)		E [y5] - 594.2552+ (rank 3)				
	692.8318++ (heavy)		567.2912++ (heavy)				
	P [y8] - 1051.5085+ (rank 1)		Y [y7] - 878.4168+ (rank 2)				
	V [y6] - 825.4131+ (rank 2)		L [y6] - 715.3535+ (rank 1)				
	T [y5] - 726.3447+ (rank 3)		E [y5] - 602.2694+ (rank 3)				
RAB34	IPI: IPI00328180.4 SWISS-PROT: Q9BZG1-1 RAB34 Isoform 1 of Ras-related protein Rab-34						
	K.VIVVGDLSVKG.T [54, 64]		R.FEVLGIPFSLQLWDTAGQER.F [93, 11]			K.ENDPSSVLLFLVGSK.K [152, 166]	
	543.3319++		1153.5944++			802.9301++	
	V [y9] - 873.5040+ (rank 1)		Q [y10] - 1203.5753+ (rank 5)			L [y8] - 876.5553+ (rank 1)	
	V [y8] - 774.4356+ (rank 2)		L [y9] - 1075.5167+ (rank 4)			L [y7] - 763.4713+ (rank 2)	
	G [y7] - 675.3672+ (rank 3)		W [y8] - 962.4326+ (rank 1)			F [y6] - 650.3872+ (rank 3)	
	547.3390++ (heavy)		1156.6045++ (heavy)			806.9372++ (heavy)	
	V [y9] - 881.5182+ (rank 1)		Q [y10] - 1209.5954+ (rank 5)			L [y8] - 884.5695+ (rank 1)	
	V [y8] - 782.4498+ (rank 2)		L [y9] - 1081.5368+ (rank 4)			L [y7] - 771.4855+ (rank 2)	
	G [y7] - 683.3814+ (rank 3)		W [y8] - 968.4528+ (rank 1)			F [y6] - 658.4014+ (rank 3)	
	K.AEYWAVSSLTGENVR.E [191, 205]		R.INSDDSNLYLTASK.K [238, 251]				
	841.4127++		770.8781++				
	S [y9] - 962.4901+ (rank 3)		Y [y6] - 682.3770+ (rank 3)				
	T [y6] - 675.3420+ (rank 2)		L [y5] - 519.3137+ (rank 4)				
	G [y5] - 574.2944+ (rank 1)		T [y4] - 406.2296+ (rank 2)				
	844.4227++ (heavy)		774.8852++ (heavy)				
	S [y9] - 968.5103+ (rank 3)		Y [y6] - 690.3912+ (rank 3)				
	T [y6] - 681.3622+ (rank 2)		L [y5] - 527.3279+ (rank 4)				
	G [y5] - 580.3145+ (rank 1)		T [y4] - 414.2438+ (rank 2)				
RAB43	IPI: IPI00329441.1 SWISS-PROT: Q86YS6 RAB43; ISY1 Ras-related protein Rab-43						
	K.YAGSNIVQLLIGNK.S [118, 131]		K.DSSNVEEAFLR.V [164, 174]			K.SPDHIQLNSK.D [192, 201]	
	745.4223++		633.8017++			569.7962++	
	V [y8] - 884.5564+ (rank 1)		E [y6] - 764.3937+ (rank 1)			D [y8] - 954.5003+ (rank 5)	
	Q [y7] - 785.4880+ (rank 2)		A [y4] - 506.3085+ (rank 3)			H [y7] - 839.4734+ (rank 1)	
	I [y4] - 431.2613+ (rank 3)		F [y3] - 435.2714+ (rank 2)			I [y6] - 702.4145+ (rank 2)	
	749.4294++ (heavy)		636.8117++ (heavy)			573.8033++ (heavy)	
	V [y8] - 892.5706+ (rank 1)		E [y6] - 770.4139+ (rank 1)			D [y8] - 962.5145+ (rank 5)	
	Q [y7] - 793.5022+ (rank 2)		A [y4] - 512.3287+ (rank 3)			H [y7] - 847.4876+ (rank 1)	
	I [y4] - 439.2755+ (rank 3)		F [y3] - 441.2916+ (rank 2)			I [y6] - 710.4287+ (rank 2)	
	R.VATELIMR.H [175, 182]					380.1999+++	
	466.7653++					P [y9] - 1051.5531+ (rank 2)	
	T [y6] - 762.4178+ (rank 1)					I [y6] - 702.4145+ (rank 4)	
	L [y4] - 532.3276+ (rank 2)					Q [y5] - 589.3304+ (rank 5)	
	I [y3] - 419.2435+ (rank 3)					382.8713+++ (heavy)	
	469.7754++ (heavy)					P [y9] - 1059.5673+ (rank 2)	
	T [y6] - 768.4380+ (rank 1)					I [y6] - 710.4287+ (rank 4)	
	L [y4] - 538.3477+ (rank 2)					Q [y5] - 597.3446+ (rank 5)	
	I [y3] - 425.2636+ (rank 3)						
NKIRAS1	IPI: IPI00410705.2 SWISS-PROT: Q9NYS0 NKIRAS1 NF-kappa-B inhibitor-interacting Ras-like protein 1						
	K.VVVCGLLSVKG.T [6, 16]		R.QVDAEVAQQWAK.S [128, 139]			K.TLIEPFTLLASK.L [155, 166]	
	565.8337++		686.8464++			666.8923++	
	V [y9] - 932.5234+ (rank 1)		V [y7] - 830.4519+ (rank 2)			I [y10] - 1118.6456+ (rank 2)	
	C [y8] - 833.4550+ (rank 2)		A [y6] - 731.3835+ (rank 1)			E [y9] - 1005.5615+ (rank 3)	
	S [y4] - 390.2347+ (rank 3)		Q [y5] - 660.3464+ (rank 3)			P [y8] - 876.5189+ (rank 1)	
	569.8408++ (heavy)		690.8535++ (heavy)			670.8994++ (heavy)	
	V [y9] - 940.5376+ (rank 1)		V [y7] - 838.4661+ (rank 2)			I [y10] - 1126.6598+ (rank 2)	
	C [y8] - 841.4691+ (rank 2)		A [y6] - 739.3977+ (rank 1)			E [y9] - 1013.5757+ (rank 3)	
	S [y4] - 398.2489+ (rank 3)		Q [y5] - 668.3606+ (rank 3)			P [y8] - 884.5331+ (rank 1)	
RAB12	IPI: IPI00419932.5 SWISS-PROT: Q6IQ22 RAB12 Ras-related protein Rab-12						
	R.AGGGGGLGAGSPALSGGQGR.R [10,		K.LQVLIIGSR.G [42, 50]			R.FTDDTFCEACK.S [61, 71]	
	792.3979++		499.8215++			697.2736++	
	G [y13] - 1114.5600+ (rank 3)		V [y7] - 757.4930+ (rank 1)			D [y9] - 1145.4238+ (rank 1)	
	G [y11] - 986.5014+ (rank 2)		I [y6] - 658.4246+ (rank 2)			F [y6] - 814.3222+ (rank 3)	

	P [y9] - 842.4479+ (rank 1)	I [y5] - 545.3406+ (rank 3)	C [y5] - 667.2538+ (rank 2)
	795.4079++ (heavy)	502.8315++ (heavy)	701.2807++ (heavy)
	G [y13] - 1120.5801+ (rank 3)	V [y7] - 763.5132+ (rank 1)	D [y9] - 1153.4380+ (rank 1)
	G [y11] - 992.5215+ (rank 2)	I [y6] - 664.4448+ (rank 2)	F [y6] - 822.3364+ (rank 3)
	P [y9] - 848.4680+ (rank 1)	I [y5] - 551.3607+ (rank 3)	C [y5] - 675.2680+ (rank 2)
	R.FNSITSAYR.S [103, 112]	K.FAQQITGMR.F [172, 180]	
	611.2986++	526.2713++	
	S [y8] - 960.4785+ (rank 2)	Q [y6] - 705.3712+ (rank 1)	
	T [y6] - 760.3624+ (rank 1)	I [y5] - 577.3126+ (rank 3)	
	S [y5] - 659.3148+ (rank 3)	T [y4] - 464.2286+ (rank 2)	
	614.3086++ (heavy)	529.2814++ (heavy)	
	S [y8] - 966.4987+ (rank 2)	Q [y6] - 711.3913+ (rank 1)	
	T [y6] - 766.3826+ (rank 1)	I [y5] - 583.3328+ (rank 3)	
	S [y5] - 665.3349+ (rank 3)	T [y4] - 470.2487+ (rank 2)	
KRAS	IPI:IP100423568.1 SWISS-PROT:P01116-1 KRAS Isoform 2A of GTPase KRas		
	K.DSEDVPMVLVGNK.C [104, 116]	R.QRVEDAFYTLVR.E [149, 160] (missed)	R.VEDAFYTLVR.E [151, 160]
	701.8478++	499.6001+++	606.8166++
	P [y8] - 857.4913+ (rank 1)	Y [y5] - 651.3824+ (rank 2)	D [y8] - 984.5149+ (rank 1)
	V [y4] - 417.2456+ (rank 3)	T [y4] - 488.3191+ (rank 1)	A [y7] - 869.4880+ (rank 2)
	G [y3] - 318.1772+ (rank 4)	L [y3] - 387.2714+ (rank 4)	F [y6] - 798.4509+ (rank 3)
	705.8549++ (heavy)	503.6135+++ (heavy)	609.8267++ (heavy)
	P [y8] - 865.5055+ (rank 1)	Y [y5] - 657.4026+ (rank 2)	D [y8] - 990.5350+ (rank 1)
	V [y4] - 425.2598+ (rank 3)	T [y4] - 494.3392+ (rank 1)	A [y7] - 875.5081+ (rank 2)
	G [y3] - 326.1914+ (rank 4)	L [y3] - 393.2916+ (rank 4)	F [y6] - 804.4710+ (rank 3)
KRAS	IPI:IP100423570.3 SWISS-PROT:P01116-2 KRAS Isoform 2B of GTPase KRas		
	R.SYGIPFIETSAK.T [135, 146]	K.TRQGVDDAFYTLVR.E [147, 160] (miss)	R.QGVDDAFYTLVR.E [149, 160]
	656.8428++	547.6179+++	692.3488++
	P [y8] - 892.4775+ (rank 1)	F [y6] - 798.4509+ (rank 4)	A [y7] - 869.4880+ (rank 3)
	F [y7] - 795.4247+ (rank 4)	Y [y5] - 651.3824+ (rank 1)	F [y6] - 798.4509+ (rank 2)
	I [y6] - 648.3563+ (rank 3)	T [y4] - 488.3191+ (rank 3)	Y [y5] - 651.3824+ (rank 1)
	660.8499++ (heavy)	551.6313+++ (heavy)	695.3589++ (heavy)
	P [y8] - 900.4917+ (rank 1)	F [y6] - 804.4710+ (rank 4)	A [y7] - 875.5081+ (rank 3)
	F [y7] - 803.4389+ (rank 4)	Y [y5] - 657.4026+ (rank 1)	F [y6] - 804.4710+ (rank 2)
	I [y6] - 656.3705+ (rank 3)	T [y4] - 494.3392+ (rank 3)	Y [y5] - 657.4026+ (rank 1)
RAB11A	IPI:IP100429190.4 TREMBL:B4DMN1 RAB11A cDNA FLJ61136, highly similar to Ras-related protein Rab-11A		
	K.NGLSFIETSAALDSTNVEAAFQILTILTEIYR.I [190, 218]		
	1068.5417+++		
	L [y6] - 794.4407+ (rank 1)		
	T [y5] - 681.3566+ (rank 2)		
	E [y4] - 580.3089+ (rank 3)		
	1070.5484+++ (heavy)		
	L [y6] - 800.4608+ (rank 1)		
	T [y5] - 687.3767+ (rank 2)		
	E [y4] - 586.3291+ (rank 3)		
RHOT2	IPI:IP100465059.4 SWISS-PROT:Q8IX11-1 RHOT2 Isoform 1 of Mitochondrial Rho GTPase 2		
	K.WIPLVNGGTTQGP.R.V [96, 109]	K.SAFLQAFLGR.G [429, 438]	K.ADLPEGVAVSGPSPAEFGR.K [525, 543]
	748.4044++	555.3087++	979.9675++
	P [y12] - 1196.6382+ (rank 1)	Q [y6] - 691.3886+ (rank 1)	S [y10] - 1107.4888+ (rank 1)
	N [y9] - 887.4330+ (rank 2)	A [y5] - 563.3300+ (rank 2)	G [y9] - 1020.4567+ (rank 2)
	G [y8] - 773.3900+ (rank 3)	F [y4] - 492.2929+ (rank 3)	P [y8] - 963.4353+ (rank 4)
	751.4145++ (heavy)	558.3188++ (heavy)	982.9775++ (heavy)
	P [y12] - 1202.6583+ (rank 1)	Q [y6] - 697.4087+ (rank 1)	S [y10] - 1113.5089+ (rank 1)
	N [y9] - 893.4531+ (rank 2)	A [y5] - 569.3501+ (rank 2)	G [y9] - 1026.4769+ (rank 2)
	G [y8] - 779.4102+ (rank 3)	F [y4] - 498.3130+ (rank 3)	P [y8] - 969.4554+ (rank 4)
RAB19	IPI:IP100478209.6 SWISS-PROT:A4D1S5-1 RAB19 Isoform 1 of Ras-related protein Rab-19		
	R.AADENFDYLFK.I [76, 86]	K.IILIGDSNVGK.T [87, 97]	K.MQVWDTAGQER.F [135, 145]
	666.8090++	564.8348++	660.8037++
	N [y7] - 946.4669+ (rank 3)	L [y9] - 902.4942+ (rank 2)	V [y9] - 1061.5010+ (rank 2)
	D [y5] - 685.3556+ (rank 4)	I [y8] - 789.4101+ (rank 3)	W [y8] - 962.4326+ (rank 1)
	Y [y4] - 570.3286+ (rank 5)	G [y7] - 676.3260+ (rank 1)	D [y7] - 776.3533+ (rank 3)
	670.8161++ (heavy)	568.8419++ (heavy)	663.8138++ (heavy)
	N [y7] - 954.4811+ (rank 3)	L [y9] - 910.5084+ (rank 2)	V [y9] - 1067.5212+ (rank 2)
	D [y5] - 693.3698+ (rank 4)	I [y8] - 797.4243+ (rank 3)	W [y8] - 968.4528+ (rank 1)
	Y [y4] - 578.3428+ (rank 5)	G [y7] - 684.3402+ (rank 1)	D [y7] - 782.3735+ (rank 3)
	R.SAHAALAYDLTR.R [156, 168]	R.HVLFEDACTLAEK.Y [205, 217]	
	467.9210+++	511.5853+++	
	Y [y5] - 667.3410+ (rank 4)	C [y6] - 721.3549+ (rank 4)	
	D [y4] - 504.2776+ (rank 2)	T [y5] - 561.3243+ (rank 3)	
	L [y3] - 389.2507+ (rank 3)	A [y3] - 347.1925+ (rank 2)	
	469.9277+++ (heavy)	514.2567+++ (heavy)	
	Y [y5] - 673.3611+ (rank 4)	C [y6] - 729.3691+ (rank 4)	
	D [y4] - 510.2978+ (rank 2)	T [y5] - 569.3385+ (rank 3)	
	L [y3] - 395.2708+ (rank 3)	A [y3] - 355.2067+ (rank 2)	
RHOA	IPI:IP100478231.2 SWISS-PROT:P61586 RHOA Transforming protein RhoA		
	K.QEPVKPEEGR.D [135, 144]	R.IGAFGYMECSAK.T [150, 161]	R.IGAFGYMECSAK.T [150, 161]
	584.8015++	667.2994++	675.2969++
	P [y8] - 911.4945+ (rank 1)	G [y8] - 945.3805+ (rank 1)	G [y8] - 961.3754+ (rank 1)

	K [y6] - 715.3733+ (rank 4)		Y [y7] - 888.3590+ (rank 3)		Y [y7] - 904.3539+ (rank 2)
	E [y3] - 361.1830+ (rank 3)		M [y6] - 725.2957+ (rank 2)		M [y6] - 741.2906+ (rank 3)
	591.8186++ (heavy)		671.3065++ (heavy)		679.3040++ (heavy)
	P [y8] - 925.5288+ (rank 1)		G [y8] - 953.3947+ (rank 1)		G [y8] - 969.3896+ (rank 1)
	K [y6] - 729.4077+ (rank 4)		Y [y7] - 896.3732+ (rank 3)		Y [y7] - 912.3681+ (rank 2)
	E [y3] - 367.2031+ (rank 3)		M [y6] - 733.3099+ (rank 2)		M [y6] - 749.3048+ (rank 3)
RAB4A	IPI:IP100480056.8 SWISS-PROT:P20338 RAB4A RAB4A, member RAS oncogene family variant				
	K.FLVIGNAGTGK.S [15, 25]		K.IESGELDPER.M [177, 186]		R.MGSGIQYGDAAALR.Q [187, 199]
	538.8086++		572.7777++		669.8272++
	V [y9] - 816.4574+ (rank 2)		S [y8] - 902.4214+ (rank 1)		Q [y8] - 893.4476+ (rank 1)
	I [y8] - 717.3890+ (rank 1)		D [y4] - 516.2413+ (rank 2)		Y [y7] - 765.3890+ (rank 2)
	G [y7] - 604.3049+ (rank 3)		P [y3] - 401.2143+ (rank 3)		G [y6] - 602.3257+ (rank 3)
	542.8157++ (heavy)		E [y9] - 516.2356++ (rank 2)		672.8372++ (heavy)
	V [y9] - 824.4716+ (rank 2)		575.7877++ (heavy)		Q [y8] - 899.4677+ (rank 1)
	I [y8] - 725.4032+ (rank 1)		S [y8] - 908.4415+ (rank 1)		Y [y7] - 771.4091+ (rank 2)
	G [y7] - 612.3191+ (rank 3)		D [y4] - 522.2614+ (rank 2)		G [y6] - 608.3458+ (rank 3)
			P [y3] - 407.2344+ (rank 3)		
			E [y9] - 519.2457++ (rank 2)		
RAN	IPI:IP100643041.3 SWISS-PROT:P62826 RANP1;RAN GTP-binding nuclear protein Ran				
	K.FNVWDTAGQEK.F [60, 70]		R.VCENIPIVLCGNK.V [110, 122]		K.NLQYYDISAK.S [142, 151]
	647.8068++		758.3865++		607.8062++
	V [y9] - 1033.4949+ (rank 3)		P [y8] - 900.4971+ (rank 1)		Q [y8] - 987.4782+ (rank 1)
	W [y8] - 934.4265+ (rank 1)		V [y6] - 690.3603+ (rank 3)		Y [y7] - 859.4196+ (rank 2)
	D [y7] - 748.3472+ (rank 2)		L [y5] - 591.2919+ (rank 2)		Y [y6] - 696.3563+ (rank 3)
	651.8139++ (heavy)		762.3936++ (heavy)		611.8133++ (heavy)
	V [y9] - 1041.5091+ (rank 3)		P [y8] - 908.5113+ (rank 1)		Q [y8] - 995.4924+ (rank 1)
	W [y8] - 942.4407+ (rank 1)		V [y6] - 698.3745+ (rank 3)		Y [y7] - 867.4338+ (rank 2)
	D [y7] - 756.3614+ (rank 2)		L [y5] - 599.3061+ (rank 2)		Y [y6] - 704.3705+ (rank 3)
RAB34	IPI:IP100788998.3 TREMBL:B4DNC0 RAB34 ras-related protein Rab-34 isoform 2				
	-MSHLPGLELR.R [0, 9]		R.VLAELPQCLR.K [68, 77]		
	390.2096+++		599.8343++		
	L [y4] - 530.3297+ (rank 1)		A [y8] - 986.5088+ (rank 2)		
	E [y3] - 417.2456+ (rank 3)		L [y6] - 786.4291+ (rank 3)		
	L [y2] - 288.2030+ (rank 2)		P [y5] - 673.3450+ (rank 1)		
	392.2163+++ (heavy)		602.8443++ (heavy)		
	L [y4] - 536.3498+ (rank 1)		A [y8] - 992.5289+ (rank 2)		
	E [y3] - 423.2657+ (rank 3)		L [y6] - 792.4492+ (rank 3)		
	L [y2] - 294.2231+ (rank 2)		P [y5] - 679.3651+ (rank 1)		
RAB11A	IPI:IP100795676.1 VEGA:OTTHUMP00000175895 RAB11A 22 kDa protein				
	R.ENDMSPSNVPIHVPPTTENKPK.V [167, 190]		R.ENDMSPSNVPIHVPPTTENKPK.V [167, 190]		
	882.1060+++		887.4377+++		
	H [y11] - 1247.6743+ (rank 4)		P [y13] - 1457.8111+ (rank 3)		
	P [y9] - 1011.5469+ (rank 1)		P [y9] - 1011.5469+ (rank 1)		
	T [y7] - 817.4414+ (rank 2)		E [y5] - 615.3461+ (rank 2)		
	887.4488+++ (heavy)		892.7805+++ (heavy)		
	H [y11] - 1263.7027+ (rank 4)		P [y13] - 1473.8395+ (rank 3)		
	P [y9] - 1027.5753+ (rank 1)		P [y9] - 1027.5753+ (rank 1)		
	T [y7] - 833.4698+ (rank 2)		E [y5] - 631.3744+ (rank 2)		
RABL4/IFT27	IPI:IP100872292.1 SWISS-PROT:Q9BW83-1 IFT27 Isoform 1 of Intraflagellar transport protein 27 homolog				
	K.CILAGDPAVVGK.T [7, 17]		K.TALAQIFR.S [18, 25]		R.SQAPGISLPGVLVGNK.T [108, 123]
	550.7921++		460.2716++		768.9408++
	L [y9] - 827.4621+ (rank 1)		L [y6] - 747.4512+ (rank 1)		P [y13] - 1250.7467+ (rank 3)
	A [y8] - 714.3781+ (rank 3)		A [y5] - 634.3671+ (rank 2)		S [y10] - 983.5884+ (rank 2)
	G [y7] - 643.3410+ (rank 2)		Q [y4] - 563.3300+ (rank 3)		P [y8] - 783.4723+ (rank 1)
	554.7992++ (heavy)		463.2817++ (heavy)		772.9479++ (heavy)
	L [y9] - 835.4763+ (rank 1)		L [y6] - 753.4713+ (rank 1)		P [y13] - 1258.7609+ (rank 3)
	A [y8] - 722.3923+ (rank 3)		A [y5] - 640.3873+ (rank 2)		S [y10] - 991.6026+ (rank 2)
	G [y7] - 651.3552+ (rank 2)		Q [y4] - 569.3501+ (rank 3)		P [y8] - 791.4865+ (rank 1)

Table S3B. A complete list of quantified small GTPase peptides and proteins in three sets of SILAC experiments for WM, IGR and WMLu paired melanoma cell lines.

			$R_{WM115/WM266}$			WM, Mean	WM, S.D.
			WM, F1	WM, F2	WM, R		
NRAS		NRAS protein ratio				0.64	0.04
	R.TGEGFLCVFAINNSK.S [73, 87]	NRAS peptide ratio, 1	0.68	0.67	0.57	0.64	0.05
	K.SFADINLYR.E [88, 96]	NRAS peptide ratio, 2	0.68	0.68	0.58	0.64	0.04
	R.QGVEDAFYTLVR.E [149, 160]	NRAS peptide ratio, 3	0.76	0.74	0.67	0.72	0.04
HRAS		HRAS protein ratio				1.20	0.03
	R.TGEGFLCVFAINNTK.S [73, 87]	HRAS peptide ratio, 1	1.14	1.21	1.12	1.16	0.04
	K.SFEDIHQYR.E [88, 96]	HRAS peptide ratio, 2	1.36	1.38	0.99	1.21	0.18
	R.SYGIPYIETSAK.T [135, 146]	HRAS peptide ratio, 3	1.25	1.25	1.17	1.22	0.04
RHOB		RHOB protein ratio				2.13	0.00
	K.LVVVGDGACGK.T [7, 17]	RHOB peptide ratio, 1	2.43	3.09	1.48	2.13	0.66
	K.DEFPEVYVPTVFENYVADIEVDGK.	RHOB peptide ratio, 2	ND	ND	ND	ND	ND
	R.IQAYDYLCQSAK.T [150, 161]	RHOB peptide ratio, 3	ND	ND	ND	ND	ND
	R.EVFETATRA.A [168, 175]	RHOB peptide ratio, 4	ND	ND	ND	ND	ND
RND3		RND3 protein ratio				0.44	0.04
	K.IVVVGDSDQCGK.T [25, 35]	RND3 peptide ratio, 1	0.40	0.43	0.45	0.42	0.02
	K.TALLHVFAK.D [36, 44]	RND3 peptide ratio, 2	0.58	0.54	0.43	0.51	0.06
	K.GEIQEFQCPNTK.M [118, 128]	RND3 peptide ratio, 3	0.41	0.41	0.61	0.46	0.10
	R.TDVSTLVLSNHR.Q [140, 152]	RND3 peptide ratio, 4	0.81	0.57	0.53	0.62	0.12
	R.DIFHVATLACVVK.T [187, 199]	RND3 peptide ratio, 5	ND	ND	ND	ND	ND
RAB39		RAB39 protein ratio				0.84	0.00
	R.LIVIGDSTVVK.S [10, 20]	RAB39 peptide ratio, 1	1.14	1.22	0.85	1.05	0.16
	R.IKLQLWDTAGQER.F [61, 73] (missed)	RAB39 peptide ratio, 2	1.14	1.22	0.85	1.05	0.16
	K.LQLWDTAGQER.F [63, 73]	RAB39 peptide ratio, 3	0.94	1.05	1.14	1.04	0.08
ARL5A		ARL5A protein ratio				1.32	0.43
	R.FLMWDIGGQESLR.S [24, 36]	ARL5A peptide ratio, 1	ND	ND	ND	ND	ND
	K.MLAHEDLR.K [71, 78]	ARL5A peptide ratio, 2	3.28	4.12	0.31	0.78	1.64
	K.AGLLIFANK.Q [80, 88]	ARL5A peptide ratio, 3	3.99	3.85	0.77	1.65	1.49
SAR1B		SAR1B protein ratio				0.84	0.22
	K.IDRPEAISEER.L [135, 145]	SAR1B peptide ratio, 1	0.68	0.76	0.91	0.77	0.09
	R.EMFGLYGQTTGK.G [148, 159]	SAR1B peptide ratio, 2	2.05	0.88	0.99	1.14	0.53
	K.ELNARPLEVFMCSVLK.R [166, 181]	SAR1B peptide ratio, 3	1.24	2.18	0.95	1.29	0.53
RABL2A		RABL2A protein ratio				0.85	0.26
	K.TKPSELDQGK.Y [5, 14]	RABL2A peptide ratio, 1	12.85	2.43	0.12	0.34	5.54
	K.IICLGDSAVGK.S [23, 33]	RABL2A peptide ratio, 2	0.56	0.98	1.34	0.84	0.32
	R.NLSTWYTELR.E [110, 119]	RABL2A peptide ratio, 3	0.10	0.67	17.49	0.26	8.06
	R.EFRPEIPCIVVANK.I [120, 133]	RABL2A peptide ratio, 4	3.63	3.14	0.19	0.51	1.52
DIRAS1		DIRAS1 protein ratio				0.97	0.26
	R.VVVFAGGGVVK.S [9, 19]	DIRAS1 peptide ratio, 1	1.58	1.20	0.65	1.00	0.38
	R.DTYIPTIEDTYR.Q [33, 44]	DIRAS1 peptide ratio, 2	1.07	0.91	1.32	1.07	0.17
	K.GSVEDIPVMLVGNK.C [108, 121]	DIRAS1 peptide ratio, 3	2.09	1.09	0.21	0.48	0.77
	R.EAQAVAEWVK.C [133, 142]	DIRAS1 peptide ratio, 4	2.98	2.02	0.32	0.76	1.10
ARL2		ARL2 protein ratio				0.82	0.12
	R.ELQSLLEER.L [104, 113]	ARL2 peptide ratio, 1	0.93	0.85	1.41	1.01	0.25
	R.LAGATLLIFANK.Q [114, 125]	ARL2 peptide ratio, 2	0.79	0.81	0.71	0.77	0.04
	R.EVLELDSIR.S [139, 147]	ARL2 peptide ratio, 3	0.77	0.79	0.66	0.74	0.06
ARL3		ARL3 protein ratio				1.04	0.04
	R.ILLLGLDNAGK.T [19, 29]	ARL3 peptide ratio, 1	1.03	1.05	1.13	1.07	0.05
	K.QLASEDISHITPTQGFNIK.S [35, 53]	ARL3 peptide ratio, 2	1.01	0.99	1.21	1.06	0.10
	K.LSCVPVLIFANK.Q [115, 126]	ARL3 peptide ratio, 3	0.83	0.91	1.37	0.99	0.24
TRIM23		TRIM23 protein ratio				0.96	0.18
	R.DALLLIFANK.Q [504, 513]	TRIM23 peptide ratio, 1	0.93	0.95	1.00	0.96	0.03
RALB		RALB protein ratio				0.97	0.31
	K.GQSSLALHK.V [29, 37]	RALB peptide ratio, 1	1.47	1.50	1.12	1.34	0.17
	R.QVPVEEAR.S [158, 165]	RALB peptide ratio, 2	1.12	1.22	1.15	1.16	0.04
	K.AEEWGVQYVETSAK.T [168, 181]	RALB peptide ratio, 3	0.29	1.24	1.46	0.61	0.50
ARL15		ARL15 protein ratio				1.19	0.24
	K.LCSESPDNVVSTTGFSIK.A [51, 68]	ARL15 peptide ratio, 1	1.35	2.23	1.27	1.52	0.44
	K.AVPFQNAILNVK.E [69, 80]	ARL15 peptide ratio, 2	0.90	0.87	1.36	1.00	0.23
	K.ELGGADNIR.K [81, 89]	ARL15 peptide ratio, 3	1.23	1.18	0.78	1.02	0.20
	K.YFELEPLAR.G [157, 165]	ARL15 peptide ratio, 4	4.78	0.99	0.86	1.26	1.82
	K.DSFSQLINLLEEK.D [184, 196]	ARL15 peptide ratio, 5	ND	ND	ND	ND	ND
RAB1A		RAB1A protein ratio				1.00	0.03
	R.GAHGIIVVYDVTQESFNNVK.Q [82, 91]	RAB1A peptide ratio, 1	0.91	0.80	1.19	0.94	0.17
	K.NATNVEQSFMTMAAEIK.K [156, 171]	RAB1A peptide ratio, 2	0.89	0.98	1.17	1.00	0.11
	R.MGPGATAGGAEK.S [175, 186]	RAB1A peptide ratio, 3	0.93	0.99	1.14	1.01	0.09
CDC42		CDC42 protein ratio				0.83	0.01
Isoform 1	K.TCLLISYTTNK.F [16, 26]	CDC42 peptide ratio, 1	0.92	0.83	0.75	0.83	0.07
Isoform 1	K.WVPEITHHCQPK.T [96, 106]	CDC42 peptide ratio, 2	0.68	0.73	1.06	0.80	0.17

Isoform 1	K.TPFLLVGTQIDLR.D [107, 119]	CDC42 peptide ratio, 3	0.76	0.80	0.92	0.82	0.07
RAB21		RAB21 protein ratio				0.96	0.14
	K.VVLLGEGCVGK.T [21, 31]	RAB21 peptide ratio, 1	0.98	2.76	0.98	1.25	0.84
	R.VNLAIWDTAGQER.F [67, 79]	RAB21 peptide ratio, 2	0.91	0.83	1.12	0.94	0.12
	R.HVSIQEAESYAESVGAH.K [140, 15]	RAB21 peptide ratio, 3	0.77	0.88	1.34	0.94	0.25
RAB22A		RAB22A protein ratio				1.55	0.00
	K.TVQYQNELHK.F [45, 54]	RAB22A peptide ratio, 1	1.44	1.44	1.87	1.56	0.20
	K.EETFSTLKN [89, 96]	RAB22A peptide ratio, 2	ND	ND	ND	ND	ND
	K.DYADSIHAIFVETSAKN.N [134, 149]	RAB22A peptide ratio, 3	ND	ND	ND	ND	ND
	R.IPSTDANLPSGGK.G [165, 177]	RAB22A peptide ratio, 4	1.43	1.39	1.54	1.45	0.06
RAB17		RAB17 protein ratio				1.65	0.01
	K.SILPTVGC ^C AFFTK.V [45, 57]	RAB17 peptide ratio, 1	1.67	2.95	1.11	1.63	0.77
	K.LEIWDTAGQEK.Y [68, 78]	RAB17 peptide ratio, 2	2.05	1.20	2.03	1.66	0.40
	K.YHSV ^C CHLYFR.G [79, 88]	RAB17 peptide ratio, 3	ND	ND	ND	ND	ND
	R.SDEEGQALR.G [183, 191]	RAB17 peptide ratio, 4	ND	ND	ND	ND	ND
RAB23		RAB23 protein ratio				0.96	0.06
	K.TIGVDFLER.Q [40, 48]	RAB23 peptide ratio, 1	0.91	0.93	1.19	0.99	0.13
	R.QIQVND ^E EDVRL.L [49, 58]	RAB23 peptide ratio, 2	0.95	1.07	1.06	1.02	0.05
	K.EDLNVNEVFK.Y [153, 162]	RAB23 peptide ratio, 3	0.75	0.71	1.45	0.87	0.34
RAB1B		RAB1B protein ratio				1.31	0.20
	-MNPEYDYLFLK.L [0, 9]	RAB1B peptide ratio, 1	0.85	29.67	1.14	1.44	13.52
	K.NATNVEQAFMTMAAEIK.K [153, 16]	RAB1B peptide ratio, 2	1.20	1.33	1.45	1.32	0.10
	R.MGPGAASGG ^E RPNLK.I [172, 186]	RAB1B peptide ratio, 3	0.72	0.76	2.50	0.97	0.83
RABL2B		RABL2B protein ratio				ND	0.00
	K.AHA ^C IMVFDVQR.K [93, 104]	RABL2B peptide ratio, 1	ND	ND	ND	ND	ND
RAP2C		RAP2C protein ratio				0.99	0.00
	K.VPLILVGNK.V [108, 116]	RAP2C peptide ratio, 1	0.86	0.93	1.28	0.99	0.18
	K.VDLEPER.E [117, 123]	RAP2C peptide ratio, 2	1.02	3.21	0.57	0.98	1.15
	R.EVMSSEGR.A [124, 131]	RAP2C peptide ratio, 3	ND	ND	ND	ND	ND
	R.ALAQEWG ^C PFMETS ^A KS.S [132, 14]	RAP2C peptide ratio, 4	ND	ND	ND	ND	ND
	R.QMNYSSLPEK.Q [162, 171]	RAP2C peptide ratio, 5	1.40	1.36	1.10	1.27	0.13
RHOU		RHOU protein ratio				0.79	0.05
	K. ^C VLVGDGAVGK.T [51, 61]	RHOU peptide ratio, 1	0.73	0.79	0.85	0.79	0.05
RABL5		RABL5 protein ratio				0.69	#DIV/0!
	K.ILFVG ^C PCESGK.T [5, 15]	RABL5 peptide ratio, 1	0.65	0.77	0.64	0.68	0.06
	R.ILEFENPHVTSNNK.G [39, 52]	RABL5 peptide ratio, 2	ND	ND	ND	ND	ND
	K.FESC ^C WPALMK.D [69, 78]	RABL5 peptide ratio, 3	0.69	0.61	0.73	0.67	0.05
	K.SIINSMSES ^R .D [166, 175]	RABL5 peptide ratio, 4	0.50	0.64	0.95	0.65	0.19
RRAGD		RRAGD protein ratio				0.69	0.53
	K.MSPNETLFLESTNK.I [85, 98]	RRAGD peptide ratio, 1	1.64	1.00	1.14	1.21	0.27
	K.LNNTTVLYLK.E [320, 329]	RRAGD peptide ratio, 2	0.08	0.13	5.16	0.15	2.38
ARL4C		ARL4C protein ratio				ND	#DIV/0!
	K.GIS ^C HFWDVGGQEK.L [60, 73]	ARL4C peptide ratio, 1	ND	ND	ND	ND	ND
	K.FAENQGTPLLVIANK.Q [113, 127]	ARL4C peptide ratio, 2	ND	ND	ND	ND	ND
	K.LYEMILK.R [174, 180]	ARL4C peptide ratio, 3	ND	ND	ND	ND	ND
RAC2		RAC2 protein ratio				0.75	0.11
	R.HH ^C PSTPIILVGT ^K .L [102, 115]	RAC2 peptide ratio, 1	0.27	0.68	1.79	0.52	0.64
	K.LAPITYPQGLALAK.E [133, 146]	RAC2 peptide ratio, 2	0.57	0.59	3.21	0.80	1.24
	R.AVLC ^C PQPTR.Q [174, 182]	RAC2 peptide ratio, 3	0.48	0.46	3.40	0.66	1.38
RAC1		RAC1 protein ratio				0.87	0.01
	R.HH ^C PNTPIILVGT ^K .L [102, 115]	RAC1 peptide ratio, 1	0.67	0.77	1.33	0.85	0.29
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 2	0.82	0.85	0.93	0.87	0.05
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 3	0.74	0.83	1.11	0.87	0.16
RRAGB		RRAGB protein ratio				1.49	0.15
	R.SIIFANYIAR.D [57, 66]	RRAGB peptide ratio, 1	1.42	1.87	0.85	1.24	0.42
	R.NFAEII ^E ADEVLLFER.A [253, 268]	RRAGB peptide ratio, 2	1.19	1.46	1.16	1.26	0.13
	K.LAASFQSMEVR.N [305, 315]	RRAGB peptide ratio, 3	1.32	3.22	1.16	1.56	0.93
RAB27B		RAB27B protein ratio				ND	#DIV/0!
	K.LLALGD ^S GVGK.T [11, 21]	RAB27B peptide ratio, 1	ND	ND	ND	ND	ND
	R.VVYNAQGPN ^G SSGK.A [50, 63]	RAB27B peptide ratio, 2	ND	ND	ND	ND	ND
	K.VHLQLWDTAGQER.F [67, 79]	RAB27B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YGIPYFETSAATGQNVEK.A [154, 1]	RAB27B peptide ratio, 4	ND	ND	ND	ND	ND
RHOD		RHOD protein ratio				ND	#DIV/0!
	K.GKPVHLHIWDTAGQDDYDR.L [61,	RHOD peptide ratio, 1	ND	ND	ND	ND	ND
	R.WYPEVNHFK.K [110, 119]	RHOD peptide ratio, 2	ND	ND	ND	ND	ND
	R.SVGAVAYLE ^C SAR.L [161, 173]	RHOD peptide ratio, 3	ND	ND	ND	ND	ND
RHOQ		RHOQ protein ratio				ND	#DIV/0!
	K.EEWVPELK.E [100, 107]	RHOQ peptide ratio, 1	ND	ND	ND	ND	ND
	K.EIGACC ^C YVECSALTQK.G [153, 168]	RHOQ peptide ratio, 2	ND	ND	ND	ND	ND
	K.TVFDEAIIAILTPK.K [172, 185]	RHOQ peptide ratio, 3	ND	ND	ND	ND	ND
RRAS2		RRAS2 protein ratio				1.39	0.25
	R.LVVVGGGGV ^G GK.S [16, 26]	RRAS2 peptide ratio, 1	2.71	1.53	1.07	1.53	0.69
	R.LDILD ^T AGQEEFGAMRE.E [69, 84]	RRAS2 peptide ratio, 2	0.71	0.89	1.57	0.95	0.37
	R.TGEGFLLVFSVTDR.G [90, 103]	RRAS2 peptide ratio, 3	1.83	0.86	2.30	1.40	0.60

	R.QVTQEEGQQLAR.Q [141, 152]	RRAS2 peptide ratio, 4	1.11	1.30	1.94	1.37	0.35
RAB31		RAB31 protein ratio				0.25	0.61
	R.FHSLAPMYR.G [67, 76]	RAB31 peptide ratio, 1	1.74	1.49	1.64	1.62	0.10
	R.GSAAVIVYDITK.Q [77, 89]	RAB31 peptide ratio, 2	0.25	0.24	0.27	0.25	0.01
	K.QDSFYTLK.K [90, 97]	RAB31 peptide ratio, 3	0.45	0.46	0.33	0.40	0.06
RAB32		RAB32 protein ratio				1.15	0.00
	K.VLVIGELGVGK.T [27, 37]	RAB32 peptide ratio, 1	1.28	1.14	1.05	1.15	0.09
	R.SSTFEAVLK.W [110, 118]	RAB32 peptide ratio, 2	1.20	1.27	1.01	1.15	0.11
	K.DNINIEEAR.F [176, 185]	RAB32 peptide ratio, 3	1.17	1.23	1.05	1.15	0.07
RAB18		RAB18 protein ratio				1.48	0.06
	K.IIIGESGVGK.S [10, 20]	RAB18 peptide ratio, 1	1.57	1.63	1.50	1.56	0.05
	K.LAIWDTAGQER.F [58, 68]	RAB18 peptide ratio, 2	1.50	1.49	1.52	1.50	0.02
	R.TLTPSYR.G [71, 78]	RAB18 peptide ratio, 3	1.41	1.43	1.39	1.41	0.02
	R.NDIVNMLVGNK.I [112, 122]	RAB18 peptide ratio, 4	1.44	1.59	1.57	1.53	0.07
RAB9B		RAB9B protein ratio				1.02	0.03
	K.VILLGDGGVVK.S [9, 19]	RAB9B peptide ratio, 1	1.10	1.12	0.96	1.05	0.07
	R.QSFENLGNWQK.E [92, 102]	RAB9B peptide ratio, 2	1.78	0.86	0.77	0.99	0.45
	K.EFIYYADV.K.D [103, 111]	RAB9B peptide ratio, 3	ND	ND	ND	ND	ND
RAP1B		RAP1B protein ratio				0.78	0.15
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 1	0.57	0.71	1.00	0.72	0.18
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 2	1.98	0.86	0.89	1.07	0.52
	R.QWNNCAFLESSAK.S [136, 148]	RAP1B peptide ratio, 3	0.75	0.77	0.81	0.78	0.03
ARFRP1		ARFRP1 protein ratio				0.98	0.07
	K.TTFLEQSK.T [30, 37]	ARFRP1 peptide ratio, 1	0.98	1.04	0.93	0.98	0.05
	K.ITTVGLNIGTVDVGK.A [52, 67]	ARFRP1 peptide ratio, 2	1.61	1.33	0.81	1.15	0.33
	K.QDVETCLSIDIK.T [135, 147]	ARFRP1 peptide ratio, 3	0.77	1.04	1.66	1.05	0.37
	K.TAFSDCTSK.I [148, 156]	ARFRP1 peptide ratio, 4	1.02	3.46	0.44	0.84	1.31
	R.DCLTQACSALTGK.G [161, 173]	ARFRP1 peptide ratio, 5	0.52	0.49	1.20	0.63	0.33
RAB20		RAB20 protein ratio				ND	#DIV/0!
	K.IVLLGDMNVGK.T [7, 17]	RAB20 peptide ratio, 1	ND	ND	ND	ND	ND
	R.GAAAILTYDVNHR.Q [71, 84]	RAB20 peptide ratio, 2	ND	ND	ND	ND	ND
	R.FLGLTDTASK.D [94, 103]	RAB20 peptide ratio, 3	ND	ND	ND	ND	ND
	K.QVQLEDAVALYK.K [147, 158]	RAB20 peptide ratio, 4	ND	ND	ND	ND	ND
SAR1A		SAR1A protein ratio				1.63	0.04
	K.NYLPAINGIVFLVDCADHSR.L [87, 100]	SAR1A peptide ratio, 1	1.42	1.47	1.90	1.57	0.22
	R.TDAISEEK.L [138, 145]	SAR1A peptide ratio, 2	1.47	1.52	1.78	1.58	0.14
	R.EIFGLYGQTTGK.G [148, 159]	SAR1A peptide ratio, 3	1.60	1.74	1.65	1.66	0.06
RAB5C		RAB5C protein ratio				1.04	0.05
	R.QASPNIVIALAGNK.A [121, 134]	RAB5C peptide ratio, 1	1.09	1.19	1.12	1.13	0.04
	K.NEPQATGAPGR.N [184, 195]	RAB5C peptide ratio, 2	0.87	0.95	1.33	1.02	0.20
	R.GVDLQENNPASR.S [198, 209]	RAB5C peptide ratio, 3	0.98	1.03	1.19	1.06	0.09
RAB7A		RAB7A protein ratio				1.25	0.04
	R.FQSLGVAFYR.G [69, 78]	RAB7A peptide ratio, 1	1.29	1.34	1.09	1.23	0.11
	R.DEFLIQASPR.D [103, 112]	RAB7A peptide ratio, 2	1.13	1.24	1.28	1.21	0.06
	R.AQAWCYSK.N [138, 145]	RAB7A peptide ratio, 3	1.29	1.47	1.19	1.30	0.12
	K.NNIPYFETSAK.E [146, 156]	RAB7A peptide ratio, 4	1.25	1.33	1.18	1.25	0.06
RAB9A		RAB9A protein ratio				1.03	0.12
	R.QVSTEEAQAWCR.D [131, 142]	RAB9A peptide ratio, 1	1.20	1.27	1.17	1.21	0.04
	K.DATNVAAAFEEAVR.R [156, 169]	RAB9A peptide ratio, 2	0.96	1.18	0.75	0.93	0.18
	R.SDHLIQDTDTVNLHR.K [178, 191]	RAB9A peptide ratio, 3	0.95	1.02	0.98	0.98	0.03
RAB13		RAB13 protein ratio				0.97	0.37
	K.LQVWDTAGQER.F [58, 68]	RAB13 peptide ratio, 1	0.80	11.43	1.69	1.56	4.81
	K.SFENIQNWMS.K [94, 103]	RAB13 peptide ratio, 2	0.40	0.79	1.63	0.68	0.51
	K.ENASAGVER.L [107, 115]	RAB13 peptide ratio, 3	0.74	0.84	1.67	0.95	0.42
RAB28		RAB28 protein ratio				0.64	0.02
	K.IVVLGDGASGK.T [14, 24]	RAB28 peptide ratio, 1	0.40	0.79	1.63	0.68	0.51
	K.TSLTTCFAQETFGK.Q [25, 38]	RAB28 peptide ratio, 2	0.76	0.69	0.75	0.73	0.03
	K.VSEESQPLVALVGNK.I [113, 129]	RAB28 peptide ratio, 3	0.75	0.67	0.65	0.69	0.05
	K.VAAEILGIK.L [172, 180]	RAB28 peptide ratio, 4	0.65	0.56	1.01	0.70	0.20
	K.AEIEQSQR.V [184, 191]	RAB28 peptide ratio, 5	0.52	0.81	0.68	0.65	0.12
RAB27A		RAB27A protein ratio				2.21	0.01
	K.FLALGDSGVGK.T [11, 21]	RAB27A peptide ratio, 1	2.44	2.50	1.84	2.22	0.30
	K.TSVLYQYTDGK.F [22, 32]	RAB27A peptide ratio, 2	2.31	2.71	1.76	2.19	0.39
	R.IHLQLWDTAGQER.F [67, 79]	RAB27A peptide ratio, 3	ND	ND	ND	ND	ND
	K.SDLEDQR.V [134, 140]	RAB27A peptide ratio, 4	2.43	2.52	1.66	2.13	0.38
	K.SWIPEGVVR.S [191, 199]	RAB27A peptide ratio, 5	2.17	2.28	1.97	2.13	0.13
RAB10		RAB10 protein ratio				1.21	0.04
	K.TYDLLFK.L [4, 10]	RAB10 peptide ratio, 1	1.26	1.27	1.15	1.23	0.05
	R.FHTITTSYYR.G [70, 79]	RAB10 peptide ratio, 2	1.20	1.27	1.18	1.21	0.04
	R.NIDEHANEDVER.M [105, 116]	RAB10 peptide ratio, 3	1.00	1.09	1.40	1.14	0.17
RHEB		RHEB protein ratio				0.75	0.02
	K.IAILGYR.S [8, 14]	RHEB peptide ratio, 1	ND	ND	ND	ND	ND
	K.VQIPIMLVGNK.K [109, 119]	RHEB peptide ratio, 2	0.80	0.84	0.74	0.79	0.04
	K.ALAESWNAAFLESSAK.E [135, 150]	RHEB peptide ratio, 3	0.73	0.75	0.77	0.75	0.01

	K.ENQTAVDVFR.R [151, 160]	RHEB peptide ratio, 4	0.70	0.68	0.76	0.71	0.03
CDC42		CDC42 protein ratio				0.86	0.08
Isoform 2	K.YVECSALTQK.G [153, 162]	CDC42 peptide ratio, 1	0.85	0.93	0.79	0.86	0.06
Isoform 2	K.NVFDAILAALPEPEPK.K [166, 182]	CDC42 peptide ratio, 2	0.55	0.65	0.97	0.68	0.18
RAB6B		RAB6B protein ratio				0.69	0.22
	R.QITIEEGEQR.A [134, 143]	RAB6B peptide ratio, 1	0.75	0.75	0.58	0.68	0.08
	K.ELSVMFIETSAK.T [146, 157]	RAB6B peptide ratio, 2	1.92	0.95	0.95	1.14	0.46
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 3	0.73	0.83	0.53	0.67	0.12
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 4	0.79	0.48	1.17	0.71	0.28
RHOG		RHOG protein ratio				0.96	0.02
	R.TVNLNLWDTAGQEEYDR.L [49, 65]	RHOG peptide ratio, 1	0.84	0.86	1.18	0.94	0.15
	K.EQGQAPITPQQGQALAK.Q [130, 146]	RHOG peptide ratio, 2	0.79	0.92	1.35	0.97	0.24
	R.YLECSALQQDGVK.E [153, 165]	RHOG peptide ratio, 3	0.86	0.96	1.12	0.97	0.11
RAB5B		RAB5B protein ratio				0.93	0.01
	R.QASPSIVIALAGNK.A [120, 133]	RAB5B peptide ratio, 1	1.04	0.93	0.92	0.96	0.05
	K.TAMNVNDLFLAIK.K [165, 178]	RAB5B peptide ratio, 2	0.96	1.01	0.85	0.94	0.07
	K.SEPQNLGGAAGR.S [183, 194]	RAB5B peptide ratio, 3	0.85	0.92	1.06	0.93	0.09
	R.GVDLHEQSQQNK.S [197, 208]	RAB5B peptide ratio, 4	0.89	0.94	0.96	0.93	0.03
RAP2B		RAP2B protein ratio				1.15	0.20
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 1	0.81	1.31	1.31	1.09	0.24
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 2	ND	ND	ND	ND	ND
	K.VDLEGER.E [117, 123]	RAP2B peptide ratio, 3	0.48	0.51	2.64	0.68	1.01
	K.ASVDELFAEIVR.Q [150, 161]	RAP2B peptide ratio, 4	1.20	1.31	1.00	1.16	0.13
ARL8B		ARL8B protein ratio				1.31	0.17
	R.DLPNALDEK.Q [184, 192]	ARL8B peptide ratio, 1	1.77	1.67	1.47	1.63	0.12
	K.MNLSAIQDR.E [198, 206]	ARL8B peptide ratio, 2	1.23	1.33	1.20	1.25	0.06
	R.EICCSYSISCK.E [207, 216]	ARL8B peptide ratio, 3	1.33	1.47	1.14	1.30	0.13
RHOH		RHOH protein ratio				ND	#DIV/0!
	R.SNLPCTPVLVVATQTDQR.E [103, 116]	RHOH peptide ratio, 1	ND	ND	ND	ND	ND
	R.ASCVNAMEGK.K [127, 136]	RHOH peptide ratio, 2	ND	ND	ND	ND	ND
	K.GYLECSALSNR.G [146, 156]	RHOH peptide ratio, 3	ND	ND	ND	ND	ND
	R.GVQQVFEC AVR.T [157, 167]	RHOH peptide ratio, 4	ND	ND	ND	ND	ND
RAP1A		RAP1A protein ratio				1.02	0.34
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 1	0.89	18.35	1.25	1.52	8.15
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 2	0.86	0.38	2.12	0.70	0.73
	K.DTEDVPMILVGNK.C [104, 116]	RAP1A peptide ratio, 3	0.87	1.01	1.16	1.00	0.12
	R.QWCNCAFLESSAK.S [136, 148]	RAP1A peptide ratio, 4	0.97	1.12	1.08	1.05	0.06
RAP2A		RAP2A protein ratio				0.89	0.08
	K.VPVILVGNK.V [108, 116]	RAP2A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ALAEWGCPCPFMETS AK.S [132, 147]	RAP2A peptide ratio, 2	1.29	1.23	0.67	0.98	0.28
	K.TMVDLFAEIVR.Q [150, 161]	RAP2A peptide ratio, 3	0.76	0.97	0.78	0.82	0.09
RRAS		RRAS protein ratio				0.67	0.00
	K.ICSVDGIPAR.L [68, 77]	RRAS peptide ratio, 1	ND	ND	ND	ND	ND
	R.QSFNEVGK.L [113, 120]	RRAS peptide ratio, 2	ND	ND	ND	ND	ND
	K.LFTQILR.V [121, 127]	RRAS peptide ratio, 3	0.64	0.37	0.91	0.56	0.22
	K.ADLESQR.Q [143, 149]	RRAS peptide ratio, 4	1.70	1.36	0.57	0.98	0.47
RAB11B		RAB11B protein ratio				1.22	0.21
	K.AQIWDTAGQERY.Y [61, 71]	RAB11B peptide ratio, 1	1.39	1.51	1.44	1.45	0.05
	R.GAVGALLVYDI AK.H [82, 94]	RAB11B peptide ratio, 2	1.63	1.78	1.33	1.56	0.19
	K.NILTEIYR.I [166, 173]	RAB11B peptide ratio, 3	1.28	0.78	1.31	1.06	0.24
NKIRAS2		NKIRAS2 protein ratio				0.90	0.00
	K.VVVCQGQASV GK.T [6, 16]	NKIRAS2 peptide ratio, 1	0.88	0.83	0.82	0.84	0.03
	K.EVTIVVLGNK.C [111, 120]	NKIRAS2 peptide ratio, 2	ND	ND	ND	ND	ND
	R.VDPDVAQHWAK.S [129, 139]	NKIRAS2 peptide ratio, 3	ND	ND	ND	ND	ND
	R.SLLEPFVYLASK.M [155, 166]	NKIRAS2 peptide ratio, 4	0.80	0.95	0.97	0.90	0.08
RAB33B		RAB33B protein ratio				0.93	0.04
	K.IIVIGDSNVGK.T [35, 45]	RAB33B peptide ratio, 1	2.04	1.52	0.54	1.00	0.62
	R.AVEIDGER.I [73, 80]	RAB33B peptide ratio, 2	ND	ND	ND	ND	ND
	R.SAIQVPTDLAQK.F [153, 164]	RAB33B peptide ratio, 3	0.85	0.86	1.09	0.92	0.11
ARL6		ARL6 protein ratio				0.71	0.00
	R.NLWEHYK.E [77, 84]	ARL6 peptide ratio, 1	ND	ND	ND	ND	ND
	K.EELDTLLNHPDIK.H [106, 118]	ARL6 peptide ratio, 2	ND	ND	ND	ND	ND
	R.IPILFFANK.M [122, 130]	ARL6 peptide ratio, 3	0.74	0.81	0.62	0.71	0.08
	K.VSQLLCLENIK.D [142, 152]	ARL6 peptide ratio, 4	ND	ND	ND	ND	ND
RAC3		RAC3 protein ratio				0.43	0.00
	K.LAPITYPQGLAMAR.E [133, 146]	RAC3 peptide ratio, 1	0.40	0.52	0.39	0.43	0.06
	K.LAPITYPQGLAMAR.E [133, 146]	RAC3 peptide ratio, 2	ND	ND	ND	ND	ND
	R.AVLCPPPVK.K [174, 182]	RAC3 peptide ratio, 3	ND	ND	ND	ND	ND
RAB3A		RAB3A protein ratio				0.44	0.01
	K.ESSDQNFDMFK.I [12, 23]	RAB3A peptide ratio, 1	0.61	0.31	0.50	0.43	0.13
	K.TYSWDNAQVLLVGNK.C [121, 135]	RAB3A peptide ratio, 2	0.45	0.47	0.36	0.42	0.05
	R.LVDVICEK.M [178, 185]	RAB3A peptide ratio, 3	ND	ND	ND	ND	ND
	K.MSES�DTADPAVTGAK.Q [186, 201]	RAB3A peptide ratio, 4	ND	ND	ND	ND	ND
RAB5A		RAB5A protein ratio				0.82	0.02

	R.QASPNIVIALSGNK.A [120, 133]	RAB5A peptide ratio, 1	0.87	0.81	0.87	0.85	0.03
	K.NEPQNPGANSAR.G [183, 194]	RAB5A peptide ratio, 2	0.72	0.74	1.04	0.81	0.14
	R.GVDLTEPTQPTR.N [197, 208]	RAB5A peptide ratio, 3	0.69	0.74	1.00	0.79	0.14
RAB6C		RAB6C protein ratio				1.25	0.02
	R.QVSIIEGER.K [134, 142]	RAB6C peptide ratio, 1	1.12	1.19	1.35	1.21	0.09
	K.ELNVMFIETSAK.A [146, 157]	RAB6C peptide ratio, 2	1.22	1.23	1.35	1.26	0.06
	R.VAAALPGMESTQDR.S [169, 182]	RAB6C peptide ratio, 3	1.11	1.19	1.44	1.23	0.14
MRAS		MRAS protein ratio				ND	0.01
	K.IFVPDYDPTIEDSYLK.H [36, 51]	MRAS peptide ratio, 1	ND	ND	ND	ND	ND
RAB8B		RAB8B protein ratio				2.65	0.03
	R.NIEEHASSDVER.M [104, 115]	RAB8B peptide ratio, 1	2.31	2.47	3.52	2.67	0.54
	K.SSANVEEAFFTLAR.D [153, 166]	RAB8B peptide ratio, 2	2.24	2.52	3.18	2.59	0.40
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 3	3.22	3.18	1.96	2.64	0.58
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 4	1.29	1.38	0.76	1.07	0.27
RAB7L1		RAB7L1 protein ratio				1.04	0.14
	K.VLQWSDYEIVR.L [47, 57]	RAB7L1 peptide ratio, 1	1.03	1.42	1.16	1.18	0.16
	K.CDLSPWAVSR.D [126, 135]	RAB7L1 peptide ratio, 2	0.77	0.66	1.39	0.85	0.32
	K.ENGFTGWTTETSVK.E [144, 156]	RAB7L1 peptide ratio, 3	1.38	1.05	0.96	1.10	0.18
RHOC		RHOC protein ratio				0.84	0.07
	K.HFCPNVPIILVGNK.K [104, 117]	RHOC peptide ratio, 1	0.70	0.77	1.16	0.83	0.20
	K.HFCPNVPIILVGNKK.D [104, 118] (n	RHOC peptide ratio, 2	0.86	0.95	0.95	0.92	0.04
	R.ISAFGYLECSAK.T [150, 161]	RHOC peptide ratio, 3	0.63	0.77	0.86	0.74	0.10
RHOJ		RHOJ protein ratio				0.28	0.00
	K.AIGAQCYLECSALTQK.G [165, 180]	RHOJ peptide ratio, 1	0.21	0.36	0.33	0.28	0.06
	K.AVFDEAILTIFHPK.K [184, 197]	RHOJ peptide ratio, 2	ND	ND	ND	ND	ND
RAB38		RAB38 protein ratio				12.12	1.37
	K.LLVIGDLGVGK.T [11, 21]	RAB38 peptide ratio, 1	12.95	13.81	12.71	13.14	0.47
	K.VLHWDPETVVR.L [49, 59]	RAB38 peptide ratio, 2	8.96	12.76	15.85	11.85	2.82
	K.LSLPNGKPVSVLLANK.C [111, 12	RAB38 peptide ratio, 3	8.22	8.06	16.69	9.81	4.03
	K.ENINIDEASR.C [161, 170]	RAB38 peptide ratio, 4	ND	ND	ND	ND	ND
RAB25		RAB25 protein ratio				ND	#DIV/0!
	K.VVLIGESGVGK.T [14, 24]	RAB25 peptide ratio, 1	ND	ND	ND	ND	ND
	R.TTIGVEFSTR.T [42, 51]	RAB25 peptide ratio, 2	ND	ND	ND	ND	ND
	K.AQIWDTAGLER.Y [62, 72]	RAB25 peptide ratio, 3	ND	ND	ND	ND	ND
	R.EVPTEEAR.M [133, 140]	RAB25 peptide ratio, 4	ND	ND	ND	ND	ND
RAB8A		RAB8A protein ratio				0.98	#DIV/0!
	R.NIEEHASADVEK.M [104, 115]	RAB8A peptide ratio, 1	0.82	0.89	1.11	0.93	0.12
	K.LALDYGIK.F [138, 145]	RAB8A peptide ratio, 2	1.00	1.11	0.99	1.03	0.05
	K.LEGNSPQGSNQGVI.I [176, 189]	RAB8A peptide ratio, 3	0.88	0.95	1.17	0.99	0.12
ARL4A		ARL4A protein ratio				ND	#DIV/0!
	K.TVTFHFWDVGGQEK.L [67, 80]	ARL4A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ISENQGVPLIVANK.Q [120, 134]	ARL4A peptide ratio, 2	ND	ND	ND	ND	ND
	R.NLSLSLSEIEK.L [139, 148]	ARL4A peptide ratio, 3	ND	ND	ND	ND	ND
RAB6A		RAB6A protein ratio				1.06	#DIV/0!
	R.DSAAAVVVYDITNVNSFQQTTK.W	RAB6A peptide ratio, 1	0.99	1.03	1.60	1.15	0.28
	K.WIDDVRTER.G [106, 114] (missed 1	RAB6A peptide ratio, 2	ND	ND	ND	ND	ND
	R.TDLADKR.Q [127, 133] (missed 1)	RAB6A peptide ratio, 3	1.04	1.07	1.25	1.11	0.09
RAB2A		RAB2A protein ratio				0.77	#DIV/0!
	R.MITIDGK.Q [46, 52]	RAB2A peptide ratio, 1	0.77	0.83	0.76	0.78	0.03
	K.KEEGEAFAR.E [130, 138] (missed 1	RAB2A peptide ratio, 2	0.75	0.76	0.82	0.78	0.03
	K.TASNVEEAFINTAK.E [151, 164]	RAB2A peptide ratio, 3	0.77	0.72	0.79	0.76	0.03
	K.IQEGVFDINNEANGIK.I [170, 185]	RAB2A peptide ratio, 4	0.74	0.72	0.81	0.75	0.04
RAB3D		RAB3D protein ratio				0.69	#DIV/0!
	R.DAADQNFDYMFK.L [12, 23]	RAB3D peptide ratio, 1	0.96	0.99	0.61	0.81	0.17
	K.LLLIGNSSVGK.T [24, 34]	RAB3D peptide ratio, 2	0.76	0.61	0.57	0.64	0.08
	R.LADDLGFEFFFEASAK.E [152, 166]	RAB3D peptide ratio, 3	0.86	0.87	0.62	0.76	0.12
RAB36		RAB36 protein ratio				ND	#DIV/0!
	R.EHFHGQVSAACQR.R [100, 112]	RAB36 peptide ratio, 1	ND	ND	ND	ND	ND
	R.FEAGIPYSLQIWDTAGQEK.F [164,	RAB36 peptide ratio, 2	ND	ND	ND	ND	ND
	R.VAALAFEQSVLQDLER.Q [282, 297]	RAB36 peptide ratio, 3	ND	ND	ND	ND	ND
RAN		RAN protein ratio				1.04	#DIV/0!
	K.LVLVGDGGTGK.T [12, 22]	RAN peptide ratio, 1	1.01	1.11	0.95	1.02	0.07
	K.YVATLGVEVHPLVFHTNR.G [38, 55]	RAN peptide ratio, 2	0.87	1.09	1.24	1.04	0.15
	K.NVPNWHR.D [99, 105]	RAN peptide ratio, 3	1.02	1.06	0.99	1.02	0.03
RAB40C		RAB40C protein ratio				ND	#DIV/0!
	R.VFSLQDLCCR.A [188, 197]	RAB40C peptide ratio, 1	ND	ND	ND	ND	ND
	R.SYSLASGAGGGGSK.G [239, 252]	RAB40C peptide ratio, 2	ND	ND	ND	ND	ND
ARL11		ARL11 protein ratio				ND	#DIV/0!
	R.GCSALTGEGLPEALQSLWSLLK.S	ARL11 peptide ratio, 1	ND	ND	ND	ND	ND
RAB24		RAB24 protein ratio				1.07	#DIV/0!
	R.SLEEGCQIYLCGTK.S [107, 120]	RAB24 peptide ratio, 1	0.53	2.14	0.55	0.72	0.75
	R.VDFHVDVQDYADNIK.A [133, 146]	RAB24 peptide ratio, 2	1.11	2.35	0.99	1.29	0.62
	K.AQLFETSSK.T [147, 155]	RAB24 peptide ratio, 3	0.96	0.91	0.85	0.90	0.05
	K.TGQSVDELQK.V [156, 166]	RAB24 peptide ratio, 4	1.08	1.17	0.84	1.01	0.14

RAB7B		RAB7B protein ratio				3.07	#DIV/0!
	K.IIILGDTTLK.L [48, 57]	RAB7B peptide ratio, 1	4.10	7.54	2.40	3.78	2.14
	K.LQIWDGTGGQER.F [58, 68]	RAB7B peptide ratio, 2	3.97	7.01	1.75	3.11	2.15
	R.YQSILENHLTESIK.L [174, 187]	RAB7B peptide ratio, 3	3.46	1.47	5.02	2.56	1.45
ARL8A		ARL8A protein ratio				0.65	#DIV/0!
	K.LWDIGGQPR.F [68, 76]	ARL8A peptide ratio, 1	ND	ND	ND	ND	ND
	R.GVSAIVYMVDAADQEK.I [87, 102]	ARL8A peptide ratio, 2	0.72	0.67	0.59	0.66	0.06
	R.DLPGALDEKELIEK.M [132, 145] (m	ARL8A peptide ratio, 3	0.73	0.49	0.98	0.68	0.20
RAB39B		RAB39B protein ratio				5.60	#DIV/0!
	R.SFQNVHEWLEETK.V [95, 107]	RAB39B peptide ratio, 1	7.66	3.28	1.06	2.18	2.74
	K.CDLDTQR.Q [124, 130]	RAB39B peptide ratio, 2	ND	ND	ND	ND	ND
	K.LAAAYGMK.Y [140, 147]	RAB39B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YIETSAR.D [148, 154]	RAB39B peptide ratio, 4	1.67	2.27	7.15	2.55	2.45
	K.SGFVFNVVHSSEEVVK.S [190, 205]	RAB39B peptide ratio, 5	5.83	1.33	1.64	1.96	2.05
DIRAS2		DIRAS2 protein ratio				0.06	#DIV/0!
	R.VAVFGAGGVGK.S [9, 19]	DIRAS2 peptide ratio, 1	0.41	3.23	0.83	0.76	1.24
	K.SICTLQITDTTGS HQFPAMQR.L [52	DIRAS2 peptide ratio, 2	1.41	0.87	0.58	0.84	0.35
RAB2B		RAB2B protein ratio				0.92	#DIV/0!
	R.ETFNHLTSWLEDAR.Q [26, 39]	RAB2B peptide ratio, 1	0.79	0.84	1.09	0.89	0.13
	K.REEGEAFAR.E [65, 73] (missed 1)	RAB2B peptide ratio, 2	2.39	0.70	4.25	1.44	1.45
	K.TACNVVEAFINTAK.E [86, 99]	RAB2B peptide ratio, 3	0.70	0.69	1.28	0.82	0.28
RAB37		RAB37 protein ratio				ND	#DIV/0!
	R.SPPCSPSYDLTGK.V [18, 30]	RAB37 peptide ratio, 1	ND	ND	ND	ND	ND
	K.VMLLGDTGVGK.T [31, 41]	RAB37 peptide ratio, 2	ND	ND	ND	ND	ND
	K.TCFLIQFK.D [42, 49]	RAB37 peptide ratio, 3	ND	ND	ND	ND	ND
	R.AGHQADEPSFQIR.D [194, 206]	RAB37 peptide ratio, 4	ND	ND	ND	ND	ND
ARL5B		ARL5B protein ratio				1.04	#DIV/0!
	K.LWSLFCNQEHK.V [7, 17]	ARL5B peptide ratio, 1	4.84	2.70	0.24	0.63	1.88
	K.NTHFLMWDIGGQESLR.S [58, 73]	ARL5B peptide ratio, 2	2.08	1.34	0.67	1.11	0.58
	K.AAVLIFANK.Q [117, 125]	ARL5B peptide ratio, 3	3.99	2.21	0.77	1.49	1.32
	K.GCMTAAEISK.Y [130, 139]	ARL5B peptide ratio, 4	2.15	1.19	0.95	1.27	0.52
RAB2B		RAB2B protein ratio				0.86	#DIV/0!
	R.MVNIDGK.Q [46, 52]	RAB2B peptide ratio, 1	0.84	0.82	0.84	0.84	0.01
	K.IQQGLFDVHNEANGIK.I [170, 185]	RAB2B peptide ratio, 2	0.85	1.04	0.80	0.88	0.10
	K.IGPQQSISTSVGSPASQR.N [186, 2	RAB2B peptide ratio, 3	0.61	0.72	1.18	0.77	0.25
RABL3		RABL3 protein ratio				0.82	#DIV/0!
	R.WSLEALNR.D [108, 115]	RABL3 peptide ratio, 1	0.84	0.82	0.84	0.84	0.01
	R.YLAAGSSNAVK.L [184, 194]	RABL3 peptide ratio, 2	0.85	1.04	0.80	0.88	0.10
	R.EGNQIPGFDR.K [211, 221]	RABL3 peptide ratio, 3	0.61	0.72	1.18	0.77	0.25
RRAGA		RRAGA protein ratio				1.27	#DIV/0!
	R.LGATIDVEHSHVR.F [38, 50]	RRAGA peptide ratio, 1	1.93	8.05	0.79	1.58	3.18
	R.NFAQIIEADEVLLFER.A [192, 207]	RRAGA peptide ratio, 2	1.36	1.35	0.94	1.18	0.19
RABL6		RABL6 protein ratio					#DIV/0!
	K.LVGSDQAPGR.D [7, 16]	RABL6 peptide ratio, 1	1.92	0.73	0.33	0.61	0.68
	K.NIPAGLQSMNQALQR.R [19, 33]	RABL6 peptide ratio, 2	2.43	1.56	1.20	1.59	0.52
	K.FFNIPFLQLQR.E [226, 236]	RABL6 peptide ratio, 3	1.69	0.56	2.34	1.07	0.74
RAB4B		RAB4B protein ratio				0.73	#DIV/0!
	K.FLVIGSAGTGK.S [45, 55]	RAB4B peptide ratio, 1	0.66	0.71	0.77	0.71	0.04
	K.SCLLHQFIENK.F [56, 66]	RAB4B peptide ratio, 2	3.22	20.45	0.35	0.92	8.88
	K.IDSGELDPER.M [207, 216]	RAB4B peptide ratio, 3	ND	ND	ND	ND	ND
	R.MGSGIQYGDASLR.Q [217, 229]	RAB4B peptide ratio, 4	0.58	0.61	0.86	0.66	0.12
ARF1		ARF1 protein ratio				1.01	#DIV/0!
	K.NISFTVWDVGGQDK.I [59, 72]	ARF1 peptide ratio, 1	1.09	1.14	1.02	1.08	0.05
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 2	0.76	0.82	1.34	0.92	0.26
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 3	0.85	1.12	1.31	1.06	0.19
ARF3		ARF3 protein ratio				1.05	#DIV/0!
	R.VNEAREELMR.M [99, 108] (missed	ARF3 peptide ratio, 1	0.66	0.90	1.27	0.88	0.25
	R.VNEAREELMR.M [99, 108] (missed	ARF3 peptide ratio, 2	ND	ND	ND	ND	ND
	K.LGLHSLR.H [142, 148]	ARF3 peptide ratio, 3	1.05	1.08	1.00	1.04	0.03
ARF4		ARF4 protein ratio				1.05	#DIV/0!
	K.NICFTVWDVGGQDR.I [59, 72]	ARF4 peptide ratio, 1	0.93	0.99	1.21	1.03	0.12
	R.IQEVADELQK.M [99, 108]	ARF4 peptide ratio, 2	0.97	1.03	1.24	1.07	0.11
	R.DAVLLL FANK.Q [117, 126]	ARF4 peptide ratio, 3	0.99	1.04	1.19	1.07	0.08
	K.LGLQSLR.N [142, 148]	ARF4 peptide ratio, 4	0.97	1.05	1.15	1.05	0.07
ARF5		ARF5 protein ratio				1.13	#DIV/0!
	K.NICFTVWDVGGQDK.I [59, 72]	ARF5 peptide ratio, 1	1.13	1.17	1.10	1.13	0.03
	R.VQESADELQK.M [99, 108]	ARF5 peptide ratio, 2	1.80	1.17	0.58	0.96	0.49
	K.LGLQHLSR.S [142, 148]	ARF5 peptide ratio, 3	1.22	1.17	0.91	1.08	0.13
ARF6		ARF6 protein ratio				0.90	#DIV/0!
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 1	ND	ND	ND	ND	ND
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 2	ND	ND	ND	ND	ND
	K.LGQSVTTIPTVGFNVETVTK.N [34	ARF6 peptide ratio, 3	0.85	0.81	1.12	0.90	0.14
	K.FNVWDVGGQDK.I [58, 68]	ARF6 peptide ratio, 4	0.82	0.91	1.10	0.93	0.12
RALA		RALA protein ratio				1.05	#DIV/0!

	K.GQNSLALHK.V [7, 15]	RALA peptide ratio, 1	1.09	1.22	0.88	1.05	0.14
	K.EDENVPFLLVGNK.S [115, 127]	RALA peptide ratio, 2	ND	ND	ND	ND	ND
	R.QVSVEEAQN [135, 142]	RALA peptide ratio, 3	1.00	1.05	1.01	1.02	0.02
	R.AEQWNVNYVETSAK.T [145, 158]	RALA peptide ratio, 4	0.89	0.99	1.06	0.98	0.07
RHOT1		RHOT1 protein ratio				ND	#DIV/0!
	R.LPLILVGNK.S [110, 118]	RHOT1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.AVLHPTGPLYCPEEK.E [164, 178]	RHOT1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.ICFNTPLAPQALEDVK.N [214, 229]	RHOT1 peptide ratio, 3	ND	ND	ND	ND	ND
ARL1		ARL1 protein ratio				1.17	#DIV/0!
	R.ILILGLDGAGK.T [19, 29]	ARL1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.FQVWDLGGQTSIRPYWR.C [62, 78]	ARL1 peptide ratio, 2	0.69	0.63	1.23	0.78	0.27
	K.AILVVFANK.Q [118, 126]	ARL1 peptide ratio, 3	1.32	1.14	1.25	1.23	0.07
RAC1		RAC1 protein ratio				ND	#DIV/0!
	R.LRPLSYPQTVGETYGK.D [66, 81]	RAC1 peptide ratio, 1	ND	ND	ND	ND	ND
RABL2B		RABL2B protein ratio				0.84	#DIV/0!
	K.IDADINVTQK.S [134, 143]	RABL2B peptide ratio, 1	0.77	0.97	0.80	0.84	0.09
ARL16		ARL16 protein ratio				ND	#DIV/0!
	K.GDLGEPPTTRPTVGTNLTDIVAQR.R [166, 176]	ARL16 peptide ratio, 1	ND	ND	ND	ND	ND
	K.QNITAEISAR.E [166, 176]	ARL16 peptide ratio, 2	ND	ND	ND	ND	ND
	R.EGTGLAGVLAWLQATHR.A [177, 193]	ARL16 peptide ratio, 3	ND	ND	ND	ND	ND
REM1		REM1 protein ratio				ND	#DIV/0!
	R.LSTVPSTQSQHPR.L [32, 44]	REM1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.TSLASLFAGK.Q [93, 102]	REM1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.DLHEQLGEDVYER.T [106, 118]	REM1 peptide ratio, 3	ND	ND	ND	ND	ND
	R.GSFESASELR.I [166, 175]	REM1 peptide ratio, 4	ND	ND	ND	ND	ND
RAB14		RAB14 protein ratio				0.55	#DIV/0!
	K.YIIIGDMGVGK.S [13, 23]	RAB14 peptide ratio, 1	0.57	0.61	0.50	0.56	0.05
	R.STYNHLSSWLTAR.N [96, 109]	RAB14 peptide ratio, 2	0.54	0.58	0.52	0.54	0.02
	K.TGENVEDAFLEAAK.K [156, 169]	RAB14 peptide ratio, 3	0.48	0.49	0.59	0.52	0.05
SRPRB		SRPRB protein ratio				1.51	#DIV/0!
	R.AVLLVGLCDSGK.T [65, 76]	SRPRB peptide ratio, 1	0.97	1.07	1.69	1.17	0.32
	R.DTQTSITDSCAVYR.V [90, 103]	SRPRB peptide ratio, 2	1.16	1.40	1.73	1.40	0.23
	K.LIQQQLEK.E [191, 198]	SRPRB peptide ratio, 3	1.38	1.54	1.69	1.53	0.13
RAB35		RAB35 protein ratio				1.13	#DIV/0!
	R.TITSTYYR.G [71, 78]	RAB35 peptide ratio, 1	1.01	1.20	1.21	1.13	0.09
	R.WLHEINQNCDDVCR.I [101, 114]	RAB35 peptide ratio, 2	0.74	0.81	1.65	0.94	0.41
	K.VVETEDAYK.F [128, 136]	RAB35 peptide ratio, 3	1.01	1.20	1.21	1.13	0.09
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 4	1.00	1.33	1.57	1.26	0.23
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 5	ND	ND	ND	ND	ND
RAB3B		RAB3B protein ratio				ND	#DIV/0!
	K.DASDQNFDFYMFK.L [12, 23]	RAB3B peptide ratio, 1	ND	ND	ND	ND	ND
	K.GQLLAEQLGFDFFEASAK.E [149, 164]	RAB3B peptide ratio, 2	ND	ND	ND	ND	ND
	K.MSDSLDTPSMLGSSK.N [186, 201]	RAB3B peptide ratio, 3	ND	ND	ND	ND	ND
RAB30		RAB30 protein ratio				2.96	#DIV/0!
	K.IVLIGNAGVGK.T [11, 21]	RAB30 peptide ratio, 1	2.53	1.50	5.17	2.39	1.55
	R.EIEQYASNK.V [105, 113]	RAB30 peptide ratio, 2	2.91	1.92	5.80	2.89	1.64
	K.VITVLVGNK.I [114, 122]	RAB30 peptide ratio, 3	1.18	1.37	2.46	1.51	0.56
	K.LFLDLACR.L [161, 168]	RAB30 peptide ratio, 4	6.05	5.59	1.19	2.54	2.19
	R.QNTLVNNSVSSPLPGEK.S [175, 190]	RAB30 peptide ratio, 5	2.10	2.23	4.81	2.65	1.25
RHOF		RHOF protein ratio				ND	#DIV/0!
	K.IVIVGDGGCGK.T [21, 31]	RHOF peptide ratio, 1	ND	ND	ND	ND	ND
	K.YTASVTVGSK.E [55, 64]	RHOF peptide ratio, 2	ND	ND	ND	ND	ND
	K.EVTLNLYDTAGQEDYDR.L [65, 81]	RHOF peptide ratio, 3	ND	ND	ND	ND	ND
	K.WFPEVTHFCR.G [112, 121]	RHOF peptide ratio, 4	ND	ND	ND	ND	ND
	R.AALYLECSAK.F [166, 175]	RHOF peptide ratio, 5	ND	ND	ND	ND	ND
RAB34		RAB34 protein ratio				1.71	#DIV/0!
	K.VIVVGDLVSVGK.T [54, 64]	RAB34 peptide ratio, 1	2.62	1.44	1.48	1.71	0.55
	R.FEVLGIPFSLQLWDTAGQER.F [93, 103]	RAB34 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ENDPSSVLLFLVGSK.K [152, 166]	RAB34 peptide ratio, 3	1.61	1.23	1.89	1.53	0.27
	K.AEYWAVSSLTGENVR.E [191, 205]	RAB34 peptide ratio, 4	1.71	1.69	1.78	1.72	0.04
	R.INSDDSNLYLTASK.K [238, 251]	RAB34 peptide ratio, 5	ND	ND	ND	ND	ND
RAB43		RAB43 protein ratio				0.62	#DIV/0!
	K.YAGSNIVQLLIGNK.S [118, 131]	RAB43 peptide ratio, 1	0.65	0.63	0.58	0.62	0.03
	K.DSSNVEEAFLR.V [164, 174]	RAB43 peptide ratio, 2	0.50	0.67	0.92	0.66	0.17
	R.VATELIMR.H [175, 182]	RAB43 peptide ratio, 3	ND	ND	ND	ND	ND
	K.SPDIQLNSK.D [192, 201]	RAB43 peptide ratio, 4	0.46	0.64	2.04	0.71	0.71
NKIRAS1		NKIRAS1 protein ratio				1.87	#DIV/0!
	K.VVVCGLLSVGK.T [6, 16]	NKIRAS1 peptide ratio, 1	0.98	1.22	0.97	1.04	0.12
	R.QVDAEVAQQWAK.S [128, 139]	NKIRAS1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.TLIEPFTLLASK.L [155, 166]	NKIRAS1 peptide ratio, 3	1.67	2.02	1.74	1.80	0.15
RAB12		RAB12 protein ratio				0.54	#DIV/0!
	R.AGGGGGLGAGSPALSGGQGR.R [155, 166]	RAB12 peptide ratio, 1	0.48	0.53	0.58	0.53	0.04
	K.LQVIIIIGSR.G [42, 50]	RAB12 peptide ratio, 2	0.77	0.87	0.38	0.59	0.21
	R.FTDDTFCEACK.S [61, 71]	RAB12 peptide ratio, 3	0.50	0.58	0.45	0.50	0.06

	K.AGLLIFANK.Q [80, 88]	ARL5A peptide ratio, 3	ND	ND	ND	ND	ND
SAR1B		SAR1B protein ratio				1.06	#DIV/0!
	K.IDRPEAISEER.L [135, 145]	SAR1B peptide ratio, 1	0.83	0.70	1.45	0.90	0.33
	R.EMFGLYGQTTGK.G [148, 159]	SAR1B peptide ratio, 2	1.21	0.83	0.51	0.75	0.28
	K.ELNARPLEVFMCSVLK.R [166, 181]	SAR1B peptide ratio, 3	ND	ND	ND	ND	ND
RABL2A		RABL2A protein ratio				0.88	#DIV/0!
	K.TKPSELDQGK.Y [5, 14]	RABL2A peptide ratio, 1	ND	ND	ND	ND	ND
	K.IICLGDSAVGK.S [23, 33]	RABL2A peptide ratio, 2	0.75	0.65	1.53	0.85	0.39
	R.NLSTWYTELR.E [110, 119]	RABL2A peptide ratio, 3	0.82	0.64	1.74	0.89	0.48
	R.EFRPEIPCIVVANK.I [120, 133]	RABL2A peptide ratio, 4	10.79	20.16	0.32	0.91	8.11
DIRAS1		DIRAS1 protein ratio				ND	#DIV/0!
	R.VVVFAGGGVVGK.S [9, 19]	DIRAS1 peptide ratio, 1	ND	ND	ND	ND	ND
	R.DTYIPTIEDTYR.Q [33, 44]	DIRAS1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.GSVEDIPVMLVGNK.C [108, 121]	DIRAS1 peptide ratio, 3	ND	ND	ND	ND	ND
	R.EAQAVAQEWK.C [133, 142]	DIRAS1 peptide ratio, 4	ND	ND	ND	ND	ND
ARL2		ARL2 protein ratio				1.10	#DIV/0!
	R.ELQSLLEVEER.L [104, 113]	ARL2 peptide ratio, 1	0.65	0.65	2.50	0.86	0.87
	R.LAGATLLIFANK.Q [114, 125]	ARL2 peptide ratio, 2	0.95	0.94	1.50	1.08	0.26
	R.EVLELDSIR.S [139, 147]	ARL2 peptide ratio, 3	1.41	1.53	0.86	1.19	0.29
ARL3		ARL3 protein ratio				0.66	#DIV/0!
	R.ILLLGLDNAGK.T [19, 29]	ARL3 peptide ratio, 1	0.65	0.66	1.67	0.82	0.48
	K.QLASEDISHITPTQGFNIK.S [35, 53]	ARL3 peptide ratio, 2	0.64	0.92	0.95	0.81	0.14
	K.LSCVPVLIFANK.Q [115, 126]	ARL3 peptide ratio, 3	1.23	0.99	0.77	0.96	0.19
TRIM23		TRIM23 protein ratio				0.79	#DIV/0!
	R.DALLLIFANK.Q [504, 513]	TRIM23 peptide ratio, 1	0.78	0.71	0.89	0.79	0.07
RALB		RALB protein ratio				0.66	#DIV/0!
	K.GQSSLALHK.V [29, 37]	RALB peptide ratio, 1	0.97	4.50	0.99	1.32	1.66
	R.QVPVEEAR.S [158, 165]	RALB peptide ratio, 2	0.39	0.40	1.77	0.53	0.65
	K.AEEWGVQYVETSAK.T [168, 181]	RALB peptide ratio, 3	0.95	0.21	1.68	0.47	0.60
ARL15		ARL15 protein ratio				0.51	#DIV/0!
	K.LCSESPDNVSTTGFSIK.A [51, 68]	ARL15 peptide ratio, 1	0.29	0.82	1.29	0.55	0.41
	K.AVPFQNAILNVK.E [69, 80]	ARL15 peptide ratio, 2	0.49	0.30	0.52	0.41	0.10
	K.ELGGADNIR.K [81, 89]	ARL15 peptide ratio, 3	0.30	0.45	0.44	0.38	0.07
	K.YFELEPLAR.G [157, 165]	ARL15 peptide ratio, 4	0.38	0.32	0.89	0.44	0.25
	K.DSFSQLINLLEEK.D [184, 196]	ARL15 peptide ratio, 5	ND	ND	ND	ND	ND
RAB1A		RAB1A protein ratio				1.43	#DIV/0!
	R.GAHGIIVVYDVTQESFNNVK.Q [82, 91]	RAB1A peptide ratio, 1	1.64	2.80	0.83	1.38	0.81
	K.NATNVEQSFMTMAAEIK.K [156, 171]	RAB1A peptide ratio, 2	0.85	0.98	2.10	1.12	0.56
	R.MGPGATAGGAEK.S [175, 186]	RAB1A peptide ratio, 3	0.98	0.97	1.54	1.11	0.26
CDC42		CDC42 protein ratio				1.31	#DIV/0!
Isoform 1	K.TCLLISYTTNK.F [16, 26]	CDC42 peptide ratio, 1	0.78	0.76	1.15	0.87	0.18
Isoform 1	K.WVPEITHHCPK.T [96, 106]	CDC42 peptide ratio, 2	0.59	0.55	1.02	0.67	0.21
Isoform 1	K.TPFLLVGTQIDLR.D [107, 119]	CDC42 peptide ratio, 3	0.51	0.50	1.61	0.65	0.52
RAB21		RAB21 protein ratio				0.87	#DIV/0!
	K.VVLLGEGCVGK.T [21, 31]	RAB21 peptide ratio, 1	0.52	1.28	0.94	0.79	0.31
	R.VNLAIWDTAGQER.F [67, 79]	RAB21 peptide ratio, 2	0.35	0.38	1.25	0.48	0.42
	R.HVSIQEAESYAESVGAK.H [140, 155]	RAB21 peptide ratio, 3	3.18	0.35	0.48	0.57	1.30
RAB22A		RAB22A protein ratio				ND	#DIV/0!
	K.TVQYQNELHK.F [45, 54]	RAB22A peptide ratio, 1	ND	ND	ND	ND	ND
	K.EETFSTLK.N [89, 96]	RAB22A peptide ratio, 2	ND	ND	ND	ND	ND
	K.DYADSIHAIFVETSAK.N [134, 149]	RAB22A peptide ratio, 3	ND	ND	ND	ND	ND
	R.IPSTDANLPSGGK.G [165, 177]	RAB22A peptide ratio, 4	ND	ND	ND	ND	ND
RAB17		RAB17 protein ratio				1.73	#DIV/0!
	K.SILPTVGC ^{CA} FFTK.V [45, 57]	RAB17 peptide ratio, 1	1.69	0.83	0.26	0.53	0.59
	K.LEIWDTAGQEK.Y [68, 78]	RAB17 peptide ratio, 2	1.07	1.14	2.25	1.33	0.54
	K.YHSV ^{CH} LYFR.G [79, 88]	RAB17 peptide ratio, 3	0.57	2.07	0.48	0.69	0.73
	R.SDEEGQALR.G [183, 191]	RAB17 peptide ratio, 4	1.92	6.18	0.59	1.27	2.38
RAB23		RAB23 protein ratio				0.47	#DIV/0!
	K.TIGVDFLER.Q [40, 48]	RAB23 peptide ratio, 1	0.28	0.26	0.57	0.33	0.14
	R.QIQVND ^{ED} VR.L [49, 58]	RAB23 peptide ratio, 2	0.45	0.43	0.69	0.50	0.12
	K.EDLNVNEVF ^K .Y [153, 162]	RAB23 peptide ratio, 3	0.29	1.12	0.80	0.54	0.34
RAB1B		RAB1B protein ratio				0.78	#DIV/0!
	-.MNPEYDYLF ^K .L [0, 9]	RAB1B peptide ratio, 1	0.81	0.68	1.01	0.81	0.14
	K.NATNVEQAFMTMAAEIK.K [153, 168]	RAB1B peptide ratio, 2	0.48	0.57	1.72	0.68	0.57
	R.MGPGAASGG ^{ER} PNLK.I [172, 186]	RAB1B peptide ratio, 3	1.38	1.19	1.08	1.20	0.12
RABL2B		RABL2B protein ratio				1.16	#DIV/0!
	K.AHAC ^{IM} VFDVQR.K [93, 104]	RABL2B peptide ratio, 1	1.08	1.20	1.22	1.16	0.06
RAP2C		RAP2C protein ratio				0.45	#DIV/0!
	K.VPLILVGNK.V [108, 116]	RAP2C peptide ratio, 1	ND	ND	ND	ND	ND
	K.VDLEPER.E [117, 123]	RAP2C peptide ratio, 2	0.28	0.41	0.97	0.43	0.30
	R.EVMSSEGR.A [124, 131]	RAP2C peptide ratio, 3	0.90	0.96	0.51	0.73	0.20
	R.ALAQEWG ^{CP} PFMETS ^K .S [132, 147]	RAP2C peptide ratio, 4	0.72	13.99	1.36	1.37	6.11
	R.QMNYSSLPEK.Q [162, 171]	RAP2C peptide ratio, 5	4.10	0.67	0.08	0.22	1.77
RHO		RHO protein ratio				ND	#DIV/0!

	K.CVLVGDGAVGK.T [51, 61]	RHO peptide ratio, 1	ND	ND	ND	ND	ND
RABL5		RABL5 protein ratio				1.11	#DIV/0!
	K.ILFVGPCEESGK.T [5, 15]	RABL5 peptide ratio, 1	0.72	0.69	2.74	0.94	0.96
	R.ILEFENPHVTSNNK.G [39, 52]	RABL5 peptide ratio, 2	ND	ND	ND	ND	ND
	K.FESCWPALMK.D [69, 78]	RABL5 peptide ratio, 3	ND	ND	ND	ND	ND
	K.SIINSMSES.R.D [166, 175]	RABL5 peptide ratio, 4	2.73	1.19	0.47	0.90	0.95
RRAGD		RRAGD protein ratio				ND	#DIV/0!
	K.MSPNETLFLESTNK.I [85, 98]	RRAGD peptide ratio, 1	ND	ND	ND	ND	ND
	K.LNNTTVLYLK.E [320, 329]	RRAGD peptide ratio, 2	ND	ND	ND	ND	ND
ARL4C		ARL4C protein ratio				ND	#DIV/0!
	K.GISCHFWDVGGQEK.L [60, 73]	ARL4C peptide ratio, 1	ND	ND	ND	ND	ND
	K.FAENQGTPLLVIANK.Q [113, 127]	ARL4C peptide ratio, 2	ND	ND	ND	ND	ND
	K.LYEMILK.R [174, 180]	ARL4C peptide ratio, 3	ND	ND	ND	ND	ND
RAC2		RAC2 protein ratio				ND	#DIV/0!
	R.HHCPTPIILVGTK.L [102, 115]	RAC2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.LAPITYPQGLALAK.E [133, 146]	RAC2 peptide ratio, 2	ND	ND	ND	ND	ND
	R.AVLCPQPTR.Q [174, 182]	RAC2 peptide ratio, 3	ND	ND	ND	ND	ND
RAC1		RAC1 protein ratio				1.03	#DIV/0!
	R.HHCPTPIILVGTK.L [102, 115]	RAC1 peptide ratio, 1	0.81	0.83	2.04	1.02	0.57
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 2	0.60	0.58	1.92	0.77	0.63
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 3	0.64	0.57	2.17	0.79	0.74
RRAGB		RRAGB protein ratio				0.95	#DIV/0!
	R.SIIFANYIAR.D [57, 66]	RRAGB peptide ratio, 1	0.84	0.88	1.72	1.03	0.41
	R.NFAEIIEADEVLLFER.A [253, 268]	RRAGB peptide ratio, 2	0.87	0.85	0.81	0.84	0.02
	K.LAASFQSMEV.R.N [305, 315]	RRAGB peptide ratio, 3	0.71	0.62	2.04	0.85	0.65
RAB27B		RAB27B protein ratio				ND	#DIV/0!
	K.LLALGDSGVGK.T [11, 21]	RAB27B peptide ratio, 1	ND	ND	ND	ND	ND
	R.VVYNAQGPNGSSGK.A [50, 63]	RAB27B peptide ratio, 2	ND	ND	ND	ND	ND
	K.VHLQLWDTAGQER.F [67, 79]	RAB27B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YGIPYFETSAAATGQNVK.A [154, 168]	RAB27B peptide ratio, 4	ND	ND	ND	ND	ND
RHOD		RHOD protein ratio				ND	#DIV/0!
	K.GKPVHLHIWDTAGQDDYDR.L [61, 75]	RHOD peptide ratio, 1	ND	ND	ND	ND	ND
	R.WYPEVNHFCCK.K [110, 119]	RHOD peptide ratio, 2	ND	ND	ND	ND	ND
	R.SVGAVAYLECSAR.L [161, 173]	RHOD peptide ratio, 3	ND	ND	ND	ND	ND
RHOQ		RHOQ protein ratio				ND	#DIV/0!
	K.EEWVPELK.E [100, 107]	RHOQ peptide ratio, 1	ND	ND	ND	ND	ND
	K.EIGACCYVECSALTQK.G [153, 168]	RHOQ peptide ratio, 2	ND	ND	ND	ND	ND
	K.TVFDEAIIAILTPK.K [172, 185]	RHOQ peptide ratio, 3	ND	ND	ND	ND	ND
RRAS2		RRAS2 protein ratio				0.40	#DIV/0!
	R.LVVVGGGGVGVK.S [16, 26]	RRAS2 peptide ratio, 1	0.71	0.76	0.21	0.40	0.25
	R.LDILDTAGQEEFGAMR.E [69, 84]	RRAS2 peptide ratio, 2	0.11	0.11	0.64	0.15	0.25
	R.TGEGFLLVFSVTD.R.G [90, 103]	RRAS2 peptide ratio, 3	ND	ND	ND	ND	ND
	R.QVTQEEGQQLAR.Q [141, 152]	RRAS2 peptide ratio, 4	0.16	0.17	0.98	0.23	0.38
RAB31		RAB31 protein ratio				0.48	#DIV/0!
	R.FHSLAPMYR.G [67, 76]	RAB31 peptide ratio, 1	0.37	0.42	1.08	0.50	0.32
	R.GSAAAVIVYDITK.Q [77, 89]	RAB31 peptide ratio, 2	0.30	0.34	0.40	0.34	0.04
	K.QDSFYTLK.K [90, 97]	RAB31 peptide ratio, 3	0.63	0.69	0.62	0.65	0.03
RAB32		RAB32 protein ratio				3.60	#DIV/0!
	K.VLVIGELGVGK.T [27, 37]	RAB32 peptide ratio, 1	2.13	1.99	3.54	2.39	0.70
	R.SSTFEAVLK.W [110, 118]	RAB32 peptide ratio, 2	1.94	1.95	3.69	2.31	0.82
	K.DNINIEEAAR.F [176, 185]	RAB32 peptide ratio, 3	2.06	2.13	4.01	2.49	0.90
RAB18		RAB18 protein ratio				1.39	#DIV/0!
	K.ILIIGESGVGK.S [10, 20]	RAB18 peptide ratio, 1	0.81	0.78	1.49	0.94	0.33
	K.LAIWDTAGQER.F [58, 68]	RAB18 peptide ratio, 2	0.55	0.49	1.69	0.67	0.55
	R.TLTPSYR.G [71, 78]	RAB18 peptide ratio, 3	0.81	0.79	1.29	0.91	0.23
	R.NDIVNMLVGNK.I [112, 122]	RAB18 peptide ratio, 4	0.83	0.81	1.50	0.97	0.32
RAB9B		RAB9B protein ratio				3.34	#DIV/0!
	K.VILLGDGGVGVK.S [9, 19]	RAB9B peptide ratio, 1	2.00	1.96	3.12	2.25	0.54
	R.QSFENLGNWQK.E [92, 102]	RAB9B peptide ratio, 2	1.55	1.17	3.54	1.68	1.04
	K.EFIYADV.K.D [103, 111]	RAB9B peptide ratio, 3	1.44	1.57	2.45	1.72	0.45
RAP1B		RAP1B protein ratio				0.48	#DIV/0!
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 1	0.39	0.29	1.17	0.44	0.39
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 2	0.40	0.36	0.70	0.45	0.15
	R.QWNNCAFLESSAK.S [136, 148]	RAP1B peptide ratio, 3	0.28	0.29	0.80	0.36	0.24
ARFRP1		ARFRP1 protein ratio				0.79	#DIV/0!
	K.TTFLEQSK.T [30, 37]	ARFRP1 peptide ratio, 1	0.58	0.78	1.34	0.80	0.32
	K.ITTTVGLNIGTVDVGK.A [52, 67]	ARFRP1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.QDVETCLSIDIK.T [135, 147]	ARFRP1 peptide ratio, 3	ND	ND	ND	ND	ND
	K.TAFSDCTSK.I [148, 156]	ARFRP1 peptide ratio, 4	0.75	2.04	1.09	1.09	0.55
	R.DCLTQACQSALTGK.G [161, 173]	ARFRP1 peptide ratio, 5	0.55	0.65	2.01	0.78	0.66
RAB20		RAB20 protein ratio				ND	#DIV/0!
	K.IVLLGDMNVGK.T [7, 17]	RAB20 peptide ratio, 1	ND	ND	ND	ND	ND
	R.GAAAILTYDVNHR.Q [71, 84]	RAB20 peptide ratio, 2	ND	ND	ND	ND	ND
	R.FLGLTDTASK.D [94, 103]	RAB20 peptide ratio, 3	ND	ND	ND	ND	ND

	K.QVQLEDAVALYK.K [147, 158]	RAB20 peptide ratio, 4	ND	ND	ND	ND	ND
SAR1A		SAR1A protein ratio				0.85	#DIV/0!
	K.NYLPAINGIVFLVDCADHSR.L [87, 1	SAR1A peptide ratio, 1	0.86	1.01	0.98	0.95	0.06
	R.TDAISEEK.L [138, 145]	SAR1A peptide ratio, 2	ND	ND	ND	ND	ND
	R.EIFGLYGQTTGK.G [148, 159]	SAR1A peptide ratio, 3	ND	ND	ND	ND	ND
RAB5C		RAB5C protein ratio				1.52	#DIV/0!
	R.QASPNIVIALAGNK.A [121, 134]	RAB5C peptide ratio, 1	0.91	0.87	2.14	1.10	0.59
	K.NEPQNATGAPGR.N [184, 195]	RAB5C peptide ratio, 2	1.17	0.68	2.32	1.09	0.68
	R.GVDLQENNPASR.S [198, 209]	RAB5C peptide ratio, 3	0.75	0.71	2.62	0.96	0.89
RAB7A		RAB7A protein ratio				3.46	#DIV/0!
	R.FQSLGVAFYR.G [69, 78]	RAB7A peptide ratio, 1	2.07	2.08	4.04	2.48	0.92
	R.DEFLIQASPR.D [103, 112]	RAB7A peptide ratio, 2	2.06	1.99	3.76	2.39	0.82
	R.AQAWCYSK.N [138, 145]	RAB7A peptide ratio, 3	1.89	1.92	4.28	2.34	1.12
	K.NNIPYFETSARK.E [146, 156]	RAB7A peptide ratio, 4	1.28	1.20	5.54	1.67	2.03
RAB9A		RAB9A protein ratio				1.72	#DIV/0!
	R.QVSTEEAQAWCR.D [131, 142]	RAB9A peptide ratio, 1	1.02	1.00	4.82	1.37	1.79
	K.DATNVAAAFEEAVR.R [156, 169]	RAB9A peptide ratio, 2	1.07	0.94	3.75	1.32	1.30
	R.SDHLIQTDTVNLHR.K [178, 191]	RAB9A peptide ratio, 3	3.32	1.66	2.90	2.40	0.70
RAB13		RAB13 protein ratio				1.80	#DIV/0!
	K.LQVWDTAGQER.F [58, 68]	RAB13 peptide ratio, 1	ND	ND	ND	ND	ND
	K.SFENIQNWMK.S [94, 103]	RAB13 peptide ratio, 2	1.95	2.01	10.77	2.72	4.14
	K.ENASAGVER.L [107, 115]	RAB13 peptide ratio, 3	1.11	1.75	3.32	1.69	0.93
RAB28		RAB28 protein ratio				0.25	#DIV/0!
	K.IVVLGDGASGK.T [14, 24]	RAB28 peptide ratio, 1	0.27	0.96	4.62	0.60	1.91
	K.TSLTTCFAQETFGK.Q [25, 38]	RAB28 peptide ratio, 2	0.37	0.28	2.54	0.45	1.05
	K.VSEESQPLVALVGNK.I [113, 129]	RAB28 peptide ratio, 3	ND	ND	ND	ND	ND
	K.VAAEILGIK.L [172, 180]	RAB28 peptide ratio, 4	ND	ND	ND	ND	ND
	K.AEIEQSQR.V [184, 191]	RAB28 peptide ratio, 5	0.86	0.33	0.16	0.29	0.30
RAB27A		RAB27A protein ratio				8.49	#DIV/0!
	K.FLALGDSGVGK.T [11, 21]	RAB27A peptide ratio, 1	5.13	5.31	12.63	6.49	3.50
	K.TSVLYQYTDGK.F [22, 32]	RAB27A peptide ratio, 2	4.57	5.10	10.70	5.91	2.77
	R.IHLQLWDTAGQER.F [67, 79]	RAB27A peptide ratio, 3	ND	ND	ND	ND	ND
	K.SDLEDQR.V [134, 140]	RAB27A peptide ratio, 4	3.49	4.95	0.70	1.56	1.76
	K.SWIPEGVVR.S [191, 199]	RAB27A peptide ratio, 5	4.73	4.92	13.28	6.12	3.99
RAB10		RAB10 protein ratio				1.67	#DIV/0!
	K.TYDLLFK.L [4, 10]	RAB10 peptide ratio, 1	1.01	0.94	1.36	1.07	0.19
	R.FHTITTSYYR.G [70, 79]	RAB10 peptide ratio, 2	0.98	0.95	1.35	1.07	0.18
	R.NIDEHANEDVER.M [105, 116]	RAB10 peptide ratio, 3	1.19	0.51	1.59	0.87	0.45
RHEB		RHEB protein ratio				1.56	#DIV/0!
	K.IAILGYR.S [8, 14]	RHEB peptide ratio, 1	0.95	0.74	0.15	0.33	0.34
	K.VQIPIMLVGNK.K [109, 119]	RHEB peptide ratio, 2	0.94	1.10	2.73	1.28	0.81
	K.ALAESWNAAFLESSAK.E [135, 150]	RHEB peptide ratio, 3	0.75	0.72	2.22	0.95	0.70
	K.ENQTAVDVFR.R [151, 160]	RHEB peptide ratio, 4	0.80	0.81	2.10	1.02	0.61
CDC42		CDC42 protein ratio				0.93	#DIV/0!
Isoform 2	K.YVECSALTQK.G [153, 162]	CDC42 peptide ratio, 1	0.56	0.56	1.24	0.68	0.32
Isoform 2	K.NVFDEAILAALPEPEPK.K [166, 182]	CDC42 peptide ratio, 2	0.74	0.85	1.02	0.86	0.11
RAB6B		RAB6B protein ratio				1.45	#DIV/0!
	R.QITIEEGEQR.A [134, 143]	RAB6B peptide ratio, 1	ND	ND	ND	ND	ND
	K.ELSVMFIETSAK.T [146, 157]	RAB6B peptide ratio, 2	1.52	1.18	2.68	1.60	0.64
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 3	1.03	1.07	1.05	1.05	0.01
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 4	ND	ND	ND	ND	ND
RHOG		RHOG protein ratio				0.63	#DIV/0!
	R.TVNLNLWDTAGQEEYDR.L [49, 65]	RHOG peptide ratio, 1	0.37	0.41	1.30	0.51	0.43
	K.EQGQAPITPQQGQALAK.Q [130, 14	RHOG peptide ratio, 2	0.17	0.19	3.40	0.26	1.52
	R.YLECSALQQDGVK.E [153, 165]	RHOG peptide ratio, 3	0.40	0.31	1.37	0.47	0.48
RAB5B		RAB5B protein ratio				1.54	#DIV/0!
	R.QASPSIVIALAGNK.A [120, 133]	RAB5B peptide ratio, 1	0.78	0.69	1.79	0.91	0.50
	K.TAMNVNDLFLAIK.K [165, 178]	RAB5B peptide ratio, 2	0.91	0.88	1.69	1.06	0.38
	K.SEPQNLGGAAGR.S [183, 194]	RAB5B peptide ratio, 3	0.98	0.92	1.65	1.11	0.33
	R.GVDLHEQSQQNK.S [197, 208]	RAB5B peptide ratio, 4	ND	ND	ND	ND	ND
RAP2B		RAP2B protein ratio				1.43	#DIV/0!
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 1	ND	ND	ND	ND	ND
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 2	0.46	0.51	3.22	0.67	1.29
	K.VDLEGER.E [117, 123]	RAP2B peptide ratio, 3	ND	ND	ND	ND	ND
	K.ASVDELFAEIVR.Q [150, 161]	RAP2B peptide ratio, 4	0.77	0.78	3.25	1.04	1.16
ARL8B		ARL8B protein ratio				1.72	#DIV/0!
	R.DLPNALDEK.Q [184, 192]	ARL8B peptide ratio, 1	0.86	0.97	3.04	1.19	1.00
	K.MNLSAIQDR.E [198, 206]	ARL8B peptide ratio, 2	1.09	1.06	2.98	1.36	0.90
	R.EICCYSSICK.E [207, 216]	ARL8B peptide ratio, 3	1.44	1.39	2.62	1.67	0.57
RHOH		RHOH protein ratio				ND	#DIV/0!
	R.SNLPCTPVLVVATQTDQR.E [103, 1	RHOH peptide ratio, 1	ND	ND	ND	ND	ND
	R.ASCVNAMEGK.K [127, 136]	RHOH peptide ratio, 2	ND	ND	ND	ND	ND
	K.GYLECSALSNR.G [146, 156]	RHOH peptide ratio, 3	ND	ND	ND	ND	ND
	R.GVQQVFECAVR.T [157, 167]	RHOH peptide ratio, 4	ND	ND	ND	ND	ND

RAP1A		RAP1A protein ratio				1.59	#DIV/0!
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 1	0.76	0.35	1.66	0.63	0.55
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 2	2.25	2.66	2.21	2.36	0.20
	K.DTEDVPMILVGNK.C [104, 116]	RAP1A peptide ratio, 3	2.03	0.80	2.85	1.43	0.85
	R.QWCNCAFLESSAK.S [136, 148]	RAP1A peptide ratio, 4	0.95	1.00	2.69	1.24	0.81
RAP2A		RAP2A protein ratio				1.18	#DIV/0!
	K.VPVILVGNK.V [108, 116]	RAP2A peptide ratio, 1	5.21	5.20	0.20	0.56	2.36
	R.ALAEWGWCPFMETSAK.S [132, 147]	RAP2A peptide ratio, 2	1.25	3.45	3.46	2.17	1.04
	K.TMVDELFAEIVR.Q [150, 161]	RAP2A peptide ratio, 3	0.60	0.74	1.41	0.81	0.35
RRAS		RRAS protein ratio				0.20	#DIV/0!
	K.ICSVDGIPAR.L [68, 77]	RRAS peptide ratio, 1	0.12	0.12	0.43	0.16	0.14
	R.QSFNEVGK.L [113, 120]	RRAS peptide ratio, 2	0.14	0.17	1.60	0.22	0.68
	K.LFTQILR.V [121, 127]	RRAS peptide ratio, 3	0.49	8.21	0.11	0.26	3.73
	K.ADLESQR.Q [143, 149]	RRAS peptide ratio, 4	ND	ND	ND	ND	ND
RAB11B		RAB11B protein ratio				1.48	#DIV/0!
	K.AQIWDTAGQERY.Y [61, 71]	RAB11B peptide ratio, 1	0.69	0.66	2.71	0.90	0.96
	R.GAVGALLVYDIAKH.H [82, 94]	RAB11B peptide ratio, 2	1.05	1.01	1.96	1.22	0.44
	K.NILTEIYR.I [166, 173]	RAB11B peptide ratio, 3	0.88	0.85	1.64	1.03	0.36
NKIRAS2		NKIRAS2 protein ratio				0.99	#DIV/0!
	K.VVVCQGQASVKG.T [6, 16]	NKIRAS2 peptide ratio, 1	0.59	1.16	1.08	0.87	0.25
	K.EVTIVVLGNK.C [111, 120]	NKIRAS2 peptide ratio, 2	0.29	0.87	5.40	0.63	2.28
	R.VDPDVAQHWAK.S [129, 139]	NKIRAS2 peptide ratio, 3	3.86	0.47	1.18	0.92	1.46
	R.SLLEPFVYLASK.M [155, 166]	NKIRAS2 peptide ratio, 4	0.59	0.55	1.73	0.73	0.55
RAB33B		RAB33B protein ratio				3.55	#DIV/0!
	K.IIVIGDSNVGK.T [35, 45]	RAB33B peptide ratio, 1	2.32	1.73	1.72	1.88	0.28
	R.AVEIDGER.I [73, 80]	RAB33B peptide ratio, 2	0.37	1.35	1.38	0.71	0.47
	R.SAIQVPTDLAQK.F [153, 164]	RAB33B peptide ratio, 3	0.66	0.75	3.00	0.94	1.08
ARL6		ARL6 protein ratio				1.16	#DIV/0!
	R.NLWEHYK.E [77, 84]	ARL6 peptide ratio, 1	5.78	0.49	0.73	0.84	2.44
	K.EELDTLLNHPDIKH.H [106, 118]	ARL6 peptide ratio, 2	ND	ND	ND	ND	ND
	R.IPILFFANK.M [122, 130]	ARL6 peptide ratio, 3	0.69	0.64	2.44	0.88	0.84
	K.VSQLLCLENIK.D [142, 152]	ARL6 peptide ratio, 4	ND	ND	ND	ND	ND
RAC3		RAC3 protein ratio				1.27	#DIV/0!
	K.LAPITYPQGLAMARE.E [133, 146]	RAC3 peptide ratio, 1	1.46	0.82	1.64	1.19	0.35
	K.LAPITYPQGLAMARE.E [133, 146]	RAC3 peptide ratio, 2	1.41	1.41	1.34	1.39	0.03
	R.AVLCPPPVK.K [174, 182]	RAC3 peptide ratio, 3	0.76	0.75	1.66	0.92	0.43
RAB3A		RAB3A protein ratio				3.58	#DIV/0!
	K.ESSDQNFDMFK.I [12, 23]	RAB3A peptide ratio, 1	5.52	0.20	0.15	0.25	2.52
	K.TYSWDNAQVLLVGNK.C [121, 135]	RAB3A peptide ratio, 2	0.42	0.35	0.95	0.48	0.27
	R.LVDVICEK.M [178, 185]	RAB3A peptide ratio, 3	1.67	1.24	3.26	1.75	0.87
	K.MSESLDTADPAVTGAK.Q [186, 201]	RAB3A peptide ratio, 4	2.93	1.91	1.36	1.87	0.65
RAB5A		RAB5A protein ratio				1.30	#DIV/0!
	R.QASPNIVIALSGNKA.A [120, 133]	RAB5A peptide ratio, 1	1.23	0.86	1.96	1.21	0.45
	K.NEPQNPANSAR.G [183, 194]	RAB5A peptide ratio, 2	0.92	2.35	5.94	1.78	2.11
	R.GVDLTEPTQPTR.N [197, 208]	RAB5A peptide ratio, 3	0.78	0.77	3.00	1.03	1.05
RAB6C		RAB6C protein ratio				0.86	#DIV/0!
	R.QVSIEEGER.K [134, 142]	RAB6C peptide ratio, 1	0.89	0.88	0.82	0.86	0.03
	K.ELNVMFIETSAK.A [146, 157]	RAB6C peptide ratio, 2	ND	ND	ND	ND	ND
	R.VAAALPGMESTQDR.S [169, 182]	RAB6C peptide ratio, 3	ND	ND	ND	ND	ND
MRAS		MRAS protein ratio				ND	#DIV/0!
	K.IFVPDYDPTIEDSYLKH.H [36, 51]	MRAS peptide ratio, 1	ND	ND	ND	ND	ND
RAB8B		RAB8B protein ratio				1.15	#DIV/0!
	R.NIEEHASSDVER.M [104, 115]	RAB8B peptide ratio, 1	0.52	0.31	3.65	0.56	1.53
	K.SSANVEEAFFTLAR.D [153, 166]	RAB8B peptide ratio, 2	0.69	0.70	1.82	0.87	0.53
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 3	ND	ND	ND	ND	ND
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 4	ND	ND	ND	ND	ND
RAB7L1		RAB7L1 protein ratio				3.68	#DIV/0!
	K.VLQWSDYEIVR.L [47, 57]	RAB7L1 peptide ratio, 1	0.88	0.66	2.48	0.98	0.81
	K.CDLSPWAVSR.D [126, 135]	RAB7L1 peptide ratio, 2	2.10	2.53	3.95	2.67	0.79
	K.ENGFTGWTETSVK.E [144, 156]	RAB7L1 peptide ratio, 3	0.52	0.26	5.80	0.51	2.55
RHOC		RHOC protein ratio				1.09	#DIV/0!
	K.HFCPNVPIILVGNK.K [104, 117]	RHOC peptide ratio, 1	0.85	0.90	1.20	0.96	0.15
	K.HFCPNVPIILVGNKK.D [104, 118] (n	RHOC peptide ratio, 2	0.70	0.67	1.19	0.80	0.24
	R.ISAFGYLECSAK.T [150, 161]	RHOC peptide ratio, 3	0.66	0.64	1.09	0.75	0.21
RHOJ		RHOJ protein ratio				ND	#DIV/0!
	K.AIGAQCYLECSALTQKG.G [165, 180]	RHOJ peptide ratio, 1	ND	ND	ND	ND	ND
	K.AVFDEAILTIFHPK.K [184, 197]	RHOJ peptide ratio, 2	ND	ND	ND	ND	ND
RAB38		RAB38 protein ratio				50.38	#DIV/0!
	K.LLVIGDLGVGK.T [11, 21]	RAB38 peptide ratio, 1	31.25	23.42	51.24	31.84	11.71
	K.VLHWDPETVVR.L [49, 59]	RAB38 peptide ratio, 2	ND	ND	ND	ND	ND
	K.LSLPNGKPVSVLLANK.C [111, 127]	RAB38 peptide ratio, 3	12.66	9.46	9.18	10.22	1.58
	K.ENINIDEASR.C [161, 170]	RAB38 peptide ratio, 4	18.94	18.52	11.35	15.39	3.48
RAB25		RAB25 protein ratio				ND	#DIV/0!
	K.VVLIGESGVGK.T [14, 24]	RAB25 peptide ratio, 1	ND	ND	ND	ND	ND

	R.TTIGVEFSTR.T [42, 51]	RAB25 peptide ratio, 2	ND	ND	ND	ND	ND
	K.AQIWDTAGLER.Y [62, 72]	RAB25 peptide ratio, 3	ND	ND	ND	ND	ND
	R.EVPTEEAR.M [133, 140]	RAB25 peptide ratio, 4	ND	ND	ND	ND	ND
RAB8A		RAB8A protein ratio				1.29	#DIV/0!
	R.NIEEHASADVEK.M [104, 115]	RAB8A peptide ratio, 1	0.40	0.34	2.38	0.51	0.95
	K.LALDYGIK.F [138, 145]	RAB8A peptide ratio, 2	0.80	0.72	1.22	0.87	0.22
	K.LEGNPQGSNQGVI.I [176, 189]	RAB8A peptide ratio, 3	0.42	0.35	1.58	0.51	0.56
ARL4A		ARL4A protein ratio				ND	#DIV/0!
	K.TVTFHFWDVGGQEK.L [67, 80]	ARL4A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ISENQGVPLIVANK.Q [120, 134]	ARL4A peptide ratio, 2	ND	ND	ND	ND	ND
	R.NLSLSLSEIEK.L [139, 148]	ARL4A peptide ratio, 3	ND	ND	ND	ND	ND
RAB6A		RAB6A protein ratio				0.88	#DIV/0!
	R.DSAAAVVYDITNVNSFQQTTK.W	RAB6A peptide ratio, 1	0.57	0.45	2.09	0.67	0.75
	K.WIDDVTER.G [106, 114] (missed 1)	RAB6A peptide ratio, 2	ND	ND	ND	ND	ND
	R.TDLADKR.Q [127, 133] (missed 1)	RAB6A peptide ratio, 3	0.79	0.54	1.95	0.83	0.61
RAB2A		RAB2A protein ratio				1.75	#DIV/0!
	R.MITIDGK.Q [46, 52]	RAB2A peptide ratio, 1	1.05	1.05	1.11	1.07	0.03
	K.KEEGEAFAR.E [130, 138] (missed 1)	RAB2A peptide ratio, 2	0.64	0.62	2.10	0.82	0.70
	K.TASNVEEAFINTAK.E [151, 164]	RAB2A peptide ratio, 3	0.79	0.75	1.80	0.95	0.49
	K.IQEGVFDINNEANGIK.I [170, 185]	RAB2A peptide ratio, 4	0.63	0.72	1.97	0.86	0.61
RAB3D		RAB3D protein ratio				7.09	#DIV/0!
	R.DAADQNFDYMFK.L [12, 23]	RAB3D peptide ratio, 1	0.26	1.49	0.74	0.52	0.51
	K.LLLIGNSSVGK.T [24, 34]	RAB3D peptide ratio, 2	0.13	0.15	3.66	0.20	1.66
	R.LADDLGFEFFEASAK.E [152, 166]	RAB3D peptide ratio, 3	1.22	1.16	3.37	1.52	1.03
RAB36		RAB36 protein ratio				ND	#DIV/0!
	R.EHFHGQVSAACQR.R [100, 112]	RAB36 peptide ratio, 1	ND	ND	ND	ND	ND
	R.FEAGIPYSLQIWDTAGQEK.F [164, 177]	RAB36 peptide ratio, 2	ND	ND	ND	ND	ND
	R.VAALAFEQSVLQDLER.Q [282, 297]	RAB36 peptide ratio, 3	ND	ND	ND	ND	ND
RAN		RAN protein ratio				1.60	#DIV/0!
	K.LVLVGDGGTGK.T [12, 22]	RAN peptide ratio, 1	1.63	0.96	3.70	1.55	1.17
	K.YVATLGVEVHPLVFHTNR.G [38, 55]	RAN peptide ratio, 2	1.66	1.87	2.82	2.01	0.51
	K.NVPNWHR.D [99, 105]	RAN peptide ratio, 3	0.99	0.99	1.81	1.17	0.39
RAB40C		RAB40C protein ratio				ND	#DIV/0!
	R.VFSLQDLCCR.A [188, 197]	RAB40C peptide ratio, 1	ND	ND	ND	ND	ND
	R.SYSLASGAGGGGSK.G [239, 252]	RAB40C peptide ratio, 2	ND	ND	ND	ND	ND
ARL11		ARL11 protein ratio				ND	#DIV/0!
	R.GCSALTGEGLEALQSLWSLLK.S	ARL11 peptide ratio, 1	ND	ND	ND	ND	ND
RAB24		RAB24 protein ratio				1.28	#DIV/0!
	R.SLEEGCQIYLCGTK.S [107, 120]	RAB24 peptide ratio, 1	0.78	0.74	2.63	1.00	0.88
	R.VDFHDVQDYADNIK.A [133, 146]	RAB24 peptide ratio, 2	2.78	1.04	0.75	1.13	0.89
	K.AQLFETSSK.T [147, 155]	RAB24 peptide ratio, 3	0.74	0.83	2.28	1.00	0.70
	K.TGQSVDELQK.V [156, 166]	RAB24 peptide ratio, 4	0.81	0.69	1.79	0.92	0.49
RAB7B		RAB7B protein ratio				ND	#DIV/0!
	K.IIILGDTTLK.L [48, 57]	RAB7B peptide ratio, 1	ND	ND	ND	ND	ND
	K.LQIWDTGGQER.F [58, 68]	RAB7B peptide ratio, 2	ND	ND	ND	ND	ND
	R.YQSILENHLTESIK.L [174, 187]	RAB7B peptide ratio, 3	ND	ND	ND	ND	ND
ARL8A		ARL8A protein ratio				1.79	#DIV/0!
	K.LWDIGGQPR.F [68, 76]	ARL8A peptide ratio, 1	1.09	1.04	3.82	1.40	1.30
	R.GVSAIVYMVDAADQEK.I [87, 102]	ARL8A peptide ratio, 2	0.81	0.95	1.40	1.00	0.25
	R.DLPGALDEKELIEK.M [132, 145] (m	ARL8A peptide ratio, 3	5.38	6.20	2.48	4.00	1.60
RAB39B		RAB39B protein ratio				ND	#DIV/0!
	R.SFQNVHEWLEETK.V [95, 107]	RAB39B peptide ratio, 1	ND	ND	ND	ND	ND
	K.CDLDTQR.Q [124, 130]	RAB39B peptide ratio, 2	ND	ND	ND	ND	ND
	K.LAAAYGMK.Y [140, 147]	RAB39B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YIETSAR.D [148, 154]	RAB39B peptide ratio, 4	ND	ND	ND	ND	ND
	K.SGFVPPNVVHSSEEVK.S [190, 205]	RAB39B peptide ratio, 5	ND	ND	ND	ND	ND
DIRAS2		DIRAS2 protein ratio				ND	#DIV/0!
	R.VAVFGAGGVGK.S [9, 19]	DIRAS2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.SICTLQITDTTGSHPAMQR.L [52, 65]	DIRAS2 peptide ratio, 2	ND	ND	ND	ND	ND
RAB2B		RAB2B protein ratio				0.69	#DIV/0!
	R.ETFNHLTSWLEDAR.Q [26, 39]	RAB2B peptide ratio, 1	0.50	0.89	0.77	0.68	0.16
	K.REEGEAFAR.E [65, 73] (missed 1)	RAB2B peptide ratio, 2	0.70	0.49	0.42	0.51	0.12
	K.TACNVVEEAFINTAK.E [86, 99]	RAB2B peptide ratio, 3	0.42	0.39	2.47	0.56	0.97
RAB37		RAB37 protein ratio				ND	#DIV/0!
	R.SPPCSPSYDLTGK.V [18, 30]	RAB37 peptide ratio, 1	ND	ND	ND	ND	ND
	K.VMLLGDTGVGK.T [31, 41]	RAB37 peptide ratio, 2	ND	ND	ND	ND	ND
	K.TCFLIQFK.D [42, 49]	RAB37 peptide ratio, 3	ND	ND	ND	ND	ND
	R.AGHQADEPSFQIR.D [194, 206]	RAB37 peptide ratio, 4	ND	ND	ND	ND	ND
ARL5B		ARL5B protein ratio				ND	#DIV/0!
	K.LWSLFCNQEHK.V [7, 17]	ARL5B peptide ratio, 1	ND	ND	ND	ND	ND
	K.NTHFLMWDIGGQESLR.S [58, 73]	ARL5B peptide ratio, 2	ND	ND	ND	ND	ND
	K.AAVLIFANK.Q [117, 125]	ARL5B peptide ratio, 3	ND	ND	ND	ND	ND
	K.GCMTAAEISK.Y [130, 139]	ARL5B peptide ratio, 4	ND	ND	ND	ND	ND
RAB2B		RAB2B protein ratio				1.48	#DIV/0!

	R.MVNIDGK.Q [46, 52]	RAB2B peptide ratio, 1	1.48	1.16	2.23	1.51	0.45
	K.IQQGLFDVHNEANGIK.I [170, 185]	RAB2B peptide ratio, 2	1.75	1.08	1.74	1.45	0.31
	K.IGPQQSISTSVGPSASQR.N [186, 201]	RAB2B peptide ratio, 3	ND	ND	ND	ND	ND
RABL3		RABL3 protein ratio				1.16	#DIV/0!
	R.WSLEALNR.D [108, 115]	RABL3 peptide ratio, 1	0.70	0.75	1.32	0.85	0.28
	R.YLAAGSSNAVK.L [184, 194]	RABL3 peptide ratio, 2	0.71	0.68	1.22	0.81	0.25
	R.EGNQIPGFDR.K [211, 221]	RABL3 peptide ratio, 3	0.86	0.80	1.02	0.88	0.09
RRAGA		RRAGA protein ratio				1.15	#DIV/0!
	R.LGATIDVEHSHVR.F [38, 50]	RRAGA peptide ratio, 1	0.87	0.86	1.60	1.02	0.35
	R.NFAQIIEADEVLLFER.A [192, 207]	RRAGA peptide ratio, 2	0.70	0.68	2.51	0.91	0.85
RABL6		RABL6 protein ratio				0.87	#DIV/0!
	K.LVGSQAPGR.D [7, 16]	RABL6 peptide ratio, 1	1.05	1.90	3.06	1.66	0.83
	K.NIPAGLQSMNQALQR.R [19, 33]	RABL6 peptide ratio, 2	0.56	0.39	1.30	0.59	0.39
	K.FFNIPFLQLQR.E [226, 236]	RABL6 peptide ratio, 3	0.50	1.11	1.36	0.83	0.36
RAB4B		RAB4B protein ratio				1.02	#DIV/0!
	K.FLVIGSAGTGK.S [45, 55]	RAB4B peptide ratio, 1	0.58	0.64	1.31	0.74	0.33
	K.SCLLHQFIENK.F [56, 66]	RAB4B peptide ratio, 2	6.10	12.63	0.23	0.64	5.06
	K.IDSGELDPER.M [207, 216]	RAB4B peptide ratio, 3	0.88	0.82	1.08	0.92	0.11
	R.MGSGIQYGDAASLR.Q [217, 229]	RAB4B peptide ratio, 4	0.51	0.55	1.29	0.66	0.36
ARF1		ARF1 protein ratio				1.30	#DIV/0!
	K.NISFTVWDVGGQDK.I [59, 72]	ARF1 peptide ratio, 1	0.78	0.78	1.90	0.97	0.53
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 2	0.58	0.57	2.52	0.78	0.92
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 3	0.49	0.50	2.75	0.68	1.06
ARF3		ARF3 protein ratio				1.87	#DIV/0!
	R.VNEAREELMR.M [99, 108] (missed)	ARF3 peptide ratio, 1	1.94	1.87	3.30	2.21	0.66
	R.VNEAREELMR.M [99, 108] (missed)	ARF3 peptide ratio, 2	2.99	2.76	3.59	3.08	0.35
	K.LGLHSLR.H [142, 148]	ARF3 peptide ratio, 3	1.11	1.14	1.62	1.26	0.23
ARF4		ARF4 protein ratio				2.76	#DIV/0!
	K.NICFTVWDVGGQDR.I [59, 72]	ARF4 peptide ratio, 1	1.27	1.28	3.10	1.58	0.86
	R.IQEVADQLK.M [99, 108]	ARF4 peptide ratio, 2	1.89	0.94	3.58	1.60	1.09
	R.DAVLLLFANK.Q [117, 126]	ARF4 peptide ratio, 3	1.68	1.60	2.63	1.87	0.47
	K.LGLQSLR.N [142, 148]	ARF4 peptide ratio, 4	1.59	1.59	2.74	1.85	0.54
ARF5		ARF5 protein ratio				0.60	#DIV/0!
	K.NICFTVWDVGGQDK.I [59, 72]	ARF5 peptide ratio, 1	0.55	0.70	1.03	0.71	0.20
	R.VQESADELQK.M [99, 108]	ARF5 peptide ratio, 2	0.35	0.38	1.41	0.49	0.49
	K.LGLQHLR.S [142, 148]	ARF5 peptide ratio, 3	1.05	0.86	0.25	0.49	0.34
ARF6		ARF6 protein ratio				0.68	#DIV/0!
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 1	5.86	0.41	0.41	0.60	2.57
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 2	3.02	1.24	0.43	0.87	1.08
	K.LGQSVTTIPTVGFNVETVTK.N [34, 44]	ARF6 peptide ratio, 3	0.39	1.02	1.05	0.67	0.30
	K.FNVWDVGGQDK.I [58, 68]	ARF6 peptide ratio, 4	0.35	0.32	0.95	0.43	0.29
RALA		RALA protein ratio				1.10	#DIV/0!
	K.GQNSLALHK.V [7, 15]	RALA peptide ratio, 1	1.21	1.18	1.30	1.23	0.05
	K.EDENVPFLLVGNK.S [115, 127]	RALA peptide ratio, 2	ND	ND	ND	ND	ND
	R.QVSVEEAK.N [135, 142]	RALA peptide ratio, 3	0.76	0.83	1.37	0.92	0.27
	R.AEQWNVNYVETSAK.T [145, 158]	RALA peptide ratio, 4	0.65	0.67	2.04	0.85	0.65
RHOT1		RHOT1 protein ratio				ND	#DIV/0!
	R.LPLILVGNK.S [110, 118]	RHOT1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.AVLHPTGPLYCPEEK.E [164, 178]	RHOT1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.ICFNTPLAPQALEDVK.N [214, 229]	RHOT1 peptide ratio, 3	ND	ND	ND	ND	ND
ARL1		ARL1 protein ratio				2.65	#DIV/0!
	R.ILILGLDGAGK.T [19, 29]	ARL1 peptide ratio, 1	1.59	1.60	2.98	1.89	0.65
	K.FQVWDLGGQTSIRPYWR.C [62, 78]	ARL1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.AILVVFANK.Q [118, 126]	ARL1 peptide ratio, 3	2.03	1.84	2.56	2.10	0.31
RAC1		RAC1 protein ratio				1.14	#DIV/0!
	R.LRPLSYPQTVGETYGK.D [66, 81]	RAC1 peptide ratio, 1	1.11	1.08	0.59	0.85	0.24
RABL2B		RABL2B protein ratio				1.37	#DIV/0!
	K.IDADINVTQK.S [134, 143]	RABL2B peptide ratio, 1	0.96	0.78	1.06	0.92	0.11
ARL16		ARL16 protein ratio				ND	#DIV/0!
	K.GDLGEPPTRPVTGNTLTDIVAQR.R [166, 176]	ARL16 peptide ratio, 1	ND	ND	ND	ND	ND
	K.QNITTAEISAR.E [166, 176]	ARL16 peptide ratio, 2	ND	ND	ND	ND	ND
	R.EGTGLAGVLAWLQATHR.A [177, 192]	ARL16 peptide ratio, 3	ND	ND	ND	ND	ND
REM1		REM1 protein ratio				ND	#DIV/0!
	R.LSTVPSTQSQHPR.L [32, 44]	REM1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.TSLASLFAGK.Q [93, 102]	REM1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.DLHEQLGEDVYER.T [106, 118]	REM1 peptide ratio, 3	ND	ND	ND	ND	ND
	R.GSFESASELR.I [166, 175]	REM1 peptide ratio, 4	ND	ND	ND	ND	ND
RAB14		RAB14 protein ratio				0.68	#DIV/0!
	K.YIIIGDMGVGK.S [13, 23]	RAB14 peptide ratio, 1	0.77	0.73	1.27	0.87	0.24
	R.STYNHLSSWLTDAR.N [96, 109]	RAB14 peptide ratio, 2	0.77	0.62	1.44	0.83	0.36
	K.TGENVEDAFLEAAK.K [156, 169]	RAB14 peptide ratio, 3	0.42	0.38	2.18	0.55	0.84
SRPRB		SRPRB protein ratio				2.82	#DIV/0!
	R.AVLLVGLCDSGK.T [65, 76]	SRPRB peptide ratio, 1	1.53	1.34	2.55	1.67	0.53
	R.DTQTSITDSCAVYR.V [90, 103]	SRPRB peptide ratio, 2	1.20	1.07	3.46	1.46	1.10

	K.LIQQQLEK.E [191, 198]	SRPRB peptide ratio, 3	1.05	0.93	2.35	1.23	0.64
RAB35		RAB35 protein ratio				1.22	#DIV/0!
	R.TITSTYYR.G [71, 78]	RAB35 peptide ratio, 1	0.69	0.73	1.46	0.86	0.35
	R.WLHEINQNCDDVCR.I [101, 114]	RAB35 peptide ratio, 2	0.95	0.63	1.10	0.85	0.20
	K.VVETEDAYK.F [128, 136]	RAB35 peptide ratio, 3	0.68	0.55	1.27	0.74	0.31
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 4	ND	ND	ND	ND	ND
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 5	ND	ND	ND	ND	ND
RAB3B		RAB3B protein ratio				ND	#DIV/0!
	K.DASDQNFDFYMFK.L [12, 23]	RAB3B peptide ratio, 1	ND	ND	ND	ND	ND
	K.GQLLAELGDFDFEASAK.E [149, 161]	RAB3B peptide ratio, 2	ND	ND	ND	ND	ND
	K.MSDSLDTPSMLGSSK.N [186, 201]	RAB3B peptide ratio, 3	ND	ND	ND	ND	ND
RAB30		RAB30 protein ratio				0.77	#DIV/0!
	K.IVLIGNAGVVK.T [11, 21]	RAB30 peptide ratio, 1	1.25	0.86	1.07	1.03	0.16
	R.EIEQYASNK.V [105, 113]	RAB30 peptide ratio, 2	3.58	2.81	0.36	0.87	1.37
	K.VITVLVGNK.I [114, 122]	RAB30 peptide ratio, 3	1.13	0.47	1.14	0.77	0.31
	K.LFLDLACR.L [161, 168]	RAB30 peptide ratio, 4	ND	ND	ND	ND	ND
	R.QNTLVNNVSSPLPGEK.S [175, 199]	RAB30 peptide ratio, 5	ND	ND	ND	ND	ND
RHOF		RHOF protein ratio				ND	#DIV/0!
	K.IVIVGDGGCGK.T [21, 31]	RHOF peptide ratio, 1	ND	ND	ND	ND	ND
	K.YTASVTVGSK.E [55, 64]	RHOF peptide ratio, 2	ND	ND	ND	ND	ND
	K.EVTLNLYDTAGQEDYDR.L [65, 81]	RHOF peptide ratio, 3	ND	ND	ND	ND	ND
	K.WFPEVTHFCR.G [112, 121]	RHOF peptide ratio, 4	ND	ND	ND	ND	ND
	R.AALYLECSAK.F [166, 175]	RHOF peptide ratio, 5	ND	ND	ND	ND	ND
RAB34		RAB34 protein ratio				ND	#DIV/0!
	K.VIVVGDLSVVK.T [54, 64]	RAB34 peptide ratio, 1	ND	ND	ND	ND	ND
	R.FEVLGIPFSLQLWDTAGQER.F [93, 103]	RAB34 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ENDPSSVLLFLVGSK.K [152, 166]	RAB34 peptide ratio, 3	ND	ND	ND	ND	ND
	K.AEYWAVSSLTGENVR.E [191, 205]	RAB34 peptide ratio, 4	ND	ND	ND	ND	ND
	R.INSDDSNLYLTASK.K [238, 251]	RAB34 peptide ratio, 5	ND	ND	ND	ND	ND
RAB43		RAB43 protein ratio				2.44	#DIV/0!
	K.YAGSNIVQLLIGNK.S [118, 131]	RAB43 peptide ratio, 1	1.40	1.54	2.25	1.66	0.37
	K.DSSNVEEAFLR.V [164, 174]	RAB43 peptide ratio, 2	1.29	1.50	2.36	1.61	0.46
	R.VATELIMR.H [175, 182]	RAB43 peptide ratio, 3	1.45	1.34	1.11	1.29	0.14
	K.SPDIHLNSK.D [192, 201]	RAB43 peptide ratio, 4	1.98	1.21	2.74	1.77	0.62
NKIRAS1		NKIRAS1 protein ratio				1.62	#DIV/0!
	K.VVVCGLLSVVK.T [6, 16]	NKIRAS1 peptide ratio, 1	0.53	0.78	0.99	0.72	0.19
	R.QVDAEVAQQWAK.S [128, 139]	NKIRAS1 peptide ratio, 2	2.96	5.62	0.74	1.61	1.99
	K.TLIEPFTLLASK.L [155, 166]	NKIRAS1 peptide ratio, 3	0.97	0.72	2.10	1.03	0.60
RAB12		RAB12 protein ratio				0.92	#DIV/0!
	R.AGGGGGLGAGSPALSGGQGR.R [10, 20]	RAB12 peptide ratio, 1	0.71	0.55	1.18	0.74	0.27
	K.LQVIIIGSR.G [42, 50]	RAB12 peptide ratio, 2	0.97	0.67	1.10	0.87	0.18
	R.FTDDTFCEACK.S [61, 71]	RAB12 peptide ratio, 3	0.65	0.85	1.76	0.92	0.48
	R.FNSITSAYYR.S [103, 112]	RAB12 peptide ratio, 4	1.55	1.50	0.82	1.19	0.33
	K.FAQQITGMR.F [172, 180]	RAB12 peptide ratio, 5	ND	ND	ND	ND	ND
KRAS		KRAS(4A) protein ratio				ND	#DIV/0!
Isoform 2A	K.DSEDVPMVLVGNK.C [104, 116]	KRAS(4A) peptide ratio, 1	ND	ND	ND	ND	ND
Isoform 2A	R.QRVEDAFYTLVR.E [149, 160] (miss)	KRAS(4A) peptide ratio, 2	ND	ND	ND	ND	ND
Isoform 2A	R.VEDAFYTLVR.E [151, 160]	KRAS(4A) peptide ratio, 3	ND	ND	ND	ND	ND
KRAS		KRAS(4B) protein ratio				0.98	#DIV/0!
Isoform 2B	R.SYGIPFIETSAK.T [135, 146]	KRAS(4B) peptide ratio, 1	0.47	0.51	1.39	0.62	0.43
Isoform 2B	K.TRQGVDDAFYTLVR.E [147, 160] (n)	KRAS(4B) peptide ratio, 2	1.58	0.33	3.27	0.75	1.21
Isoform 2B	R.QGVDDAFYTLVR.E [149, 160]	KRAS(4B) peptide ratio, 3	0.61	0.55	1.18	0.70	0.29
RAB11A		RAB11A protein ratio				ND	#DIV/0!
	K.NGLSFIETSALDSTNVEAAFQILT	RAB11A peptide ratio, 1	ND	ND	ND	ND	ND
RHOT2		RHOT2 protein ratio				ND	#DIV/0!
	K.WIPLVNGGTTQGPR.V [96, 109]	RHOT2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.SAFLQAFLGR.G [429, 438]	RHOT2 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ADLPEGVAVSGPSPAEFCR.K [525, 535]	RHOT2 peptide ratio, 3	ND	ND	ND	ND	ND
RAB19		RAB19 protein ratio				ND	#DIV/0!
	R.AADENFDYLFK.I [76, 86]	RAB19 peptide ratio, 1	ND	ND	ND	ND	ND
	K.IILIGDSNVGK.T [87, 97]	RAB19 peptide ratio, 2	ND	ND	ND	ND	ND
	K.MQVWDTAGQER.F [135, 145]	RAB19 peptide ratio, 3	ND	ND	ND	ND	ND
	R.SAHAAIIAYDLTR.R [156, 168]	RAB19 peptide ratio, 4	ND	ND	ND	ND	ND
	R.HVLFEDACTLAEK.Y [205, 217]	RAB19 peptide ratio, 5	ND	ND	ND	ND	ND
RHOA		RHOA protein ratio				1.07	#DIV/0!
	K.QEPVKPEEGR.D [135, 144]	RHOA peptide ratio, 1	ND	ND	ND	ND	ND
	R.IGAFGYMECSAK.T [150, 161]	RHOA peptide ratio, 2	0.64	0.63	1.13	0.74	0.23
	R.IGAFGYMECSAK.T [150, 161]	RHOA peptide ratio, 3	0.58	0.67	1.07	0.73	0.21
RAB4A		RAB4A protein ratio				3.16	#DIV/0!
	K.FLVIGNAGTGK.S [15, 25]	RAB4A peptide ratio, 1	2.02	1.65	3.09	2.11	0.61
	K.IESGELDPER.M [177, 186]	RAB4A peptide ratio, 2	1.47	1.40	4.49	1.86	1.44
	R.MGSGIQYGDAALR.Q [187, 199]	RAB4A peptide ratio, 3	1.58	1.41	4.26	1.90	1.31
RAN		RAN protein ratio				1.24	#DIV/0!
	K.FNVWDTAGQEK.F [60, 70]	RAN peptide ratio, 1	0.75	0.71	1.79	0.91	0.50

	R.VCENIPIVL \underline{C} GNK.V [110, 122]	RAN peptide ratio, 2	0.92	0.95	1.71	1.10	0.37
	K.NLQYYDISAK.S [142, 151]	RAN peptide ratio, 3	0.83	0.82	1.71	1.00	0.42
RAB34		RAB34 protein ratio				ND	#DIV/0!
	- \underline{M} SHLPGLELR.R [0, 9]	RAB34 peptide ratio, 1	ND	ND	ND	ND	ND
	R.VLAELPQC \underline{L} R.K [68, 77]	RAB34 peptide ratio, 2	ND	ND	ND	ND	ND
RAB11A		RAB11A protein ratio				ND	#DIV/0!
	R.ENDMSPSNV \underline{V} PIHVPPTTEN \underline{KPK}	RAB11A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ENDMSPSNV \underline{V} PIHVPPTTEN \underline{KPK}	RAB11A peptide ratio, 2	ND	ND	ND	ND	ND
RABL4/IFT27		RABL4 protein ratio				1.24	#DIV/0!
	K. \underline{C} ILAGDPAVGK.T [7, 17]	RABL4 peptide ratio, 1	0.70	0.50	2.77	0.79	1.02
	K.TALAQIFR.S [18, 25]	RABL4 peptide ratio, 2	0.95	0.96	0.83	0.91	0.06
	R.SQAPGISLPGVLVGNK.T [108, 123]	RABL4 peptide ratio, 3	0.77	0.70	2.18	0.94	0.68
			R_{WM793/1205Lu}				
			WMLu, F1	WMLu, F2	WMLu, R	WMLu, Mean	WM/Lu, S.D.
NRAS		NRAS protein ratio				0.62	#DIV/0!
	R.TGEGFL \underline{C} VFAINNSK.S [73, 87]	NRAS peptide ratio, 1	9.78	10.40	0.16	0.48	4.69
	K.SFADINLYR.E [88, 96]	NRAS peptide ratio, 2	1.28	0.73	0.20	0.42	0.44
	R.QGVEDAFYTLVR.E [149, 160]	NRAS peptide ratio, 3	1.69	1.93	0.39	0.81	0.68
HRAS		HRAS protein ratio				1.07	#DIV/0!
	R.TGEGFL \underline{C} VFAINNTK.S [73, 87]	HRAS peptide ratio, 1	2.02	1.07	0.51	0.88	0.62
	K.SFEDIHQYR.E [88, 96]	HRAS peptide ratio, 2	1.45	1.36	1.24	1.34	0.08
	R.SYGIPYIETSAK.T [135, 146]	HRAS peptide ratio, 3	0.78	1.12	1.29	1.01	0.21
RHOB		RHOB protein ratio				0.25	#DIV/0!
	K.LVVVGDGAC \underline{C} GK.T [7, 17]	RHOB peptide ratio, 1	0.24	0.22	0.18	0.21	0.03
	K.DEFPEVYVPTVFENYVADIEVDGK.	RHOB peptide ratio, 2	0.48	0.25	0.24	0.29	0.11
	R.IQAYDYLE \underline{C} SAK.T [150, 161]	RHOB peptide ratio, 3	0.44	0.55	0.28	0.39	0.11
	R.EVFETATR.A [168, 175]	RHOB peptide ratio, 4	0.23	0.26	0.30	0.26	0.03
RND3		RND3 protein ratio				1.65	#DIV/0!
	K.IVVVGDSD \underline{C} Q \underline{C} GK.T [25, 35]	RND3 peptide ratio, 1	0.49	0.77	0.77	0.65	0.13
	K.TALLHVFAK.D [36, 44]	RND3 peptide ratio, 2	ND	ND	ND	ND	ND
	K.GEIQEF \underline{C} PNTK.M [118, 128]	RND3 peptide ratio, 3	0.39	0.56	2.11	0.62	0.78
	R.TDVSTLVELSNHR.Q [140, 152]	RND3 peptide ratio, 4	ND	ND	ND	ND	ND
	R.DIFHVATLAC \underline{V} NK.T [187, 199]	RND3 peptide ratio, 5	0.38	3.18	1.92	0.87	1.14
RAB39		RAB39 protein ratio				1.02	#DIV/0!
	R.LIVIGDSTV \underline{G} K.S [10, 20]	RAB39 peptide ratio, 1	ND	ND	ND	ND	ND
	R.IKLQLWDTAGQER.F [61, 73] (miss)	RAB39 peptide ratio, 2	6.80	4.81	0.13	0.36	2.80
	K.LQLWDTAGQER.F [63, 73]	RAB39 peptide ratio, 3	1.31	1.29	1.22	1.27	0.04
ARL5A		ARL5A protein ratio				0.55	#DIV/0!
	R.FLMWDIGGQESLR.S [24, 36]	ARL5A peptide ratio, 1	ND	ND	ND	ND	ND
	K.MLAHEDLR.K [71, 78]	ARL5A peptide ratio, 2	5.59	0.09	0.25	0.20	2.56
	K.AGLLIFANK.Q [80, 88]	ARL5A peptide ratio, 3	0.55	1.06	0.55	0.66	0.24
SAR1B		SAR1B protein ratio				1.17	#DIV/0!
	K.IDRPEAISEER.L [135, 145]	SAR1B peptide ratio, 1	ND	ND	ND	ND	ND
	R.EMFGLYGQTTGK.G [148, 159]	SAR1B peptide ratio, 2	2.79	1.39	0.44	0.89	0.97
	K.ELNARPLEVFM \underline{C} SVLK.R [166, 181]	SAR1B peptide ratio, 3	2.11	2.15	0.58	1.13	0.73
RABL2A		RABL2A protein ratio				0.89	#DIV/0!
	K.TKPSELDQ \underline{G} K.Y [5, 14]	RABL2A peptide ratio, 1	1.72	3.01	0.60	1.16	0.99
	K.II \underline{C} LGDSAVGK.S [23, 33]	RABL2A peptide ratio, 2	0.89	0.82	0.94	0.88	0.05
	R.NLSTWYTELR.E [110, 119]	RABL2A peptide ratio, 3	0.85	1.20	1.17	1.04	0.16
	R.EFRPEIPC \underline{V} VANK.I [120, 133]	RABL2A peptide ratio, 4	0.77	2.77	0.49	0.81	1.01
DIRAS1		DIRAS1 protein ratio				0.52	#DIV/0!
	R.VVVFAGG \underline{V} GK.S [9, 19]	DIRAS1 peptide ratio, 1	0.79	0.89	0.55	0.71	0.14
	R.DTYIPTIEDTYR.Q [33, 44]	DIRAS1 peptide ratio, 2	0.67	0.66	0.86	0.72	0.10
	K.GSVEDIPVMLVGNK.C [108, 121]	DIRAS1 peptide ratio, 3	0.47	0.68	0.42	0.50	0.11
	R.EAQAVAQEWK.C [133, 142]	DIRAS1 peptide ratio, 4	0.75	0.56	0.91	0.71	0.14
ARL2		ARL2 protein ratio				1.00	#DIV/0!
	R.ELQSLLEER.L [104, 113]	ARL2 peptide ratio, 1	0.97	0.92	1.06	0.98	0.06
	R.LAGATLLIFANK.Q [114, 125]	ARL2 peptide ratio, 2	0.84	0.85	1.36	0.97	0.24
	R.EVLELDSIR.S [139, 147]	ARL2 peptide ratio, 3	2.12	0.98	0.74	1.05	0.60
ARL3		ARL3 protein ratio				1.23	#DIV/0!
	R.ILLLGLDNAGK.T [19, 29]	ARL3 peptide ratio, 1	1.47	1.50	0.31	0.66	0.55
	K.QLASEDISHITPTQGFK.S [35, 53]	ARL3 peptide ratio, 2	1.76	0.86	0.37	0.67	0.57
	K.LSC \underline{V} PVLIFANK.Q [115, 126]	ARL3 peptide ratio, 3	1.51	1.37	0.90	1.20	0.26
TRIM23		TRIM23 protein ratio				ND	#DIV/0!
	R.DALLLIFANK.Q [504, 513]	TRIM23 peptide ratio, 1	ND	ND	ND	ND	ND
RALB		RALB protein ratio				0.90	#DIV/0!
	K.GQSSLALHK.V [29, 37]	RALB peptide ratio, 1	2.19	7.14	0.72	1.51	2.75
	R.QVPVEEAR.S [158, 165]	RALB peptide ratio, 2	ND	ND	ND	ND	ND
	K.AEEWGVQYVETSAK.T [168, 181]	RALB peptide ratio, 3	1.97	0.30	5.24	0.75	2.05
ARL15		ARL15 protein ratio				0.47	#DIV/0!
	K.L \underline{C} SESPDNVSTTGFSIK.A [51, 68]	ARL15 peptide ratio, 1	0.97	3.98	0.49	0.91	1.54
	K.AVPFQNAILNVK.E [69, 80]	ARL15 peptide ratio, 2	2.89	0.36	0.81	0.68	1.10
	K.ELGGADNIR.K [81, 89]	ARL15 peptide ratio, 3	1.73	0.88	1.29	1.20	0.35

	K.YFELEPLAR.G [157, 165]	ARL15 peptide ratio, 4	0.97	2.35	0.92	1.18	0.66
	K.DSFSQLINLLEEK.D [184, 196]	ARL15 peptide ratio, 5	ND	ND	ND	ND	ND
RAB1A		RAB1A protein ratio				1.07	#DIV/0!
	R.GAHGIIVVYDVTQESFNNV.K.Q [82, 117]	RAB1A peptide ratio, 1	1.29	1.42	0.77	1.08	0.28
	K.NATNVEQSFMTMAAEIK.K [156, 171]	RAB1A peptide ratio, 2	1.38	0.76	1.38	1.09	0.29
	R.MGPGATAGGAEK.S [175, 186]	RAB1A peptide ratio, 3	1.15	1.55	0.74	1.04	0.33
CDC42		CDC42 protein ratio				1.00	#DIV/0!
Isoform 1	K.TCLLISYTTNK.F [16, 26]	CDC42 peptide ratio, 1	1.07	1.07	0.89	1.00	0.08
Isoform 1	K.WVPEITHHC.PK.T [96, 106]	CDC42 peptide ratio, 2	1.02	0.99	0.87	0.96	0.07
Isoform 1	K.TPFLLVGTQIDLR.D [107, 119]	CDC42 peptide ratio, 3	2.19	0.86	0.61	0.92	0.70
RAB21		RAB21 protein ratio				0.99	#DIV/0!
	K.VVLLGEGCVGK.T [21, 31]	RAB21 peptide ratio, 1	0.88	1.55	1.18	1.14	0.28
	R.VNLAIWDTAGQER.F [67, 79]	RAB21 peptide ratio, 2	0.64	1.63	1.01	0.95	0.41
	R.HVSIQEAESYAESVGAK.H [140, 155]	RAB21 peptide ratio, 3	ND	ND	ND	ND	ND
RAB22A		RAB22A protein ratio				1.84	#DIV/0!
	K.TVQYQNELHK.F [45, 54]	RAB22A peptide ratio, 1	ND	ND	ND	ND	ND
	K.EETFSTLKN.N [89, 96]	RAB22A peptide ratio, 2	1.75	1.23	2.23	1.64	0.41
	K.DYADSIHAIFVETSAKN.N [134, 149]	RAB22A peptide ratio, 3	4.39	2.08	0.33	0.81	1.66
	R.IPSTDANLPSGGK.G [165, 177]	RAB22A peptide ratio, 4	2.45	3.15	0.45	1.02	1.15
RAB17		RAB17 protein ratio				ND	#DIV/0!
	K.SILPTVGC.AFFT.K.V [45, 57]	RAB17 peptide ratio, 1	ND	ND	ND	ND	ND
	K.LEIWDTAGQEK.Y [68, 78]	RAB17 peptide ratio, 2	ND	ND	ND	ND	ND
	K.YHSVCHLYFR.G [79, 88]	RAB17 peptide ratio, 3	ND	ND	ND	ND	ND
	R.SDEEGQALR.G [183, 191]	RAB17 peptide ratio, 4	ND	ND	ND	ND	ND
RAB23		RAB23 protein ratio				0.98	#DIV/0!
	K.TIGVDFLE.R.Q [40, 48]	RAB23 peptide ratio, 1	ND	ND	ND	ND	ND
	R.QIQVNDDEDVR.L [49, 58]	RAB23 peptide ratio, 2	2.82	0.46	1.20	0.89	0.99
	K.EDLNVNEVF.K.Y [153, 162]	RAB23 peptide ratio, 3	1.33	0.82	1.25	1.08	0.22
RAB1B		RAB1B protein ratio				ND	#DIV/0!
	-.MNPEYDYLFK.L [0, 9]	RAB1B peptide ratio, 1	ND	ND	ND	ND	ND
	K.NATNVEQAFMTMAAEIK.K [153, 168]	RAB1B peptide ratio, 2	ND	ND	ND	ND	ND
	R.MGPGAASGGERP.NLK.I [172, 186]	RAB1B peptide ratio, 3	ND	ND	ND	ND	ND
RABL2B		RABL2B protein ratio				0.56	#DIV/0!
	K.AHACIMVFDVQR.K [93, 104]	RABL2B peptide ratio, 1	1.00	0.59	0.38	0.56	0.26
RAP2C		RAP2C protein ratio				ND	#DIV/0!
	K.VPLILVGNK.V [108, 116]	RAP2C peptide ratio, 1	ND	ND	ND	ND	ND
	K.VDLEPER.E [117, 123]	RAP2C peptide ratio, 2	ND	ND	ND	ND	ND
	R.EVMSSEGR.A [124, 131]	RAP2C peptide ratio, 3	ND	ND	ND	ND	ND
	R.ALAQEWGCPFMETSAK.S [132, 147]	RAP2C peptide ratio, 4	ND	ND	ND	ND	ND
	R.QMNYSSLPEK.Q [162, 171]	RAP2C peptide ratio, 5	ND	ND	ND	ND	ND
RHO		RHO protein ratio				ND	#DIV/0!
	K.CVLVGDGAVGK.T [51, 61]	RHO peptide ratio, 1	ND	ND	ND	ND	ND
RABL5		RABL5 protein ratio				0.58	#DIV/0!
	K.ILFVGPCESGK.T [5, 15]	RABL5 peptide ratio, 1	0.43	0.32	0.48	0.40	0.07
	R.ILEFENPHVTSNNK.G [39, 52]	RABL5 peptide ratio, 2	0.48	0.45	0.25	0.36	0.10
	K.FESCWPALMK.D [69, 78]	RABL5 peptide ratio, 3	1.53	0.56	0.52	0.69	0.47
	K.SIINSMSES.R.D [166, 175]	RABL5 peptide ratio, 4	2.57	1.13	0.75	1.15	0.78
RRAGD		RRAGD protein ratio				ND	#DIV/0!
	K.MSPNETLFLESTNK.I [85, 98]	RRAGD peptide ratio, 1	ND	ND	ND	ND	ND
	K.LNNTTVLYLK.E [320, 329]	RRAGD peptide ratio, 2	ND	ND	ND	ND	ND
ARL4C		ARL4C protein ratio				ND	#DIV/0!
	K.GISCHFWDVGGQEK.L [60, 73]	ARL4C peptide ratio, 1	ND	ND	ND	ND	ND
	K.FAENQGTPLLVIANK.Q [113, 127]	ARL4C peptide ratio, 2	ND	ND	ND	ND	ND
	K.LYEMILK.R [174, 180]	ARL4C peptide ratio, 3	ND	ND	ND	ND	ND
RAC2		RAC2 protein ratio				ND	#DIV/0!
	R.HHC.PSTPIILVGT.K.L [102, 115]	RAC2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.LAPITYPQGLALAK.E [133, 146]	RAC2 peptide ratio, 2	ND	ND	ND	ND	ND
	R.AVLCPQPTR.Q [174, 182]	RAC2 peptide ratio, 3	ND	ND	ND	ND	ND
RAC1		RAC1 protein ratio				0.63	#DIV/0!
	R.HHC.PNTPIILVGT.K.L [102, 115]	RAC1 peptide ratio, 1	0.75	0.48	1.26	0.71	0.33
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 2	0.49	0.42	1.69	0.60	0.59
	K.LTPITYPQGLAMAK.E [133, 146]	RAC1 peptide ratio, 3	0.44	0.65	8.20	0.76	3.61
RRAGB		RRAGB protein ratio				0.76	#DIV/0!
	R.SIIFANYIAR.D [57, 66]	RRAGB peptide ratio, 1	3.51	1.29	1.03	1.48	1.11
	R.NFAEIIAEDEVLLFER.A [253, 268]	RRAGB peptide ratio, 2	0.85	0.64	0.55	0.66	0.12
	K.LAASFQSMEVR.N [305, 315]	RRAGB peptide ratio, 3	2.51	1.31	0.20	0.49	0.94
RAB27B		RAB27B protein ratio				ND	#DIV/0!
	K.LLALGDSGVGK.T [11, 21]	RAB27B peptide ratio, 1	ND	ND	ND	ND	ND
	R.VVYNAQGPNGSSGK.A [50, 63]	RAB27B peptide ratio, 2	ND	ND	ND	ND	ND
	K.VHLQLWDTAGQER.F [67, 79]	RAB27B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YGIPYFETSAATGQNVEK.A [154, 169]	RAB27B peptide ratio, 4	ND	ND	ND	ND	ND
RHOD		RHOD protein ratio				ND	#DIV/0!
	K.GKPVHLHIWDTAGQDDYDR.L [61, 74]	RHOD peptide ratio, 1	ND	ND	ND	ND	ND
	R.WYPEVNHFC.K.K [110, 119]	RHOD peptide ratio, 2	ND	ND	ND	ND	ND

	R.SVGAVAYLECSAR.L [161, 173]	RHOD peptide ratio, 3	ND	ND	ND	ND	ND
RHOQ		RHOQ protein ratio				ND	#DIV/0!
	K.EEWVPELK.E [100, 107]	RHOQ peptide ratio, 1	ND	ND	ND	ND	ND
	K.EIGACCYVECSALTQK.G [153, 168]	RHOQ peptide ratio, 2	ND	ND	ND	ND	ND
	K.TVFDEAIIAILTPK.K [172, 185]	RHOQ peptide ratio, 3	ND	ND	ND	ND	ND
RRAS2		RRAS2 protein ratio				1.14	#DIV/0!
	R.LVVVGGGGVGVK.S [16, 26]	RRAS2 peptide ratio, 1	2.57	1.97	0.66	1.24	0.80
	R.LDILDTAGQEEFGAMR.E [69, 84]	RRAS2 peptide ratio, 2	ND	ND	ND	ND	ND
	R.TGEGFLLVFSVTDGR.G [90, 103]	RRAS2 peptide ratio, 3	ND	ND	ND	ND	ND
	R.QVTQEEGQQLAR.Q [141, 152]	RRAS2 peptide ratio, 4	1.67	1.21	1.21	1.33	0.22
RAB31		RAB31 protein ratio				0.52	#DIV/0!
	R.FHSLAPMYR.G [67, 76]	RAB31 peptide ratio, 1	0.44	0.43	0.09	0.19	0.16
	R.GSAAAVIVYDITK.Q [77, 89]	RAB31 peptide ratio, 2	0.75	0.51	0.42	0.53	0.14
	K.QDSFYTLK.K [90, 97]	RAB31 peptide ratio, 3	0.76	1.00	0.97	0.90	0.10
RAB32		RAB32 protein ratio				1.99	#DIV/0!
	K.VLVIGELGVGK.T [27, 37]	RAB32 peptide ratio, 1	3.28	3.69	7.95	4.27	2.11
	R.SSTFEAVLK.W [110, 118]	RAB32 peptide ratio, 2	2.65	2.21	1.34	1.91	0.55
	K.DNINIEEAAR.F [176, 185]	RAB32 peptide ratio, 3	2.30	2.64	2.48	2.46	0.14
RAB18		RAB18 protein ratio				1.09	#DIV/0!
	K.ILIIGESGVGK.S [10, 20]	RAB18 peptide ratio, 1	1.16	0.98	1.34	1.14	0.15
	K.LAIWDTAGQER.F [58, 68]	RAB18 peptide ratio, 2	1.17	1.16	0.84	1.03	0.15
	R.TLTPSYR.G [71, 78]	RAB18 peptide ratio, 3	0.97	0.96	1.40	1.08	0.21
	R.NDIVNMLVGNK.I [112, 122]	RAB18 peptide ratio, 4	0.40	0.72	0.66	0.56	0.14
RAB9B		RAB9B protein ratio				0.57	#DIV/0!
	K.VILLGDGGVGVK.S [9, 19]	RAB9B peptide ratio, 1	0.51	0.57	0.86	0.62	0.15
	R.QSFENLGNWQK.E [92, 102]	RAB9B peptide ratio, 2	0.51	0.53	0.67	0.56	0.07
	K.EFIYYADV.K.D [103, 111]	RAB9B peptide ratio, 3	ND	ND	ND	ND	ND
RAP1B		RAP1B protein ratio				1.20	#DIV/0!
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 1	1.40	1.97	1.26	1.49	0.30
	K.DTDDVPMILVGNK.C [104, 116]	RAP1B peptide ratio, 2	ND	ND	ND	ND	ND
	R.QWNNCAFLESSAK.S [136, 148]	RAP1B peptide ratio, 3	1.34	1.23	1.50	1.35	0.11
ARFRP1		ARFRP1 protein ratio				1.06	#DIV/0!
	K.TTFLEQSK.T [30, 37]	ARFRP1 peptide ratio, 1	0.92	1.07	1.23	1.06	0.13
	K.ITTTVGLNIGTVDVGK.A [52, 67]	ARFRP1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.QDVETCLSIDIK.T [135, 147]	ARFRP1 peptide ratio, 3	ND	ND	ND	ND	ND
	K.TAFSDCTSK.I [148, 156]	ARFRP1 peptide ratio, 4	ND	ND	ND	ND	ND
	R.DCLTQACCSALTGK.G [161, 173]	ARFRP1 peptide ratio, 5	ND	ND	ND	ND	ND
RAB20		RAB20 protein ratio				ND	#DIV/0!
	K.IVLLGDMNVGK.T [7, 17]	RAB20 peptide ratio, 1	ND	ND	ND	ND	ND
	R.GAAIILTYDVNHR.Q [71, 84]	RAB20 peptide ratio, 2	ND	ND	ND	ND	ND
	R.FLGLTDTASK.D [94, 103]	RAB20 peptide ratio, 3	ND	ND	ND	ND	ND
	K.QVQLEDAVALYK.K [147, 158]	RAB20 peptide ratio, 4	ND	ND	ND	ND	ND
SAR1A		SAR1A protein ratio				0.56	#DIV/0!
	K.NYLPAINGIVFLVDCADHSR.L [87, 100]	SAR1A peptide ratio, 1	1.08	1.07	0.97	1.04	0.05
	R.TDAISEEK.L [138, 145]	SAR1A peptide ratio, 2	4.40	3.94	0.93	1.93	1.54
	R.EIFGLYGQTTGK.G [148, 159]	SAR1A peptide ratio, 3	0.39	0.40	0.92	0.49	0.25
RAB5C		RAB5C protein ratio				0.50	#DIV/0!
	R.QASPNIVIALAGNK.A [121, 134]	RAB5C peptide ratio, 1	6.44	1.05	0.24	0.57	2.75
	K.NEPQATGAPGR.N [184, 195]	RAB5C peptide ratio, 2	0.94	2.21	0.27	0.58	0.80
	R.GVDLQENNPASR.S [198, 209]	RAB5C peptide ratio, 3	0.42	0.51	0.30	0.39	0.09
RAB7A		RAB7A protein ratio				1.07	#DIV/0!
	R.FQSLGVAFYR.G [69, 78]	RAB7A peptide ratio, 1	0.81	0.99	0.98	0.92	0.08
	R.DEFLIQASPR.D [103, 112]	RAB7A peptide ratio, 2	ND	ND	ND	ND	ND
	R.AQAWCYSK.N [138, 145]	RAB7A peptide ratio, 3	0.83	0.95	0.88	0.88	0.05
	K.NNIPYFETSAK.E [146, 156]	RAB7A peptide ratio, 4	0.80	0.82	1.48	0.95	0.32
RAB9A		RAB9A protein ratio				0.56	#DIV/0!
	R.QVSTEEAQAWCR.D [131, 142]	RAB9A peptide ratio, 1	0.61	0.50	0.21	0.35	0.17
	K.DATNVAAAFEEAVR.R [156, 169]	RAB9A peptide ratio, 2	5.96	4.90	0.25	0.70	2.48
	R.SDHLIQTDTVNLHR.K [178, 191]	RAB9A peptide ratio, 3	0.15	4.50	0.43	0.33	1.99
RAB13		RAB13 protein ratio				0.98	#DIV/0!
	K.LQVWDTAGQER.F [58, 68]	RAB13 peptide ratio, 1	0.93	0.95	1.01	0.96	0.04
	K.SFENIQNWMK.S [94, 103]	RAB13 peptide ratio, 2	0.54	0.50	1.29	0.65	0.36
	K.ENASAGVER.L [107, 115]	RAB13 peptide ratio, 3	1.33	2.12	0.90	1.29	0.50
RAB28		RAB28 protein ratio				1.13	#DIV/0!
	K.IVVLGDGASGK.T [14, 24]	RAB28 peptide ratio, 1	0.72	0.73	0.87	0.77	0.07
	K.TSLTTCFAQETFGK.Q [25, 38]	RAB28 peptide ratio, 2	1.88	2.30	0.97	1.50	0.56
	K.VSEESQPLVALVGNK.I [113, 129]	RAB28 peptide ratio, 3	ND	ND	ND	ND	ND
	K.VAAEILGK.L [172, 180]	RAB28 peptide ratio, 4	1.34	1.06	1.14	1.17	0.12
	K.AEIEQSQR.V [184, 191]	RAB28 peptide ratio, 5	0.78	0.78	0.76	0.77	0.01
RAB27A		RAB27A protein ratio				1.09	#DIV/0!
	K.FLALGDSGVGK.T [11, 21]	RAB27A peptide ratio, 1	1.07	1.16	1.17	1.13	0.05
	K.TSVLYQYTDGK.F [22, 32]	RAB27A peptide ratio, 2	1.17	1.01	1.28	1.15	0.11
	R.IHLQLWDTAGQER.F [67, 79]	RAB27A peptide ratio, 3	ND	ND	ND	ND	ND
	K.SDLEDQR.V [134, 140]	RAB27A peptide ratio, 4	ND	ND	ND	ND	ND

	K.SWIPEGVVR.S [191, 199]	RAB27A peptide ratio, 5	1.33	1.14	1.17	1.21	0.08
RAB10		RAB10 protein ratio				1.02	#DIV/0!
	K.TYDLLFK.L [4, 10]	RAB10 peptide ratio, 1	1.12	1.16	0.96	1.07	0.09
	R.FHTITTSYYR.G [70, 79]	RAB10 peptide ratio, 2	1.47	1.41	0.48	0.87	0.45
	R.NIDEHANEDVER.M [105, 116]	RAB10 peptide ratio, 3	1.39	4.60	0.53	1.07	1.75
RHEB		RHEB protein ratio				0.69	#DIV/0!
	K.IAILGYR.S [8, 14]	RHEB peptide ratio, 1	ND	ND	ND	ND	ND
	K.VQIPIMLVGNK.K [109, 119]	RHEB peptide ratio, 2	ND	ND	ND	ND	ND
	K.ALAESWNAAFLESSAK.E [135, 150]	RHEB peptide ratio, 3	ND	ND	ND	ND	ND
	K.ENQTAVDVFR.R [151, 160]	RHEB peptide ratio, 4	0.68	0.68	0.70	0.69	0.01
CDC42		CDC42 protein ratio				0.99	#DIV/0!
Isoform 2	K.YVECSALTQK.G [153, 162]	CDC42 peptide ratio, 1	1.06	1.10	1.09	1.08	0.02
Isoform 2	K.NVFDEAILAALPEPEPK.K [166, 182]	CDC42 peptide ratio, 2	1.82	1.07	0.41	0.76	0.58
RAB6B		RAB6B protein ratio				1.70	#DIV/0!
	R.QITIEEGEQR.A [134, 143]	RAB6B peptide ratio, 1	2.04	2.17	1.22	1.69	0.42
	K.ELSMFIETSAK.T [146, 157]	RAB6B peptide ratio, 2	1.62	2.89	1.51	1.85	0.62
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 3	ND	ND	ND	ND	ND
	R.VASALPGMENVQEK.S [169, 182]	RAB6B peptide ratio, 4	ND	ND	ND	ND	ND
RHOG		RHOG protein ratio				1.33	#DIV/0!
	R.TVNLNLWDTAGQEEYDR.L [49, 65]	RHOG peptide ratio, 1	ND	ND	ND	ND	ND
	K.EQGQAPITPQQGQALAK.Q [130, 146]	RHOG peptide ratio, 2	4.74	1.27	0.80	1.33	1.76
	R.YLECSALQQDGVK.E [153, 165]	RHOG peptide ratio, 3	1.23	1.29	2.31	1.48	0.49
RAB5B		RAB5B protein ratio				0.87	#DIV/0!
	R.QASPSIVIALAGNK.A [120, 133]	RAB5B peptide ratio, 1	1.09	1.14	1.04	1.09	0.04
	K.TAMNVNDLFLAIK.K [165, 178]	RAB5B peptide ratio, 2	1.01	0.91	0.63	0.82	0.16
	K.SEPQNLGGAAGR.S [183, 194]	RAB5B peptide ratio, 3	ND	ND	ND	ND	ND
	R.GVDLHEQSQQNK.S [197, 208]	RAB5B peptide ratio, 4	ND	ND	ND	ND	ND
RAP2B		RAP2B protein ratio				0.96	#DIV/0!
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 1	0.61	0.80	0.95	0.76	0.14
	R.VPMILVGNK.V [108, 116]	RAP2B peptide ratio, 2	0.95	0.91	0.82	0.89	0.05
	K.VDLEGER.E [117, 123]	RAP2B peptide ratio, 3	ND	ND	ND	ND	ND
	K.ASVDELFAEIVR.Q [150, 161]	RAP2B peptide ratio, 4	1.94	1.13	1.31	1.39	0.35
ARL8B		ARL8B protein ratio				0.89	#DIV/0!
	R.DLPNALDEK.Q [184, 192]	ARL8B peptide ratio, 1	0.69	0.67	1.26	0.80	0.27
	K.MNLSAIQDR.E [198, 206]	ARL8B peptide ratio, 2	0.75	0.83	1.37	0.92	0.27
	R.EICCYSSISCK.E [207, 216]	ARL8B peptide ratio, 3	0.86	0.80	0.51	0.69	0.15
RHOH		RHOH protein ratio				ND	#DIV/0!
	R.SNLPCTPVLVVATQTDQR.E [103, 119]	RHOH peptide ratio, 1	ND	ND	ND	ND	ND
	R.ASCVNAMEGK.K [127, 136]	RHOH peptide ratio, 2	ND	ND	ND	ND	ND
	K.GYLECSALSNR.G [146, 156]	RHOH peptide ratio, 3	ND	ND	ND	ND	ND
	R.GVQQVFEC AVR.T [157, 167]	RHOH peptide ratio, 4	ND	ND	ND	ND	ND
RAP1A		RAP1A protein ratio				0.65	#DIV/0!
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 1	34.97	17.70	0.26	0.77	14.17
	R.VKDTEDEVPMILVGNK.C [102, 116]	RAP1A peptide ratio, 2	1.90	3.69	0.24	0.61	1.41
	K.DTEDEVPMILVGNK.C [104, 116]	RAP1A peptide ratio, 3	1.98	6.32	0.25	0.64	2.55
	R.QWCNCAFLESSAK.S [136, 148]	RAP1A peptide ratio, 4	ND	ND	ND	ND	ND
RAP2A		RAP2A protein ratio				0.88	#DIV/0!
	K.VPVILVGNK.V [108, 116]	RAP2A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ALAEWGC PFMETSAK.S [132, 147]	RAP2A peptide ratio, 2	0.84	1.12	0.83	0.91	0.13
	K.TMVDELFAEIVR.Q [150, 161]	RAP2A peptide ratio, 3	0.86	0.89	0.75	0.83	0.06
RRAS		RRAS protein ratio				1.61	#DIV/0!
	K.ICSVDGIPAR.L [68, 77]	RRAS peptide ratio, 1	1.39	1.44	1.44	1.42	0.02
	R.QSFNEVGK.L [113, 120]	RRAS peptide ratio, 2	ND	ND	ND	ND	ND
	K.LFTQILR.V [121, 127]	RRAS peptide ratio, 3	1.60	1.58	1.46	1.54	0.07
	K.ADLESQR.Q [143, 149]	RRAS peptide ratio, 4	ND	ND	ND	ND	ND
RAB11B		RAB11B protein ratio				0.90	#DIV/0!
	K.AQIWDTAGQER.Y [61, 71]	RAB11B peptide ratio, 1	0.86	0.87	1.04	0.92	0.08
	R.GAVGALLVYDIK.H [82, 94]	RAB11B peptide ratio, 2	1.71	0.40	0.60	0.63	0.58
	K.NILTEIYR.I [166, 173]	RAB11B peptide ratio, 3	ND	ND	ND	ND	ND
NKIRAS2		NKIRAS2 protein ratio				0.76	#DIV/0!
	K.VVVCQGQASVKG.T [6, 16]	NKIRAS2 peptide ratio, 1	3.03	0.80	0.87	1.09	1.04
	K.EVTIVVLGNK.C [111, 120]	NKIRAS2 peptide ratio, 2	0.45	0.98	0.74	0.66	0.21
	R.VDPDVAQHWAK.S [129, 139]	NKIRAS2 peptide ratio, 3	1.15	0.48	1.24	0.80	0.34
	R.SLLEPFVYLASK.M [155, 166]	NKIRAS2 peptide ratio, 4	0.98	0.68	1.08	0.88	0.17
RAB33B		RAB33B protein ratio				1.01	#DIV/0!
	K.IIVIGDSNVGK.T [35, 45]	RAB33B peptide ratio, 1	0.82	0.81	2.34	1.04	0.72
	R.AVEIDGER.I [73, 80]	RAB33B peptide ratio, 2	3.97	0.35	9.12	0.94	3.60
	R.SAIQVPTDLAQK.F [153, 164]	RAB33B peptide ratio, 3	1.15	0.59	6.51	1.11	2.67
ARL6		ARL6 protein ratio				1.24	#DIV/0!
	R.NLWEHYK.E [77, 84]	ARL6 peptide ratio, 1	ND	ND	ND	ND	ND
	K.EELDTLLNHPDIK.H [106, 118]	ARL6 peptide ratio, 2	1.51	4.12	0.65	1.23	1.48
	R.IPILFFANK.M [122, 130]	ARL6 peptide ratio, 3	1.30	1.95	0.90	1.26	0.43
	K.VSQLLCLENIK.D [142, 152]	ARL6 peptide ratio, 4	1.06	1.23	1.19	1.16	0.07
RAC3		RAC3 protein ratio				0.87	#DIV/0!

	K.LAPITYPQGLAMAR.E [133, 146]	RAC3 peptide ratio, 1	2.71	4.12	0.24	0.63	1.60
	K.LAPITYPQGLAMAR.E [133, 146]	RAC3 peptide ratio, 2	1.41	1.97	1.71	1.67	0.23
	R.AVLCPPPVK.K [174, 182]	RAC3 peptide ratio, 3	0.64	0.64	1.52	0.80	0.42
RAB3A		RAB3A protein ratio				0.64	#DIV/0!
	K.ESSDQNFDFYMF.K.I [12, 23]	RAB3A peptide ratio, 1	0.41	0.61	0.12	0.24	0.20
	K.TYSWDNAQVLLVGNK.C [121, 135]	RAB3A peptide ratio, 2	0.37	0.46	0.97	0.51	0.27
	R.LVDVIC.EK.M [178, 185]	RAB3A peptide ratio, 3	0.69	0.75	0.89	0.77	0.08
	K.MSESLDTADPAVTGAK.Q [186, 201]	RAB3A peptide ratio, 4	6.00	1.96	0.23	0.59	2.42
RAB5A		RAB5A protein ratio				0.56	#DIV/0!
	R.QASPNIVIALSGNK.A [120, 133]	RAB5A peptide ratio, 1	0.99	0.89	1.15	1.00	0.11
	K.NEPQNPANSAR.G [183, 194]	RAB5A peptide ratio, 2	0.60	0.66	0.74	0.66	0.06
	R.GVDLTEPTQPTR.N [197, 208]	RAB5A peptide ratio, 3	0.49	0.44	0.71	0.52	0.12
RAB6C		RAB6C protein ratio				ND	#DIV/0!
	R.QVSIEEGER.K [134, 142]	RAB6C peptide ratio, 1	ND	ND	ND	ND	ND
	K.ELNVMFIETSAK.A [146, 157]	RAB6C peptide ratio, 2	ND	ND	ND	ND	ND
	R.VAAALPGMESTQDR.S [169, 182]	RAB6C peptide ratio, 3	0.94	1.12	0.96	1.00	0.08
MRAS		MRAS protein ratio				ND	#DIV/0!
	K.IFVPDYDPTIEDSYLK.H [36, 51]	MRAS peptide ratio, 1	ND	ND	ND	ND	ND
RAB8B		RAB8B protein ratio				ND	#DIV/0!
	R.NIEEHASSDVER.M [104, 115]	RAB8B peptide ratio, 1	ND	ND	ND	ND	ND
	K.SSANVEEAFFTLAR.D [153, 166]	RAB8B peptide ratio, 2	ND	ND	ND	ND	ND
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 3	ND	ND	ND	ND	ND
	K.MNDSNSAGAGGPVK.I [176, 189]	RAB8B peptide ratio, 4	ND	ND	ND	ND	ND
RAB7L1		RAB7L1 protein ratio				0.91	#DIV/0!
	K.VLQWSDYEIVR.L [47, 57]	RAB7L1 peptide ratio, 1	1.37	1.71	0.64	1.04	0.45
	K.CDLSPWAVSR.D [126, 135]	RAB7L1 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ENGFTGWTETSVK.E [144, 156]	RAB7L1 peptide ratio, 3	0.84	0.70	1.13	0.86	0.18
RHOC		RHOC protein ratio				1.65	#DIV/0!
	K.HFCPNVPIILVGNK.K [104, 117]	RHOC peptide ratio, 1	0.73	0.92	1.35	0.94	0.26
	K.HFCPNVPIILVGNKK.D [104, 118] (n	RHOC peptide ratio, 2	1.72	0.74	1.32	1.12	0.40
	R.ISAFGYLECSAK.T [150, 161]	RHOC peptide ratio, 3	1.10	1.05	1.09	1.08	0.02
RHOJ		RHOJ protein ratio				ND	#DIV/0!
	K.AIGAQCYLECSALTQK.G [165, 180]	RHOJ peptide ratio, 1	ND	ND	ND	ND	ND
	K.AVFDEAILTIFHPK.K [184, 197]	RHOJ peptide ratio, 2	ND	ND	ND	ND	ND
RAB38		RAB38 protein ratio				ND	#DIV/0!
	K.LLVIGDLGVGK.T [11, 21]	RAB38 peptide ratio, 1	ND	ND	ND	ND	ND
	K.VLHWDPETVVR.L [49, 59]	RAB38 peptide ratio, 2	ND	ND	ND	ND	ND
	K.LSLPNGKPVSVLLANK.C [111, 121]	RAB38 peptide ratio, 3	ND	ND	ND	ND	ND
	K.ENINIDEASR.C [161, 170]	RAB38 peptide ratio, 4	ND	ND	ND	ND	ND
RAB25		RAB25 protein ratio				ND	#DIV/0!
	K.VVLIGESGVGK.T [14, 24]	RAB25 peptide ratio, 1	ND	ND	ND	ND	ND
	R.TTIGVEFSTR.T [42, 51]	RAB25 peptide ratio, 2	ND	ND	ND	ND	ND
	K.AQIWDTAGLER.Y [62, 72]	RAB25 peptide ratio, 3	ND	ND	ND	ND	ND
	R.EVPTTEEAR.M [133, 140]	RAB25 peptide ratio, 4	ND	ND	ND	ND	ND
RAB8A		RAB8A protein ratio				0.93	#DIV/0!
	R.NIEEHASADVEK.M [104, 115]	RAB8A peptide ratio, 1	1.14	1.04	1.06	1.08	0.04
	K.LALDYGIK.F [138, 145]	RAB8A peptide ratio, 2	0.73	0.71	1.40	0.86	0.32
	K.LEGNSPQGSNQGK.V.I [176, 189]	RAB8A peptide ratio, 3	ND	ND	ND	ND	ND
ARL4A		ARL4A protein ratio				ND	#DIV/0!
	K.TVTFHFWDVGGQEK.L [67, 80]	ARL4A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ISENQGVPLIVANK.Q [120, 134]	ARL4A peptide ratio, 2	ND	ND	ND	ND	ND
	R.NSLSLSEIEK.L [139, 148]	ARL4A peptide ratio, 3	ND	ND	ND	ND	ND
RAB6A		RAB6A protein ratio				1.14	#DIV/0!
	R.DSAAAVVYDITNVNSFQQTTK.W	RAB6A peptide ratio, 1	1.66	0.76	0.71	0.90	0.43
	K.WIDDVTER.G [106, 114] (missed 1)	RAB6A peptide ratio, 2	1.20	14.20	1.13	1.68	6.15
	R.TDLADKR.Q [127, 133] (missed 1)	RAB6A peptide ratio, 3	0.76	1.12	1.18	0.98	0.19
RAB2A		RAB2A protein ratio				1.54	#DIV/0!
	R.MITIDGK.Q [46, 52]	RAB2A peptide ratio, 1	1.33	1.49	1.59	1.46	0.11
	K.KEEGEAFAR.E [130, 138] (missed 1)	RAB2A peptide ratio, 2	1.20	0.81	1.65	1.13	0.34
	K.TASNVEEAFINTAK.E [151, 164]	RAB2A peptide ratio, 3	1.65	1.60	1.15	1.43	0.22
	K.IQEGVFDINNEANGIK.I [170, 185]	RAB2A peptide ratio, 4	1.87	5.53	1.54	2.20	1.81
RAB3D		RAB3D protein ratio				0.74	#DIV/0!
	R.DAADQNFDFYMF.K.L [12, 23]	RAB3D peptide ratio, 1	12.80	19.69	0.85	2.30	7.78
	K.LLLIGNSSVGK.T [24, 34]	RAB3D peptide ratio, 2	0.65	0.71	0.82	0.72	0.07
	R.LADDLGFEEFEASAK.E [152, 166]	RAB3D peptide ratio, 3	1.33	1.53	0.61	0.98	0.39
RAB36		RAB36 protein ratio				ND	#DIV/0!
	R.EHFHGQVSAACQR.R [100, 112]	RAB36 peptide ratio, 1	ND	ND	ND	ND	ND
	R.FEAGIPYSLQIWDTAGQEK.F [164, 177]	RAB36 peptide ratio, 2	ND	ND	ND	ND	ND
	R.VAALAFEQSVLQDLER.Q [282, 297]	RAB36 peptide ratio, 3	ND	ND	ND	ND	ND
RAN		RAN protein ratio				0.66	#DIV/0!
	K.LVLVGDGGTGK.T [12, 22]	RAN peptide ratio, 1	0.72	0.73	0.88	0.77	0.07
	K.YVATLGVEVHPLVFHTNR.G [38, 55]	RAN peptide ratio, 2	1.60	0.21	9.08	0.54	3.90
	K.NVPNWHR.D [99, 105]	RAN peptide ratio, 3	ND	ND	ND	ND	ND
RAB40C		RAB40C protein ratio				ND	#DIV/0!

	R.VFSLQDLCCR.A [188, 197]	RAB40C peptide ratio, 1	ND	ND	ND	ND	ND
	R.SYSLASGAGGGGSK.G [239, 252]	RAB40C peptide ratio, 2	ND	ND	ND	ND	ND
ARL11		ARL11 protein ratio				ND	#DIV/0!
	R.GCSALTGEGEGLPEALQSLWSLLK.S	ARL11 peptide ratio, 1	ND	ND	ND	ND	ND
RAB24		RAB24 protein ratio				ND	#DIV/0!
	R.SLEEGCQIYLCGTK.S [107, 120]	RAB24 peptide ratio, 1	ND	ND	ND	ND	ND
	R.VDFHVDVQDYADNIK.A [133, 146]	RAB24 peptide ratio, 2	ND	ND	ND	ND	ND
	K.AQLFETSSK.T [147, 155]	RAB24 peptide ratio, 3	ND	ND	ND	ND	ND
	K.TGQSVDELDFQK.V [156, 166]	RAB24 peptide ratio, 4	ND	ND	ND	ND	ND
RAB7B		RAB7B protein ratio				0.92	#DIV/0!
	K.IIILGDTTLK.L [48, 57]	RAB7B peptide ratio, 1	ND	ND	ND	ND	ND
	K.LQIWDVTGGQER.F [58, 68]	RAB7B peptide ratio, 2	0.89	0.97	0.76	0.86	0.09
	R.YQSILENHLTESIK.L [174, 187]	RAB7B peptide ratio, 3	1.52	0.71	0.89	0.94	0.35
ARL8A		ARL8A protein ratio				ND	#DIV/0!
	K.LWDIGGQPR.F [68, 76]	ARL8A peptide ratio, 1	ND	ND	ND	ND	ND
	R.GVSAIVYMVDAADQEK.I [87, 102]	ARL8A peptide ratio, 2	ND	ND	ND	ND	ND
	R.DLPGALDEKELIEK.M [132, 145] (m	ARL8A peptide ratio, 3	ND	ND	ND	ND	ND
RAB39B		RAB39B protein ratio				ND	#DIV/0!
	R.SFQNVHEWLEETK.V [95, 107]	RAB39B peptide ratio, 1	ND	ND	ND	ND	ND
	K.CDLDTQR.Q [124, 130]	RAB39B peptide ratio, 2	ND	ND	ND	ND	ND
	K.LAAAYGMK.Y [140, 147]	RAB39B peptide ratio, 3	ND	ND	ND	ND	ND
	K.YIETSAR.D [148, 154]	RAB39B peptide ratio, 4	ND	ND	ND	ND	ND
	K.SGFVFPNVVHSSEEVK.S [190, 205]	RAB39B peptide ratio, 5	ND	ND	ND	ND	ND
DIRAS2		DIRAS2 protein ratio				ND	#DIV/0!
	R.VAVFGAGGVGK.S [9, 19]	DIRAS2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.SICTLQITDTTGGSHQFPAMQR.L [52	DIRAS2 peptide ratio, 2	ND	ND	ND	ND	ND
RAB2B		RAB2B protein ratio				0.85	#DIV/0!
	R.ETFNHLTSWLEDAR.Q [26, 39]	RAB2B peptide ratio, 1	ND	ND	ND	ND	ND
	K.REEGEAFAR.E [65, 73] (missed 1)	RAB2B peptide ratio, 2	0.89	0.97	1.36	1.04	0.20
	K.TACNVVEAFINTAK.E [86, 99]	RAB2B peptide ratio, 3	1.82	1.76	1.26	1.57	0.25
RAB37		RAB37 protein ratio				ND	#DIV/0!
	R.SPPCSPSYDLTGK.V [18, 30]	RAB37 peptide ratio, 1	ND	ND	ND	ND	ND
	K.VMLLGDGTGVGK.T [31, 41]	RAB37 peptide ratio, 2	ND	ND	ND	ND	ND
	K.TCFLIQFK.D [42, 49]	RAB37 peptide ratio, 3	ND	ND	ND	ND	ND
	R.AGHQADEPSFQIR.D [194, 206]	RAB37 peptide ratio, 4	ND	ND	ND	ND	ND
ARL5B		ARL5B protein ratio				0.51	#DIV/0!
	K.LWSLFCNQEHK.V [7, 17]	ARL5B peptide ratio, 1	0.74	0.97	0.56	0.72	0.17
	K.NTHFLMWDIGGQESLR.S [58, 73]	ARL5B peptide ratio, 2	1.39	0.85	0.50	0.77	0.37
	K.AAVLIFANK.Q [117, 125]	ARL5B peptide ratio, 3	0.65	0.66	0.74	0.68	0.04
	K.GCMTAAEISK.Y [130, 139]	ARL5B peptide ratio, 4	1.48	0.84	1.04	1.06	0.27
RAB2B		RAB2B protein ratio				0.85	#DIV/0!
	R.MVNIDGK.Q [46, 52]	RAB2B peptide ratio, 1	0.84	0.62	1.60	0.87	0.42
	K.IQQGLFDVHNEANGIK.I [170, 185]	RAB2B peptide ratio, 2	0.53	1.06	1.18	0.82	0.28
	K.IGPQQSISTSVGSPASQR.N [186, 2	RAB2B peptide ratio, 3	0.90	0.93	1.16	0.98	0.12
RABL3		RABL3 protein ratio				1.41	#DIV/0!
	R.WSLEALNR.D [108, 115]	RABL3 peptide ratio, 1	ND	ND	ND	ND	ND
	R.YLAAGSSNAVK.L [184, 194]	RABL3 peptide ratio, 2	2.74	3.07	1.98	2.51	0.45
	R.EGNQIPGFPDR.K [211, 221]	RABL3 peptide ratio, 3	0.80	0.85	3.50	1.10	1.26
RRAGA		RRAGA protein ratio				ND	#DIV/0!
	R.LGATIDVEHSHVR.F [38, 50]	RRAGA peptide ratio, 1	ND	ND	ND	ND	ND
	R.NFAQIIEADEVLLFER.A [192, 207]	RRAGA peptide ratio, 2	ND	ND	ND	ND	ND
RABL6		RABL6 protein ratio				ND	#DIV/0!
	K.LVGSQAPGR.D [7, 16]	RABL6 peptide ratio, 1	ND	ND	ND	ND	ND
	K.NIPAGLQSMNQALQR.R [19, 33]	RABL6 peptide ratio, 2	ND	ND	ND	ND	ND
	K.FFNIPFLQLQR.E [226, 236]	RABL6 peptide ratio, 3	ND	ND	ND	ND	ND
RAB4B		RAB4B protein ratio				0.74	#DIV/0!
	K.FLVIGSAGTGK.S [45, 55]	RAB4B peptide ratio, 1	ND	ND	ND	ND	ND
	K.SCLLHQFIENK.F [56, 66]	RAB4B peptide ratio, 2	1.73	3.55	0.57	1.15	1.23
	K.IDSGELDPER.M [207, 216]	RAB4B peptide ratio, 3	0.67	0.54	0.66	0.62	0.06
	R.MGSGIQYGDAASLR.Q [217, 229]	RAB4B peptide ratio, 4	3.05	6.82	0.24	0.65	2.69
ARF1		ARF1 protein ratio				0.84	#DIV/0!
	K.NISFTVWDVGGQDK.I [59, 72]	ARF1 peptide ratio, 1	0.96	0.92	0.91	0.93	0.02
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 2	1.67	2.07	0.65	1.14	0.60
	K.QDLPNAMNAAEITDK.L [127, 141]	ARF1 peptide ratio, 3	0.79	0.79	0.87	0.81	0.04
ARF3		ARF3 protein ratio				1.06	#DIV/0!
	R.VNEAREELMR.M [99, 108] (missed	ARF3 peptide ratio, 1	ND	ND	ND	ND	ND
	R.VNEAREELMR.M [99, 108] (missed	ARF3 peptide ratio, 2	1.00	0.99	1.60	1.14	0.29
	K.LGLHSLR.H [142, 148]	ARF3 peptide ratio, 3	1.08	1.09	1.00	1.05	0.04
ARF4		ARF4 protein ratio				0.86	#DIV/0!
	K.NICFTVWDVGGQDR.I [59, 72]	ARF4 peptide ratio, 1	0.89	1.26	0.87	0.98	0.18
	R.IQEVADLQK.M [99, 108]	ARF4 peptide ratio, 2	0.84	0.85	1.12	0.92	0.13
	R.DAVLLLLFANK.Q [117, 126]	ARF4 peptide ratio, 3	0.81	4.91	1.24	1.34	1.84
	K.LGLQSLR.N [142, 148]	ARF4 peptide ratio, 4	0.94	0.95	0.87	0.92	0.03
ARF5		ARF5 protein ratio				1.14	#DIV/0!

	K.NICFTVWDVGGQDK.I [59, 72]	ARF5 peptide ratio, 1	2.21	3.16	0.37	0.86	1.16
	R.VQESADELQK.M [99, 108]	ARF5 peptide ratio, 2	2.37	2.68	0.34	0.80	1.04
	K.LGLQLHLR.S [142, 148]	ARF5 peptide ratio, 3	1.47	1.29	1.17	1.30	0.12
ARF6		ARF6 protein ratio				1.12	#DIV/0!
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 1	0.97	0.67	1.06	0.86	0.17
	R.ILMLGLDAAGK.T [15, 25]	ARF6 peptide ratio, 2	4.42	1.60	1.12	1.72	1.45
	K.LGQSVTTIPTVGFNVETVTK.N [34, 34]	ARF6 peptide ratio, 3	0.65	1.69	1.10	0.99	0.43
	K.FNVWDVGGQDK.I [58, 68]	ARF6 peptide ratio, 4	ND	ND	ND	ND	ND
RALA		RALA protein ratio				0.55	#DIV/0!
	K.GQNSLALHK.V [7, 15]	RALA peptide ratio, 1	0.10	0.43	0.17	0.17	0.14
	K.EDENVPFLLVGNK.S [115, 127]	RALA peptide ratio, 2	0.42	0.56	1.04	0.59	0.26
	R.QVSVEEAK.N [135, 142]	RALA peptide ratio, 3	1.25	4.71	1.08	1.55	1.67
	R.AEQWNVNYVETSAK.T [145, 158]	RALA peptide ratio, 4	0.92	0.93	0.52	0.73	0.19
RHOT1		RHOT1 protein ratio				ND	#DIV/0!
	R.LPLILVGNK.S [110, 118]	RHOT1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.AVLHPTGPLYCPEEK.E [164, 178]	RHOT1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.ICFNTPLAPQALEDVK.N [214, 229]	RHOT1 peptide ratio, 3	ND	ND	ND	ND	ND
ARL1		ARL1 protein ratio				1.24	#DIV/0!
	R.ILILGLDGAGK.T [19, 29]	ARL1 peptide ratio, 1	0.98	2.01	3.30	1.65	0.95
	K.FQVWDLGGQTSIRPYWR.C [62, 78]	ARL1 peptide ratio, 2	2.14	0.24	0.78	0.50	0.80
	K.AILVVFANK.Q [118, 126]	ARL1 peptide ratio, 3	0.79	0.60	1.89	0.86	0.57
RAC1		RAC1 protein ratio				0.50	#DIV/0!
	R.LRPLSYPQTVGETYK.D [66, 81]	RAC1 peptide ratio, 1	0.50	0.55	0.45	0.50	0.04
RABL2B		RABL2B protein ratio				1.50	#DIV/0!
	K.IDADINVTQK.S [134, 143]	RABL2B peptide ratio, 1	1.53	1.69	1.33	1.50	0.15
ARL16		ARL16 protein ratio				ND	#DIV/0!
	K.GDLGEPPTRPTVGTNLTDIVAQR.R [177, 184]	ARL16 peptide ratio, 1	ND	ND	ND	ND	ND
	K.QNITTAEISAR.E [166, 176]	ARL16 peptide ratio, 2	ND	ND	ND	ND	ND
	R.EGTGLAGVLAWLQATHR.A [177, 184]	ARL16 peptide ratio, 3	ND	ND	ND	ND	ND
REM1		REM1 protein ratio				ND	#DIV/0!
	R.LSTVPSTQSQHPR.L [32, 44]	REM1 peptide ratio, 1	ND	ND	ND	ND	ND
	K.TSLASLFAGK.Q [93, 102]	REM1 peptide ratio, 2	ND	ND	ND	ND	ND
	R.DLHEQLGEDVYER.T [106, 118]	REM1 peptide ratio, 3	ND	ND	ND	ND	ND
	R.GSFESASELR.I [166, 175]	REM1 peptide ratio, 4	ND	ND	ND	ND	ND
RAB14		RAB14 protein ratio				0.89	#DIV/0!
	K.YIIIGDMGVGK.S [13, 23]	RAB14 peptide ratio, 1	1.20	1.16	1.19	1.18	0.01
	R.STYNHLSSWLTAR.N [96, 109]	RAB14 peptide ratio, 2	0.90	0.86	1.25	0.98	0.17
	K.TGENVEDAFLEAAK.K [156, 169]	RAB14 peptide ratio, 3	1.71	0.84	0.64	0.90	0.47
SRPRB		SRPRB protein ratio				1.00	#DIV/0!
	R.AVLLVGLCDSGK.T [65, 76]	SRPRB peptide ratio, 1	1.88	3.84	1.12	1.78	1.15
	R.DTQTSITDSCAVYR.V [90, 103]	SRPRB peptide ratio, 2	0.90	0.78	0.60	0.74	0.12
	K.LIQQQLEK.E [191, 198]	SRPRB peptide ratio, 3	1.02	0.91	1.05	0.99	0.06
RAB35		RAB35 protein ratio				0.74	#DIV/0!
	R.TITSTYYR.G [71, 78]	RAB35 peptide ratio, 1	0.77	0.79	0.70	0.75	0.04
	R.WLHEINQNCDDVCR.I [101, 114]	RAB35 peptide ratio, 2	0.66	0.78	0.66	0.70	0.05
	K.VVETEDAYK.F [128, 136]	RAB35 peptide ratio, 3	ND	ND	ND	ND	ND
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 4	ND	ND	ND	ND	ND
	K.FAGQMGIQLFETSAK.E [137, 151]	RAB35 peptide ratio, 5	ND	ND	ND	ND	ND
RAB3B		RAB3B protein ratio				ND	#DIV/0!
	K.DASDQNFDFYMFK.L [12, 23]	RAB3B peptide ratio, 1	ND	ND	ND	ND	ND
	K.GQLLAEQLGFDFFEASAK.E [149, 162]	RAB3B peptide ratio, 2	ND	ND	ND	ND	ND
	K.MSDSLDTPSMLGSSK.N [186, 201]	RAB3B peptide ratio, 3	ND	ND	ND	ND	ND
RAB30		RAB30 protein ratio				1.87	#DIV/0!
	K.IVLIGNAGVGK.T [11, 21]	RAB30 peptide ratio, 1	2.17	2.09	3.20	2.39	0.50
	R.EIEQYASNK.V [105, 113]	RAB30 peptide ratio, 2	1.59	4.96	2.84	2.54	1.39
	K.VITVLVGNK.I [114, 122]	RAB30 peptide ratio, 3	3.11	2.62	1.62	2.27	0.62
	K.LFLDLACR.L [161, 168]	RAB30 peptide ratio, 4	ND	ND	ND	ND	ND
	R.QNTLVNNSPLPGEK.S [175, 190]	RAB30 peptide ratio, 5	ND	ND	ND	ND	ND
RHOF		RHOF protein ratio				ND	#DIV/0!
	K.IVIVGDGGCGK.T [21, 31]	RHOF peptide ratio, 1	ND	ND	ND	ND	ND
	K.YTASVTVGSK.E [55, 64]	RHOF peptide ratio, 2	ND	ND	ND	ND	ND
	K.EVTLNLYDTAGQEDYDR.L [65, 81]	RHOF peptide ratio, 3	ND	ND	ND	ND	ND
	K.WFPEVTHFCR.G [112, 121]	RHOF peptide ratio, 4	ND	ND	ND	ND	ND
	R.AALYLECSAK.F [166, 175]	RHOF peptide ratio, 5	ND	ND	ND	ND	ND
RAB34		RAB34 protein ratio				ND	#DIV/0!
	K.VIVVGDLSVGK.T [54, 64]	RAB34 peptide ratio, 1	ND	ND	ND	ND	ND
	R.FEVLGIPFSLQLWDTAGQER.F [93, 103]	RAB34 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ENDPSSVLLFLVGSK.K [152, 166]	RAB34 peptide ratio, 3	ND	ND	ND	ND	ND
	K.AEYWAVSSLTGENVR.E [191, 205]	RAB34 peptide ratio, 4	ND	ND	ND	ND	ND
	R.INSDDSNLYLTASK.K [238, 251]	RAB34 peptide ratio, 5	ND	ND	ND	ND	ND
RAB43		RAB43 protein ratio				1.08	#DIV/0!
	K.YAGSNIVQLLIGNK.S [118, 131]	RAB43 peptide ratio, 1	0.86	1.00	1.23	1.01	0.15
	K.DSSNVEEAFLR.V [164, 174]	RAB43 peptide ratio, 2	ND	ND	ND	ND	ND
	R.VATELIMR.H [175, 182]	RAB43 peptide ratio, 3	ND	ND	ND	ND	ND

	K.SPDHIQLNSK.D [192, 201]	RAB43 peptide ratio, 4	1.30	0.69	1.48	1.04	0.34
NKIRAS1		NKIRAS1 protein ratio				0.62	#DIV/0!
	K.VVVCGLLSVVGK.T [6, 16]	NKIRAS1 peptide ratio, 1	0.93	0.86	0.75	0.84	0.07
	R.QVDAEVAQQWAK.S [128, 139]	NKIRAS1 peptide ratio, 2	0.11	6.87	0.43	0.25	3.12
	K.TLIEPFTLLASK.L [155, 166]	NKIRAS1 peptide ratio, 3	0.99	0.83	1.17	0.98	0.14
RAB12		RAB12 protein ratio				0.29	#DIV/0!
	R.AGGGGGLGAGSPALSGGQGR.R [RAB12 peptide ratio, 1	0.30	0.24	0.44	0.30	0.08
	K.LQVIIIGSR.G [42, 50]	RAB12 peptide ratio, 2	0.43	0.39	0.37	0.40	0.03
	R.FTDDTFCEACK.S [61, 71]	RAB12 peptide ratio, 3	3.18	0.39	0.37	0.54	1.32
	R.FNSITSAYYR.S [103, 112]	RAB12 peptide ratio, 4	0.59	0.63	0.44	0.54	0.08
	K.FAQQITGMR.F [172, 180]	RAB12 peptide ratio, 5	ND	ND	ND	ND	ND
KRAS		KRAS(4A) protein ratio				ND	#DIV/0!
Isoform 2A	K.DSEDVPMVLVGNK.C [104, 116]	KRAS(4A) peptide ratio, 1	ND	ND	ND	ND	ND
Isoform 2A	R.QRVEDAFYTLVR.E [149, 160] (miss	KRAS(4A) peptide ratio, 2	ND	ND	ND	ND	ND
Isoform 2A	R.VEDAFYTLVR.E [151, 160]	KRAS(4A) peptide ratio, 3	ND	ND	ND	ND	ND
KRAS		KRAS(4B) protein ratio				0.88	#DIV/0!
Isoform 2B	R.SYGIPFIETSAK.T [135, 146]	KRAS(4B) peptide ratio, 1	1.31	0.61	1.02	0.89	0.29
Isoform 2B	K.TRQGVDDAFYTLVR.E [147, 160] (n	KRAS(4B) peptide ratio, 2	3.18	4.02	0.42	1.02	1.54
Isoform 2B	R.QGVDDAFYTLVR.E [149, 160]	KRAS(4B) peptide ratio, 3	2.76	0.67	2.02	1.28	0.86
RAB11A		RAB11A protein ratio				ND	#DIV/0!
	K.NGLSFIETSALDSTNVEAAFQILTET	RAB11A peptide ratio, 1	ND	ND	ND	ND	ND
RHOT2		RHOT2 protein ratio				ND	#DIV/0!
	K.WIPLVNGGTTQGPR.V [96, 109]	RHOT2 peptide ratio, 1	ND	ND	ND	ND	ND
	K.SAFLQAFLGR.G [429, 438]	RHOT2 peptide ratio, 2	ND	ND	ND	ND	ND
	K.ADLPEGVAVSGPSPAEFQR.K [525,	RHOT2 peptide ratio, 3	ND	ND	ND	ND	ND
RAB19		RAB19 protein ratio				ND	#DIV/0!
	R.AADENFDYLFK.I [76, 86]	RAB19 peptide ratio, 1	ND	ND	ND	ND	ND
	K.IILIGDSNVGK.T [87, 97]	RAB19 peptide ratio, 2	ND	ND	ND	ND	ND
	K.MQVWDTAGQER.F [135, 145]	RAB19 peptide ratio, 3	ND	ND	ND	ND	ND
	R.SAHAIIAYDLTR.R [156, 168]	RAB19 peptide ratio, 4	ND	ND	ND	ND	ND
	R.HVLFEDACTLAEK.Y [205, 217]	RAB19 peptide ratio, 5	ND	ND	ND	ND	ND
RHOA		RHOA protein ratio				0.73	#DIV/0!
	K.QEPVKPEEGR.D [135, 144]	RHOA peptide ratio, 1	ND	ND	ND	ND	ND
	R.IGAFGYMECSAK.T [150, 161]	RHOA peptide ratio, 2	0.78	0.81	0.41	0.60	0.18
	R.IGAFGYMECSAK.T [150, 161]	RHOA peptide ratio, 3	0.82	0.81	1.12	0.89	0.14
RAB4A		RAB4A protein ratio				0.95	#DIV/0!
	K.FLVIGNAGTGK.S [15, 25]	RAB4A peptide ratio, 1	0.89	0.95	1.11	0.98	0.09
	K.IESGELDPER.M [177, 186]	RAB4A peptide ratio, 2	0.81	0.86	1.28	0.95	0.21
	R.MGSGIQYGDAALR.Q [187, 199]	RAB4A peptide ratio, 3	ND	ND	ND	ND	ND
RAN		RAN protein ratio				0.80	#DIV/0!
	K.FNVWDTAGQEK.F [60, 70]	RAN peptide ratio, 1	0.74	0.69	0.80	0.74	0.04
	R.VCENIPIVLCGNK.V [110, 122]	RAN peptide ratio, 2	0.88	1.31	2.39	1.30	0.63
	K.NLQYYDISAK.S [142, 151]	RAN peptide ratio, 3	0.75	0.74	1.01	0.82	0.13
RAB34		RAB34 protein ratio				ND	#DIV/0!
	-.MSHLPGLELR.R [0, 9]	RAB34 peptide ratio, 1	ND	ND	ND	ND	ND
	R.VLAELPQCLR.K [68, 77]	RAB34 peptide ratio, 2	ND	ND	ND	ND	ND
RAB11A		RAB11A protein ratio				ND	#DIV/0!
	R.ENDMSPSNNVVPIHVPPTTENKPK	RAB11A peptide ratio, 1	ND	ND	ND	ND	ND
	R.ENDMSPSNNVVPIHVPPTTENKPK	RAB11A peptide ratio, 2	ND	ND	ND	ND	ND
RABL4/IFT27		RABL4 protein ratio				2.29	#DIV/0!
	K.CILAGDPAVGK.T [7, 17]	RABL4 peptide ratio, 1	ND	ND	ND	ND	ND
	K.TALAQIFR.S [18, 25]	RABL4 peptide ratio, 2	2.37	2.40	2.12	2.29	0.13
	R.SQAPGISLPGVLVGNK.T [108, 123]	RABL4 peptide ratio, 3	ND	ND	ND	ND	ND