Title page

ARHGAP24 represses β-catenin transactivation-induced invasiveness in hepatocellular carcinoma mainly by acting as a GTPase-independent scaffold

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Supplementary Figures

Supplementary figure 1. Low ARHGAP24 expression indicates the poorer prognosis of HCC patients. A. Kaplan-Meier analysis of the overall survival (OS) in HCC patients stratified by ARHGAP24 expression according to K-M plotter dataset. **B.** Kaplan-Meier analysis of the relapse-free survival (RFS) in HCC patients stratified by ARHGAP24 expression according to K-M plotter dataset. **C.** Kaplan-Meier analysis of the progression-free survival (PFS) in HCC patients stratified by ARHGAP24 expression according to K-M plotter dataset. **D.** Kaplan-Meier analysis of the disease-specific survival (DSS) in HCC patients stratified by ARHGAP24 expression according to K-M plotter dataset.

Supplementary figure 2. ARHGAP24 expression could predict the prognosis of HCC patients with high risk of recurrence. A. Kaplan-Meier analysis of progression-free survival (PFS) of HCC patients with tumor size < 5 cm, with single tumor number, and with early tumor differentiation. **B.** Kaplan-Meier analysis of progression-free survival (PFS) of HCC patients with early tumor stage (Chinese liver tumor stage), without satellite lesions and without microvascular invasion. **C.** Univariate cox proportional regression analysis of factors associated with HCC tumor recurrence.

Supplementary figure 3. Kaplan-Meier analysis for OS in other tumors. A.

Kaplan-Meier analysis of the OS of kidney renal clear cell carcinoma in ARHGAP24 high expression group and ARHGAP24 low expression group. **B.** Kaplan-Meier analysis of the OS of lung adenocarcinoma in ARHGAP24 high expression group and ARHGAP24 low expression group. **C.** Kaplan-Meier analysis of the OS of pancreatic ductal adenocarcinoma in ARHGAP24 high expression group and ARHGAP24 low expression group. **D.** Kaplan-Meier analysis of the OS of kidney renal papillary cell carcinoma in ARHGAP24 high expression group and ARHGAP24 low expression group. **E.** Kaplan-Meier analysis of the OS of lung squamous cell carcinoma in ARHGAP24 high expression group and ARHGAP24 low expression group.

Supplementary figure 4. ARHGAP24 overexpression inhibits huh7 cell proliferation. A. Cell proliferation-related molecules were detected by WB assays in ARHGAP24 overexpressed-Huh7 cells. **B.** Effects of ARHGAP24 overexpression on huh7 cell proliferation using colony formation assays. **C.** Effects of ARHGAP24 overexpression on huh7 cell proliferation using CCK8 assays. **D.** Effects of ARHGAP24 knockdown on Li-7 cell cycle using flow cytometry. **E.** Effects of ARHGAP24 overexpression on Huh7 cell cycle using flow cytometry. **F.** Effects of ARHGAP24 overexpression on HCCLM3 cell cycle using flow cytometry. **G.** Effects of ARHGAP24 overexpression on Huh7 cell apoptosis using flow cytometry.

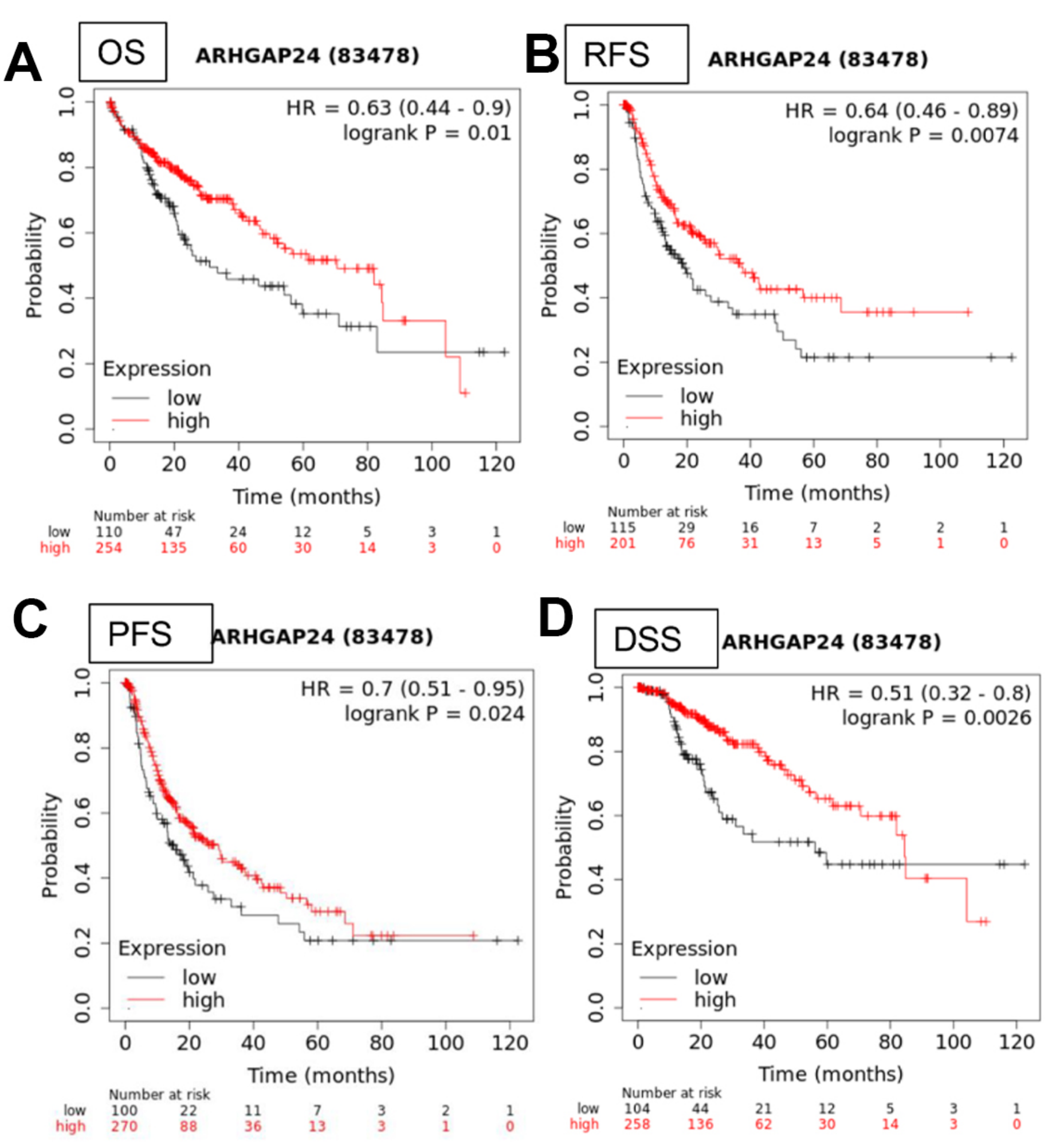
Supplementary figure 5. ARHGAP24 inhibits cell invasiveness via inactivating wnt/β-catenin signaling pathway. A. Effects of ARHGAP24 overexpression on Huh7 cell migration and invasion using Transwell assays. **B.** Effects of ARHGAP24 overexpression on Huh7 cell migration using scratch wound healing assays. **C.** qRT-PCR analysis of EMT-related markers in ARHGAP24 overexpressed Huh7 cells. **D.** Protein expression of EMT-related markers in ARHGAP24 overexpressed Huh7 cells. **E.** Protein expression of downstream target genes of β-catenin in ARHGAP24 overexpression and knockdown cells. **F.** Effects of ICG-001 on HCCLM3 cell proliferation using CCK8 assays. **G.** Effects of ICG-001 on sh-ARH Li-7 cell proliferation using CCK8 assays.

Supplementary figure 6. ARHGAP24 inhibits cell invasiveness independent of Rho GTPase activity. A. Q158R plasmids were successfully constructed and confirmed by sanger sequence analysis. **B.** Protein expressions of EMT-related markers in HCCLM3 cells transfected with the indicated plasmids. **C.** Protein expressions of EMT-related markers in Huh7 cells transfected with the indicated plasmids.

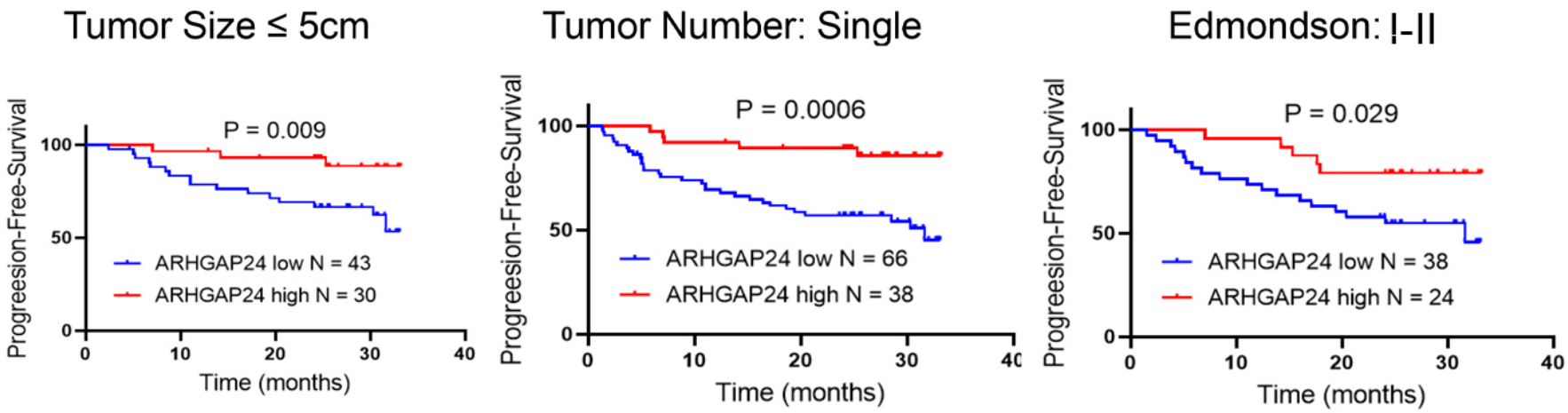
Supplementary figure 7. ARHGAP24 inhibits HCC progression by degradation of PKM2. A. PKM2 was successfully silenced in ARHGAP24 knockdown cells. **B.** Protein expressions of EMT-related markers were detected

by WB assays. **C.** Silenced PKM2 have no effects on increased Rho GTPase activity caused by knockdown ARHGAP24 in Li-7 cells. **D.** Effects of PKM2 silencing on HCCLM3 cell proliferation using CCK8 assays. **E.** Effects of PKM2 silencing on sh-ARH Li-7 cell proliferation using CCK8 assays.

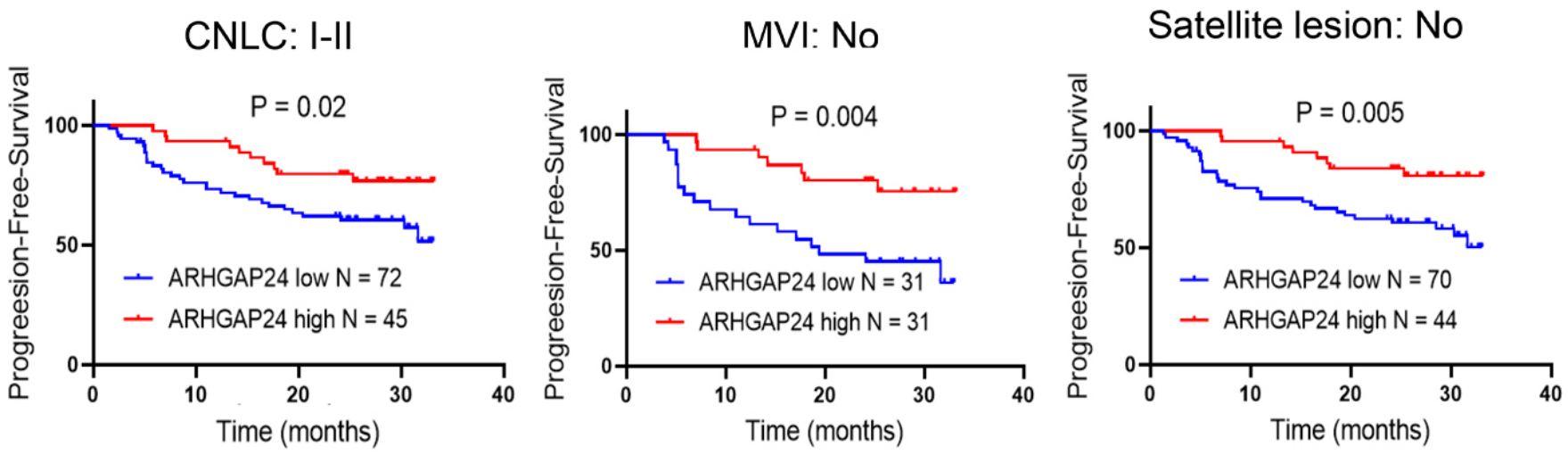
Supplementary figure 8. ARHGAP24 recruits WWP1 to degrade PKM2. A. IP and WB analyses of PKM2, WWP1 and ARHGAP24 protein expression in HCCLM3 and MHCC97H cells transfected with the numbers of ARHGAP24-HA plasmids. **B.** Representative pictures of the binding domain of the ARHGAP24 and PKM2 structure. **C.** IP and WB analyses and Ubiquitination assays of PKM2 in the presence or absence of ARHGAP24 C-terminal domain.


A
OS
ARHGAP24 (83478)
HR = 0.63 (0.44 - 0.9)
logrank P = 0.01
Probability
Expression
low
high
Time (months)
Number at risk
low 110 47 24 12 5 3 1
high 254 135 60 30 14 3 0
B
RFS
ARHGAP24 (83478)
HR = 0.64 (0.46 - 0.89)
logrank P = 0.0074
Probability
Expression
low
high
Time (months)
Number at risk
low 115 29 16 7 2 2 1
high 201 76 31 13 5 1 0
C
PFS
ARHGAP24 (83478)
HR = 0.7 (0.51 - 0.95)
logrank P = 0.024
Probability
Expression
low
high
Time (months)
Number at risk
low 100 22 11 7 3 2 1
high 270 88 36 13 3 1 0
D
DSS
ARHGAP24 (83478)
HR = 0.51 (0.32 - 0.8)
logrank P = 0.0026
Probability
Expression
low
high
Time (months)
Number at risk
low 104 44 21 12 5 3 1
high 258 136 62 30 14 3 0

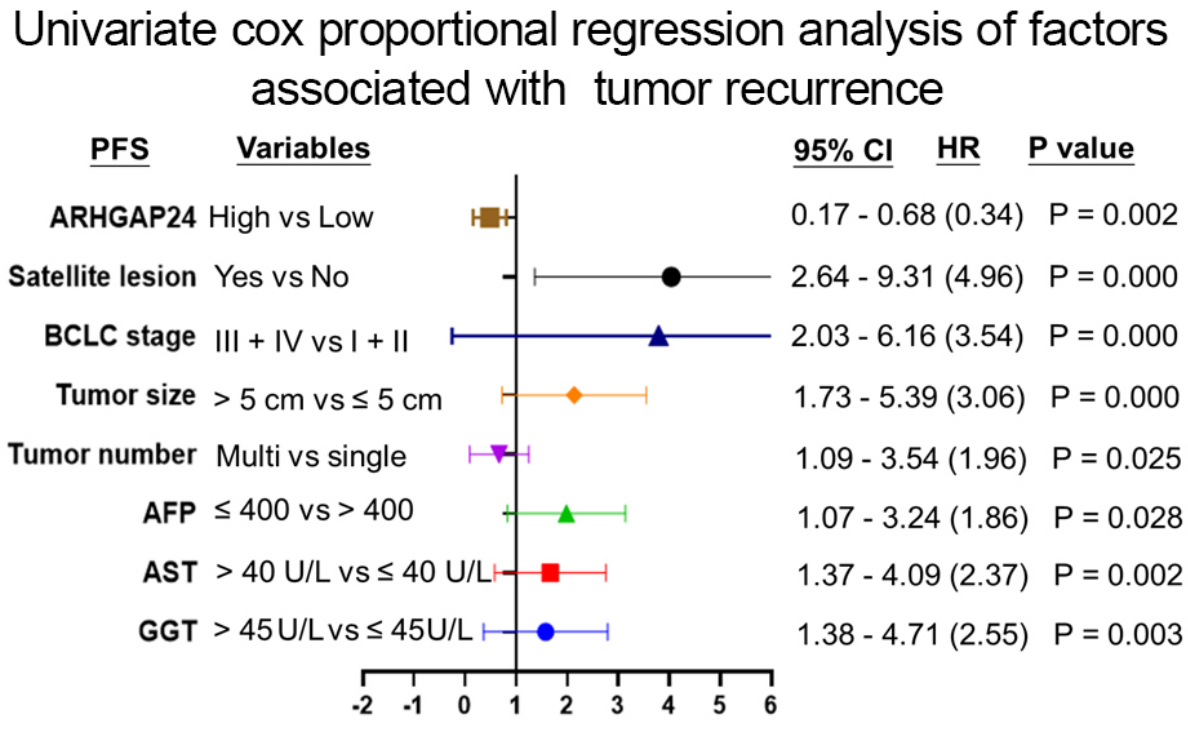
A


Tumor Size ≤ 5cm
P = 0.009
ARHGAP24 low N = 43
ARHGAP24 high N = 30
Tumor Number: Single
P = 0.0006
ARHGAP24 low N = 66
ARHGAP24 high N = 38
Edmondson: I-II
P = 0.029
ARHGAP24 low N = 38
ARHGAP24 high N = 24
Progreesion-Free-Survival
Time (months)

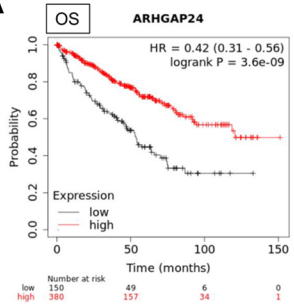
B


CNLC: I-II
P = 0.02
ARHGAP24 low N = 72
ARHGAP24 high N = 45
MVI: No
P = 0.004
ARHGAP24 low N = 31
ARHGAP24 high N = 31
Satellite lesion: No
P = 0.005
ARHGAP24 low N = 70
ARHGAP24 high N = 44
Progreesion-Free-Survival
Time (months)

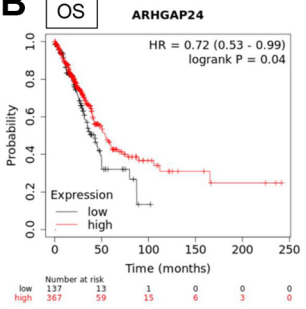
C


Univariate cox proportional regression analysis of factors associated with tumor recurrence
PFS
Variables
95% CI
HR
P value
ARHGAP24 High vs Low 0.17 - 0.68 (0.34) P = 0.002
Satellite lesion Yes vs No 2.64 - 9.31 (4.96) P = 0.000
BCLC stage III + IV vs I + II 2.03 - 6.16 (3.54) P = 0.000
Tumor size > 5 cm vs ≤ 5 cm 1.73 - 5.39 (3.06) P = 0.000
Tumor number Multi vs single 1.09 - 3.54 (1.96) P = 0.025
AFP ≤ 400 vs > 400 1.07 - 3.24 (1.86) P = 0.028
AST > 40 U/L vs ≤ 40 U/L 1.37 - 4.09 (2.37) P = 0.002
GGT > 45 U/L vs ≤ 45 U/L 1.38 - 4.71 (2.55) P = 0.003
-2 -1 0 1 2 3 4 5 6

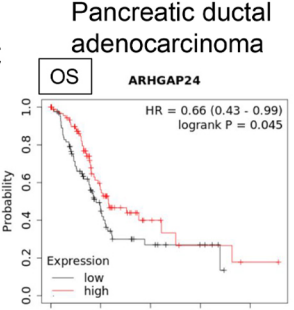
A


Kidney renal clear cell carcinoma
OS
ARHGAP24
HR = 0.42 (0.31 - 0.56)
logrank P = 3.6e-09
Probability
Expression
low
high
Time (months)
Number at risk
low 150 49 6 0
high 380 157 34 1

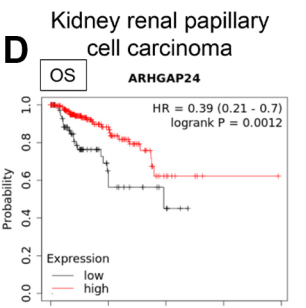
B


Lung adenocarcinoma
OS
ARHGAP24
HR = 0.72 (0.53 - 0.99)
logrank P = 0.04
Probability
Expression
low
high
Time (months)
Number at risk
low 137 13 1 0 0 0
high 367 59 15 6 3 0

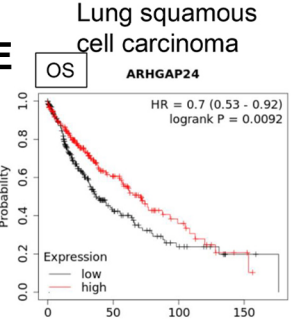
C

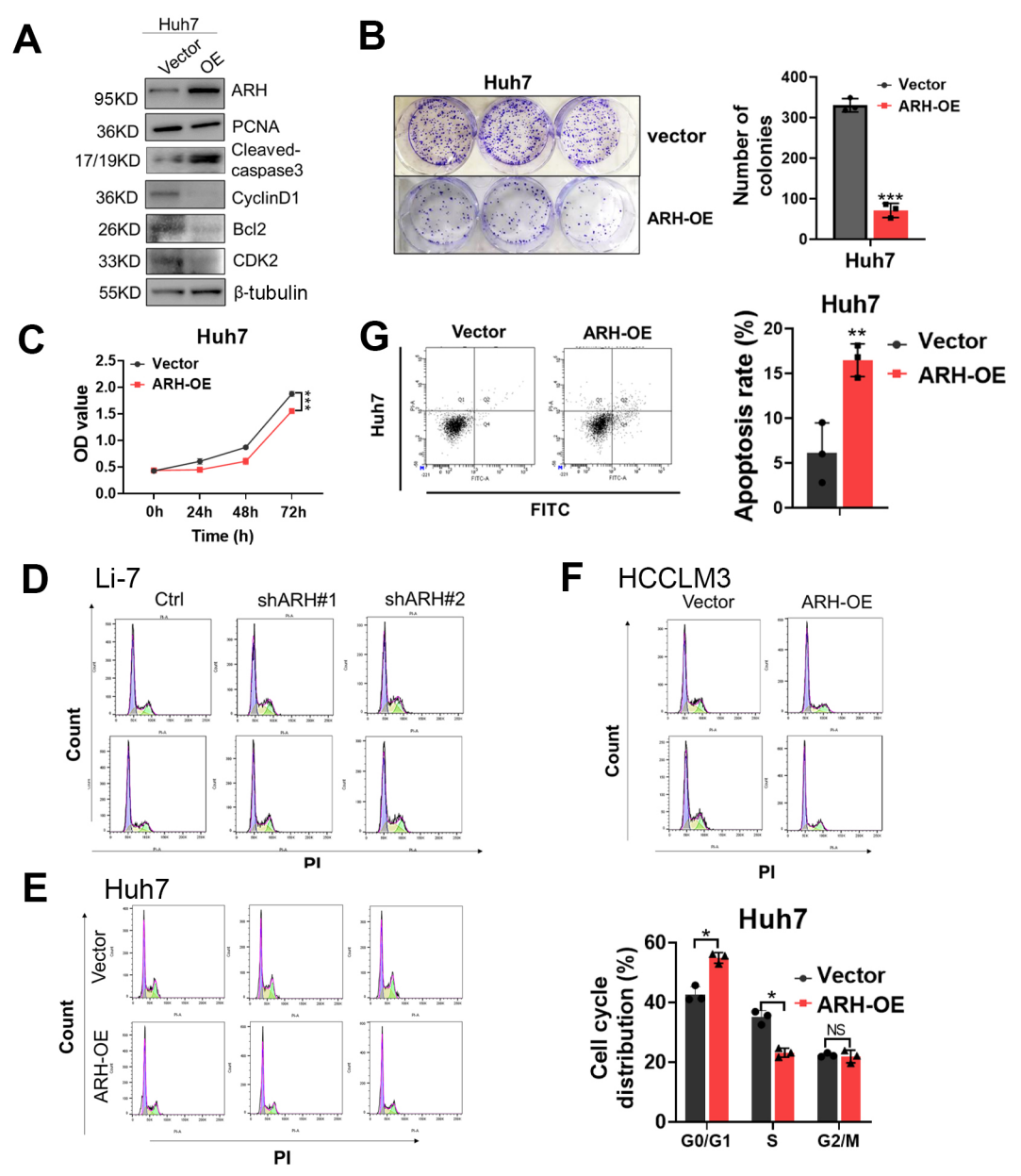

Pancreatic ductal adenocarcinoma
OS
ARHGAP24
HR = 0.66 (0.43 - 0.99)
logrank P = 0.045
Probability
Expression
low
high
Time (months)
Number at risk
low 84 25 9 5 0
high 93 33 8 3 1

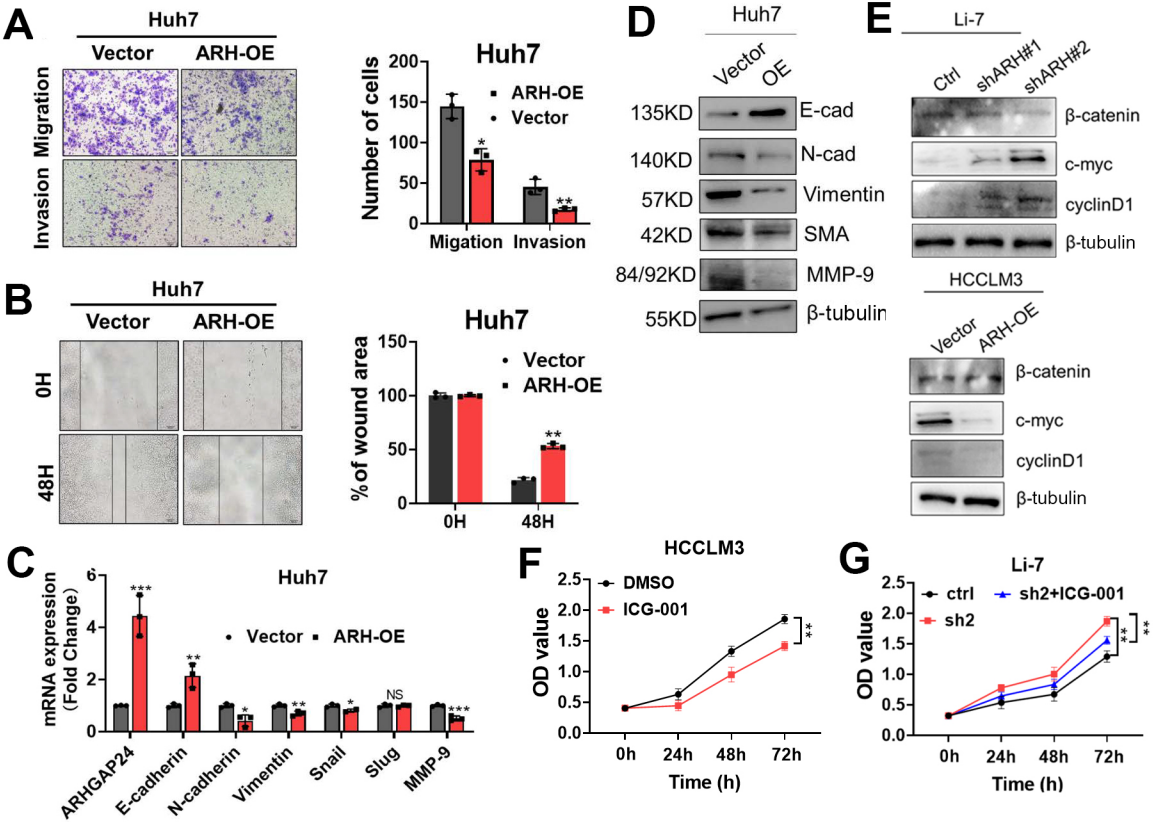
D

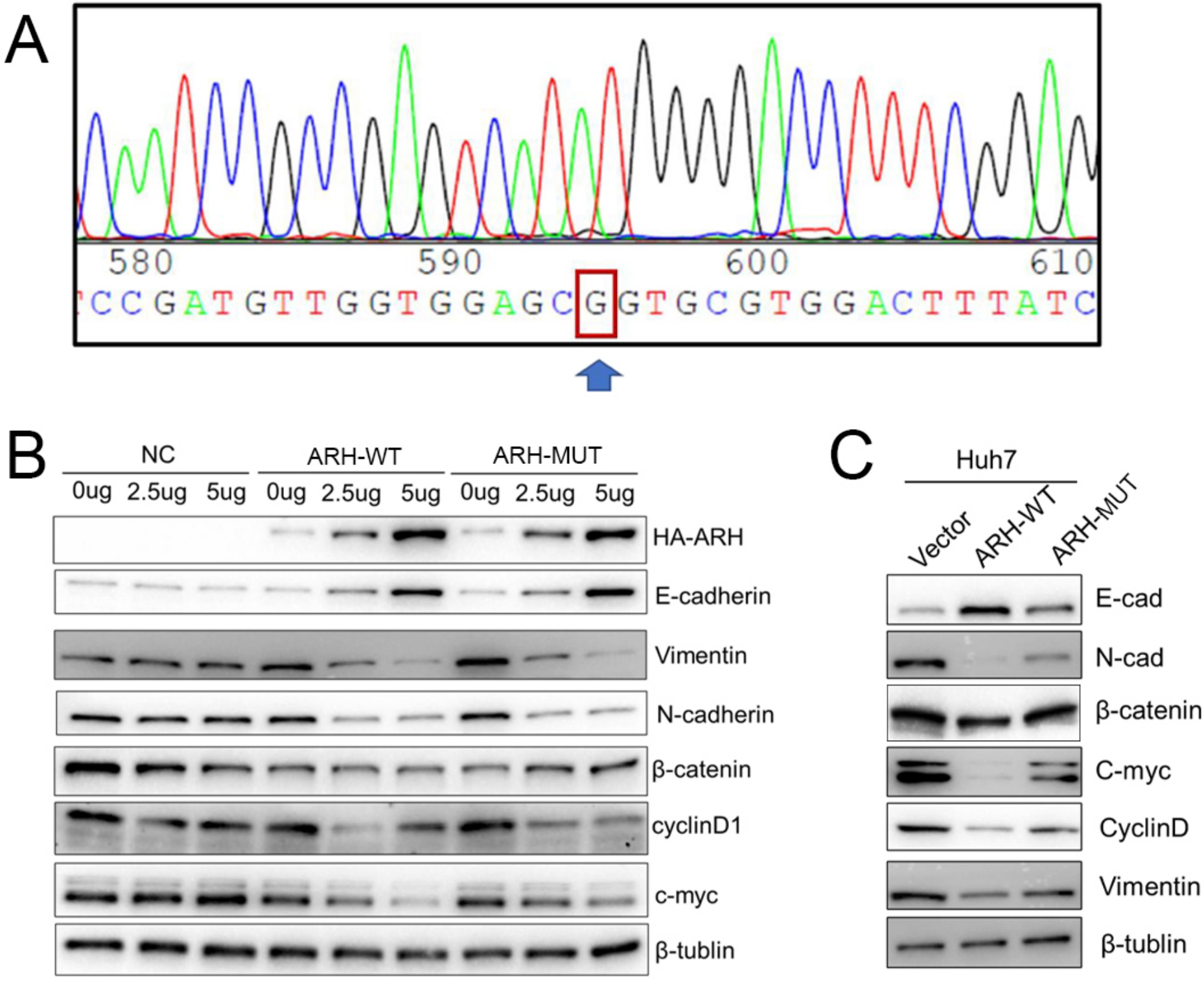

Kidney renal papillary cell carcinoma
OS
ARHGAP24
HR = 0.39 (0.21 - 0.7)
logrank P = 0.0012
Probability
Expression
low
high
Time (months)
Number at risk
low 77 14 4 0 0
high 210 59 8 1 0

E


Lung squamous cell carcinoma
OS
ARHGAP24
HR = 0.7 (0.53 - 0.92)
logrank P = 0.0092
Probability
Expression
low
high
Time (months)
Number at risk
low 261 42 12 2
high 234 63 15 3


A
Huh7
Vector
OE
95KD
ARH
36KD
PCNA
17/19KD
Cleaved-caspase3
36KD
CyclinD1
26KD
Bcl2
33KD
CDK2
55KD
β-tubulin
B
Huh7
vector
ARH-OE
Number of colonies
Vector
ARH-OE
***
Huh7
C
Huh7
Vector
ARH-OE
OD value
***
0h
24h
48h
72h
Time (h)
G
Vector
ARH-OE
Huh7
FITC
Huh7
Apoptosis rate (%)
**
Vector
ARH-OE
D
Li-7
Ctrl
shARH#1
shARH#2
Count
PI
F
HCCLM3
Vector
ARH-OE
Count
PI
E
Huh7
Vector
ARH-OE
Count
PI
Huh7
Cell cycle distribution (%)
*
*
NS
Vector
ARH-OE
G0/G1
S
G2/M


A
Huh7
Vector
ARH-OE
Migration
Invasion
Huh7
Number of cells
ARH-OE
Vector
Migation
Invasion
B
Huh7
Vector
ARH-OE
0H
48H
Huh7
% of wound area
Vector
ARH-OE
0H
48H
C
Huh7
mRNA expression (Fold Change)
Vector
ARH-OE
ARHGAP24
E-cadherin
N-cadherin
Vimentin
Snail
Slug
MMP-9
NS
D
Huh7
Vector
OE
135KD
E-cad
140KD
N-cad
57KD
Vimentin
42KD
SMA
84/92KD
MMP-9
55KD
β-tubulin
E
Li-7
Ctrl
shARH#1
shARH#2
β-catenin
c-myc
cyclinD1
β-tubulin
HCCLM3
Vector
ARH-OE
β-catenin
c-myc
cyclinD1
β-tubulin
F
HCCLM3
DMSO
ICG-001
OD value
0h
24h
48h
72h
Time (h)
G
Li-7
ctrl
sh2
sh2+ICG-001
OD value
0h
24h
48h
72h
Time (h)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580
590
600
610
CCGATGTTGGTGGAGCGGTGCGTGGACTTTATC
B
NC
ARH-WT
ARH-MUT
0ug 2.5ug 5ug 0ug 2.5ug 5ug 0ug 2.5ug 5ug
HA-ARH
E-cadherin
Vimentin
N-cadherin
β-catenin
cyclinD1
c-myc
β-tublin
C
Huh7
Vector
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ARH-MUT
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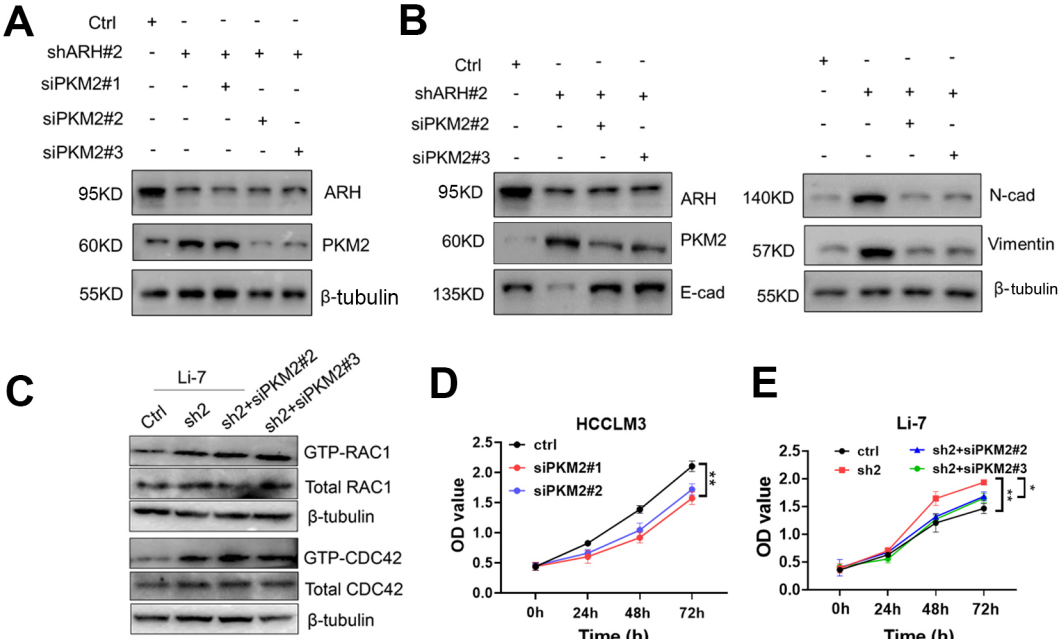
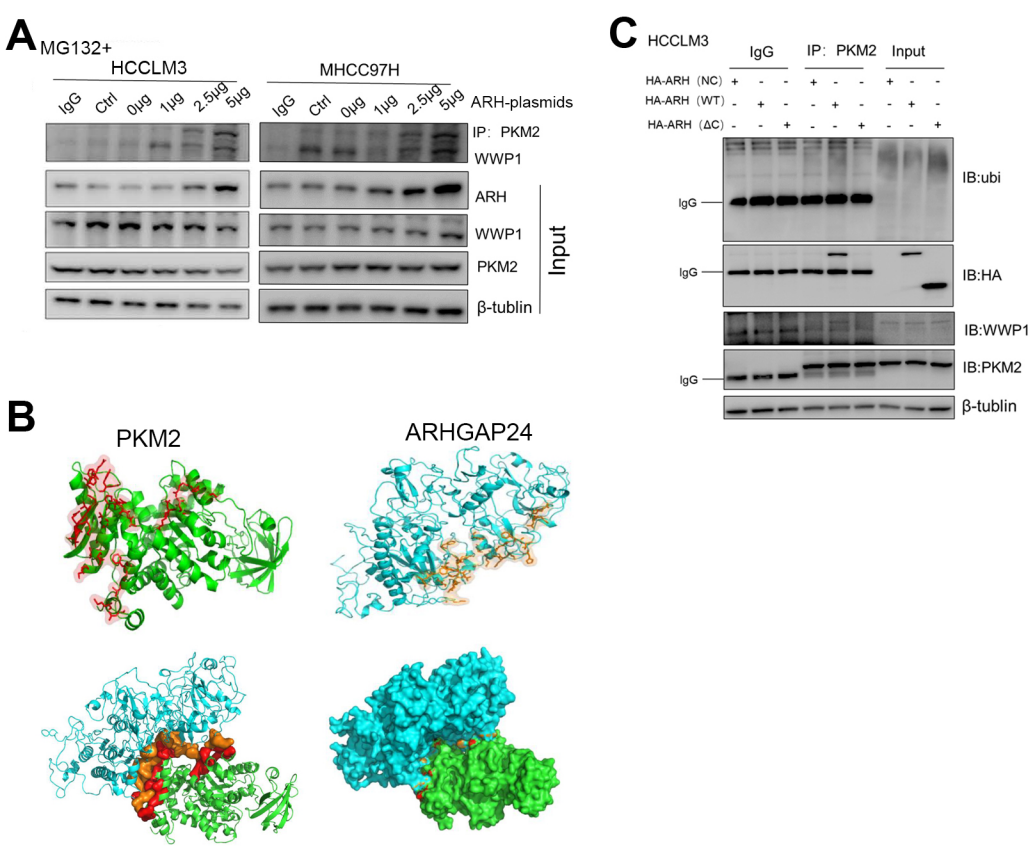
N-cad
β-catenin
C-myc
CyclinD
Vimentin
β-tublin


A
Ctrl
shARH#2
siPKM2#1
siPKM2#2
siPKM2#3
95KD
ARH
60KD
PKM2
55KD
β-tubulin
B
Ctrl
shARH#2
siPKM2#2
siPKM2#3
95KD
ARH
60KD
PKM2
135KD
E-cad
140KD
N-cad
57KD
Vimentin
55KD
β-tubulin
C
Li-7
Ctrl
sh2
sh2+siPKM2#2
sh2+siPKM2#3
GTP-RAC1
Total RAC1
β-tubulin
GTP-CDC42
Total CDC42
β-tubulin
D
HCCLM3
ctrl
siPKM2#1
siPKM2#2
OD value
Time (h)
0h
24h
48h
72h
E
Li-7
ctrl
sh2
sh2+siPKM2#2
sh2+siPKM2#3
OD value
Time (h)


A
MG132+
HCCLM3
MHCC97H
IgG
Ctrl
0μg
1μg
2.5μg
5μg
ARH-plasmids
IP: PKM2
WWP1
ARH
WWP1
PKM2
β-tublin
Input
B
PKM2
ARHGAP24
C
HCCLM3
IgG
IP: PKM2
Input
HA-ARH (NC)
HA-ARH (WT)
HA-ARH (ΔC)
IgG
IB:ubi
IB:HA
IB:WWP1
IB:PKM2
β-tublin

Supplementary Tables

Supplementary Table 1. List of potential interactors of ARHGAP24 identified by IP-MS.

Supplementary Table 2. The correlations between ARHGAP24 expression and clinicopathological characteristics in HCC.

Supplementary Table 3. Univariate cox proportional regression analysis of factors associated with recurrence and overall survival.

Number	Accession	-10lgP	Avg. Mass	Description
1	sp|Q8N264|RHG24_HUMAN	476.95	84258	Rho GTPase-activating protein 24 OS=Homo sapiens OX=9606 GN=ARHGAP24 PE=1 SV=2
2	tr|D6RCP5|D6RCP5_HUMAN	447.89	69481	Rho GTPase-activating protein 24 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGAP24 PE=1 SV=1
3	sp|P07900|HS90A_HUMAN	408.91	84660	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5
4	sp|P04264|K2C1_HUMAN	405.95	66039	Keratin type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6
5	sp|P08238|HS90B_HUMAN	397.88	83264	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4
6	sp|P14618|KPYM_HUMAN	388.63	57937	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4
7	sp|P35527|K1C9_HUMAN	378.05	62064	Keratin type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3
8	sp|Q9H0M0|WWP1_HUMAN	334.02	105202	NEDD4-like E3 ubiquitin-protein ligase WWP1 OS=Homo sapiens OX=9606 GN=WWP1 PE=1 SV=1
9	sp|P13639|EF2_HUMAN	326.51	95338	Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4
10	sp|P23246|SFPQ_HUMAN	321.83	76150	Splicing factor proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2
11	sp|P10809|CH60_HUMAN	320.54	61055	60 kDa heat shock protein mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2
12	sp|P13645|K1C10_HUMAN	318.53	58827	Keratin type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6
13	sp|P0DMV8|HS71A_HUMAN	304.36	70052	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1
14	sp|P0DMV9|HS71B_HUMAN	304.36	70052	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1
15	tr|A0A0G2JIW1|A0A0G2JIW1_HUMAN	304.36	70109	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1
16	sp|P35908|K22E_HUMAN	303.27	65433	Keratin type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2
17	sp|P27824|CALX_HUMAN	300.52	67568	Calnexin OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=2
18	sp|P09874|PARP1_HUMAN	298.49	113084	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4
19	sp|P13010|XRCC5_HUMAN	283.79	82705	X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3
20	sp|Q00839|HNRPU_HUMAN	280.32	90585	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6
21	sp|P55072|TERA_HUMAN	277.94	89322	Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4
22	sp|Q9NR30|DDX21_HUMAN	276.45	87344	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5
23	tr|B9A067|B9A067_HUMAN	275.06	78974	MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=2
24	sp|Q16891|MIC60_HUMAN	275.06	83678	MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1
25	sp|P31948|STIP1_HUMAN	271.16	62639	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1
26	sp|P33993|MCM7_HUMAN	270.96	81308	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4
27	sp|O43143|DHX15_HUMAN	268	90933	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2
28	sp|Q01813|PFKAP_HUMAN	264.17	85596	ATP-dependent 6-phosphofructokinase platelet type OS=Homo sapiens OX=9606 GN=PFKP PE=1 SV=2
29	sp|P22314|UBA1_HUMAN	262.3	117849	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3
30	sp|P11142|HSP7C_HUMAN	261.73	70898	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1
31	sp|Q12906|ILF3_HUMAN	259.29	95339	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3
32	sp|P49368|TCPG_HUMAN	258.11	60534	T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=4
33	sp|P47897|SYQ_HUMAN	256.49	87799	Glutamine--tRNA ligase OS=Homo sapiens OX=9606 GN=QARS PE=1 SV=1
34	sp|P38646|GRP75_HUMAN	256.08	73681	Stress-70 protein mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2
35	sp|P19338|NUCL_HUMAN	254.37	76615	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3
36	sp|P53396|ACLY_HUMAN	254.33	120839	ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3
37	sp|P33992|MCM5_HUMAN	252.29	82286	DNA replication licensing factor MCM5 OS=Homo sapiens OX=9606 GN=MCM5 PE=1 SV=5
38	sp|O75534|CSDE1_HUMAN	251.09	88885	Cold shock domain-containing protein E1 OS=Homo sapiens OX=9606 GN=CSDE1 PE=1 SV=2
39	sp|P13797|PLST_HUMAN	250.79	70811	Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4
40	sp|P61978|HNRPK_HUMAN	240.92	50976	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1
41	sp|Q14974|IMB1_HUMAN	240.54	97170	Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2
42	sp|Q8N1F7|NUP93_HUMAN	240.08	93488	Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=2
43	sp|Q14697|GANAB_HUMAN	235.54	106874	Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=3
44	sp|P50990|TCPQ_HUMAN	230.63	59621	T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=4
45	sp|P29401|TKT_HUMAN	229.32	67878	Transketolase OS=Homo sapiens OX=9606 GN=TKT PE=1 SV=3
46	sp|Q4VCS5|AMOT_HUMAN	228.51	118085	Angiomotin OS=Homo sapiens OX=9606 GN=AMOT PE=1 SV=1
47	sp|Q99798|ACON_HUMAN	225.8	85425	Aconitate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2
48	tr|A2A274|A2A274_HUMAN	225.8	87820	Aconitate hydratase mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=1
49	sp|Q12788|TBL3_HUMAN	222.6	89035	Transducin beta-like protein 3 OS=Homo sapiens OX=9606 GN=TBL3 PE=1 SV=2
50	sp|Q9UHB6|LIMA1_HUMAN	222.03	85226	LIM domain and actin-binding protein 1 OS=Homo sapiens OX=9606 GN=LIMA1 PE=1 SV=1
51	sp|P02768|ALBU_HUMAN	221.41	69367	Serum albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2
52	sp|P14625|ENPL_HUMAN	219.92	92469	Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1
53	tr|C9J2Y9|C9J2Y9_HUMAN	219.8	133057	DNA-directed RNA polymerase subunit beta OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=2
54	sp|P30876|RPB2_HUMAN	219.8	133896	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1
55	sp|P31939|PUR9_HUMAN	217.52	64616	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3
56	sp|P78347|GTF2I_HUMAN	217.03	112416	General transcription factor II-I OS=Homo sapiens OX=9606 GN=GTF2I PE=1 SV=2
57	sp|P40227|TCPZ_HUMAN	214.56	58024	T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3
58	sp|P23921|RIR1_HUMAN	210.97	90070	Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens OX=9606 GN=RRM1 PE=1 SV=1
59	sp|P48643|TCPE_HUMAN	208.14	59671	T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1
60	sp|P05023|AT1A1_HUMAN	205.4	112896	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1
61	sp|P26639|SYTC_HUMAN	205.3	83435	Threonine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=TARS PE=1 SV=3
62	sp|P34932|HSP74_HUMAN	203.65	94331	Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4
63	tr|A0A087WYC1|A0A087WYC1_HUMAN	203.65	78606	Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=1
64	tr|J3KTA4|J3KTA4_HUMAN	200.66	69087	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1
65	sp|P17844|DDX5_HUMAN	200.66	69148	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1
66	tr|F1T0B3|F1T0B3_HUMAN	198.89	73915	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=1
67	tr|A0A087X2G1|A0A087X2G1_HUMAN	198.89	73975	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=1
68	sp|Q92499|DDX1_HUMAN	198.89	82432	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2
69	tr|A0A0A0MS51|A0A0A0MS51_HUMAN	194.07	82526	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
70	tr|A0A0A0MT01|A0A0A0MT01_HUMAN	194.07	84745	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
71	sp|P06396|GELS_HUMAN	194.07	85697	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
72	sp|P08237|PFKAM_HUMAN	193.75	85183	ATP-dependent 6-phosphofructokinase muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2
73	tr|A0A2R8Y891|A0A2R8Y891_HUMAN	193.75	96908	ATP-dependent 6-phosphofructokinase OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=1
74	sp|P30153|2AAA_HUMAN	193.62	65309	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R1A PE=1 SV=4
75	tr|M0R3F1|M0R3F1_HUMAN	193.02	71730	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=1
76	tr|A0A0A0MRA5|A0A0A0MRA5_HUMAN	193.02	85940	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=1
77	tr|B7Z4B8|B7Z4B8_HUMAN	193.02	86122	cDNA FLJ56481 highly similar to Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=1
78	sp|Q9BUJ2|HNRL1_HUMAN	193.02	95739	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2
79	sp|Q9UBT2|SAE2_HUMAN	192.31	71224	SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=2
80	sp|P60709|ACTB_HUMAN	191.68	41737	Actin cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1
81	sp|P63261|ACTG_HUMAN	191.68	41793	Actin cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1
82	sp|Q13200|PSMD2_HUMAN	191.27	100200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 PE=1 SV=3
83	sp|Q9NZI8|IF2B1_HUMAN	190.52	63481	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=1 SV=2
84	sp|Q8WUM4|PDC6I_HUMAN	188.98	96023	Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP PE=1 SV=1
85	sp|P35606|COPB2_HUMAN	188.85	102487	Coatomer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2
86	sp|P14866|HNRPL_HUMAN	187.18	64133	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=2
87	tr|M0QXS5|M0QXS5_HUMAN	187.18	58481	Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1
88	tr|A0A3B3ITJ4|A0A3B3ITJ4_HUMAN	187.18	59219	Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV=1
89	sp|Q96QK1|VPS35_HUMAN	185.58	91707	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV=2
90	sp|Q99613|EIF3C_HUMAN	180.16	105344	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1
91	sp|Q16643|DREB_HUMAN	178.98	71429	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4
92	sp|P11586|C1TC_HUMAN	178.46	101559	C-1-tetrahydrofolate synthase cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV=3
93	tr|F5H2F4|F5H2F4_HUMAN	178.46	110613	C-1-tetrahydrofolate synthase cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV=1
94	sp|P68104|EF1A1_HUMAN	178.04	50141	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1
95	sp|Q5VTE0|EF1A3_HUMAN	178.04	50185	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens OX=9606 GN=EEF1A1P5 PE=5 SV=1
96	tr|E9PK47|E9PK47_HUMAN	176.38	94070	Alpha-1 4 glucan phosphorylase OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=1
97	sp|P06737|PYGL_HUMAN	176.38	97149	Glycogen phosphorylase liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4
98	sp|Q99832|TCPH_HUMAN	174.04	59367	T-complex protein 1 subunit eta OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=2
99	sp|P13647|K2C5_HUMAN	173.77	62378	Keratin type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3
100	sp|Q9BQE3|TBA1C_HUMAN	170.62	49895	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
101	sp|Q71U36|TBA1A_HUMAN	170.62	50136	Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1
102	tr|F5H5D3|F5H5D3_HUMAN	170.62	57730	Tubulin alpha chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
103	sp|P68363|TBA1B_HUMAN	169.73	50152	Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1
104	sp|P18206|VINC_HUMAN	169.69	123799	Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4
105	sp|P02452|CO1A1_HUMAN	168.95	138942	Collagen alpha-1(I) chain OS=Homo sapiens OX=9606 GN=COL1A1 PE=1 SV=5
106	sp|P04843|RPN1_HUMAN	168.47	68569	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1
107	tr|G3V1J5|G3V1J5_HUMAN	166.33	90584	Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=1
108	sp|Q9Y2L1|RRP44_HUMAN	166.33	109003	Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=2
109	sp|P49321|NASP_HUMAN	165.45	85238	Nuclear autoantigenic sperm protein OS=Homo sapiens OX=9606 GN=NASP PE=1 SV=2
110	sp|O60506|HNRPQ_HUMAN	165.21	69603	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2
111	sp|P02533|K1C14_HUMAN	164.41	51562	Keratin type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4
112	sp|Q86VP6|CAND1_HUMAN	159.18	136375	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=2
113	sp|Q15029|U5S1_HUMAN	158.44	109436	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1
114	sp|Q92973|TNPO1_HUMAN	158.14	102355	Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=2
115	sp|Q9UBF2|COPG2_HUMAN	158.11	97622	Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1
116	sp|P04844|RPN2_HUMAN	157.43	69284	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3
117	sp|P55884|EIF3B_HUMAN	156.14	92482	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=1 SV=3
118	tr|F5GZS6|F5GZS6_HUMAN	154.61	64873	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1
119	sp|P08195|4F2_HUMAN	154.61	67994	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=3
120	tr|J3KPF3|J3KPF3_HUMAN	154.61	68101	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1
121	tr|A0A0C4DGX4|A0A0C4DGX4_HUMAN	153.92	87388	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=1
122	sp|Q13616|CUL1_HUMAN	153.92	89678	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2
123	sp|P36578|RL4_HUMAN	153.39	47697	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5
124	sp|Q08J23|NSUN2_HUMAN	152.3	86471	tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV=2
125	sp|Q08945|SSRP1_HUMAN	152.08	81075	FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=1 SV=1
126	sp|P49588|SYAC_HUMAN	151.65	106810	Alanine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=AARS PE=1 SV=2
127	sp|O43242|PSMD3_HUMAN	151.05	60978	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PSMD3 PE=1 SV=2
128	sp|O43390|HNRPR_HUMAN	150.64	70943	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1

129	sp|P08779|K1C16_HUMAN	150.05	51268	Keratin type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4
130	tr|A0A087WVC1|A0A087WVC1_HUMAN	147.5	82227	ATP-dependent RNA helicase DDX50 OS=Homo sapiens OX=9606 GN=DDX50 PE=1 SV=1
131	sp|Q9BQ39|DDX50_HUMAN	147.5	82565	ATP-dependent RNA helicase DDX50 OS=Homo sapiens OX=9606 GN=DDX50 PE=1 SV=1
132	sp|P04406|G3P_HUMAN	146.74	36053	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3
133	tr|E7EUT5|E7EUT5_HUMAN	146.74	27871	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=1
134	sp|Q92841|DDX17_HUMAN	145.74	80273	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2
135	tr|A0A1X7SBZ2|A0A1X7SBZ2_HUMAN	145.74	80255	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1
136	tr|A0A1W2PQ51|A0A1W2PQ51_HUMAN	145.74	80458	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=1
137	sp|Q13283|G3BP1_HUMAN	143.71	52164	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1
138	sp|O75131|CPNE3_HUMAN	143.28	60131	Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1
139	sp|Q15233|NONO_HUMAN	142.47	54232	Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=4
140	sp|Q9Y262|EIF3L_HUMAN	142.16	66727	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1
141	tr|B0QY89|B0QY89_HUMAN	142.16	70902	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1
142	sp|O00410|IPO5_HUMAN	141.05	123630	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4
143	tr|H0Y8C6|H0Y8C6_HUMAN	141.05	123867	Importin-5 (Fragment) OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=1
144	tr|H3BLV9|H3BLV9_HUMAN	140.42	76040	SRSF protein kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=1
145	sp|Q96SB4|SRPK1_HUMAN	140.42	74325	SRSF protein kinase 1 OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=2
146	tr|A0A0R4J2E8|A0A0R4J2E8_HUMAN	139.96	94623	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1
147	sp|P43243|MATR3_HUMAN	139.96	94623	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2
148	tr|A8MXP9|A8MXP9_HUMAN	139.96	99967	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1
149	sp|Q8WXF1|PSPC1_HUMAN	137.88	58744	Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 PE=1 SV=1
150	sp|Q7KZF4|SND1_HUMAN	137.33	101997	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SND1 PE=1 SV=1
151	tr|A0A3B3IU45|A0A3B3IU45_HUMAN	136.96	91191	DNA helicase OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=1
152	sp|P33991|MCM4_HUMAN	136.96	96558	DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=5
153	tr|A0A087WTA8|A0A087WTA8_HUMAN	136.64	129151	Collagen alpha-2(I) chain OS=Homo sapiens OX=9606 GN=COL1A2 PE=1 SV=1
154	sp|P08123|CO1A2_HUMAN	136.64	129314	Collagen alpha-2(I) chain OS=Homo sapiens OX=9606 GN=COL1A2 PE=1 SV=7
155	sp|P08133|ANXA6_HUMAN	135.68	75873	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3
156	sp|P55060|XPO2_HUMAN	135.55	110417	Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3
157	sp|P50991|TCPD_HUMAN	135.13	57924	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4
158	sp|P11021|BIP_HUMAN	134.99	72333	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2
159	sp|Q14651|PLSI_HUMAN	133.74	70254	Plastin-1 OS=Homo sapiens OX=9606 GN=PLS1 PE=1 SV=2
160	sp|O15226|NKRF_HUMAN	133.26	77673	NF-kappa-B-repressing factor OS=Homo sapiens OX=9606 GN=NKRF PE=1 SV=2
161	sp|Q9Y678|COPG1_HUMAN	133.22	97718	Coatomer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1
162	tr|A0A2R8Y804|A0A2R8Y804_HUMAN	133.08	77207	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
163	tr|A0A2R8Y543|A0A2R8Y543_HUMAN	133.08	78405	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
164	tr|B4DGU4|B4DGU4_HUMAN	133.08	84766	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
165	tr|A0A2R8YCH5|A0A2R8YCH5_HUMAN	133.08	85268	Catenin beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
166	tr|A0A2R8Y7Z0|A0A2R8Y7Z0_HUMAN	133.08	85368	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
167	sp|P35222|CTNB1_HUMAN	133.08	85497	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
168	tr|A0A2R8Y5A3|A0A2R8Y5A3_HUMAN	133.08	85681	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
169	tr|A0A2R8Y5C3|A0A2R8Y5C3_HUMAN	133.08	80699	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
170	tr|A0A2R8Y750|A0A2R8Y750_HUMAN	133.08	81430	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
171	tr|A0A2R8Y5Z1|A0A2R8Y5Z1_HUMAN	133.08	82426	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
172	sp|P51116|FXR2_HUMAN	132.38	74223	Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens OX=9606 GN=FXR2 PE=1 SV=2
173	sp|Q9ULV4|COR1C_HUMAN	132.25	53249	Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1
174	sp|P42224|STAT1_HUMAN	132.2	87335	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2
175	sp|Q09161|NCBP1_HUMAN	131.74	91839	Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1
176	sp|Q9NSD9|SYFB_HUMAN	129.52	66116	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens OX=9606 GN=FARSB PE=1 SV=3
177	tr|A0A0J9YYL3|A0A0J9YYL3_HUMAN	129.19	54627	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
178	tr|A0A0J9YXJ8|A0A0J9YXJ8_HUMAN	129.19	56331	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
179	tr|A0A0J9YVP6|A0A0J9YVP6_HUMAN	129.19	57399	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
180	tr|A0A0J9YXX5|A0A0J9YXX5_HUMAN	129.19	59103	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
181	sp|Q9UHX1|PUF60_HUMAN	129.19	59876	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
182	sp|Q96AE4|FUBP1_HUMAN	128.52	67560	Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3
183	tr|E9PEB5|E9PEB5_HUMAN	128.52	68904	Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=1
184	sp|Q9P0K7|RAI14_HUMAN	127.93	110041	Ankycorbin OS=Homo sapiens OX=9606 GN=RAI14 PE=1 SV=2
185	sp|Q14684|RRP1B_HUMAN	127.91	84428	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens OX=9606 GN=RRP1B PE=1 SV=3
186	sp|O00139|KIF2A_HUMAN	126.4	79955	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3
187	sp|P36871|PGM1_HUMAN	126.22	61449	Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3
188	tr|A0A3B3ITK7|A0A3B3ITK7_HUMAN	126.22	63958	Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=1
189	sp|O43707|ACTN4_HUMAN	125.98	104854	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2
190	sp|P22059|OSBP1_HUMAN	124.67	89421	Oxysterol-binding protein 1 OS=Homo sapiens OX=9606 GN=OSBP PE=1 SV=1
191	sp|P08621|RU17_HUMAN	124.1	51557	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP70 PE=1 SV=2
192	sp|Q9BXJ9|NAA15_HUMAN	123.11	101272	N-alpha-acetyltransferase 15 NatA auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA15 PE=1 SV=1
193	sp|Q86Y56|DAAF5_HUMAN	122.73	93521	Dynein assembly factor 5 axonemal OS=Homo sapiens OX=9606 GN=DNAAF5 PE=1 SV=4
194	sp|P61221|ABCE1_HUMAN	122.35	67314	ATP-binding cassette sub-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1 SV=1
195	tr|D6R9I9|D6R9I9_HUMAN	122.35	47037	ATP-binding cassette sub-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1 SV=1
196	sp|O00469|PLOD2_HUMAN	121.98	84686	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE=1 SV=2
197	tr|E7ETU9|E7ETU9_HUMAN	121.98	81170	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE=1 SV=1
198	sp|O43776|SYNC_HUMAN	121.98	62943	Asparagine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=NARS PE=1 SV=1
199	sp|Q13617|CUL2_HUMAN	121.86	86983	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=2
200	tr|A0A0A0MTN0|A0A0A0MTN0_HUMAN	121.86	88506	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=1
201	tr|Q5T2B5|Q5T2B5_HUMAN	121.86	82359	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=1
202	sp|P25205|MCM3_HUMAN	121.26	90981	DNA replication licensing factor MCM3 OS=Homo sapiens OX=9606 GN=MCM3 PE=1 SV=3
203	tr|A8MZH3|A8MZH3_HUMAN	120.08	19730	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=1
204	tr|J3QQK6|J3QQK6_HUMAN	120.08	27700	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=1
205	tr|E9PMR5|E9PMR5_HUMAN	120.08	10811	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=2
206	tr|H0YF02|H0YF02_HUMAN	120.08	11722	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=2
207	tr|H0YEA2|H0YEA2_HUMAN	120.08	13061	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=2
208	tr|J3QL64|J3QL64_HUMAN	120.08	17119	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=1
209	tr|J3QKL5|J3QKL5_HUMAN	120.08	18875	Myelin basic protein (Fragment) OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=1
210	tr|H7BYR8|H7BYR8_HUMAN	120.08	25742	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=1
211	sp|P02686|MBP_HUMAN	120.08	33117	Myelin basic protein OS=Homo sapiens OX=9606 GN=MBP PE=1 SV=3
212	sp|O15371|EIF3D_HUMAN	119.84	63973	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=1 SV=1
213	tr|F8WJN3|F8WJN3_HUMAN	119.78	52270	Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens OX=9606 GN=CPSF6 PE=1 SV=1
214	sp|Q16630|CPSF6_HUMAN	119.78	59210	Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens OX=9606 GN=CPSF6 PE=1 SV=2
215	tr|E7EQR4|E7EQR4_HUMAN	118.75	69372	Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=3
216	sp|P15311|EZRI_HUMAN	118.75	69413	Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4
217	sp|P10515|ODP2_HUMAN	118.51	68997	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex mitochondrial OS=Homo sapiens OX=9606 GN=DLAT P
218	tr|H0YDD4|H0YDD4_HUMAN	118.51	51201	Acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Homo sapiens OX=9606 GN=DLAT PE=1 SV=1
219	sp|P20700|LMNB1_HUMAN	118.45	66408	Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2
220	sp|P35241|RADI_HUMAN	118.12	68564	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1
221	tr|A0A2R8Y5S7|A0A2R8Y5S7_HUMAN	118.12	69336	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1
222	tr|A0A2R8Y7M3|A0A2R8Y7M3_HUMAN	118.12	62931	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1
223	tr|Q5T5C7|Q5T5C7_HUMAN	117.07	61313	Serine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=SARS PE=1 SV=1
224	sp|P49591|SYSC_HUMAN	117.07	58777	Serine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=SARS PE=1 SV=3
225	sp|P54886|P5CS_HUMAN	116.57	87302	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens OX=9606 GN=ALDH18A1 PE=1 SV=2
226	tr|H0Y8E6|H0Y8E6_HUMAN	116.52	94118	DNA helicase (Fragment) OS=Homo sapiens OX=9606 GN=MCM2 PE=1 SV=1
227	sp|P49736|MCM2_HUMAN	116.52	101896	DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 GN=MCM2 PE=1 SV=4
228	tr|H9KV75|H9KV75_HUMAN	115.95	94826	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=1
229	sp|P12814|ACTN1_HUMAN	115.95	103058	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=2
230	tr|B1AHC9|B1AHC9_HUMAN	115.46	64284	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=1
231	sp|P12956|XRCC6_HUMAN	115.46	69843	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2
232	sp|Q9NVE7|PANK4_HUMAN	114.89	85991	Pantothenate kinase 4 OS=Homo sapiens OX=9606 GN=PANK4 PE=1 SV=1
233	sp|P16402|H13_HUMAN	114.81	22350	Histone H1.3 OS=Homo sapiens OX=9606 GN=HIST1H1D PE=1 SV=2
234	sp|P10412|H14_HUMAN	114.81	21865	Histone H1.4 OS=Homo sapiens OX=9606 GN=HIST1H1E PE=1 SV=2
235	sp|P16403|H12_HUMAN	114.81	21365	Histone H1.2 OS=Homo sapiens OX=9606 GN=HIST1H1C PE=1 SV=2
236	sp|P14923|PLAK_HUMAN	113.24	81745	Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3
237	sp|P14314|GLU2B_HUMAN	112.69	59426	Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=2
238	tr|K7ELL7|K7ELL7_HUMAN	112.69	60192	Glucosidase 2 subunit beta OS=Homo sapiens OX=9606 GN=PRKCSH PE=1 SV=1
239	tr|A0A0U1RQH7|A0A0U1RQH7_HUMAN	112.58	26699	RNA-binding protein 39 (Fragment) OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1
240	tr|H0Y4X3|H0Y4X3_HUMAN	112.58	36633	RNA-binding protein 39 (Fragment) OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=8
241	tr|G3XAC6|G3XAC6_HUMAN	112.58	48024	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=1
242	sp|Q14498|RBM39_HUMAN	112.58	59380	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2
243	sp|O94874|UFL1_HUMAN	112.28	89595	E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2
244	sp|O95831|AIFM1_HUMAN	112.07	66901	Apoptosis-inducing factor 1 mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1
245	sp|Q13724|MOGS_HUMAN	111.86	91918	Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5
246	sp|P78371|TCPB_HUMAN	111.78	57488	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4
247	tr|F5GWF6|F5GWF6_HUMAN	111.78	56807	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=2
248	tr|F8VQ14|F8VQ14_HUMAN	111.78	44813	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=1
249	sp|O14556|G3PT_HUMAN	108.54	44501	Glyceraldehyde-3-phosphate dehydrogenase testis-specific OS=Homo sapiens OX=9606 GN=GAPDHS PE=1 SV=2
250	sp|O43264|ZW10_HUMAN	108.49	88830	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10 PE=1 SV=3
251	sp|Q92945|FUBP2_HUMAN	107.77	73115	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=4
252	tr|A0A087WTP3|A0A087WTP3_HUMAN	107.77	73028	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=1
253	sp|P11216|PYGB_HUMAN	106.3	96696	Glycogen phosphorylase brain form OS=Homo sapiens OX=9606 GN=PYGB PE=1 SV=5
254	sp|P33176|KINH_HUMAN	106.19	109685	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1
255	sp|O00425|IF2B3_HUMAN	105	63705	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3 PE=1 SV=2
256	sp|Q14566|MCM6_HUMAN	104.26	92889	DNA replication licensing factor MCM6 OS=Homo sapiens OX=9606 GN=MCM6 PE=1 SV=1
257	sp|O75083|WDR1_HUMAN	102.46	66194	WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4

258	sp|Q15393|SF3B3_HUMAN	102.17	135577	Splicing factor 3B subunit 3 OS=Homo sapiens OX=9606 GN=SF3B3 PE=1 SV=4
259	sp|P53597|SUCA_HUMAN	100.63	36250	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=SUCLG1 PE=1 SV=4
260	sp|Q13423|NNTM_HUMAN	99.66	113895	NAD(P) transhydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=3
261	tr|E9PCX7|E9PCX7_HUMAN	99.66	99729	NAD(P) transhydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=1
262	sp|O43395|PRPF3_HUMAN	98.24	77529	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens OX=9606 GN=PRPF3 PE=1 SV=2
263	sp|P51610|HCFC1_HUMAN	96.71	208730	Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=2
264	tr|A6NEM2|A6NEM2_HUMAN	96.71	213474	Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCFC1 PE=1 SV=2
265	sp|Q07065|CKAP4_HUMAN	93.02	66023	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2
266	sp|Q9Y697|NFS1_HUMAN	92.86	50196	Cysteine desulfurase mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3
267	tr|H7C0I5|H7C0I5_HUMAN	92.86	15422	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1
268	tr|H0YGN5|H0YGN5_HUMAN	92.86	17797	Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1
269	tr|H7BXI1|H7BXI1_HUMAN	92.14	98010	Extended synaptotagmin-2 (Fragment) OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1
270	tr|A0A087WXU3|A0A087WXU3_HUMAN	92.14	102372	Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1
271	sp|A0FGR8|ESYT2_HUMAN	92.14	102357	Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1
272	sp|P49411|EFTU_HUMAN	91.79	49542	Elongation factor Tu mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2
273	sp|Q16531|DDB1_HUMAN	90.23	126968	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1
274	tr|F5GY55|F5GY55_HUMAN	90.23	121714	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1
275	sp|Q93034|CUL5_HUMAN	89.77	90955	Cullin-5 OS=Homo sapiens OX=9606 GN=CUL5 PE=1 SV=4
276	sp|Q04727|TLE4_HUMAN	89.76	83755	Transducin-like enhancer protein 4 OS=Homo sapiens OX=9606 GN=TLE4 PE=1 SV=3
277	sp|Q04724|TLE1_HUMAN	89.76	83201	Transducin-like enhancer protein 1 OS=Homo sapiens OX=9606 GN=TLE1 PE=1 SV=2
278	tr|H3BR35|H3BR35_HUMAN	89.66	52951	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment) OS=Homo sapiens OX=9606 GN=GSPT1 PE=1 SV=1
279	sp|P15170|ERF3A_HUMAN	89.66	55756	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1 PE=1 SV=1
280	sp|Q86YZ3|HORN_HUMAN	89.6	282389	Hornerin OS=Homo sapiens OX=9606 GN=HRNR PE=1 SV=2
281	sp|Q7Z2T5|TRM1L_HUMAN	88.74	81747	TRMT1-like protein OS=Homo sapiens OX=9606 GN=TRMT1L PE=1 SV=2
282	tr|A0A3B3IS54|A0A3B3IS54_HUMAN	87.13	55163	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1
283	tr|A0A3B3IT01|A0A3B3IT01_HUMAN	87.13	67686	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1
284	tr|A0A3B3ISK7|A0A3B3ISK7_HUMAN	87.13	70987	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1
285	sp|Q6PI48|SYDM_HUMAN	87.13	73563	Aspartate--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1
286	tr|A0A2R8Y645|A0A2R8Y645_HUMAN	86.65	79475	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
287	tr|A0A2R8YDT5|A0A2R8YDT5_HUMAN	86.65	52798	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
288	tr|A0A2R8Y7T2|A0A2R8Y7T2_HUMAN	86.65	52885	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
289	tr|A0A2R8Y5G6|A0A2R8Y5G6_HUMAN	86.65	69048	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
290	tr|A0A0D9SFB3|A0A0D9SFB3_HUMAN	86.65	70840	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
291	tr|A0A2R8YF78|A0A2R8YF78_HUMAN	86.65	70940	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
292	tr|A0A2R8YCW1|A0A2R8YCW1_HUMAN	86.65	71694	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
293	tr|A0A0D9SG12|A0A0D9SG12_HUMAN	86.65	71541	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
294	sp|O15523|DDX3Y_HUMAN	86.65	73154	ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y PE=1 SV=2
295	tr|A0A2R8YFR4|A0A2R8YFR4_HUMAN	86.65	73127	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
296	tr|A0A2R8YFS5|A0A2R8YFS5_HUMAN	86.65	73156	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
297	tr|A0A2U3TZJ9|A0A2U3TZJ9_HUMAN	86.65	73215	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
298	tr|A0A2R8Y4A4|A0A2R8Y4A4_HUMAN	86.65	73244	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
299	sp|O00571|DDX3X_HUMAN	86.65	73244	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3
300	tr|A0A0D9SF53|A0A0D9SF53_HUMAN	86.65	81477	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
301	tr|F6S8Q4|F6S8Q4_HUMAN	86.65	69356	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
302	tr|A0A2R8YDH3|A0A2R8YDH3_HUMAN	86.65	56248	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1
303	sp|P21399|ACOC_HUMAN	85.04	98399	Cytoplasmic aconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3
304	sp|Q96SB3|NEB2_HUMAN	85.01	89192	Neurabin-2 OS=Homo sapiens OX=9606 GN=PPP1R9B PE=1 SV=2
305	tr|D3DTX6|D3DTX6_HUMAN	85.01	89334	Neurabin-2 OS=Homo sapiens OX=9606 GN=PPP1R9B PE=1 SV=1
306	sp|P42285|MTREX_HUMAN	84.98	117805	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTREX PE=1 SV=3
307	sp|P25705|ATPA_HUMAN	84.66	59751	ATP synthase subunit alpha mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1
308	sp|P06744|G6PI_HUMAN	83.77	63147	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4
309	tr|A0A0A0MTS2|A0A0A0MTS2_HUMAN	83.77	64825	Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1
310	tr|A0A2U3TZU2|A0A2U3TZU2_HUMAN	83.77	67286	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=1
311	tr|K7EQ48|K7EQ48_HUMAN	83.77	50210	Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=3
312	sp|Q14CN4|K2C72_HUMAN	82.24	55877	Keratin type II cytoskeletal 72 OS=Homo sapiens OX=9606 GN=KRT72 PE=1 SV=2
313	sp|P02786|TFR1_HUMAN	81.34	84871	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2
314	tr|G3V0E5|G3V0E5_HUMAN	81.34	75964	Transferrin receptor (P90 CD71) isoform CRA_c OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=1
315	sp|P31040|SDHA_HUMAN	81.15	72692	Succinate dehydrogenase [ubiquinone] flavoprotein subunit mitochondrial OS=Homo sapiens OX=9606 GN=SDHA PE=1 SV=2
316	sp|Q9Y4W2|LAS1L_HUMAN	79.5	83065	Ribosomal biogenesis protein LAS1L OS=Homo sapiens OX=9606 GN=LAS1L PE=1 SV=2
317	tr|H0YNJ6|H0YNJ6_HUMAN	78.37	46938	GMP reductase OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
318	tr|H0YLV5|H0YLV5_HUMAN	78.37	35852	GMP reductase OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
319	tr|H0YMB3|H0YMB3_HUMAN	78.37	33922	GMP reductase OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
320	tr|A0A087WWM4|A0A087WWM4_HUMA	78.37	38217	GMP reductase OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
321	sp|Q9P2T1|GMPR2_HUMAN	78.37	37874	GMP reductase 2 OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
322	tr|F8WAN9|F8WAN9_HUMAN	78.37	38269	GMP reductase OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=1
323	tr|H0YNH0|H0YNH0_HUMAN	78.37	26670	GMP reductase 2 (Fragment) OS=Homo sapiens OX=9606 GN=GMPR2 PE=1 SV=8
324	sp|Q9Y3T9|NOC2L_HUMAN	76.5	84919	Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 GN=NOC2L PE=1 SV=4
325	sp|O95373|IPO7_HUMAN	75.92	119516	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1
326	tr|G3XAH6|G3XAH6_HUMAN	74.12	80626	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=1
327	sp|P51003|PAPOA_HUMAN	74.12	82843	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOLA PE=1 SV=4
328	tr|A0A2R8Y3X5|A0A2R8Y3X5_HUMAN	73.87	99133	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1
329	sp|O60313|OPA1_HUMAN	73.87	111630	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3
330	tr|A0A2R8YE78|A0A2R8YE78_HUMAN	73.87	112063	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1
331	tr|A0A2R8YDM2|A0A2R8YDM2_HUMAN	73.87	112273	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1
332	tr|C9JMB8|C9JMB8_HUMAN	73.87	112628	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=2
333	tr|E5KLJ9|E5KLJ9_HUMAN	73.87	113681	Dynamin-like 120 kDa protein mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=1
334	tr|Q5JP53|Q5JP53_HUMAN	73.52	47767	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=1
335	sp|P07437|TBB5_HUMAN	73.52	49671	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2
336	sp|P06733|ENOA_HUMAN	73.35	47169	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2
337	tr|A0A2R8Y6G6|A0A2R8Y6G6_HUMAN	73.35	47327	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=1
338	sp|P27694|RFA1_HUMAN	73.12	68138	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2
339	sp|O14654|IRS4_HUMAN	72.82	133767	Insulin receptor substrate 4 OS=Homo sapiens OX=9606 GN=IRS4 PE=1 SV=1
340	sp|Q15758|AAAT_HUMAN	72.72	56598	Neutral amino acid transporter B(0) OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=2
341	tr|M0QXM4|M0QXM4_HUMAN	72.72	39443	Amino acid transporter OS=Homo sapiens OX=9606 GN=SLC1A5 PE=1 SV=1
342	tr|F8W6P5|F8W6P5_HUMAN	72.62	9670	Hemoglobin subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1
343	tr|A0A2R8Y7R2|A0A2R8Y7R2_HUMAN	72.62	12176	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=1
344	sp|P68871|HBB_HUMAN	72.62	15998	Hemoglobin subunit beta OS=Homo sapiens OX=9606 GN=HBB PE=1 SV=2
345	tr|A0A087X1B2|A0A087X1B2_HUMAN	71.36	56400	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=1
346	sp|Q53GS9|SNUT2_HUMAN	71.36	65381	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2
347	tr|B9A018|B9A018_HUMAN	71.36	62044	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=1
348	tr|A0A087WW31|A0A087WW31_HUMA	71.36	6756	U4/U6.U5 tri-snRNP-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=1
349	sp|Q06210|GFPT1_HUMAN	71.36	78806	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens OX=9606 GN=GFPT1 PE=1 SV=3
350	sp|Q15031|SYLM_HUMAN	70.75	101976	Probable leucine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=LARS2 PE=1 SV=2
351	sp|Q8N1G4|LRC47_HUMAN	70.35	63473	Leucine-rich repeat-containing protein 47 OS=Homo sapiens OX=9606 GN=LRRC47 PE=1 SV=1
352	sp|Q12874|SF3A3_HUMAN	69.51	58849	Splicing factor 3A subunit 3 OS=Homo sapiens OX=9606 GN=SF3A3 PE=1 SV=1
353	sp|Q969S9|RRF2M_HUMAN	69.42	86601	Ribosome-releasing factor 2 mitochondrial OS=Homo sapiens OX=9606 GN=GFM2 PE=1 SV=1
354	sp|O43747|AP1G1_HUMAN	68.96	91351	AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 PE=1 SV=5
355	sp|Q9UGP8|SEC63_HUMAN	68.33	87997	Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2
356	sp|Q01518|CAP1_HUMAN	68.31	51902	Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=5
357	tr|Q5T0R7|Q5T0R7_HUMAN	68.31	19202	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
358	tr|Q5T0R6|Q5T0R6_HUMAN	68.31	19416	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
359	tr|Q5T0R5|Q5T0R5_HUMAN	68.31	19810	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8
360	tr|Q5T0R4|Q5T0R4_HUMAN	68.31	22532	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8
361	tr|Q5T0R3|Q5T0R3_HUMAN	68.31	22734	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
362	tr|Q5T0R2|Q5T0R2_HUMAN	68.31	23249	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
363	tr|Q5T0R1|Q5T0R1_HUMAN	68.31	23930	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=1
364	tr|Q5T0R9|Q5T0R9_HUMAN	68.31	28635	Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=CAP1 PE=1 SV=8
365	sp|P54136|SYRC_HUMAN	68.26	75379	Arginine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=RARS PE=1 SV=2
366	tr|A0A0A0MSB4|A0A0A0MSB4_HUMAN	67.92	72219	Oxysterol-binding protein OS=Homo sapiens OX=9606 GN=OSBP2 PE=1 SV=1
367	tr|Q6ZN50|Q6ZN50_HUMAN	67.92	83764	Oxysterol-binding protein OS=Homo sapiens OX=9606 GN=OSBP2 PE=1 SV=1
368	sp|Q969R2|OSBP2_HUMAN	67.92	101266	Oxysterol-binding protein 2 OS=Homo sapiens OX=9606 GN=OSBP2 PE=1 SV=2
369	sp|Q9BXP5|SRRT_HUMAN	67.86	100667	Serrate RNA effector molecule homolog OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=1
370	tr|H7C3A1|H7C3A1_HUMAN	67.86	56734	Serrate RNA effector molecule homolog (Fragment) OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=1
371	tr|A0A0A0MSP6|A0A0A0MSP6_HUMAN	67.86	16435	Serrate RNA effector molecule homolog (Fragment) OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=6
372	sp|Q96HY7|DHTK1_HUMAN	67.73	103077	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 mitochondrial OS=Homo sapiens OX=9606 GN=DHTKD1 PE=1 SV=2
373	sp|Q8IXB1|DJC10_HUMAN	67.3	91080	DnaJ homolog subfamily C member 10 OS=Homo sapiens OX=9606 GN=DNAJC10 PE=1 SV=2
374	tr|K4DI93|K4DI93_HUMAN	66.71	102756	Cullin 4B isoform CRA_e OS=Homo sapiens OX=9606 GN=CUL4B PE=1 SV=1
375	sp|Q13620|CUL4B_HUMAN	66.71	103982	Cullin-4B OS=Homo sapiens OX=9606 GN=CUL4B PE=1 SV=4
376	tr|H0Y2W2|H0Y2W2_HUMAN	66.52	64363	ATPase family AAA domain-containing protein 3A (Fragment) OS=Homo sapiens OX=9606 GN=ATAD3A PE=1 SV=1
377	sp|Q9NVI7|ATD3A_HUMAN	66.52	71369	ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ATAD3A PE=1 SV=2
378	sp|Q5T9A4|ATD3B_HUMAN	66.52	72573	ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE=1 SV=1
379	sp|Q6P996|PDXD1_HUMAN	66.31	86707	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PDXDC1 PE=1 SV=2
380	tr|H3BND4|H3BND4_HUMAN	66.31	88762	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PDXDC1 PE=1 SV=1
381	tr|Q86XE2|Q86XE2_HUMAN	66.31	54982	PDXDC1 protein OS=Homo sapiens OX=9606 GN=PDXDC1 PE=1 SV=2
382	tr|Q6XYB5|Q6XYB5_HUMAN	66.31	22427	LP8165 OS=Homo sapiens OX=9606 GN=PDXDC1 PE=1 SV=1
383	sp|P11387|TOP1_HUMAN	66.2	90726	DNA topoisomerase 1 OS=Homo sapiens OX=9606 GN=TOP1 PE=1 SV=2
384	sp|Q07666|KHDR1_HUMAN	66.18	48227	KH domain-containing RNA-binding signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 PE=1 SV=1
385	sp|Q9BXB4|OSB11_HUMAN	66.11	83643	Oxysterol-binding protein-related protein 11 OS=Homo sapiens OX=9606 GN=OSBPL11 PE=1 SV=2
386	tr|Q5T760|Q5T760_HUMAN	65.92	42316	Serine/arginine-rich-splicing factor 11 (Fragment) OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1

387	sp|Q05519|SRS11_HUMAN	65.92	53542	Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1
388	sp|P23378|GCSP_HUMAN	65.88	112730	Glycine dehydrogenase (decarboxylating) mitochondrial OS=Homo sapiens OX=9606 GN=GLDC PE=1 SV=2
389	tr|A0A1W2PQV3|A0A1W2PQV3_HUMAN	65.88	42610	Glycine dehydrogenase (decarboxylating) mitochondrial OS=Homo sapiens OX=9606 GN=GLDC PE=1 SV=1
390	tr|A0A1W2PP74|A0A1W2PP74_HUMAN	65.88	46273	Glycine dehydrogenase (decarboxylating) mitochondrial OS=Homo sapiens OX=9606 GN=GLDC PE=1 SV=1
391	sp|Q9UKN8|TF3C4_HUMAN	65.44	91982	General transcription factor 3C polypeptide 4 OS=Homo sapiens OX=9606 GN=GTF3C4 PE=1 SV=2
392	sp|P62979|RS27A_HUMAN	65.32	17965	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=2
393	sp|P62987|RL40_HUMAN	65.32	14728	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=2
394	tr|M0R2S1|M0R2S1_HUMAN	65.32	15476	Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=1
395	tr|J3QTR3|J3QTR3_HUMAN	65.32	12237	Ubiquitin-40S ribosomal protein S27a (Fragment) OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=1
396	tr|J3QS39|J3QS39_HUMAN	65.32	10469	Polyubiquitin-B (Fragment) OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1
397	tr|F5H6Q2|F5H6Q2_HUMAN	65.32	13732	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=8
398	tr|F5GYU3|F5GYU3_HUMAN	65.32	15032	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1
399	tr|F5H2Z3|F5H2Z3_HUMAN	65.32	15310	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1
400	tr|F5H265|F5H265_HUMAN	65.32	16841	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=1
401	tr|B4DV12|B4DV12_HUMAN	65.32	17215	Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1
402	tr|F5H747|F5H747_HUMAN	65.32	18073	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=8
403	tr|F5GXK7|F5GXK7_HUMAN	65.32	19016	Polyubiquitin-C (Fragment) OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=2
404	tr|J3QKN0|J3QKN0_HUMAN	65.32	23163	Polyubiquitin-B (Fragment) OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1
405	sp|P0CG47|UBB_HUMAN	65.32	25762	Polyubiquitin-B OS=Homo sapiens OX=9606 GN=UBB PE=1 SV=1
406	sp|P0CG48|UBC_HUMAN	65.32	77039	Polyubiquitin-C OS=Homo sapiens OX=9606 GN=UBC PE=1 SV=3
407	sp|Q32P28|P3H1_HUMAN	65.03	83394	Prolyl 3-hydroxylase 1 OS=Homo sapiens OX=9606 GN=P3H1 PE=1 SV=2
408	tr|E9PKI2|E9PKI2_HUMAN	64.39	8602	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
409	tr|E9PNW0|E9PNW0_HUMAN	64.39	12250	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
410	tr|E9PJJ2|E9PJJ2_HUMAN	64.39	14653	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
411	tr|E9PS34|E9PS34_HUMAN	64.39	15282	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
412	tr|E9PNJ7|E9PNJ7_HUMAN	64.39	16000	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
413	tr|E9PP22|E9PP22_HUMAN	64.39	17350	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=2
414	tr|C9J6D1|C9J6D1_HUMAN	64.39	20261	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
415	sp|Q99733|NP1L4_HUMAN	64.39	42823	Nucleosome assembly protein 1-like 4 OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
416	tr|C9J1B1|C9J1B1_HUMAN	64.39	11405	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=2
417	tr|E9PKT8|E9PKT8_HUMAN	64.39	19156	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
418	tr|C9JZI7|C9JZI7_HUMAN	64.39	31840	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L4 PE=1 SV=1
419	sp|P53985|MOT1_HUMAN	63.11	53944	Monocarboxylate transporter 1 OS=Homo sapiens OX=9606 GN=SLC16A1 PE=1 SV=3
420	tr|Q5T8R3|Q5T8R3_HUMAN	63.11	31689	Monocarboxylate transporter 1 (Fragment) OS=Homo sapiens OX=9606 GN=SLC16A1 PE=1 SV=1
421	tr|Q5T8R5|Q5T8R5_HUMAN	63.11	49219	Monocarboxylate transporter 1 (Fragment) OS=Homo sapiens OX=9606 GN=SLC16A1 PE=1 SV=1
422	tr|F8VX11|F8VX11_HUMAN	62.91	41455	Eukaryotic translation initiation factor 4B (Fragment) OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=1
423	sp|P23588|IF4B_HUMAN	62.91	69151	Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=2
424	tr|E7EX17|E7EX17_HUMAN	62.91	69698	Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=1
425	sp|P08670|VIME_HUMAN	62.08	53652	Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4
426	tr|B0YJC4|B0YJC4_HUMAN	62.08	49653	Vimentin variant 3 OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=1
427	sp|Q5SY16|NOL9_HUMAN	62.01	79323	Polynucleotide 5'-hydroxyl-kinase NOL9 OS=Homo sapiens OX=9606 GN=NOL9 PE=1 SV=1
428	sp|P09960|LKHA4_HUMAN	61.62	69285	Leukotriene A-4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H PE=1 SV=2
429	sp|Q96S59|RANB9_HUMAN	61.24	77847	Ran-binding protein 9 OS=Homo sapiens OX=9606 GN=RANBP9 PE=1 SV=1
430	tr|F5H365|F5H365_HUMAN	60.15	82969	Protein transport protein SEC23 OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=1
431	sp|Q15436|SC23A_HUMAN	60.15	86161	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2
432	sp|Q9BW62|KATL1_HUMAN	59.75	55392	Katanin p60 ATPase-containing subunit A-like 1 OS=Homo sapiens OX=9606 GN=KATNAL1 PE=1 SV=1
433	tr|B7ZBC8|B7ZBC8_HUMAN	59.75	31829	Katanin p60 ATPase-containing subunit A1 (Fragment) OS=Homo sapiens OX=9606 GN=KATNA1 PE=1 SV=1
434	sp|O75449|KTNA1_HUMAN	59.75	55965	Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens OX=9606 GN=KATNA1 PE=1 SV=1
435	tr|C9J470|C9J470_HUMAN	59.32	68012	Condensin complex subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=NCAPH PE=1 SV=8
436	tr|E9PHA2|E9PHA2_HUMAN	59.32	81573	Condensin complex subunit 2 OS=Homo sapiens OX=9606 GN=NCAPH PE=1 SV=1
437	sp|Q15003|CND2_HUMAN	59.32	82563	Condensin complex subunit 2 OS=Homo sapiens OX=9606 GN=NCAPH PE=1 SV=3
438	tr|F8W7U8|F8W7U8_HUMAN	58.35	80522	Double-strand break repair protein OS=Homo sapiens OX=9606 GN=MRE11 PE=1 SV=1
439	sp|P49959|MRE11_HUMAN	58.35	80593	Double-strand break repair protein MRE11 OS=Homo sapiens OX=9606 GN=MRE11 PE=1 SV=3
440	sp|Q9Y6Y8|S23IP_HUMAN	58.34	111076	SEC23-interacting protein OS=Homo sapiens OX=9606 GN=SEC23IP PE=1 SV=1
441	tr|A0A0C4DH82|A0A0C4DH82_HUMAN	58.34	53153	SEC23-interacting protein OS=Homo sapiens OX=9606 GN=SEC23IP PE=1 SV=1
442	sp|P46977|STT3A_HUMAN	58.33	80530	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX=9606 GN=STT3A PE=1 SV=2
443	sp|Q96TA1|NIBL1_HUMAN	58.29	84138	Niban-like protein 1 OS=Homo sapiens OX=9606 GN=FAM129B PE=1 SV=3
444	tr|Q5JR04|Q5JR04_HUMAN	58.26	107210	Helicase MOV-10 OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=1
445	sp|Q9HCE1|MOV10_HUMAN	58.26	113671	Helicase MOV-10 OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=2
446	tr|B4DKY1|B4DKY1_HUMAN	57.7	84278	Cysteine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=CARS PE=1 SV=1
447	sp|P11279|LAMP1_HUMAN	57.7	44882	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9606 GN=LAMP1 PE=1 SV=3
448	sp|Q9H8H0|NOL11_HUMAN	57.62	81124	Nucleolar protein 11 OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1
449	tr|J3QLQ6|J3QLQ6_HUMAN	57.62	21313	Nucleolar protein 11 (Fragment) OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1
450	sp|O76031|CLPX_HUMAN	56.72	69224	ATP-dependent Clp protease ATP-binding subunit clpX-like mitochondrial OS=Homo sapiens OX=9606 GN=CLPX PE=1 SV=2
451	sp|P35520|CBS_HUMAN	56.56	60587	Cystathionine beta-synthase OS=Homo sapiens OX=9606 GN=CBS PE=1 SV=2
452	sp|P0DN79|CBSL_HUMAN	56.56	60587	Cystathionine beta-synthase-like protein OS=Homo sapiens OX=9606 GN=CBSL PE=1 SV=1
453	sp|P13807|GYS1_HUMAN	54.92	83786	Glycogen [starch] synthase muscle OS=Homo sapiens OX=9606 GN=GYS1 PE=1 SV=2
454	sp|A0MZ66|SHOT1_HUMAN	53.23	71640	Shootin-1 OS=Homo sapiens OX=9606 GN=SHTN1 PE=1 SV=4
455	sp|O14744|ANM5_HUMAN	53.06	72684	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4
456	tr|H0YJX6|H0YJX6_HUMAN	53.06	32312	Protein arginine N-methyltransferase 5 (Fragment) OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=1
457	tr|A0A087X0X3|A0A087X0X3_HUMAN	52.78	77570	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1
458	sp|P52272|HNRPM_HUMAN	52.78	77516	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3
459	tr|M0R019|M0R019_HUMAN	52.78	37627	Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=8
460	tr|M0R0Y6|M0R0Y6_HUMAN	52.78	10739	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1
461	tr|M0QYQ7|M0QYQ7_HUMAN	52.78	24114	Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1
462	tr|M0R0N3|M0R0N3_HUMAN	52.78	30082	Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=8
463	tr|M0R2T0|M0R2T0_HUMAN	52.78	38226	Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=1
464	sp|Q13435|SF3B2_HUMAN	51.84	100228	Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2
465	tr|E9PPJ0|E9PPJ0_HUMAN	51.84	98170	Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1
466	tr|H0YEX5|H0YEX5_HUMAN	51.84	35017	Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=1
467	sp|P07196|NFL_HUMAN	50.57	61517	Neurofilament light polypeptide OS=Homo sapiens OX=9606 GN=NEFL PE=1 SV=3
468	sp|Q9NVH1|DJC11_HUMAN	50.54	63278	DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2
469	tr|H0Y3P2|H0Y3P2_HUMAN	50.2	98118	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1
470	tr|D3DQV9|D3DQV9_HUMAN	50.2	102330	Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1
471	sp|P78344|IF4G2_HUMAN	50.2	102362	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1
472	sp|Q8TAT6|NPL4_HUMAN	49.92	68120	Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLOC4 PE=1 SV=3
473	sp|P17174|AATC_HUMAN	49.8	46248	Aspartate aminotransferase cytoplasmic OS=Homo sapiens OX=9606 GN=GOT1 PE=1 SV=3
474	sp|Q8TE77|SSH3_HUMAN	49.75	72996	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=2
475	tr|A0A087WWG1|A0A087WWG1_HUMAN	49.75	36103	Protein phosphatase Slingshot homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=1
476	tr|E9PIT5|E9PIT5_HUMAN	49.75	24747	Protein phosphatase Slingshot homolog 3 (Fragment) OS=Homo sapiens OX=9606 GN=SSH3 PE=1 SV=2
477	sp|Q99460|PSMD1_HUMAN	48.78	105836	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PSMD1 PE=1 SV=2
478	tr|A0A087WW66|A0A087WW66_HUMAN	48.78	105851	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PSMD1 PE=1 SV=1
479	sp|Q9Y2A7|NCKP1_HUMAN	48.24	128790	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1
480	sp|Q08AM6|VAC14_HUMAN	48.22	87973	Protein VAC14 homolog OS=Homo sapiens OX=9606 GN=VAC14 PE=1 SV=1
481	sp|Q13618|CUL3_HUMAN	48.06	88930	Cullin-3 OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=2
482	tr|A0A087X1R9|A0A087X1R9_HUMAN	48.06	6485	Cullin-3 (Fragment) OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=1
483	tr|H7C1L6|H7C1L6_HUMAN	48.06	22662	Cullin-3 (Fragment) OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=1
484	sp|P22102|PUR2_HUMAN	47.64	107767	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART PE=1 SV=1
485	sp|Q9NW82|WDR70_HUMAN	47.49	73201	WD repeat-containing protein 70 OS=Homo sapiens OX=9606 GN=WDR70 PE=1 SV=1
486	tr|D6RIW8|D6RIW8_HUMAN	47.49	43240	WD repeat-containing protein 70 OS=Homo sapiens OX=9606 GN=WDR70 PE=1 SV=1
487	tr|B7Z6D5|B7Z6D5_HUMAN	47.35	86605	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens OX=9606 GN=DDX27 PE=1 SV=1
488	sp|Q96GQ7|DDX27_HUMAN	47.35	89835	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens OX=9606 GN=DDX27 PE=1 SV=2
489	tr|A0A1B0GWA9|A0A1B0GWA9_HUMAN	47.3	4709	GTP-binding protein Di-Ras2 (Fragment) OS=Homo sapiens OX=9606 GN=DIRAS2 PE=1 SV=1
490	tr|A0A1B0GVC3|A0A1B0GVC3_HUMAN	47.3	12540	GTP-binding protein Di-Ras2 (Fragment) OS=Homo sapiens OX=9606 GN=DIRAS2 PE=1 SV=1
491	sp|Q96HU8|DIRA2_HUMAN	47.3	22485	GTP-binding protein Di-Ras2 OS=Homo sapiens OX=9606 GN=DIRAS2 PE=1 SV=1
492	sp|Q9UEY8|ADDG_HUMAN	46.66	79155	Gamma-adducin OS=Homo sapiens OX=9606 GN=ADD3 PE=1 SV=1
493	tr|H0YGW7|H0YGW7_HUMAN	45.83	67669	ATP-binding cassette sub-family F member 1 (Fragment) OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=1
494	sp|Q8NE71|ABCF1_HUMAN	45.83	95926	ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=2
495	tr|A0A0G2JIC2|A0A0G2JIC2_HUMAN	45.83	27218	ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV=1
496	sp|O43592|XPOT_HUMAN	45.32	109964	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2
497	tr|A0A1W2PNX8|A0A1W2PNX8_HUMAN	45.29	118395	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1
498	sp|Q9H3U1|UN45A_HUMAN	45.29	103077	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1
499	tr|H0Y8B3|H0Y8B3_HUMAN	43.84	58124	Adenosylhomocysteinase (Fragment) OS=Homo sapiens OX=9606 GN=AHCYL2 PE=1 SV=1
500	sp|O43865|SAHH2_HUMAN	43.84	58952	S-adenosylhomocysteine hydrolase-like protein 1 OS=Homo sapiens OX=9606 GN=AHCYL1 PE=1 SV=2
501	sp|Q96HN2|SAHH3_HUMAN	43.84	66721	Adenosylhomocysteinase 3 OS=Homo sapiens OX=9606 GN=AHCYL2 PE=1 SV=1
502	tr|Q3BDU5|Q3BDU5_HUMAN	43.71	55638	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1
503	sp|P02545|LMNA_HUMAN	43.71	74140	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1
504	tr|Q5TCI8|Q5TCI8_HUMAN	43.71	55762	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1
505	tr|A0A0C4DGC5|A0A0C4DGC5_HUMAN	43.71	27536	Prelamin-A/C (Fragment) OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1
506	sp|Q13263|TIF1B_HUMAN	43.37	88550	Transcription intermediary factor 1-beta OS=Homo sapiens OX=9606 GN=TRIM28 PE=1 SV=5
507	tr|M0R0K9|M0R0K9_HUMAN	43.37	48435	Transcription intermediary factor 1-beta (Fragment) OS=Homo sapiens OX=9606 GN=TRIM28 PE=1 SV=1
508	tr|A6NJA2|A6NJA2_HUMAN	42.75	51087	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens OX=9606 GN=USP14 PE=1 SV=2
509	sp|P54578|UBP14_HUMAN	42.75	56069	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens OX=9606 GN=USP14 PE=1 SV=3
510	tr|E9PRV7|E9PRV7_HUMAN	42.61	46537	G protein-coupled receptor kinase OS=Homo sapiens OX=9606 GN=GRK2 PE=1 SV=1
511	sp|P25098|ARBK1_HUMAN	42.61	79574	Beta-adrenergic receptor kinase 1 OS=Homo sapiens OX=9606 GN=GRK2 PE=1 SV=2
512	sp|O00203|AP3B1_HUMAN	42.39	121320	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3
513	tr|H0Y873|H0Y873_HUMAN	42.12	43467	Arf-GAP with GTPase ANK repeat and PH domain-containing protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=AGAP3 PE=1 SV=1
514	sp|Q96P47|AGAP3_HUMAN	42.12	95044	Arf-GAP with GTPase ANK repeat and PH domain-containing protein 3 OS=Homo sapiens OX=9606 GN=AGAP3 PE=1 SV=2
515	tr|A0A087WT27|A0A087WT27_HUMAN	42.04	49095	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1

516	tr|J3KN95|J3KN95_HUMAN	42.04	51079	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1
517	sp|O95394|AGM1_HUMAN	42.04	59852	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1
518	tr|H0Y8I3|H0Y8I3_HUMAN	42.04	12434	Phosphoacetylglucosamine mutase (Fragment) OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1
519	tr|H0Y987|H0Y987_HUMAN	42.04	21837	Phosphoacetylglucosamine mutase (Fragment) OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1
520	sp|Q9Y5J1|UTP18_HUMAN	41.66	62004	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens OX=9606 GN=UTP18 PE=1 SV=3
521	sp|Q9HCC0|MCCB_HUMAN	41.54	61333	Methylcrotonoyl-CoA carboxylase beta chain mitochondrial OS=Homo sapiens OX=9606 GN=MCCC2 PE=1 SV=1
522	tr|E9PLK3|E9PLK3_HUMAN	41.49	102988	Aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1
523	sp|P55786|PSA_HUMAN	41.49	103276	Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2
524	tr|H0YDG0|H0YDG0_HUMAN	41.49	19052	Puromycin-sensitive aminopeptidase (Fragment) OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=1
525	sp|P13473|LAMP2_HUMAN	41.28	44961	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens OX=9606 GN=LAMP2 PE=1 SV=2
526	tr|E9PD92|E9PD92_HUMAN	41.06	29503	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=1
527	tr|E7EM57|E7EM57_HUMAN	41.06	36543	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=1
528	tr|E7EUI8|E7EUI8_HUMAN	41.06	38451	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=8
529	sp|P11413|G6PD_HUMAN	41.06	59257	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=4
530	sp|P62805|H4_HUMAN	40.94	11367	Histone H4 OS=Homo sapiens OX=9606 GN=HIST1H4A PE=1 SV=2
531	tr|A0A0B4J2G4|A0A0B4J2G4_HUMAN	40.89	86239	Leucine-rich repeat-containing protein 41 OS=Homo sapiens OX=9606 GN=LRRC41 PE=1 SV=1
532	sp|Q15345|LRC41_HUMAN	40.89	88650	Leucine-rich repeat-containing protein 41 OS=Homo sapiens OX=9606 GN=LRRC41 PE=1 SV=3
533	tr|A2A2G5|A2A2G5_HUMAN	40.7	21033	Glutathione hydrolase 7 (Fragment) OS=Homo sapiens OX=9606 GN=GGT7 PE=1 SV=8
534	sp|Q9UJ14|GGT7_HUMAN	40.7	70467	Glutathione hydrolase 7 OS=Homo sapiens OX=9606 GN=GGT7 PE=1 SV=2
535	tr|E5RHJ4|E5RHJ4_HUMAN	40.38	31090	Cell cycle and apoptosis regulator protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CCAR2 PE=1 SV=1
536	tr|H0YB24|H0YB24_HUMAN	40.38	68932	Cell cycle and apoptosis regulator protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CCAR2 PE=1 SV=1
537	sp|Q8N163|CCAR2_HUMAN	40.38	102902	Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens OX=9606 GN=CCAR2 PE=1 SV=2
538	sp|Q9NTK5|OLA1_HUMAN	39.34	44744	Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=2
539	tr|J3KQ32|J3KQ32_HUMAN	39.34	46938	Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=1
540	tr|H0YLC5|H0YLC5_HUMAN	38.55	16897	POU domain class 2 transcription factor 3 (Fragment) OS=Homo sapiens OX=9606 GN=POU2F3 PE=4 SV=9
541	tr|U3KQ96|U3KQ96_HUMAN	38.55	28649	POU domain class 2 transcription factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=1
542	tr|U3KQN1|U3KQN1_HUMAN	38.55	33354	POU domain class 2 transcription factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=2
543	tr|H0YNW1|H0YNW1_HUMAN	38.55	45578	POU domain protein OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=1
544	sp|Q9UKI9|PO2F3_HUMAN	38.55	47432	POU domain class 2 transcription factor 3 OS=Homo sapiens OX=9606 GN=POU2F3 PE=2 SV=3
545	sp|P09086|PO2F2_HUMAN	38.55	51209	POU domain class 2 transcription factor 2 OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=3
546	tr|H0YLL6|H0YLL6_HUMAN	38.55	51720	POU domain protein OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=1
547	tr|A0A0C4DG88|A0A0C4DG88_HUMAN	38.55	58683	POU domain protein (Fragment) OS=Homo sapiens OX=9606 GN=POU2F1 PE=1 SV=1
548	tr|B5ME60|B5ME60_HUMAN	38.55	60436	POU domain protein OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=4
549	tr|A0A0A0MT46|A0A0A0MT46_HUMAN	38.55	61583	POU domain protein (Fragment) OS=Homo sapiens OX=9606 GN=POU2F1 PE=1 SV=1
550	tr|H0YKT2|H0YKT2_HUMAN	38.55	65144	POU domain protein (Fragment) OS=Homo sapiens OX=9606 GN=POU2F2 PE=1 SV=2
551	sp|P14859|PO2F1_HUMAN	38.55	76472	POU domain class 2 transcription factor 1 OS=Homo sapiens OX=9606 GN=POU2F1 PE=1 SV=2
552	tr|H7BXY5|H7BXY5_HUMAN	38.49	68934	Nexilin (Fragment) OS=Homo sapiens OX=9606 GN=NEXN PE=1 SV=1
553	sp|Q0ZGT2|NEXN_HUMAN	38.49	80658	Nexilin OS=Homo sapiens OX=9606 GN=NEXN PE=1 SV=1
554	sp|Q13033|STRN3_HUMAN	38.17	87209	Striatin-3 OS=Homo sapiens OX=9606 GN=STRN3 PE=1 SV=3
555	sp|Q5JRX3|PREP_HUMAN	38.13	117413	Presequence protease mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=3
556	tr|A0A0A0MRX9|A0A0A0MRX9_HUMAN	38.13	67071	Presequence protease mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=1
557	tr|B1APQ0|B1APQ0_HUMAN	38.13	20206	Presequence protease mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=1
558	sp|P35580|MYH10_HUMAN	37.74	228997	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3
559	sp|P35579|MYH9_HUMAN	37.74	226530	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4
560	sp|Q14247|SRC8_HUMAN	37.52	61586	Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN PE=1 SV=2
561	tr|F5H0C8|F5H0C8_HUMAN	37.51	34762	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1
562	sp|P09104|ENOG_HUMAN	37.51	47269	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3
563	tr|F5H1C3|F5H1C3_HUMAN	37.51	11203	Gamma-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=1
564	tr|E5RI09|E5RI09_HUMAN	37.51	15798	Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1
565	tr|E5RG95|E5RG95_HUMAN	37.51	16457	Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1
566	tr|K7EPM1|K7EPM1_HUMAN	37.51	20922	Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1
567	tr|K7EKN2|K7EKN2_HUMAN	37.51	22514	Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1
568	tr|E5RGZ4|E5RGZ4_HUMAN	37.51	30403	Beta-enolase (Fragment) OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=1
569	sp|P13929|ENOB_HUMAN	37.51	46987	Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=5
570	tr|G3V4N7|G3V4N7_HUMAN	37.46	24116	Creatine kinase B-type (Fragment) OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1
571	sp|P12277|KCRB_HUMAN	37.46	42644	Creatine kinase B-type OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1
572	sp|P85037|FOXK1_HUMAN	37.36	75457	Forkhead box protein K1 OS=Homo sapiens OX=9606 GN=FOXK1 PE=1 SV=1
573	tr|A0A0U1RRM6|A0A0U1RRM6_HUMAN	37.2	87400	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=1
574	sp|Q8N8S7|ENAH_HUMAN	37.2	66510	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=2
575	tr|A0A087WZ13|A0A087WZ13_HUMAN	37.02	77844	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1
576	tr|E9PAU2|E9PAU2_HUMAN	37.02	79579	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1
577	sp|Q8IY67|RAVR1_HUMAN	37.02	63877	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1
578	tr|K7EKR9|K7EKR9_HUMAN	37.02	10950	Ribonucleoprotein PTB-binding 1 (Fragment) OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1
579	sp|P55771|PAX9_HUMAN	36.9	36310	Paired box protein Pax-9 OS=Homo sapiens OX=9606 GN=PAX9 PE=1 SV=3
580	tr|G3V1N2|G3V1N2_HUMAN	36.73	11948	HCG1745306 isoform CRA_a OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
581	tr|A0A2R8Y7C0|A0A2R8Y7C0_HUMAN	36.73	13962	Hemoglobin subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=HBA2 PE=1 SV=1
582	sp|P69905|HBA_HUMAN	36.73	15258	Hemoglobin subunit alpha OS=Homo sapiens OX=9606 GN=HBA1 PE=1 SV=2
583	sp|P02008|HBAZ_HUMAN	36.73	15637	Hemoglobin subunit zeta OS=Homo sapiens OX=9606 GN=HBZ PE=1 SV=2
584	tr|J3QLK5|J3QLK5_HUMAN	36.46	69288	Serine/threonine-protein kinase tousled-like 2 OS=Homo sapiens OX=9606 GN=TLK2 PE=1 SV=1
585	sp|Q86UE8|TLK2_HUMAN	36.46	87661	Serine/threonine-protein kinase tousled-like 2 OS=Homo sapiens OX=9606 GN=TLK2 PE=1 SV=2
586	tr|J3KRK0|J3KRK0_HUMAN	36.46	68833	Serine/threonine-protein kinase tousled-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=TLK2 PE=1 SV=1
587	tr|J3QQN4|J3QQN4_HUMAN	36.46	4173	Serine/threonine-protein kinase tousled-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=TLK2 PE=1 SV=1
588	tr|J3QS44|J3QS44_HUMAN	36.46	19253	Serine/threonine-protein kinase tousled-like 2 (Fragment) OS=Homo sapiens OX=9606 GN=TLK2 PE=1 SV=1
589	sp|A6NNF4|ZN726_HUMAN	35.73	85539	Zinc finger protein 726 OS=Homo sapiens OX=9606 GN=ZNF726 PE=1 SV=4
590	tr|A0A0B4J2G0|A0A0B4J2G0_HUMAN	35.73	98955	Zinc finger protein 107 OS=Homo sapiens OX=9606 GN=ZNF107 PE=1 SV=1
591	sp|Q9BRH9|ZN251_HUMAN	35.73	75763	Zinc finger protein 251 OS=Homo sapiens OX=9606 GN=ZNF251 PE=1 SV=4
592	tr|A0A0A0MR57|A0A0A0MR57_HUMAN	35.73	107729	Zinc finger protein 836 OS=Homo sapiens OX=9606 GN=ZNF836 PE=1 SV=1
593	sp|Q6ZNA1|ZN836_HUMAN	35.73	107717	Zinc finger protein 836 OS=Homo sapiens OX=9606 GN=ZNF836 PE=2 SV=2
594	sp|A6NN14|ZN729_HUMAN	35.73	145021	Zinc finger protein 729 OS=Homo sapiens OX=9606 GN=ZNF729 PE=2 SV=4
595	sp|Q5JVG8|ZN506_HUMAN	35.73	51537	Zinc finger protein 506 OS=Homo sapiens OX=9606 GN=ZNF506 PE=2 SV=2
596	sp|Q05481|ZNF91_HUMAN	35.73	137217	Zinc finger protein 91 OS=Homo sapiens OX=9606 GN=ZNF91 PE=2 SV=2
597	tr|B9EG95|B9EG95_HUMAN	35.73	59133	ZNF682 protein OS=Homo sapiens OX=9606 GN=ZNF682 PE=1 SV=1
598	tr|A0A0A0MTN5|A0A0A0MTN5_HUMAN	35.73	55603	Zinc finger protein 100 OS=Homo sapiens OX=9606 GN=ZNF100 PE=1 SV=1
599	sp|Q8IYN0|ZN100_HUMAN	35.73	62745	Zinc finger protein 100 OS=Homo sapiens OX=9606 GN=ZNF100 PE=2 SV=2
600	sp|Q96N38|ZN714_HUMAN	35.73	63883	Zinc finger protein 714 OS=Homo sapiens OX=9606 GN=ZNF714 PE=2 SV=3
601	tr|A0A087WU35|A0A087WU35_HUMAN	35.73	63998	Zinc finger protein 714 OS=Homo sapiens OX=9606 GN=ZNF714 PE=1 SV=1
602	tr|A0A075B7G6|A0A075B7G6_HUMAN	35.73	65478	Zinc finger protein 100 OS=Homo sapiens OX=9606 GN=ZNF100 PE=1 SV=2
603	sp|Q9NV72|ZN701_HUMAN	35.73	60903	Zinc finger protein 701 OS=Homo sapiens OX=9606 GN=ZNF701 PE=1 SV=3
604	sp|Q6ZN06|ZN813_HUMAN	35.73	71721	Zinc finger protein 813 OS=Homo sapiens OX=9606 GN=ZNF813 PE=2 SV=2
605	sp|P17035|ZNF28_HUMAN	35.73	83659	Zinc finger protein 28 OS=Homo sapiens OX=9606 GN=ZNF28 PE=1 SV=5
606	sp|P17040|ZSC20_HUMAN	35.73	117541	Zinc finger and SCAN domain-containing protein 20 OS=Homo sapiens OX=9606 GN=ZSCAN20 PE=1 SV=3
607	sp|Q96CX3|ZN501_HUMAN	35.73	31179	Zinc finger protein 501 OS=Homo sapiens OX=9606 GN=ZNF501 PE=2 SV=2
608	sp|Q8N8J6|ZN615_HUMAN	35.73	83739	Zinc finger protein 615 OS=Homo sapiens OX=9606 GN=ZNF615 PE=2 SV=2
609	sp|P52744|ZN138_HUMAN	35.73	30591	Zinc finger protein 138 OS=Homo sapiens OX=9606 GN=ZNF138 PE=1 SV=2
610	tr|E7EWC5|E7EWC5_HUMAN	35.73	33686	Zinc finger protein 138 OS=Homo sapiens OX=9606 GN=ZNF138 PE=4 SV=1
611	tr|J3QSS9|J3QSS9_HUMAN	35.73	37395	Zinc finger protein 138 OS=Homo sapiens OX=9606 GN=ZNF138 PE=4 SV=1
612	sp|A6NP11|ZN716_HUMAN	35.73	57006	Zinc finger protein 716 OS=Homo sapiens OX=9606 GN=ZNF716 PE=2 SV=4
613	sp|Q9Y2Q1|ZN257_HUMAN	35.73	65780	Zinc finger protein 257 OS=Homo sapiens OX=9606 GN=ZNF257 PE=2 SV=2
614	sp|P35789|ZNF93_HUMAN	35.73	70971	Zinc finger protein 93 OS=Homo sapiens OX=9606 GN=ZNF93 PE=2 SV=4
615	sp|Q5JNZ3|ZN311_HUMAN	35.73	76322	Zinc finger protein 311 OS=Homo sapiens OX=9606 GN=ZNF311 PE=2 SV=2
616	sp|Q3SXZ3|ZN718_HUMAN	35.73	55359	Zinc finger protein 718 OS=Homo sapiens OX=9606 GN=ZNF718 PE=2 SV=2
617	sp|Q8N988|ZN557_HUMAN	35.73	48627	Zinc finger protein 557 OS=Homo sapiens OX=9606 GN=ZNF557 PE=2 SV=2
618	sp|Q9UEG4|ZN629_HUMAN	35.73	96620	Zinc finger protein 629 OS=Homo sapiens OX=9606 GN=ZNF629 PE=1 SV=2
619	tr|A0A087WUV0|A0A087WUV0_HUMAN	35.73	59574	Uncharacterized protein OS=Homo sapiens OX=9606 PE=1 SV=1
620	sp|Q5HY98|ZN766_HUMAN	35.73	54507	Zinc finger protein 766 OS=Homo sapiens OX=9606 GN=ZNF766 PE=1 SV=1
621	sp|Q14590|ZN235_HUMAN	35.73	83977	Zinc finger protein 235 OS=Homo sapiens OX=9606 GN=ZNF235 PE=2 SV=3
622	sp|Q9UL36|ZN236_HUMAN	35.73	203702	Zinc finger protein 236 OS=Homo sapiens OX=9606 GN=ZNF236 PE=2 SV=2
623	tr|J9JID5|J9JID5_HUMAN	35.73	203845	Zinc finger protein 236 OS=Homo sapiens OX=9606 GN=ZNF236 PE=1 SV=1
624	sp|Q8N8C0|ZN781_HUMAN	35.73	41526	Zinc finger protein 781 OS=Homo sapiens OX=9606 GN=ZNF781 PE=2 SV=1
625	sp|O95600|KLF8_HUMAN	35.73	39314	Krueppel-like factor 8 OS=Homo sapiens OX=9606 GN=KLF8 PE=1 SV=2
626	tr|G3V1M0|G3V1M0_HUMAN	35.73	49339	Zinc finger and SCAN domain-containing protein 21 OS=Homo sapiens OX=9606 GN=ZSCAN21 PE=1 SV=2
627	sp|P10073|ZSC22_HUMAN	35.73	54561	Zinc finger and SCAN domain-containing protein 22 OS=Homo sapiens OX=9606 GN=ZSCAN22 PE=1 SV=2
628	sp|P51815|ZN75D_HUMAN	35.73	59298	Zinc finger protein 75D OS=Homo sapiens OX=9606 GN=ZNF75D PE=2 SV=2
629	sp|Q8NEM1|ZN680_HUMAN	35.73	61798	Zinc finger protein 680 OS=Homo sapiens OX=9606 GN=ZNF680 PE=1 SV=2
630	tr|A0A0C4DG42|A0A0C4DG42_HUMAN	35.73	61708	Zinc finger protein 34 OS=Homo sapiens OX=9606 GN=ZNF34 PE=1 SV=1
631	sp|Q8TB69|ZN519_HUMAN	35.73	63020	Zinc finger protein 519 OS=Homo sapiens OX=9606 GN=ZNF519 PE=2 SV=2
632	sp|Q6ZMS4|ZN852_HUMAN	35.73	62084	Zinc finger protein 852 OS=Homo sapiens OX=9606 GN=ZNF852 PE=1 SV=4
633	sp|B4DU55|ZN879_HUMAN	35.73	64577	Zinc finger protein 879 OS=Homo sapiens OX=9606 GN=ZNF879 PE=2 SV=2
634	sp|Q6PDB4|ZN880_HUMAN	35.73	66762	Zinc finger protein 880 OS=Homo sapiens OX=9606 GN=ZNF880 PE=2 SV=2
635	sp|Q9P2F9|ZN319_HUMAN	35.73	65547	Zinc finger protein 319 OS=Homo sapiens OX=9606 GN=ZNF319 PE=1 SV=2
636	tr|A0A087WV98|A0A087WV98_HUMAN	35.73	67996	Zinc finger protein 429 OS=Homo sapiens OX=9606 GN=ZNF429 PE=4 SV=1
637	tr|K7EP39|K7EP39_HUMAN	35.73	68433	Zinc finger protein 570 OS=Homo sapiens OX=9606 GN=ZNF570 PE=1 SV=1
638	sp|Q08ER8|ZN543_HUMAN	35.73	68404	Zinc finger protein 543 OS=Homo sapiens OX=9606 GN=ZNF543 PE=1 SV=3
639	sp|Q7Z3V5|ZN571_HUMAN	35.73	70793	Zinc finger protein 571 OS=Homo sapiens OX=9606 GN=ZNF571 PE=2 SV=3
640	sp|Q16587|ZNF74_HUMAN	35.73	72207	Zinc finger protein 74 OS=Homo sapiens OX=9606 GN=ZNF74 PE=1 SV=3
641	sp|Q3ZCX4|ZN568_HUMAN	35.73	74369	Zinc finger protein 568 OS=Homo sapiens OX=9606 GN=ZNF568 PE=2 SV=2
642	sp|Q8NDQ6|ZN540_HUMAN	35.73	77094	Zinc finger protein 540 OS=Homo sapiens OX=9606 GN=ZNF540 PE=1 SV=1
643	sp|O43361|ZN749_HUMAN	35.73	90364	Zinc finger protein 749 OS=Homo sapiens OX=9606 GN=ZNF749 PE=1 SV=2
644	sp|Q08AN1|ZN616_HUMAN	35.73	90273	Zinc finger protein 616 OS=Homo sapiens OX=9606 GN=ZNF616 PE=2 SV=2

645	sp|Q8WXB4|ZN606_HUMAN	35.73	91812	Zinc finger protein 606 OS=Homo sapiens OX=9606 GN=ZNF606 PE=2 SV=1
646	sp|Q4V348|Z658B_HUMAN	35.73	94331	Zinc finger protein 658B OS=Homo sapiens OX=9606 GN=ZNF658B PE=2 SV=1
647	sp|Q9Y6R6|Z780B_HUMAN	35.73	96807	Zinc finger protein 780B OS=Homo sapiens OX=9606 GN=ZNF780B PE=2 SV=1
648	sp|Q8NB50|ZFP62_HUMAN	35.73	102511	Zinc finger protein 62 homolog OS=Homo sapiens OX=9606 GN=ZFP62 PE=1 SV=3
649	sp|Q96BY6|DOC10_HUMAN	35.66	249529	Dedicator of cytokinesis protein 10 OS=Homo sapiens OX=9606 GN=DOCK10 PE=1 SV=3
650	tr|A0A2R8YD85|A0A2R8YD85_HUMAN	35.66	251313	Dedicator of cytokinesis protein 10 OS=Homo sapiens OX=9606 GN=DOCK10 PE=1 SV=1
651	sp|O14974|MYPT1_HUMAN	35.62	115281	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1
652	tr|F8VZN8|F8VZN8_HUMAN	35.62	76533	Protein phosphatase 1 regulatory subunit 12A (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1
653	tr|H0YIS4|H0YIS4_HUMAN	35.62	33152	Protein phosphatase 1 regulatory subunit 12A (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1
654	tr|H0YHI8|H0YHI8_HUMAN	35.62	40623	Protein phosphatase 1 regulatory subunit 12A (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1
655	tr|A0A3B3ISH4|A0A3B3ISH4_HUMAN	35.62	40958	Protein phosphatase 1 regulatory subunit 12A (Fragment) OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1
656	sp|P54577|SYYC_HUMAN	35.44	59144	Tyrosine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=YARS PE=1 SV=4
657	tr|A0A0C4DGZ5|A0A0C4DGZ5_HUMAN	35.44	43905	Tyrosine--tRNA ligase OS=Homo sapiens OX=9606 GN=YARS PE=1 SV=1
658	sp|Q5TCS8|KAD9_HUMAN	34.92	221411	Adenylate kinase 9 OS=Homo sapiens OX=9606 GN=AK9 PE=1 SV=2
659	tr|G3V213|G3V213_HUMAN	34.92	14325	Adenylate kinase 2 isoform CRA_a OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1
660	tr|F8VZG5|F8VZG5_HUMAN	34.92	17499	Adenylate kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1
661	tr|F8VY04|F8VY04_HUMAN	34.92	21226	Adenylate kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1
662	tr|H7C505|H7C505_HUMAN	34.92	25370	Adenylate kinase 9 (Fragment) OS=Homo sapiens OX=9606 GN=AK9 PE=1 SV=1
663	tr|F8W1A4|F8W1A4_HUMAN	34.92	25631	Adenylate kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=1
664	sp|P54819|KAD2_HUMAN	34.92	26478	Adenylate kinase 2 mitochondrial OS=Homo sapiens OX=9606 GN=AK2 PE=1 SV=2
665	sp|Q96I59|SYNM_HUMAN	34.85	54090	Probable asparagine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=NARS2 PE=1 SV=3
666	tr|X6RGJ2|X6RGJ2_HUMAN	34.66	36515	Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1
667	sp|Q5SSJ5|HP1B3_HUMAN	34.66	61207	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1
668	tr|B0QZK9|B0QZK9_HUMAN	34.66	8150	Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=8
669	tr|B0QZK8|B0QZK8_HUMAN	34.66	13684	Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1
670	tr|A0A3B3ITB4|A0A3B3ITB4_HUMAN	34.55	18612	GTP-binding protein Rit2 OS=Homo sapiens OX=9606 GN=RIT2 PE=1 SV=1
671	tr|K7EMR8|K7EMR8_HUMAN	34.55	19100	GTP-binding protein Rit2 OS=Homo sapiens OX=9606 GN=RIT2 PE=1 SV=1
672	sp|Q99578|RIT2_HUMAN	34.55	24668	GTP-binding protein Rit2 OS=Homo sapiens OX=9606 GN=RIT2 PE=1 SV=1
673	sp|P53618|COPB_HUMAN	34.05	107142	Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3
674	tr|E7EPB3|E7EPB3_HUMAN	34.04	14558	60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=1
675	sp|P50914|RL14_HUMAN	34.04	23432	60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=4
676	sp|Q2NL82|TSR1_HUMAN	34	91810	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens OX=9606 GN=TSR1 PE=1 SV=1
677	tr|H0Y6U5|H0Y6U5_HUMAN	33.97	102922	Condensin-2 complex subunit G2 (Fragment) OS=Homo sapiens OX=9606 GN=NCAPG2 PE=1 SV=1
678	sp|Q86XI2|CNDG2_HUMAN	33.97	130960	Condensin-2 complex subunit G2 OS=Homo sapiens OX=9606 GN=NCAPG2 PE=1 SV=1
679	sp|P22735|TGM1_HUMAN	33.93	89787	Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens OX=9606 GN=TGM1 PE=1 SV=4
680	tr|C9JFE4|C9JFE4_HUMAN	33.84	53372	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=2
681	tr|A0A096LP07|A0A096LP07_HUMAN	33.84	54965	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=1
682	tr|A0A096LPJ3|A0A096LPJ3_HUMAN	33.84	55408	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=1
683	sp|Q13098|CSN1_HUMAN	33.84	55537	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=4
684	tr|A8K070|A8K070_HUMAN	33.84	58922	COP9 signalosome complex subunit 1 OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=1
685	tr|J3QQX0|J3QQX0_HUMAN	33.84	8709	COP9 signalosome complex subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=GPS1 PE=1 SV=1
686	sp|Q14554|PDIA5_HUMAN	33.72	59594	Protein disulfide-isomerase A5 OS=Homo sapiens OX=9606 GN=PDIA5 PE=1 SV=1
687	sp|Q6VY07|PACS1_HUMAN	33.63	104898	Phosphofurin acidic cluster sorting protein 1 OS=Homo sapiens OX=9606 GN=PACS1 PE=1 SV=2
688	sp|P46087|NOP2_HUMAN	33.29	89302	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens OX=9606 GN=NOP2 PE=1 SV=2
689	sp|P56192|SYMC_HUMAN	33.22	101116	Methionine--tRNA ligase cytoplasmic OS=Homo sapiens OX=9606 GN=MARS PE=1 SV=2
690	sp|Q6NSJ5|LRC8E_HUMAN	33.16	90247	Volume-regulated anion channel subunit LRRC8E OS=Homo sapiens OX=9606 GN=LRRC8E PE=1 SV=2
691	sp|O43719|HTSF1_HUMAN	32.93	85853	HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1
692	tr|F6VX93|F6VX93_HUMAN	32.93	62167	Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens OX=9606 GN=VPS53 PE=1 SV=1
693	sp|Q5VIR6|VPS53_HUMAN	32.93	79653	Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens OX=9606 GN=VPS53 PE=1 SV=1
694	tr|I3L184|I3L184_HUMAN	32.93	27162	Vacuolar protein sorting-associated protein 53 homolog (Fragment) OS=Homo sapiens OX=9606 GN=VPS53 PE=1 SV=1
695	sp|Q86Z14|KLOTB_HUMAN	32.89	119808	Beta-klotho OS=Homo sapiens OX=9606 GN=KLB PE=1 SV=1
696	tr|A0A087WYK2|A0A087WYK2_HUMAN	32.79	198280	Serine/threonine-protein kinase WNK3 OS=Homo sapiens OX=9606 GN=WNK3 PE=1 SV=1
697	sp|Q9BYP7|WNK3_HUMAN	32.79	198414	Serine/threonine-protein kinase WNK3 OS=Homo sapiens OX=9606 GN=WNK3 PE=1 SV=3
698	tr|F8W9F9|F8W9F9_HUMAN	32.79	234378	Serine/threonine-protein kinase WNK2 OS=Homo sapiens OX=9606 GN=WNK2 PE=1 SV=1
699	sp|Q9Y3S1|WNK2_HUMAN	32.79	242673	Serine/threonine-protein kinase WNK2 OS=Homo sapiens OX=9606 GN=WNK2 PE=1 SV=4
700	sp|Q9NVM9|INT13_HUMAN	32.78	80225	Integrator complex subunit 13 OS=Homo sapiens OX=9606 GN=INTS13 PE=1 SV=2
701	sp|P10828|THB_HUMAN	32.58	52788	Thyroid hormone receptor beta OS=Homo sapiens OX=9606 GN=THRB PE=1 SV=2
702	sp|Q86TJ2|TAD2B_HUMAN	32.58	48470	Transcriptional adapter 2-beta OS=Homo sapiens OX=9606 GN=TADA2B PE=1 SV=2
703	sp|P10827|THA_HUMAN	32.58	54816	Thyroid hormone receptor alpha OS=Homo sapiens OX=9606 GN=THRA PE=1 SV=1
704	tr|G3XAL0|G3XAL0_HUMAN	32.58	24595	Malate dehydrogenase OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=1
705	sp|P40926|MDHM_HUMAN	32.58	35503	Malate dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3
706	sp|Q9NQX3|GEPH_HUMAN	32.54	79748	Gephyrin OS=Homo sapiens OX=9606 GN=GPHN PE=1 SV=1
707	tr|H0YJ30|H0YJ30_HUMAN	32.54	30112	Gephyrin (Fragment) OS=Homo sapiens OX=9606 GN=GPHN PE=1 SV=1
708	sp|Q8N3K9|CMYA5_HUMAN	32.52	449215	Cardiomyopathy-associated protein 5 OS=Homo sapiens OX=9606 GN=CMYA5 PE=1 SV=3
709	sp|Q9NXC5|MIO_HUMAN	32.36	98584	GATOR complex protein MIOS OS=Homo sapiens OX=9606 GN=MIOS PE=1 SV=2
710	sp|P31327|CPSM_HUMAN	32.2	164939	Carbamoyl-phosphate synthase [ammonia] mitochondrial OS=Homo sapiens OX=9606 GN=CPS1 PE=1 SV=2
711	sp|Q00266|METK1_HUMAN	31.99	43648	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens OX=9606 GN=MAT1A PE=1 SV=2
712	sp|P31153|METK2_HUMAN	31.99	43661	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens OX=9606 GN=MAT2A PE=1 SV=1
713	tr|A0A3B3IRQ9|A0A3B3IRQ9_HUMAN	31.88	128389	Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=1
714	tr|H0YCK3|H0YCK3_HUMAN	31.88	132647	Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=1
715	sp|P55265|DSRAD_HUMAN	31.88	136066	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=4
716	tr|A0A3B3ISX1|A0A3B3ISX1_HUMAN	31.88	78042	Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=1
717	tr|A0A087X253|A0A087X253_HUMAN	31.82	101333	AP complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1
718	sp|P63010|AP2B1_HUMAN	31.82	104553	AP-2 complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1
719	tr|C9J1E7|C9J1E7_HUMAN	31.82	65315	AP-1 complex subunit beta-1 (Fragment) OS=Homo sapiens OX=9606 GN=AP1B1 PE=1 SV=1
720	tr|A0A087WYD1|A0A087WYD1_HUMAN	31.82	70917	AP-2 complex subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1
721	tr|A0A087WU93|A0A087WU93_HUMAN	31.82	74137	AP-2 complex subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1
722	tr|A0A087WZQ6|A0A087WZQ6_HUMAN	31.82	75276	AP-2 complex subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1
723	sp|Q10567|AP1B1_HUMAN	31.82	104637	AP-1 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP1B1 PE=1 SV=2
724	sp|Q9BX84|TRPM6_HUMAN	31.73	231706	Transient receptor potential cation channel subfamily M member 6 OS=Homo sapiens OX=9606 GN=TRPM6 PE=1 SV=2
725	tr|H3BUF6|H3BUF6_HUMAN	31.36	112714	Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1
726	sp|Q8WWM7|ATX2L_HUMAN	31.36	113374	Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=2
727	tr|H3BUE3|H3BUE3_HUMAN	31.36	23513	Ataxin-2-like protein (Fragment) OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1
728	tr|H3BSK9|H3BSK9_HUMAN	31.36	37138	Ataxin-2-like protein (Fragment) OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1
729	sp|P10155|RO60_HUMAN	30.89	60671	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=TROVE2 PE=1 SV=2
730	tr|J3KMX1|J3KMX1_HUMAN	30.81	78890	Nuclear pore complex protein Nup88 (Fragment) OS=Homo sapiens OX=9606 GN=NUP88 PE=1 SV=1
731	sp|Q99567|NUP88_HUMAN	30.81	83542	Nuclear pore complex protein Nup88 OS=Homo sapiens OX=9606 GN=NUP88 PE=1 SV=2
732	sp|Q99661|KIF2C_HUMAN	30.76	81313	Kinesin-like protein KIF2C OS=Homo sapiens OX=9606 GN=KIF2C PE=1 SV=2
733	sp|O60264|SMCA5_HUMAN	30.75	121905	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 S
734	sp|P28370|SMCA1_HUMAN	30.75	122605	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=2
735	tr|A0A0A0MRP6|A0A0A0MRP6_HUMAN	30.75	122864	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=1
736	tr|B7ZLQ5|B7ZLQ5_HUMAN	30.75	124327	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=1
737	sp|P04040|CATA_HUMAN	30.7	59756	Catalase OS=Homo sapiens OX=9606 GN=CAT PE=1 SV=3
738	sp|P30419|NMT1_HUMAN	30.66	56806	Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 PE=1 SV=2
739	tr|M0QZN2|M0QZN2_HUMAN	30.24	14763	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=1
740	tr|M0R0F0|M0R0F0_HUMAN	30.24	22391	40S ribosomal protein S5 (Fragment) OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=1
741	sp|P46782|RS5_HUMAN	30.24	22876	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=4
742	tr|M0R0R2|M0R0R2_HUMAN	30.24	25333	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=1
743	sp|O14980|XPO1_HUMAN	29.93	123386	Exportin-1 OS=Homo sapiens OX=9606 GN=XPO1 PE=1 SV=1
744	sp|P06280|AGAL_HUMAN	29.89	48767	Alpha-galactosidase A OS=Homo sapiens OX=9606 GN=GLA PE=1 SV=1
745	tr|A0A3B3IUC4|A0A3B3IUC4_HUMAN	29.89	53284	Alpha-galactosidase OS=Homo sapiens OX=9606 GN=GLA PE=1 SV=1
746	tr|A0A1C7CYX1|A0A1C7CYX1_HUMAN	29.77	120733	ELM2 and SANT domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ELMSAN1 PE=1 SV=1
747	tr|F8VPD4|F8VPD4_HUMAN	29.63	236020	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=1
748	sp|P27708|PYR1_HUMAN	29.63	242981	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=3
749	sp|Q99879|H2B1M_HUMAN	29.61	13989	Histone H2B type 1-M OS=Homo sapiens OX=9606 GN=HIST1H2BM PE=1 SV=3
750	sp|O60814|H2B1K_HUMAN	29.61	13890	Histone H2B type 1-K OS=Homo sapiens OX=9606 GN=HIST1H2BK PE=1 SV=3
751	sp|Q16778|H2B2E_HUMAN	29.61	13920	Histone H2B type 2-E OS=Homo sapiens OX=9606 GN=HIST2H2BE PE=1 SV=3
752	sp|Q93079|H2B1H_HUMAN	29.61	13892	Histone H2B type 1-H OS=Homo sapiens OX=9606 GN=HIST1H2BH PE=1 SV=3
753	sp|P33778|H2B1B_HUMAN	29.61	13950	Histone H2B type 1-B OS=Homo sapiens OX=9606 GN=HIST1H2BB PE=1 SV=2
754	sp|P62807|H2B1C_HUMAN	29.61	13906	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens OX=9606 GN=HIST1H2BC PE=1 SV=4
755	sp|P06899|H2B1J_HUMAN	29.61	13904	Histone H2B type 1-J OS=Homo sapiens OX=9606 GN=HIST1H2BJ PE=1 SV=3
756	sp|Q99880|H2B1L_HUMAN	29.61	13952	Histone H2B type 1-L OS=Homo sapiens OX=9606 GN=HIST1H2BL PE=1 SV=3
757	sp|Q8N257|H2B3B_HUMAN	29.61	13908	Histone H2B type 3-B OS=Homo sapiens OX=9606 GN=HIST3H2BB PE=1 SV=3
758	sp|P58876|H2B1D_HUMAN	29.61	13936	Histone H2B type 1-D OS=Homo sapiens OX=9606 GN=HIST1H2BD PE=1 SV=2
759	sp|P23527|H2B1O_HUMAN	29.61	13906	Histone H2B type 1-O OS=Homo sapiens OX=9606 GN=HIST1H2BO PE=1 SV=3
760	sp|Q5QNW6|H2B2F_HUMAN	29.61	13920	Histone H2B type 2-F OS=Homo sapiens OX=9606 GN=HIST2H2BF PE=1 SV=3
761	sp|Q99877|H2B1N_HUMAN	29.61	13922	Histone H2B type 1-N OS=Homo sapiens OX=9606 GN=HIST1H2BN PE=1 SV=3
762	sp|P57053|H2BFS_HUMAN	29.61	13944	Histone H2B type F-S OS=Homo sapiens OX=9606 GN=H2BFS PE=1 SV=2
763	tr|U3KQK0|U3KQK0_HUMAN	29.61	18804	Histone H2B OS=Homo sapiens OX=9606 GN=HIST1H2BN PE=1 SV=1
764	tr|A0A2R8Y619|A0A2R8Y619_HUMAN	29.61	13491	Histone H2B OS=Homo sapiens OX=9606 PE=1 SV=1
765	sp|Q96A08|H2B1A_HUMAN	29.61	14167	Histone H2B type 1-A OS=Homo sapiens OX=9606 GN=HIST1H2BA PE=1 SV=3
766	sp|Q8N3Z3|GTPB8_HUMAN	29.49	32147	GTP-binding protein 8 OS=Homo sapiens OX=9606 GN=GTPBP8 PE=2 SV=1
767	tr|A0A087WUP3|A0A087WUP3_HUMAN	29.49	34955	GTP-binding protein 8 OS=Homo sapiens OX=9606 GN=GTPBP8 PE=1 SV=1
768	tr|Q5SYV2|Q5SYV2_HUMAN	29.47	40161	Sarcosine dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=SARDH PE=1 SV=1
769	tr|A0A0A0MT55|A0A0A0MT55_HUMAN	29.47	67216	Sarcosine dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=SARDH PE=1 SV=1
770	sp|Q9UL12|SARDH_HUMAN	29.47	101037	Sarcosine dehydrogenase mitochondrial OS=Homo sapiens OX=9606 GN=SARDH PE=1 SV=1
771	sp|Q92922|SMRC1_HUMAN	29.47	122867	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens OX=9606 GN=SMARCC1 PE=1 SV=3
772	sp|Q9ULX6|AKP8L_HUMAN	29.36	71640	A-kinase anchor protein 8-like OS=Homo sapiens OX=9606 GN=AKAP8L PE=1 SV=4
773	tr|V9GZ50|V9GZ50_HUMAN	29.36	47338	A kinase (PRKA) anchor protein 8-like isoform CRA_c OS=Homo sapiens OX=9606 GN=AKAP8L PE=1 SV=1

774	tr|A0A087WVM4|A0A087WVM4_HUMAN	29.27	99312	Monofunctional C1-tetrahydrofolate synthase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1
775	sp|Q6UB35|C1TM_HUMAN	29.27	105790	Monofunctional C1-tetrahydrofolate synthase mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1
776	tr|B7ZM99|B7ZM99_HUMAN	29.27	105889	MTHFD1L protein OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1
777	tr|A0A087WTT1|A0A087WTT1_HUMAN	29.04	58536	Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1
778	tr|E7EQV3|E7EQV3_HUMAN	29.04	65748	Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1
779	sp|P11940|PABP1_HUMAN	29.04	70671	Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2
780	tr|H0YAR2|H0YAR2_HUMAN	29.04	32258	Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1
781	tr|E7ERJ7|E7ERJ7_HUMAN	29.04	67139	Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=1
782	sp|Q9H361|PABP3_HUMAN	29.04	70031	Polyadenylate-binding protein 3 OS=Homo sapiens OX=9606 GN=PABPC3 PE=1 SV=2
783	sp|Q5VTR2|BRE1A_HUMAN	28.93	113662	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens OX=9606 GN=RNF20 PE=1 SV=2
784	sp|Q9Y4C4|MFHA1_HUMAN	28.81	116950	Malignant fibrous histiocytoma-amplified sequence 1 OS=Homo sapiens OX=9606 GN=MFHAS1 PE=1 SV=2
785	tr|D6RA20|D6RA20_HUMAN	28.81	97241	Protocadherin alpha-4 OS=Homo sapiens OX=9606 GN=PCDHA4 PE=1 SV=2
786	sp|Q9UN74|PCDA4_HUMAN	28.81	102293	Protocadherin alpha-4 OS=Homo sapiens OX=9606 GN=PCDHA4 PE=1 SV=1
787	tr|A0A087WSW8|A0A087WSW8_HUMAN	28.81	83615	Protocadherin alpha-4 OS=Homo sapiens OX=9606 GN=PCDHA4 PE=1 SV=1
788	sp|P05154|IPSP_HUMAN	28.75	45675	Plasma serine protease inhibitor OS=Homo sapiens OX=9606 GN=SERPINA5 PE=1 SV=3

Supplementary Table 2. The correlations between ARHGAP24 expression and clinicopathological characteristics in HCC.

			ARHGAP24 expression		
			low (85)	High (46)	P
Gender	Male	27	18 (66.7)	9 (33.3)	0.828
	Female	104	67 (64.4)	37 (35.6)	
Age	≤50	39	28 (71.8)	11 (28.2)	0.281
	>50	92	57 (62.0)	35 (38.0)	
Liver cirrhosis	No	64	45 (70.3)	19 (29.7)	0.203
	Yes	67	40 (59.7)	27 (40.3)	
HBsAg	No	27	17 (63.0)	10 (37.0)	0.814
	Yes	104	68 (65.4)	36 (34.6)	
ALT,U/L	≤40	101	62 (61.4)	39 (38.6)	0.124
	>40	30	23 (76.7)	7 (23.3)	
AST,U/L	≤40	88	55 (62.5)	33 (37.5)	0.413
	>40	43	30 (69.8)	13 (30.2)	
AFP, ng/ml	≤400	91	57 (62.6)	34 (37.4)	0.416
	>400	40	28 (70.0)	12 (30.0)	
Tumor number	Single	104	66 (63.5)	38 (36.5)	0.503
	Multiple	27	19 (70.4)	8 (29.6)	
Tumor size, cm	≤5	73	43 (58.9)	30 (41.1)	0.108
	>5	58	42 (72.4)	16 (27.6)	
Satellite lesion	No	114	70 (61.4)	44 (38.6)	**0.031**
	Yes	17	15 (88.2)	2 (11.8)	
MVI	No	62	31 (50.0)	31 (50.0)	**0.001**
	Yes	69	54 (78.3)	15 (21.7)	
Edmondson stage	I-II	62	38 (60.9)	24 (39.1)	0.414
	III-IV	69	47 (68.1)	22 (31.9)	
BCLC stage	0+A	100	61 (61.0)	39 (39.0)	0.094
	B+C	31	24 (77.4)	7 (22.6)	
CNLC stage	I-II	117	72 (61.5)	45 (38.5)	**0.020**
	III-IV	14	13 (92.9)	1 (7.1)	
Tumor recurrence	No	79	43 (54.4)	36 (45.6)	**0.002**
	Yes	52	42 (80.8)	10 (19.2)	

Abbreviations: ALT, alanine aminotransferase; AST, aspartate transaminase; AFP, α-fetoprotein; MVI, Microvascular invasion; BCLC, Barcelona Clinic Liver Cancer; CNLC, China liver cancer staging.

Supplementary Table 3. Univariate cox proportional regression analysis of factors associated with recurrence and overall survival

Variables	Tumor Recurrence	
	HR (95% CI)	**P**
Sex (Male versus female)	0.69 (0.37-1.30)	0.255
Age (>50 versus ≤50)	1.37 (0.73-2.56)	0.331
HBsAg (Yes versus No)	1.16 (0.57-2.38)	0.683
Liver cirrhosis (Yes versus no)	1.01 (0.58-1.73)	0.986
γ-GT, U/L (>45 versus ≤45)	2.55 1.38-4.71	**0.003**
ALT (>40U/L versus ≤40U/L)	1.48 (0.81-2.69)	0.205
AST (>40U/L versus ≤40U/L)	2.37 (1.37-4.09)	**0.002**
AFP (>400ng/ml versus ≤400ng/ml)	1.86 (1.07-3.24)	**0.028**
No. of tumors (Multi versus single)	1.96 (1.09-3.54)	**0.025**
Tumor size (>5cm versus ≤5cm)	3.06 (1.73-5.39)	**0.000**
Micro vascular invasion (Yes versus no)	1.05 (0.61-1.82)	0.852
Satellite lesion (Yes versus no)	4.96 (2.64-9.31)	**0.000**
Edmondson stage (III-IV versus I-II)	1.29 (0.75-2.24)	0.358
BCLC stage (B+C versus 0+A)	3.54 (2.03-6.16)	**0.000**
ARHGAP24 (High versus low)	0.34 (0.17-0.68)	**0.002**

Abbreviations: ALT, alanine aminotransferase; AST, aspartate transaminase; AFP, α-fetoprotein; BCLC, Barcelona Clinic Liver Cancer; HR, hazard ratio.

Methods and Materials

Cell culture

Huh7, Li-7, and Hep3B cells were purchased from the Chinese Academy of Sciences Shanghai Branch Cell Bank (Shanghai, China). L02, MHCC97L, MHCC97H, and HCCLM3 cells were gifted by Professor Yang at the Liver Cancer Institute of Zhongshan Hospital, Fudan University. The cell lines were cultured in DMEM medium (Gibco, Grand Island, NY, USA) supplemented with 10% fetal bovine serum (Gibco) and penicillin/streptomycin, and maintained in an incubator at 37°C containing 5% CO_2.

Generation of lentivirus and plasmid construction

Wild-type ARHGAP24 for overexpression of ARHGAP24 (ARH-OE cells) and negative control vector (Vector) were transfected into HCCLM3 and Huh7 cells, based on the GV492 vector (Ubi-MCS-3Flag-CBh-IRES-puromycin) purchased from Shanghai Genechem Corporation (Shanghai, China). Knockdown lentiviral vector (shARH#1 and shARH#2) and negative control vector (NC) were transfected into Li-7 cells, based on the GV493 vector (Hu6-MCS-CBh-gcGFP-IRES-puromycin) purchased from Shanghai Genechem Corporation. SiPKM2 and siWWP1 were constructed by Shanghai GenePharma Corporation (Shanghai, China).

Full-length ARHGAP24, PKM2, and WWP1 plasmids were obtained by cloning cDNA into a phage vector with a corresponding HA, FLAG, or His tag. The GAP-deficient mutant of ARHGAP24 (HA-Q158R) and a series of ARHGAP24 mutations that lack different domains, including HA-ARH-PHD, HA-ARH-GAPD, HA-ARH-CD, and HA-ARH-ΔCD, and deletion mutants of PKM2, including Flag-PKM2-ΔCD, Flag-PKM2-ABD, and Flag-PKM2-CD, and deletion mutants of ARHGAP24 were constructed by Shanghai Genechem Corporation. ARHGAP24 mutants, including M1, M2, M3, and M4, were also designed by

Shanghai Genechem Corporation.

Western blot and Immunofluorescence

Western blotting and immunofluorescence assays were performed as described previously [1]. Briefly, for western blot assays, proteins were extracted from the indicated cells and fractionated by SDS-PAGE. Then, proteins were transferred to nitrocellulose membranes. After blocking with 5% milk at room temperature for 1 h, the membranes were incubated with the specific primary antibodies overnight. For immunofluorescence assay, the cells were fixed, permeabilized, and blocked. Then, the indicated primary antibodies were incubated with cells. The next day, the membranes and cells were washed three times with PBS and incubated with a horseradish peroxidase-conjugated secondary antibody and fluorescently labeled secondary antibody, respectively. To observe the cytoskeleton, phalloidin was used for immunofluorescence staining.

Immunohistochemistry

Immunohistochemical staining was performed as described previously [1]. Briefly, HCC tissues underwent the following steps: dewaxing treatment, antigen retrieval, and endogenous peroxidase blockade. The primary antibodies and dilutions used to detect the intensities of the indicated markers are listed below. Immunostaining intensities of the indicated markers were evaluated as follows: negative, weak, moderate and strong. When the intensity was negative or weak, the expression status was defined as “low expression”, while the intensity was moderate or strong, the expression status was defined as “high expression”. At least two pathology-related professionals interpreted the slices in a double-blind manner. If the results of the two personnel were disputed, other related pathology professionals examined the slice again. After discussion by all personnel, the final immunostaining group was determined.

Immunoprecipitation

The indicated plasmids were co-transfected into Li-7, HCCLM3, and HEK293T cells. After 48 h, cells were lysed with IP lysis buffer (20mM Tris-HCL, pH7.4, 150mM NaCL, 1mM EDTA, and 1% NP-40) containing protease inhibitor cocktail (Roche, USA). Immunoprecipitation assays were performed following the manufacturer's instructions (Pierce, Thermo, USA). The supernatant protein was immunoprecipitated with the indicated tagged antibodies and protein G agarose beads overnight at 4°C. Antibodies used in these experiments are listed below. The complex was washed with NaCl buffer and boiled with 1×SDS loading buffer.

Antibodies and reagents

Antibodies used in this study were ARHGAP24 (PA5-104104; Invitrogen), β-tubulin (Beyotime, Shanghai), PCNA (13110; Cell Signaling Technology), cleaved-caspase3 (9664; Cell Signaling Technology), cyclin D1 (55506; Cell Signaling Technology), BCL2 (15071; Cell Signaling Technology), CDK2 (18048; Cell Signaling Technology), E-cadherin (3195; Cell Signaling Technology), N-cadherin (13116; Cell Signaling Technology), vimentin (5741; Cell Signaling Technology), α-SMA (19245; Cell Signaling Technology), MMP-9 (13667; Cell Signaling Technology), Ki67 (9449; Cell Signaling Technology), β-catenin (8480; Cell Signaling Technology), c-MYC (18583; Cell Signaling Technology), PKM2 (4053; Cell Signaling Technology), WWP1 (ab104440; Abcam), anti-FLAG (14793; Cell Signaling Technology), anti-HA (3724; Cell Signaling Technology), and anti-His (12698; Cell Signaling Technology).

Cell proliferation, migration, and invasion assays

CCK8 and colony formation assays were used to investigate cell proliferation, which were performed as described previously [1]. Cell migration and invasion were detected using transwell chambers (BD, PharMingen, San Jose, CA), as

previously described [51]. Briefly, 5 × 10^4 cells were plated in the top chamber with Matrigel used or not, and the lower chamber was supplemented with 500 μL complete medium and incubated for 24 h. The next day, after fixing with methanol and staining with crystal violet, the cells on the membrane were counted on three inserts. Cell migration was also investigated by cell scratching assay, as previously described [1].

Cell cycle and cell apoptosis assays

Flow cytometry (Aria II flow cytometer, BD, USA) was performed to analyze cell cycle and cell apoptosis, as described previously. For cell cycle analysis, cells were harvested and fixed with 70% ethanol overnight at 4°C. The cells were then washed three times, and 50 μg/mL PI, 100 μg/mL RNase A, and 0.2% Triton X-100 were added to each sample. For cell apoptosis analysis, control cells and experimental cells were seeded into 24-well plates and cultured for 48 h. Then, the cells were collected, resuspended, and treated with the Annexin V-FITC Apoptosis Detection Kit (BD, PharMingen, San Jose, CA) following the manufacturer's instructions. Briefly, 5 μL FITC-labeled Annexin V and 5 μL PI solution were added to each sample, and the cells were incubated for 15 min at room temperature.

In vivo assays

Six-week-old BALB/C nude mice were purchased from the Shanghai Institute of Material Medicine of the Chinese Academy of Science (Shanghai, China). The committee on the use of live animals in teaching and research at Zhongshan Hospital, Fudan University, approved all animal experiments. Li-7-Ctrl, Li-7-shARH, HCCLM3-vector, and HCCLM3-ARH-OE cells (5×10^6) were suspended in 200 μL serum-free DMEM and Matrigel (BD Biosciences; 1:1), and then injected subcutaneously into the flanks of nude mice. After 4 weeks, when the tumor volume had grown to 1 cm^3, the mice were killed and the tumor tissue was stripped. Then, the center area of the tumor tissue was selected and

the necrotic tissue was removed. The tumor tissue was then cut to a size of 1–2 mm^3 for subsequent orthotopic transplantation tumor model construction. A total of 24 nude mice were selected and randomly assigned to four groups. After completion of the transplantation for 6 weeks, the mice were killed. The volume and weight of the tumor were measured. At the same time, the liver cancer tissues were embedded in paraffin for subsequent IHC analysis.

For tumor metastasis analysis, 6- to 8-week-old nude mice were selected and randomly assigned to four groups. Mice were injected with 2×10^6 of the indicated cells via the tail vein. After 8 weeks, the lung tissues were separated and stained with HE. The numbers of tumor metastasis were recorded.

Ubiquitination analysis

The indicated plasmids were co-transfected into Li-7, HCCLM3, and HEK293T cells. After incubation for 24 h, the cells were treated with 10 μM MG132 for 6 h. Then, the cells were lysed with IP lysis buffer and boiled at 100°C for 10 min. The supernatants were collected and RIPA lysis was then added to PMSF and protease inhibitor cocktail for IP with anti-PKM2, anti-FLAG, anti-HA, or anti-His.

Bioinformatics

For identification of DEGs and pathway enrichment, the FPKM and count expression profiles were obtained from the TCGA database (https://portal.gdc.cancer.gov/), UCSC Xena website (http://xena.ucsc.edu/), GEO database(https://www.ncbi.nlm.nih.gov/geo/) and the Clinical Proteomic Tumor Analysis Consortium (https://proteomic.datacommons.cancer.gov/pdc/). “limma” R package and GEO2R online tools were employed to perform differential expression analysis between tumor tissue and tumor adjacent tissues in the GSE164760, GSE76427, GSE101728, GSE101685, TCGA and CPTAC cohorts. TCGA-LIHC samples were divided into ARHGAP24 high and low expression groups based on the upper and lower quartiles of ARHGAP24

expression. Genes with an expression- p value < 0.05 and |log2 fold change (FC)| >1 were regarded as significant DEGs using “limma” R package. To explore whether genes in ARHGAP24 high and low expression groups were enriched in meaningful biological processes, gene set enrichment analysis was performed in the two groups (www.gsea-msigdb.org/gsea/index.jsp). The annotated gene set c2.cp.reactome.v7.5.1.symbols.gmt [Curated] was selected as the reference gene set. Visual analysis of data was generated by “ggplot2”, ”pheatmap” and “enrichplot” R package. Follow-up data of patients with various cancers were acquired from the K-M plot database (http://kmplot.com/analysis). The CPTAC cohort follow-up information was acquired from the website https://proteomics.cancer.gov/programs/cptac.

For the analysis of the interaction between PKM2 and ARHGAP24, the three-dimensional protein structures of PKM (Uniport ID: P14618-1) and ARHGAP24 (Uniport ID: Q8N264-1) were established by the comprehensive use of multiple protein three-dimensional structure modeling software, including I-TASSER, FR-t5-M, and FALCON. The binding amino acid positions in the constructed PKM2 and ARHGAP24 three-dimensional protein structures were predicted by tools such as SPR and ISPRED4, respectively. According to the protein interaction sites, the optimal docking model was identified using HDOCK. MEFTop and QIPI were also used to evaluate the docking conformation. ContPro was used to calculate the spatial distance of each atom in the docking model, and 4Å was selected as the threshold of the distance between atoms to select the amino acids that may have interactions in the docking model.

TOP/FOP FLASH assays

TOP/FOP flash analysis was performed in accordance with the manufacturer’s protocol (Sigma–Aldrich, USA). TOP flash (TCF reporter plasmid) and FOP flash (mutant TCF binding sites) were used. The indicated HCC cell lines were co-transfected with 100 ng reporter plasmid, 50 ng expression plasmid, and 8

ng *Renilla* luciferase plasmid with Lipo2000 in a 96-well plate. After 24 h, the luciferase reporters TOP/FOP FLASH were combined with the various expression plasmids. Finally, the indicated cells were analyzed using a luciferase reporter assay kit (Promega) and a microplate reader.

Reference

[1] Yang W, Zhang C, Li Y, et al. Phosphorylase Kinase β Represents a Novel Prognostic Biomarker and Inhibits Malignant Phenotypes of Liver Cancer Cell. Int J Biol Sci. 2019;15(12):2596-2606.

The targeting sequences of small hairpin RNAs were used in study.

Gene	Target sequences
shRNA#1 against ARHGAP24	5′- ccGAGAGAGGAAACACAATAT -3′
shRNA#2 against ARHGAP24	5′- ccAGCAGTTGATGTCAGTGAT-3′
Scrambled shRNA	5’- TTCTCCGAACGTGTCACGT-3’
SiPKM2#1	Sense: 5’- GGAUGUUGAUAUGGUGUUUTT-3’
	Anti-sense: 5’- AAACACCAUAUCAACAUCCTT-3’
SiPKM2#2	Sense: 5’- CCAUCUACCACUUGCAAUUTT-3’
	Anti-sense: 5’- AAUUGCAAGUGGUAGAUGGTT-3’
SiWWP1#1	5’-GAAGTCATCTGTAACTAAA-3′
SiWWP1#2	5’-GCAGAGAAATACTGTTTAT-3′

The primer sequences were used in study.

Gene		Sequences
ARHGAP24	Forward	5′- GAACCGTCTGGCTCCGATG -3′
	Reverse	5′- TGGCAGTCGAAAGAGACCCT -3′
CTNNB1	Forward	5′- AAAGCGGCTGTTAGTCACTGG-3′
	Reverse	5′- CGAGTCATTGCATACTGTCCAT-3′
PKM2	Forward	5’- ATGTCGAAGCCCCATAGTGAA-3’
	Reverse	5’- TGGGTGGTGAATCAATGTCCA-3’
E-cadherin	Forward	5’- CGAGAGCTACACGTTCACGG -3’
	Reverse	5’- GGGTGTCGAGGGAAAAATAGG-3’
N-cadherin	Forward	5’- TCAGGCGTCTGTAGAGGCTT-3’
	Reverse	5’- ATGCACATCCTTCGATAAGACTG-3’
vimentin	Forward	5’- GACGCCATCAACACCGAGTT-3’
	Reverse	5’- CTTTGTCGTTGGTTAGCTGGT-3’
snail	Forward	5′- TCGGAAGCCTAACTACAGCGA-3′
	Reverse	5′- AGATGAGCATTGGCAGCGAG-3′
slug	Forward	5′- CGAACTGGACACACATACAGTG-3′
	Reverse	5’- CTGAGGATCTCTGGTTGTGGT-3’
c-myc	Forward	5’- GGCTCCTGGCAAAAGGTCA-3’
	Reverse	5’- CTGCGTAGTTGTGCTGATGT-3’
cyclinD1	Forward	5’- GCTGCGAAGTGGAAACCATC-3’
	Reverse	5’- CCTCCTTCTGCACACATTTGAA-3’
β-actin	Forward	5’- CATGTACGTTGCTATCCAGGC-3’
	Reverse	5’- CTCCTTAATGTCACGCACGAT-3’