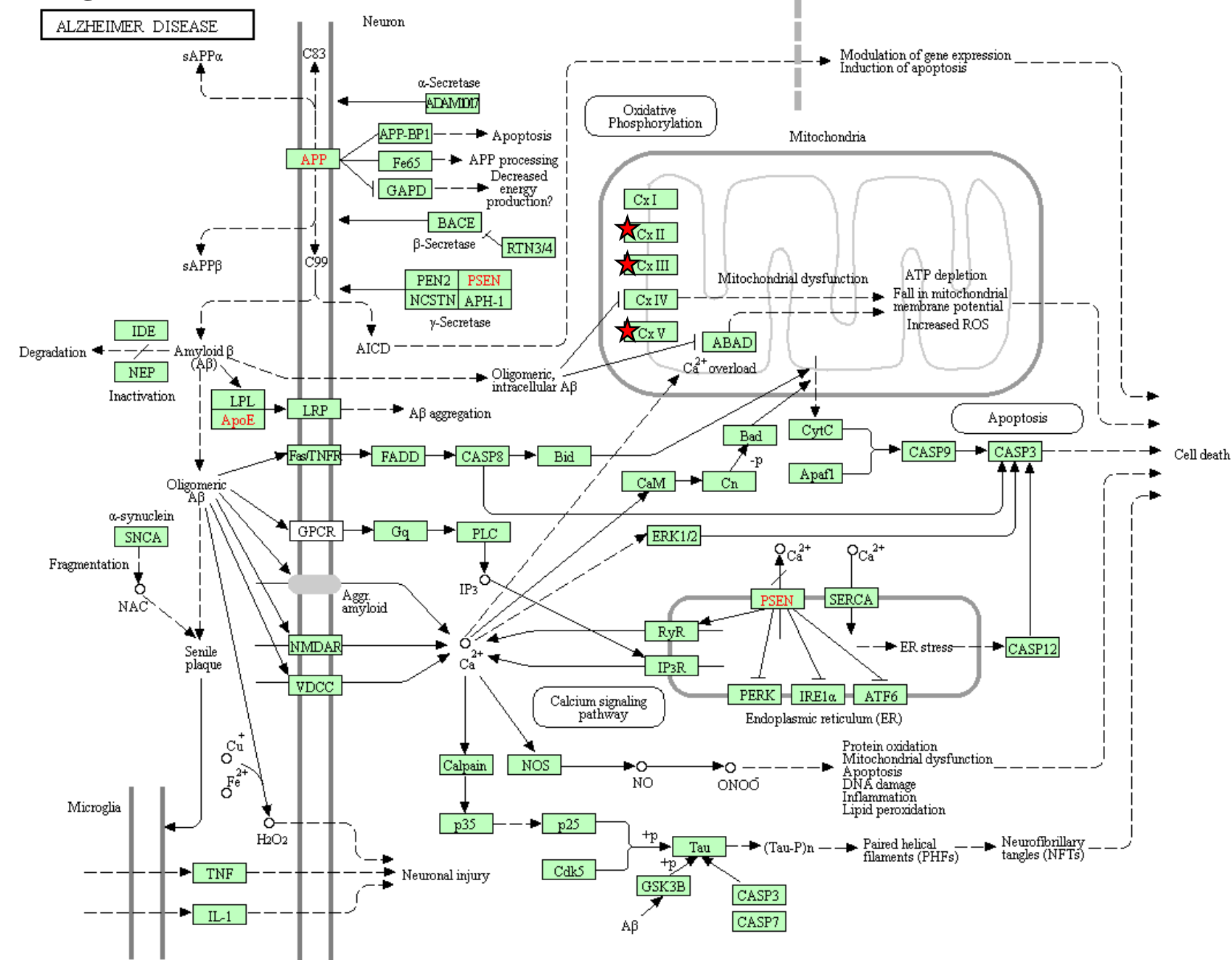


**S1 Fig.**

**Pathway diagram of differentially expressed proteins on enriched pathways using DAVID**

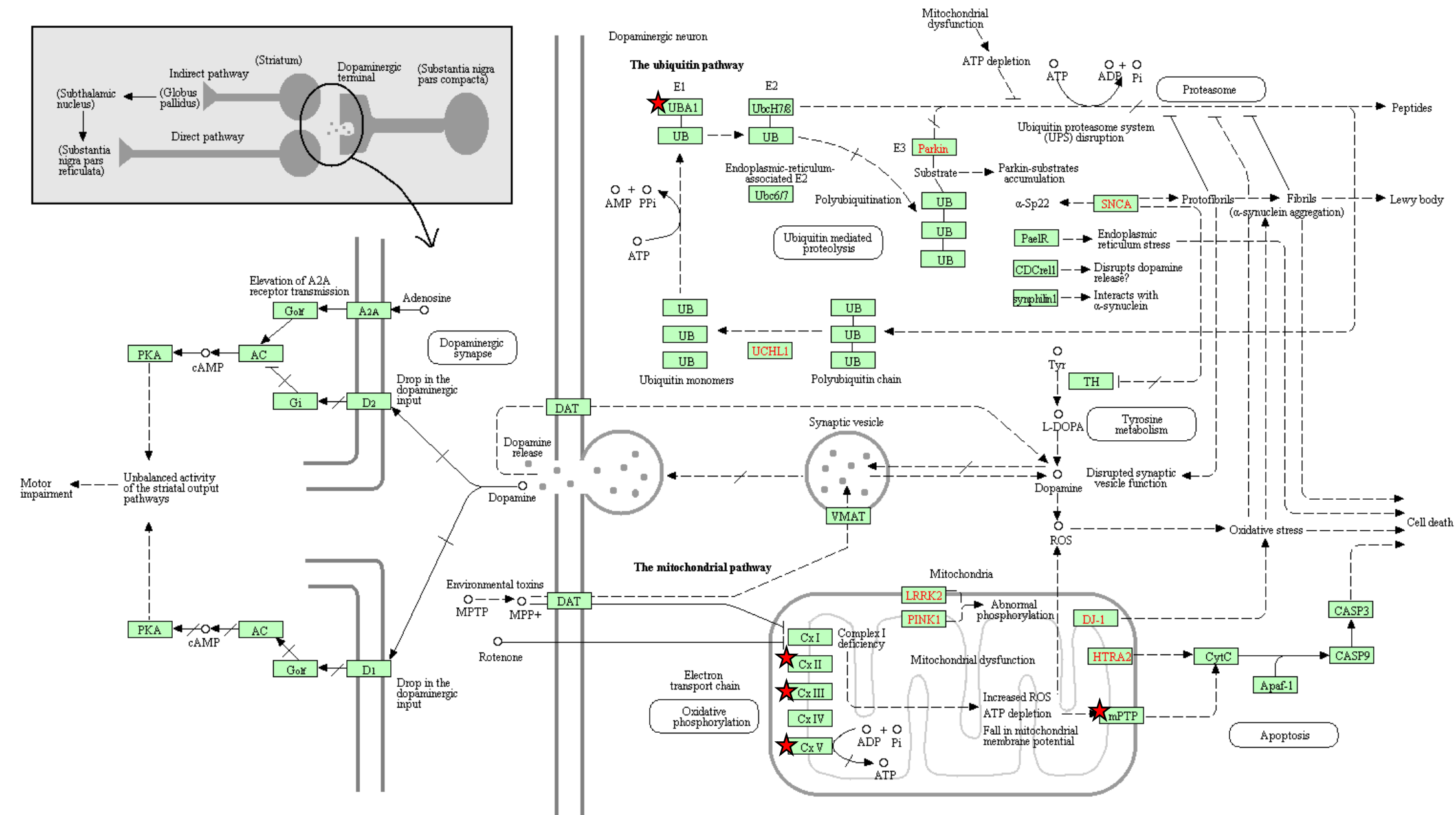
**analysis.** The red star indicates the association between pathway proteins and the differentially expressed proteins we identified (A) VPA altered the expression of 11 proteins involved in Alzheimer's disease. These include ATP5A1, ATP5B, ATP5D, ATP5F1, ATP5J, SDHA, SDHB, UQCRB, UQCRC1, UQCRC2, and UQCRH. (B) VPA altered the expression of 16 proteins involved in Parkinson's disease. These include ATP5A1, ATP5B, ATP5D, ATP5F1, ATP5J, SDHA, SDHB, SLC25A6, UBA7, UQCRB, UQCRC1, UQCRC2, UQCRFS1, UQCRH, VDAC1, and VDAC3. (C) VPA altered the expression of 15 proteins involved in oxidative phosphorylation. These include ATP5A1, ATP5B, ATP5D, ATP5F1, ATP5J, ATP5L, ATP6V1G1, SDHA, SDHB, UQCRB, UQCRC1, UQCRC2, and UQCRH. (D) VPA altered the expression of 10 proteins involved in ubiquitin mediated proteolysis. These include ANAPC4, CDC23, FBXO2, FBXO4, NEDD4, TRAF6, UBE2D1, UBE2E1, UBE2E3, and UBE2G2. (E) VPA altered the expression of 10 proteins involved in ribosome biogenesis in eukaryotes. These include BMS1, DKC1, GNL2, GTPBP4, LSG1, NOP10, ROK2, TCOF1, WDR36, and WDR75. Illustration taken from DAVID website (<http://david.abcc.ncifcrf.gov/>) and KEGG database (<http://www.kegg.jp/kegg/kegg1.html>). Reprinted with permission from KEGG.

S1 Fig. A



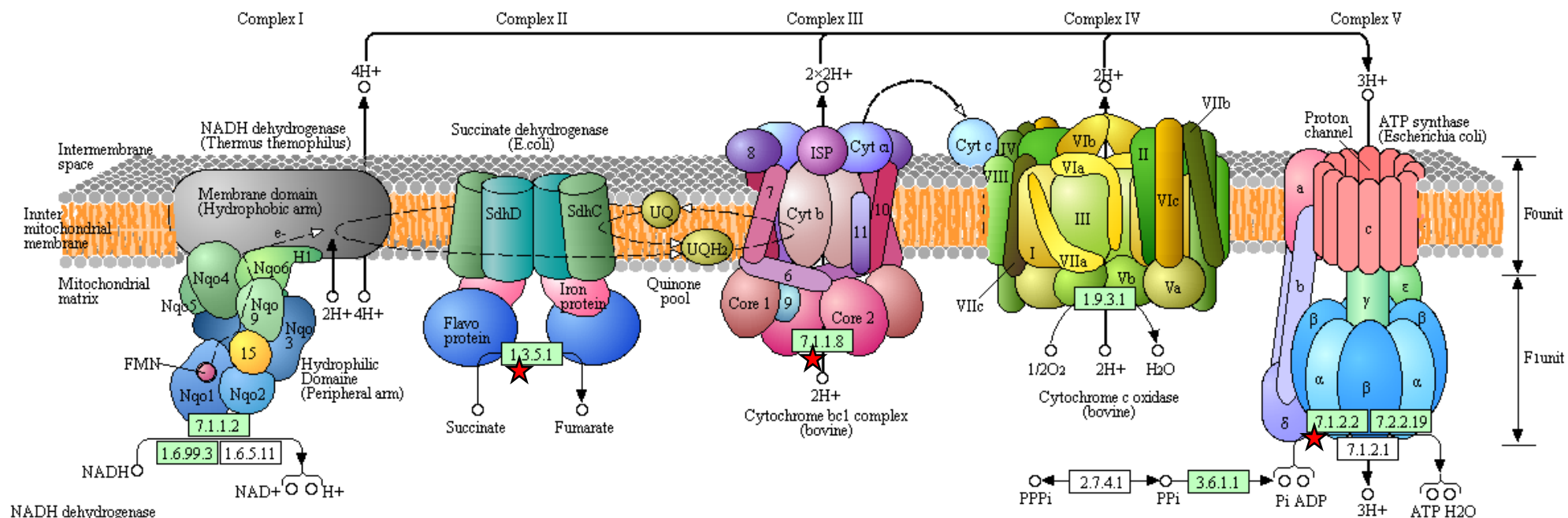
# S1 Fig. B

PARKINSON DISEASE



S1 Fig. C

## OXIDATIVE PHOSPHORYLATION



NADH dehydrogenase

E ND1 ND2 ND3 ND4 ND4L ND5 ND6

E Ndufs1 Ndufs2 Ndufs3 Ndufs4 Ndufs5 Ndufs6 Ndufs7 Ndufs8 Ndufv1 Ndufv2 Ndufv3

B/A NuoA NuoB NuoC NuoD NuoE NuoF NuoG NuoH NuoI NuoJ NuoK NuoL NuoM NuoN

B/A NdhC NdhK NdhJ NdhH NdhA NdhI NdhG NdhE NdhF NdhD NdhB NdhL NdhM NdhN HoxE HoxF HoxU

E Ndufa1 Ndufa2 Ndufa3 Ndufa4 Ndufa5 Ndufa6 Ndufa7 Ndufa8 Ndufa9 Ndufa10 Ndufab1 Ndufa11 Ndufa12 Ndufa13

E Ndubf1 Ndubf2 Ndubf3 Ndubf4 Ndubf5 Ndubf6 Ndubf7 Ndubf8 Ndubf9 Ndubf10 Ndubf11 Ndufc1 Ndufc2

Succinate dehydrogenase / Fumarate reductase

E SDHC SDHD SDHA SDHB

B/A SdhC SdhD SdhA SdhB  
FrdA FrdB FrdC FrdD

Cytochrome c reductase

E/B/A ISP Cyt b Cyt 1

E COR1 QCR2 QCR6 QCR7 QCR8 QCR9 QCR10

Cytochrome c oxidase

E COX10

B/A CyoE CyoD CyoC CyoB CyoA

CoxD CoxC CoxA CoxB  
QoxD QoxC QoxB QoxA

Cytochrome c oxidase, cbb3-type

B I II IV III

Cytochrome bd complex

B/A CydA CydB CydX

F-type ATPase (Bacteria)

alpha	beta	gamma	delta	epsilon
a	b	c		

F-type ATPase (Eukaryotes)

alpha	beta	gamma	delta	epsilon
OSCP	a	b	c	d
f	g	h6/h	j	k
				8

V/A-type ATPase (Bacteria, Archaeas)

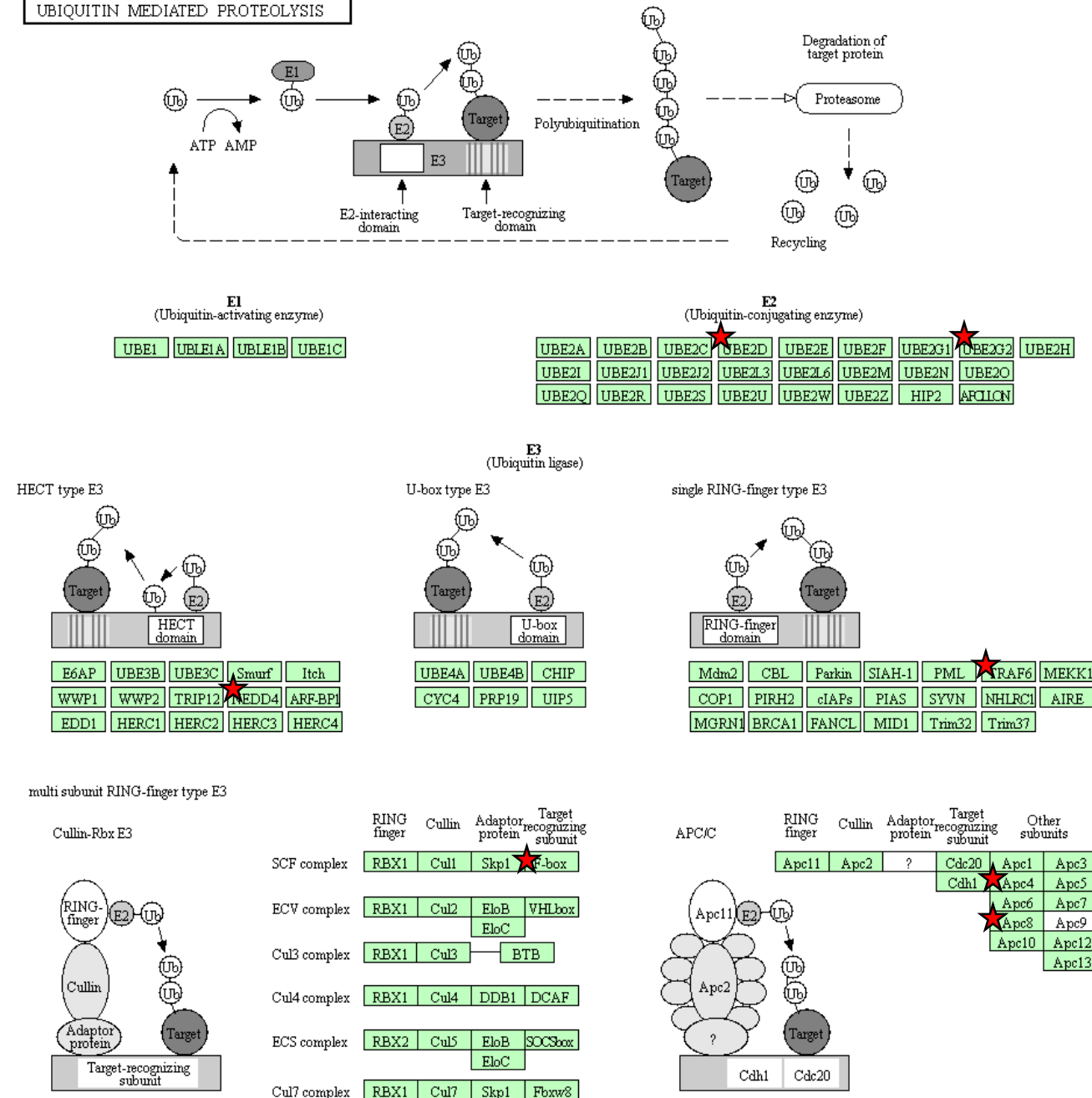
A	B	C	D	E	F	G/H
I	K					

V-type ATPase (Eukaryotes)

A	B	C	D	E	F	G	H
a	c	d	e	S1			

# S1 Fig. D

## UBIQUITIN MEDIATED PROTEOLYSIS



# S1 Fig. E

## RIBOSOME BIOGENESIS IN EUKARYOTES

