

CW-Tau fights proteinopathy by improving autophagy and diminishing Tau seeding activity

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Supplementary figure 3. Protein coverage of W-Tau peptide-binding proteins shown in Table 3. Coverage images of the eluted fraction of W-Tau peptide-binding proteins from both control and AD samples, along with their possible post-translational modifications. Proteins analyzed (as listed in Table 3) include: Rab GDP dissociation inhibitor alpha (**A**) and beta (**B**), Rab5C (**C**), Rab6B (**D**), Rab7A (**E**), Rab11B (**F**), Fatty-acid binding protein 7 (**G**), Serine-Threonine protein phosphatase 1 (**H**), Tyrosine-protein phosphatase non-receptor type substrate 1 (**I**), Apolipoprotein E (**J**), Parkinson disease protein 7 (**K**) and Ubiquitin-conjugating enzyme E2 N (**L**).

A

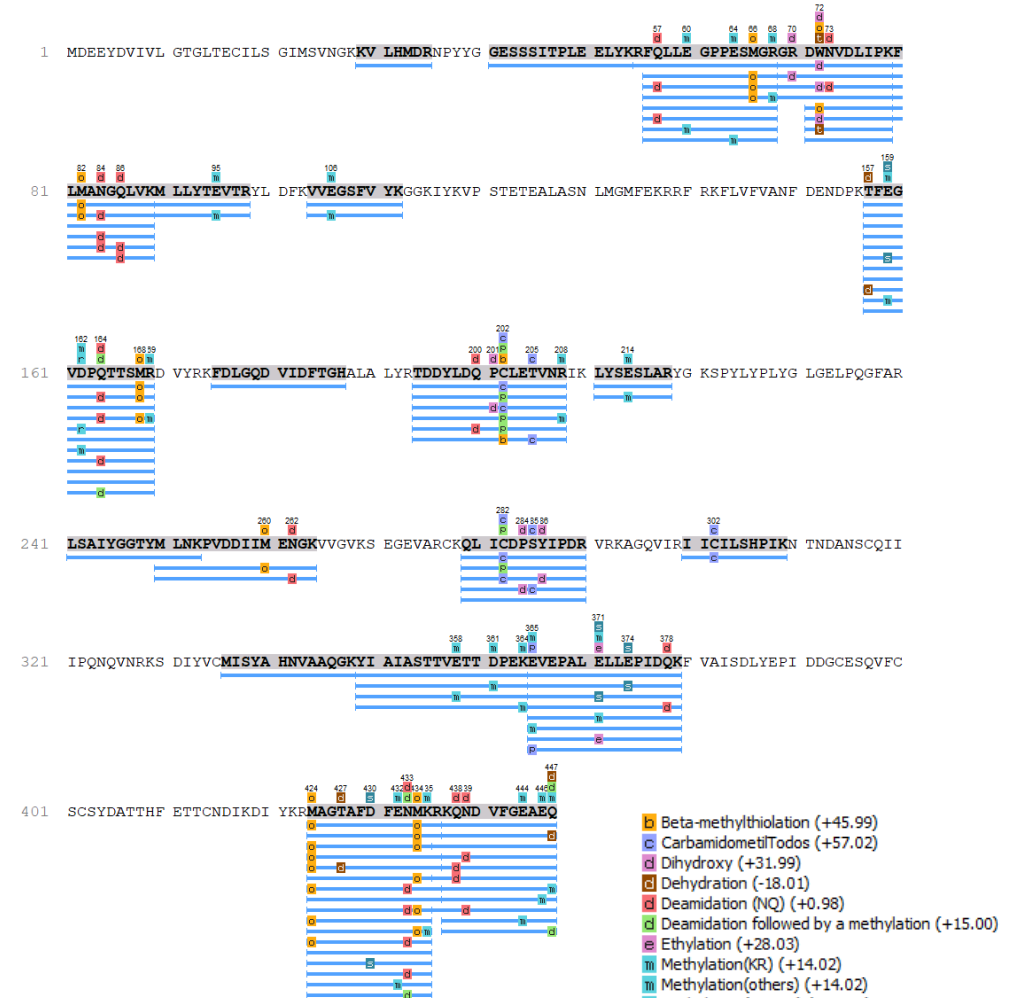
RAB GDP DISSOCIATION INHIBITOR ALPHA (GDIA_HUMAN)

Eluted control



- 2-amino-3-oxo-butanoic_acid (-2.02)
- CarbamidomethylTodos (+57.02)
- Deamidation (NQ) (+0.98)
- Dehydration (-18.01)
- Deamidation followed by a methylation (+15.00)
- Dihydroxy (+31.99)
- Half of a disulfide bridge (-1.01)
- Methylation(others) (+14.02)
- Methylation(KR) (+14.02)
- Methylation(C-term) (+14.02)
- Oxidation (M) (+15.99)
- Propionamide (+71.04)
- Tryptophan oxidation to kynurenin (+3.99)

Eluted AD

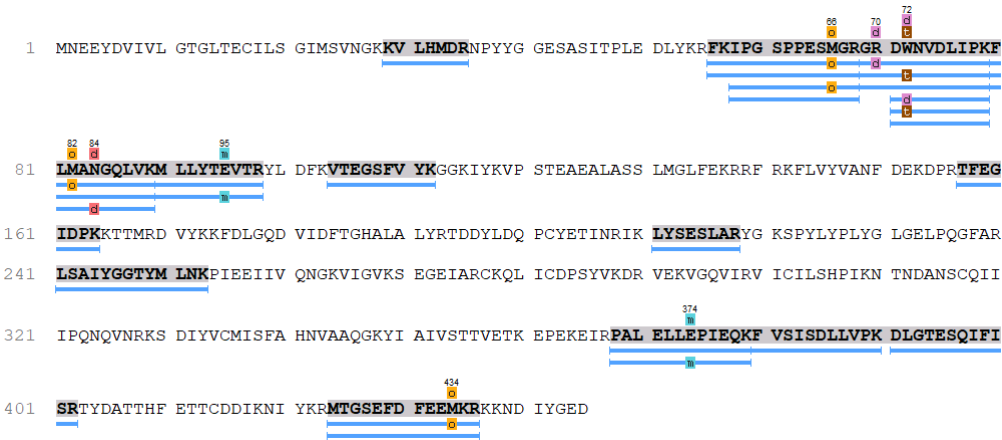


- Beta-methylthiolation (+45.99)
- CarbamidomethylTodos (+57.02)
- Dihydroxy (+31.99)
- Dehydration (-18.01)
- Deamidation (NQ) (+0.98)
- Deamidation followed by a methylation (+15.00)
- Ethylation (+28.03)
- Methylation(KR) (+14.02)
- Methylation(others) (+14.02)
- Methylation(C-term) (+14.02)
- Oxidation (M) (+15.99)
- Oxidation (H-W) (+15.99)
- Pyro-glu from E (-18.01)
- Propionamide (+71.04)
- Replacement of proton by potassium (+37.96)
- Sodium adduct (+21.98)
- Tryptophan oxidation to kynurenin (+3.99)

B

RAB GDP DISSOCIATION INHIBITOR BETA
(GDIB_HUMAN)

Eluted control



- Deamidation (NQ) (+0.98)
- Dihydroxy (+31.99)
- Methylation(others) (+14.02)
- Oxidation (M) (+15.99)
- Tryptophan oxidation to kynurenin (+3.99)

Eluted AD



- CarbamidometilTodos (+57.02)
- Dihydroxy (+31.99)
- Dehydration (-18.01)
- Deamidation (NQ) (+0.98)
- Methylation(others) (+14.02)
- Oxidation (M) (+15.99)
- Oxidation (HW) (+15.99)
- Pyro-glu from E (-18.01)
- Tryptophan oxidation to kynurenin (+3.99)

C

RAB 5C
(RAB5C_HUMAN)

Eluted control

1 MAGRGGAARP NGPAAGNKIC QFKLVLLGES AVGKSSSLVLR FVKGQFHEYQ ESTIGAAFLT QTVCLDDTTV KFEIWDTAGQ
81 ERYHSLAPMY YRGAQAAIVV YDITNTDTFA RAKNWVKELQ RQASPNIVIA LAGNKADLAS KRAVEFQEAQ AYADDNSLLF
161 METSAKTAMN VNEIFMAIAK KLPKNEPQNA TGAPGRNRGV DLQENNPASR SQCCSN

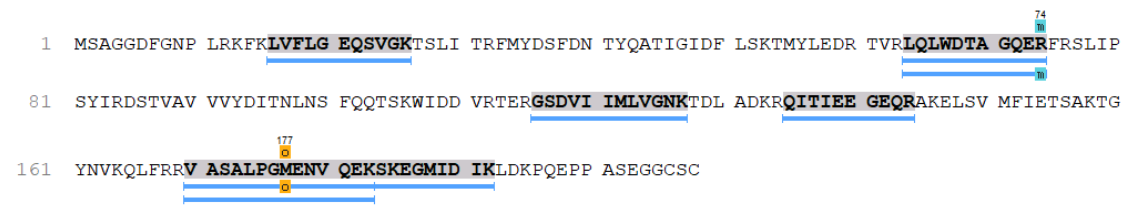
Eluted AD

1 MAGRGGAARP NGPAAGNKIC QFKLVLLGES AVGKSSSLVLR FVKGQFHEYQ ESTIGAAFLT QTVCLDDTTV KFEIWDTAGQ
81 ERYHSLAPMY YRGAQAAIVV YDITNTDTFA RAKNWVKELQ RQASPNIVIA LAGNKADLAS KRAVEFQEAQ AYADDNSLLF
161 METSAKTAMN VNEIFMAIAK KLPKNEPQNA TGAPGRNRGV DLQENNPASR SQCCSN

D

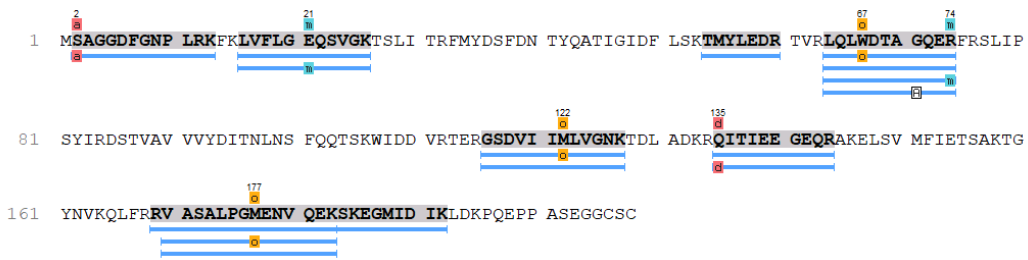
RAB 6B
(RAB6B_HUMAN)

Eluted control



Methylation(KR) (+14.02)
Oxidation (M) (+15.99)

Eluted AD



Acetylation (Protein N-term) (+42.01)
Deamidation (NQ) (+0.98)
Methylation(KR) (+14.02)
Methylation(others) (+14.02)
Oxidation (M) (+15.99)
Oxidation (HW) (+15.99)
G->A

E

RAB 7A
(RAB7A_HUMAN)

Eluted control

1 MTSRKKVLLK **VIILGDSGVG K** TSLMNQYVN KKFSNQYK**AT IGADFLTK**EV MVDDRLVTMQ IWDTAGQER**F QSLGVAFYRG**
81 ADCCVLVFDV TAPNTEKTLT SWRDEFLIQA SPR**DPENFPF VVLGNK**IDLE NRQVATKRAQ AWCYSKNNIP YFETSA**KEAI**
161 **NVEQAFQTIA R**NALKQETEV ELYNEFPEPI KLDKNDRAKA SAESCSC

Eluted AD

1 MTSRKKVLLK **VIILGDSGVG K**TSLMNQYVN **K**KKFSNQYK**AT IGADFLTK**EV MVDDRLVTMQ IWDTAGQER**F QSLGVAFYRG**
81 ADCCVLVFDV TAPNTEKTLT SWRDEFLIQA SPR**DPENFPF VVLGNK**IDLE NRQVATKRAQ AWCYSK**NNIP YFETSAKEAI**
161 **NVEQAFQTIA R**NALKQETEV ELYNEFPEPI KLDKNDRAKA SAESCSC

 Methylation(others) (+14.02)

F

RAB 11B
(RB11B_HUMAN)

Eluted control

1 MGTRDDEYDY LFKVVLLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY
81 YRGAVGALLV YDIAKHLTYE NVERWLKELR DHADSNIVIM LVGNKSDLRH LRAVPTDEAR AFAEKNNLSF IETSALDSTN
161 VEEAFKNILT EIYRIVSQKQ IADRAAHDES PGNNVVDISV PPTTDGQKPN KLQCCQNL

Eluted AD

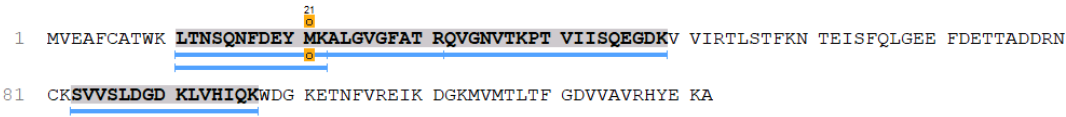
1 MGTRDDEYDY LFKVVLLIGDS GVGKSNLLSR FTRNEFNLES KSTIGVEFAT RSIQVDGKTI KAQIWDTAGQ ERYRAITSAY
81 YRGAVGALLV YDIAKHLTYE NVERWLKELR DHADSNIVIM LVGNKSDLRH LRAVPTDEAR AFAEKNNLSF IETSALDSTN
161 VEEAFKNILT EIYRIVSQKQ IADRAAHDES PGNNVVDISV PPTTDGQKPN KLQCCQNL

G

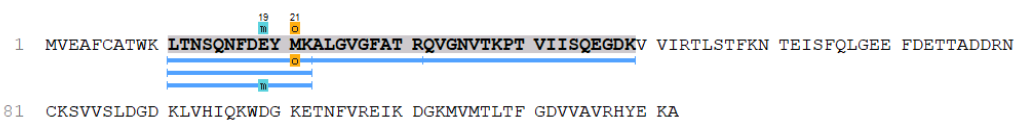
FATTY-ACID BINDING PROTEIN 7
(FABP7_HUMAN)

Eluted control

Eluted AD



□ Oxidation (M) (+15.99)



■ Methylation(others) (+14.02)
□ Oxidation (M) (+15.99)

SERINE-THREONINE-PROTEIN PHOSPHATASE 1
(CPPED_HUMAN)

Eluted control

Eluted AD

1 MSAAEAGGVF² HRARGRTLAA FPAEKESWK GPFFYFILGAD PQFGLIKAWS TGDCDNGGDE WEQEIR⁸ LTEQ AVQAIN⁷⁰KLNP
81 KPKFFVLCGD LIHAMP⁸GK⁸PW RTEQTEDLKR VLR⁸AVDRAIP LVLVSGN⁸HDI GNTPTAETVE EFCRTWGDDY FSEWVGGVLF
161 LVLNSQFYEN PSKCPSLKQA QDQWLDEQLS IARQRHCQHA IVFQHIPLFL ESIDEDDDYY FNLSKSTRKK LADKFIHAGV
241 KVVFSGHYHR NAGGTYQNLD MVVSSAIGCQ LGRDPHGLRV VVVTAEKIVH RYYSDELSE KGIEDDLMDL IKKK

 Acetylation (Protein N-term) (+42.01)

1 MSAAEAGGVF² HRARGRTLAA FPAEKESWK GPFFYFILGAD PQFGLIKAWS TGDCDNGGDE WEQEIR⁸ LTEQ AVQAIN⁷⁰KLNP
81 KPKFFVLCGD LIHAMP⁸GK⁸PW RTEQTEDLKR VLR⁸AVDRAIP LVLVSGN⁸HDI GNTPTAETVE EFCRTWGDDY FSEWVGGVLF
161 LVLNSQFYEN PSKCPSLKQA QDQWLDEQLS IARQRHCQHA IVFQHIPLFL ESIDEDDDYY FNLSKSTRKK LADKFIHAGV
241 KVVFSGHYHR NAGGTYQNLD MVVSSAIGCQ LGRDPHGLRV VVVTAEKIVH RYYSDELSE KGIEDDLMDL IKKK

 Acetylation (Protein N-term) (+42.01)
 Deamidation (NQ) (+0.98)

TYROSINE-PROTEIN PHOSPHATASE NON-RECEPTOR TYPE SUBSTRATE 1 (SHPS1_HUMAN)

Eluted control

Eluted AD

1 MEPAGPAPGR LGPLLCLLLA ASCAWSGVAG EEELQVIQPD KSVLVAAGET ATLRCTATSL IPVGPIQWFR GAGPGRELIY
81 NQKEGHFPRV TTVSDLTKRN NMDFSIRIGN ITPADAGTY Y CVKFRKGSPD DVEFKSGAGT ELSVR**AKPSA PVVSGPAARA**
161 TPQHTVSFTC ESHGFSPRDI TLKWFKNGNE LSDFQTNVDP VGESVSYSIH STAKVVLTRE DVHSQVICEV AHVTLQGDPL
241 RGTANLSETI **RVPPTLEV**TQ QPVRAENQVN VTCQVRKFYP QRLQLTWLEN GNVSR**TETAS TVTENK**DGTY NWMSWLLVNV
321 SAHRDDVKLT CQVEHDGQPA VSKSHDLKVS AHPKEQGSNT AAENTGSNER NIYIVGVVC TLLVALLMAA LYLVRIRQKK
401 AQGSTSSTRL HEPEKNAREI TQDTNDITYA DLNLPKGKKP APQAAEPNNH TEYASIQTSP QPASEDTLTY ADLDMVHLNR
481 TPKQPAPKPE PSFSEYASVQ VPRK

1 MEPAGPAPGR LGPLLCLLLA ASCAWSGVAG EEELQVIQPD KSVLVAAGET ATLRCTATSL IPVGPIQWFR GAGPGRELIY
81 NQKEGHFPRV TTVSDLTKRN NMDFSIRIGN ITPADAGTY Y CVKFRKGSPD DVEFKSGAGT ELSVR**AKPSA PVVSGPAARA**
161 TPQHTVSFTC ESHGFSPRDI TLKWFKNGNE LSDFQTNVDP VGESVSYSIH STAKVVLTRE DVHSQVICEV AHVTLQGDPL
241 RGTANLSETI RVPPTLEV**TQ** QPVRAENQVN VTCQVRKFYP QRLQLTWLEN GNVSR**TETAS TVTENK**DGTY NWMSWLLVNV
321 SAHRDDVKLT CQVEHDGQPA VSKSHDLKVS AHPKEQGSNT AAENTGSNER NIYIVGVVC TLLVALLMAA LYLVRIRQKK
401 AQGSTSSTRL HEPEKNAREI TQDTNDITYA DLNLPKGKKP APQAAEPNNH TEYASIQTSP QPASEDTLTY ADLDMVHLNR
481 TPKQPAPKPE PSFSEYASVQ VPRK

 Methylation(others) (+14.02)

J

APOLIPOPROTEIN E
(APOE_HUMAN)

Eluted control

1 MKVLWAALLV TFLAGCQAKV EQAVETEPEP ELRQQTEWQS GQRWELALGR FWDYLRWVQT LSEQVQEELL SSQVTQELRA
81 LMDETMKELK AYKSELEEQL TPVAEETRAR LSKELQAAQA RLGADMEDVC GRLVQYRGEV QAMLGQSTEE LRVRLASHLR
161 KLRKLLRDA DDLQKR**LAVY QAGAR**EGAER GLSAIRER**LG PLVEQGRVRA** ATVGSLAGQP **LQER**AQAWGE RLRARMEEMG
241 SRTDRDLDEV KEQVAEVR**AK LEEQAQQIRL** QAEAFQARLK SWFEPLVEDM QRQWAGLVEK **VQAAVGTSAA PVPSDNH**

 Deamidation (NQ) (+0.98)

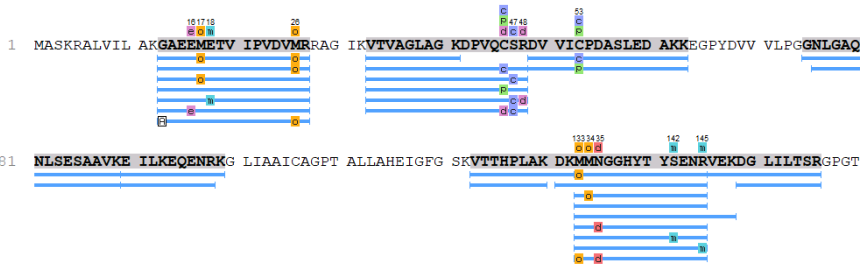
Eluted AD

1 MKVLWAALLV TFLAGCQAKV EQAVETEPEP ELRQQTEWQS GQRWELALGR FWDYLRWVQT LSEQVQEELL SSQVTQELRA
81 LMDETMKELK AYK**SELEEQL TPVAEETR**AR LSKELQAAQA RLGADMEDVC GRLVQYRGEV QAMLGQSTEE LRVRLASHLR
161 KLRKLLRDA DDLQKR**LAVY QAGAR**EGAER GLSAIRER**LG PLVEQGRVRA** ATVGSLAGQP **LQER**AQAWGE RLRARMEEMG
241 SRTDRDLDEV KEQVAEVR**AK LEEQAQQIRL** QAEAFQARLK SWFEPLVEDM QRQWAGLVEK **VQAAVGTSAA PVPSDNH**

 Deamidation (NQ) (+0.98)

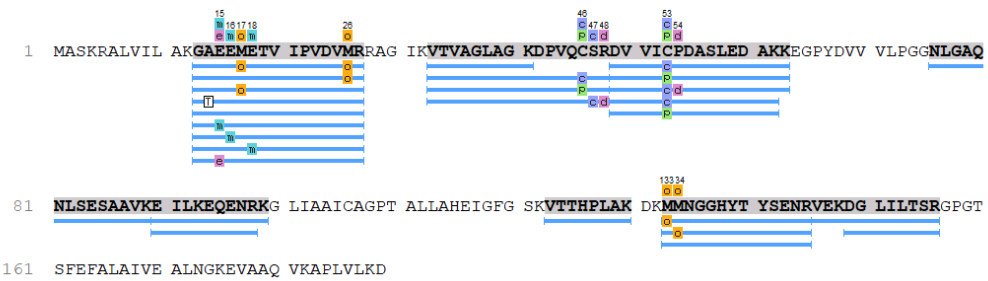
PARKINSON DISEASE PROTEIN 7
(PARK7_HUMAN)

Eluted control



- Carbamidomethyl (C) (+57.02)
- Deamidation (NQ) (+0.98)
- Dihydroxy (+31.99)
- Ethylation (+28.03)
- Methylation(others) (+14.02)
- Methylation(KR) (+14.02)
- Oxidation (M) (+15.99)
- Propionamide (+71.04)
- G->A

Eluted AD



- Carbamidomethyl (C) (+57.02)
- Dihydroxy (+31.99)
- Ethylation (+28.03)
- Methylation(others) (+14.02)
- Oxidation (M) (+15.99)
- Propionamide (+71.04)
- A->T

L

UBIQUITIN-CONGUJATING ENZYME E2 N
(UBE2N_HUMAN)

Eluted control

Eluted AD

1 MAGLPRRIIK ETQRLLAEPV PGIKAEPPDES NARYFHVVIA GPQDSPFEGG TFKLELFLPE EYPMAAPKVR FMTKIYHPNV

81 DKLGRIKLDI LKDKWSPALQ IRTVLLSIQA LLSAPNPDDP LANDVAEQWK TNEAQAIETA RAWTRLYAMN NI

Deamidation (NQ) (+0.98)

Oxidation (M) (+15.99)

1 MAGLPRRIIK ETQRLLAEPV PGIKAEPPDES NARYFHVVIA GPQDSPFEGG TFKLELFLPE EYPMAAPKVR FMTKIYHPNV

81 DKLGRIKLDI LKDKWSPALQ IRTVLLSIQA LLSAPNPDDP LANDVAEQWK TNEAQAIETA RAWTRLYAMN NI

Methylation(others) (+14.02)

Oxidation (M) (+15.99)