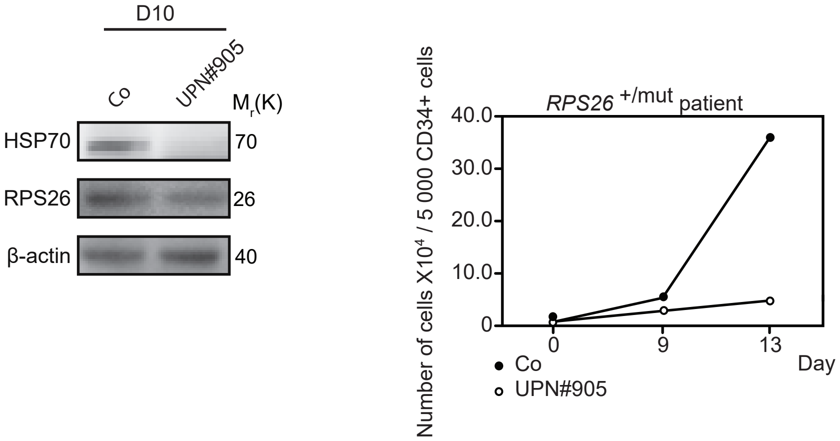
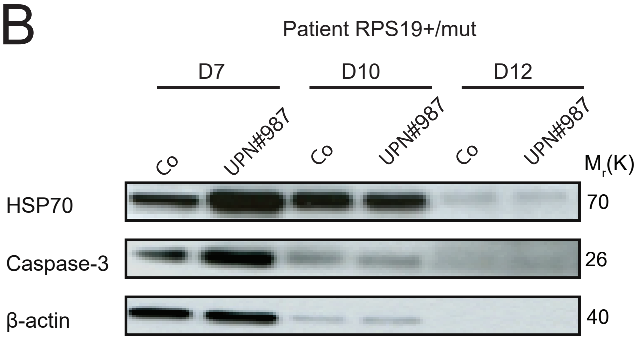
FIGURE SUPPLEMENTAL 1

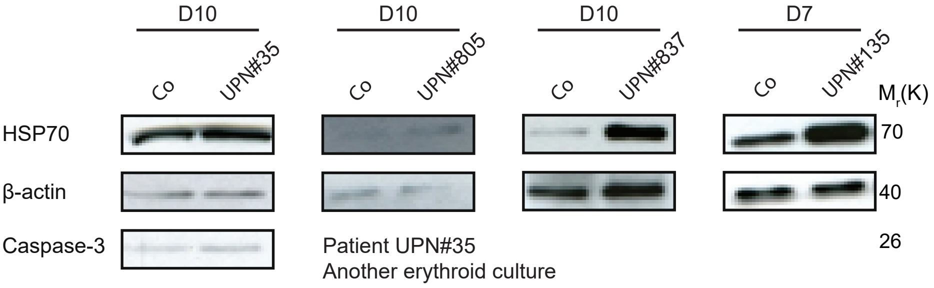
A



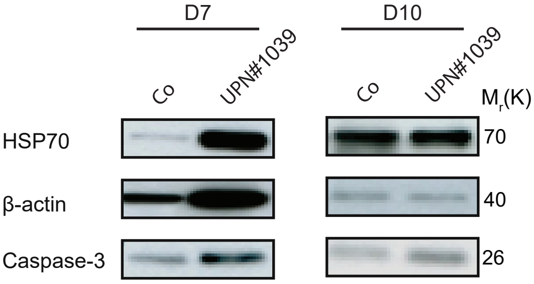
B



Patient UPN#987 during the complete erythroid time course



Patient UPN#35
Another erythroid culture



Two different erythoid cultures

FIGURE SUPPLEMENTAL 2

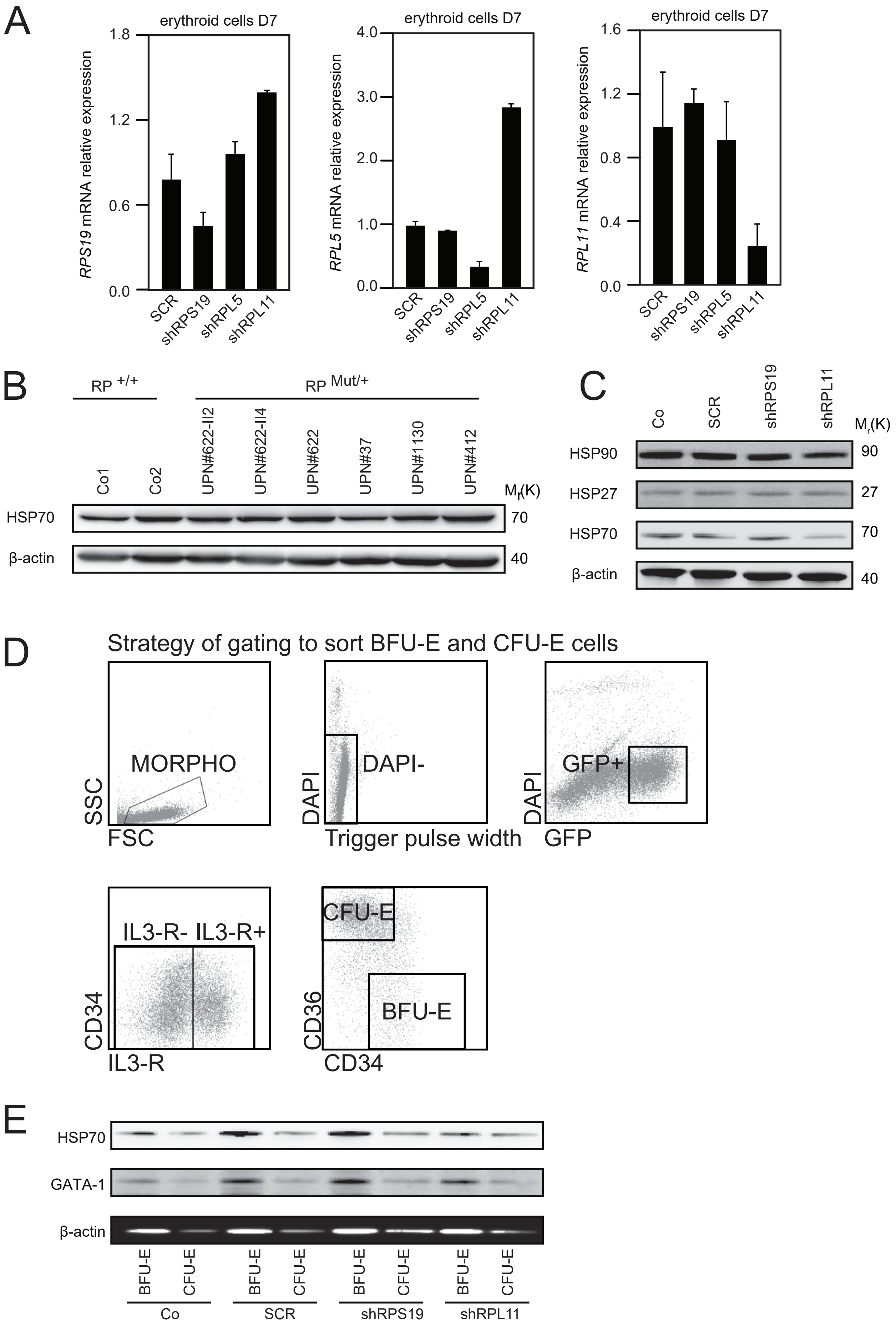


FIGURE SUPPLEMENTAL 3

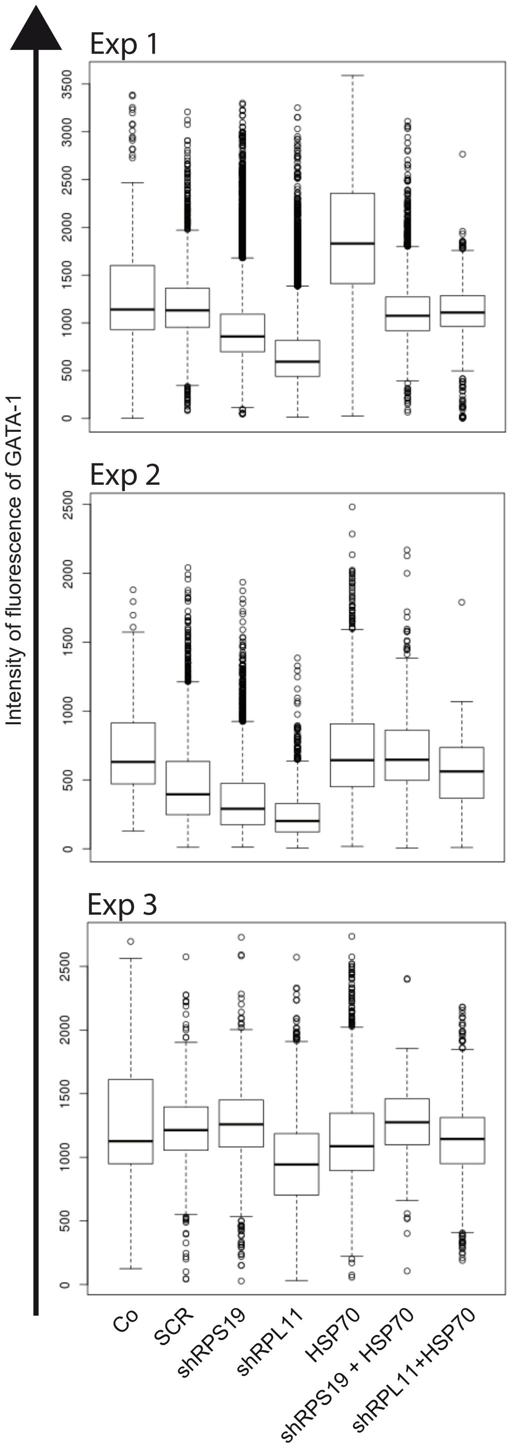


FIGURE SUPPLEMENTAL 4

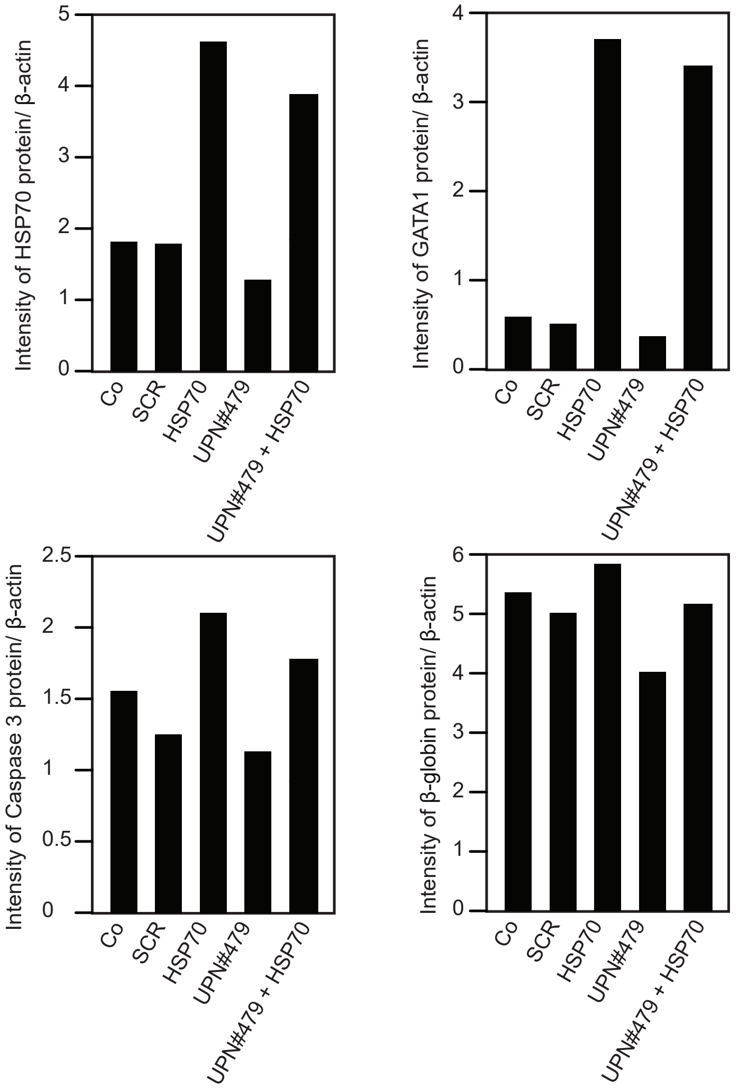
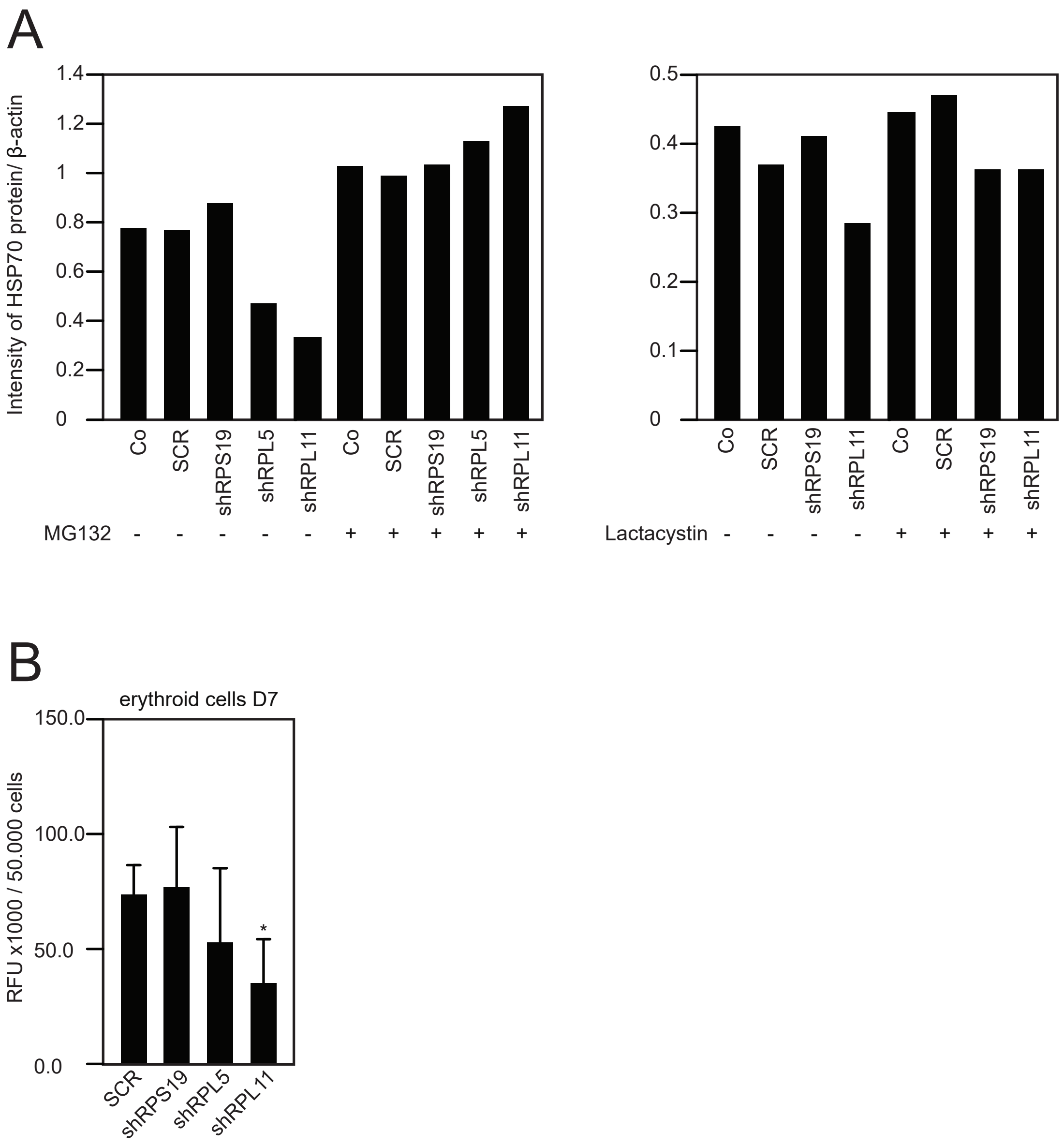


FIGURE SUPPLEMENTAL 5



Supplemental Figure 6: Putative sites of ubiquitination in Human HSP70 protein sequence.

- **Analysis Tool#1 UbPred (The Rockefeller University)**

http://www.ubpred.org/cgi-bin/ubpred/ubpred.cgi

```
>sp|P08107|HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1
MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAA
KNQVALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYK
GETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAG
VIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEV
KATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKR
TLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKA
QIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGD
KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGV
LIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKS
TGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALESYAFN
MKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQ
VCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
```

The lysin K labeled in gray has been rule out as a putative ubiquitinylation site. The table below describes only the sites from a low to high confidence in the HSP70 ubiquitination site prediction.

Residue	Score	Ubiquitinated
3	0.72	Yes Medium confidence
108	0.68	Yes Low confidence
112	0.63	Yes Low confidence
451	0.62	Yes Low confidence
512	0.65	Yes Low confidence
524	0.86	Yes High confidence
526	0.86	Yes High confidence
539	0.80	Yes Medium confidence
550	0.84	Yes High confidence
559	0.68	Yes Low confidence
561	0.69	Yes Medium confidence
589	0.75	Yes Medium confidence
595	0.69	Yes Medium confidence
597	0.68	Yes Low confidence

628	0.75	Yes Medium confidence

Legend:

Label	Score range	Sensitivity	Specificity
Low confidence	0.62 ≤ s ≤ 0.69	0.464	0.903
Medium confidence	0.69 ≤ s ≤ 0.84	0.346	0.950
High confidence	0.84 ≤ s ≤ 1.00	0.197	0.989

- **Analysis Tool#2 GGbase (Harvard University)**

https://ggbase.hms.harvard.edu/protein/view/IPI:IPI00304925.5

IPI:IPI00304925.5

Protein Information

Protein	IPI:IPI00304925.5
Gene Symbol	HSPA1A;HSPA1B
Protein Description	Heat shock 70 kDa protein 1
Sequence Length	641
Mwt	70009.037 Da
Sequence	MAKAAAIGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA LNPQNTVFDA KRLIGRKFGD PVVQSDMKHW PFQVINDGDK PKVQVSYKGE TKAFYPEEIS SMVLTKMKEI AEAYLGYPVT NAVITVPAYF NDSQRQATKD AGVIAGLNVL RIINEPTAAA IAYGLDRTGK GERNVLIFDL GGGTFDVSIL TIDDGIFEVK ATAGDTHLGG EDFDNRLVNH FVEEFKRKHK KDISQNKRAV RRLRTACERA KRTLSSSTQA SLEIDSLFEG IDFYTSITRA RFEELCSDLF RSTLEPVEKA LRDAKLDKAQ IHDLVLVGGS TRIPKVQKLL QDFFNGRDLN KSINPDEAVA YGAAVQAAIL MGDKSENVQD LLLLDVAPLS LGLETAGGVM TALIKRNSTI PTKQTQIFTT YSDNQPGVLI QVYEGERAMT KDNNLLGRFE LSGIPPAPRG VPQIEVTFDI DANGILNVTA TDKSTGKANK ITITNDKGRL SKEEIERMVQ EAEKYKAEDE VQRERVSAKN ALESYAFNMK SAVEDEGLKG KISEADKKKV LDKCQEVISW LDANTLAEKD EFEHKRKELE QVCNPIISGL YQGAGGPGPG GFGAQGPKGG SGSGPTIEEV D

The predict ubiquitination sites 108, 112, 451, 512, 524, 526, 539, 550, 559, 561, 597, and 628 are redondant in both analyses.