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Late-onset retinal degeneration pathology de to mutations in CTRP5 is mediated through HTRA1

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Figure 1:

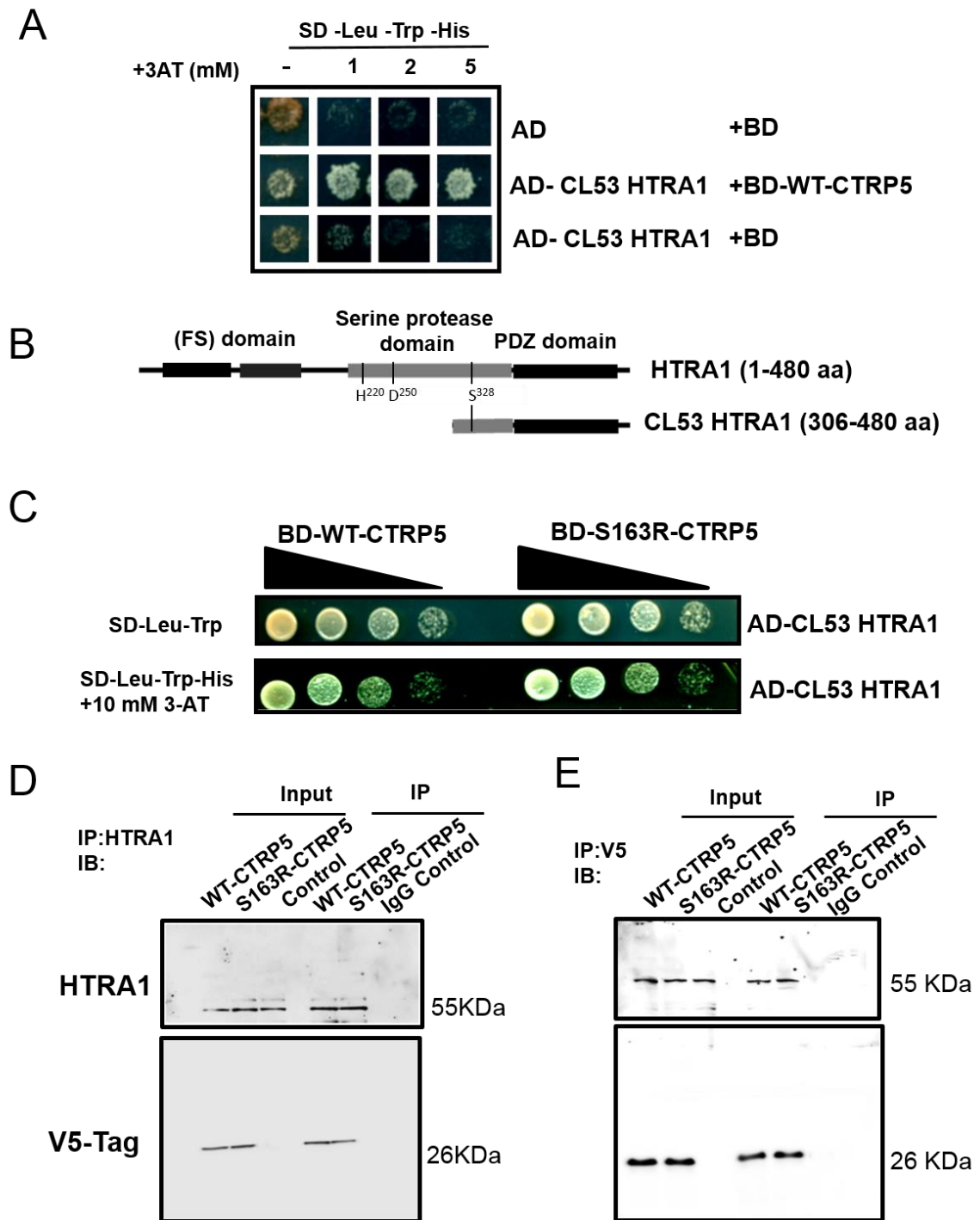


Figure 2:

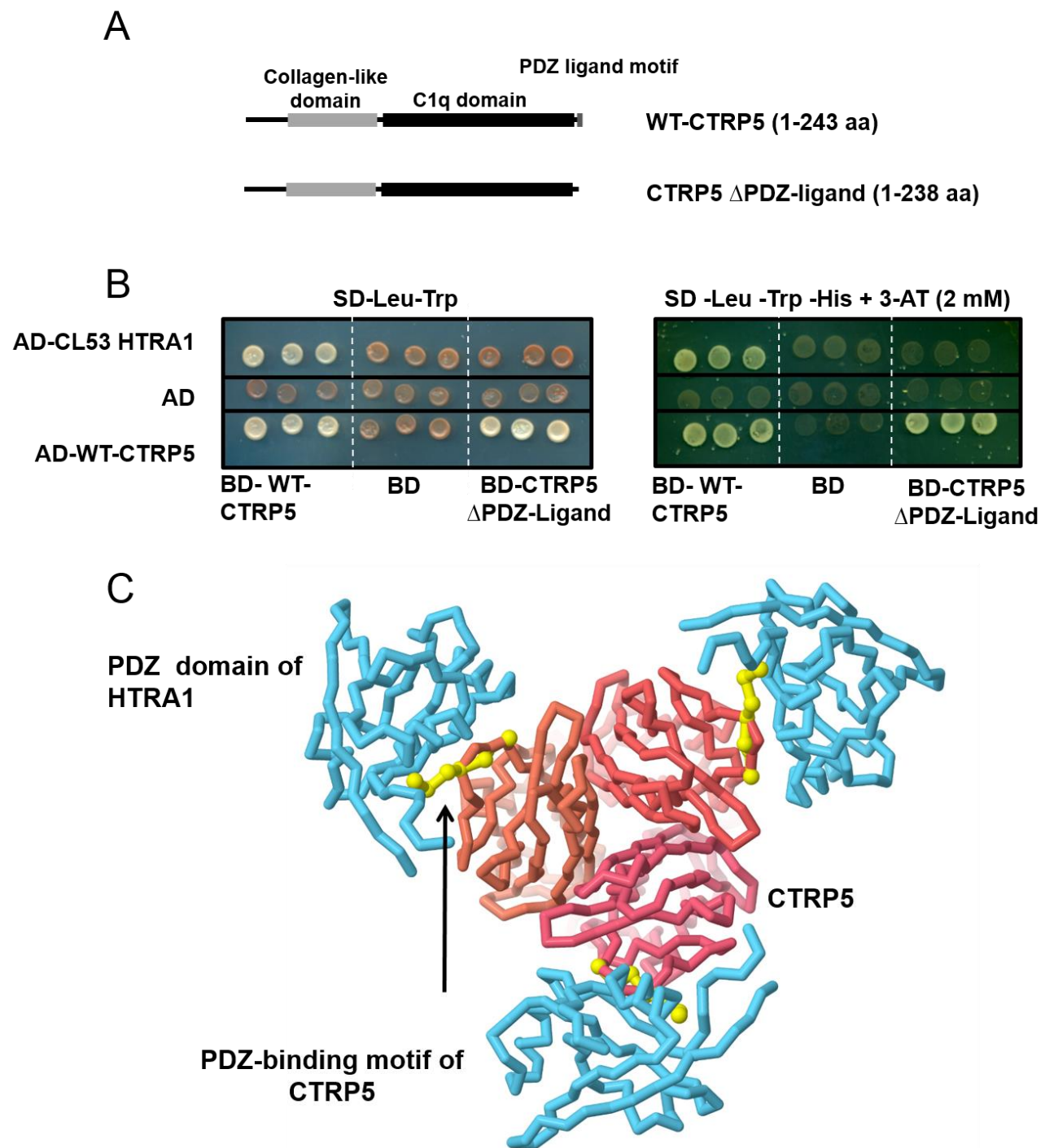


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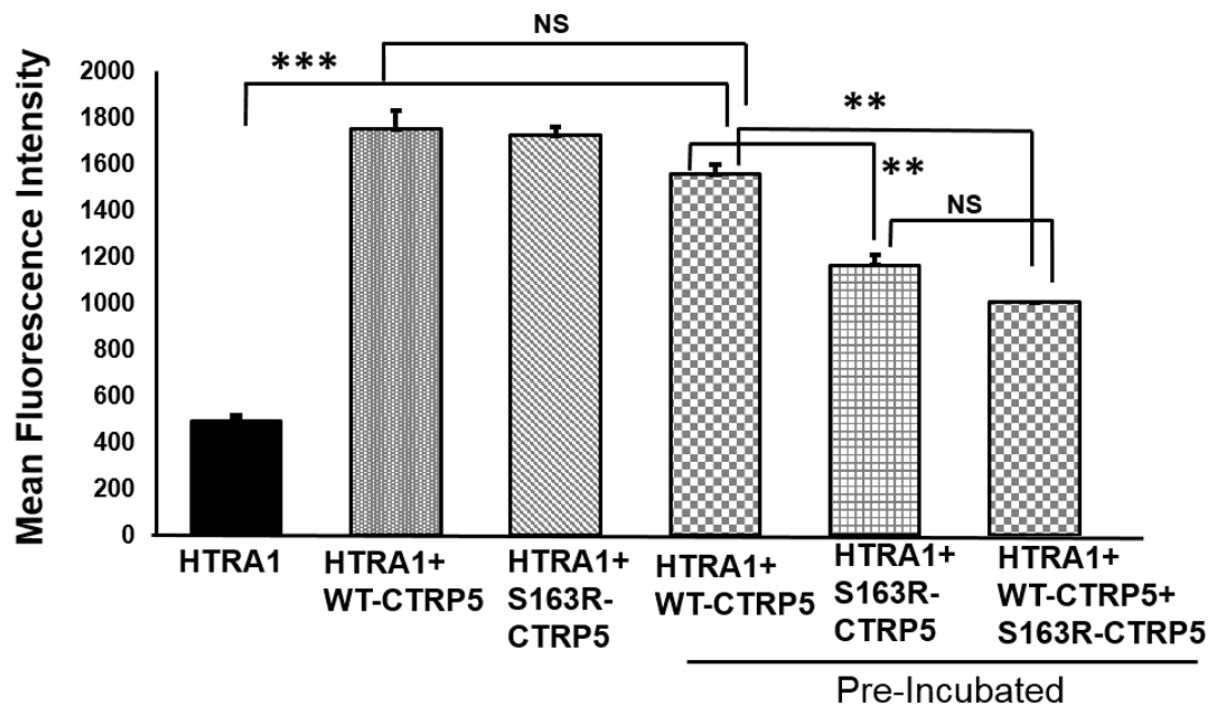
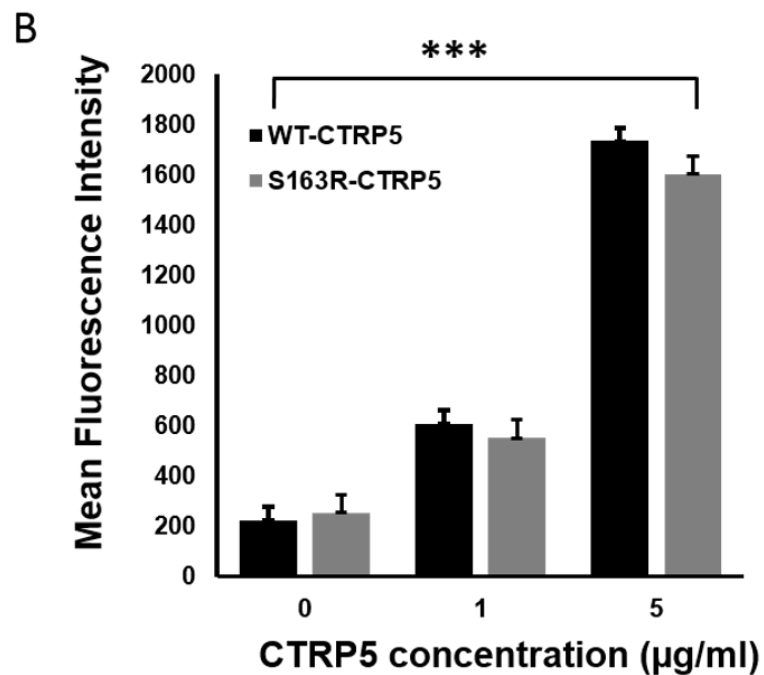
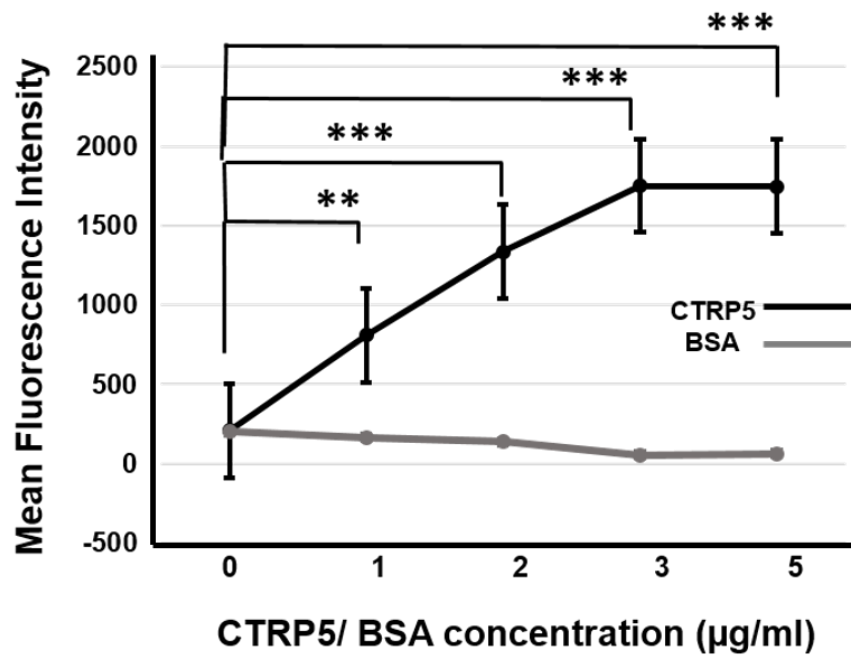
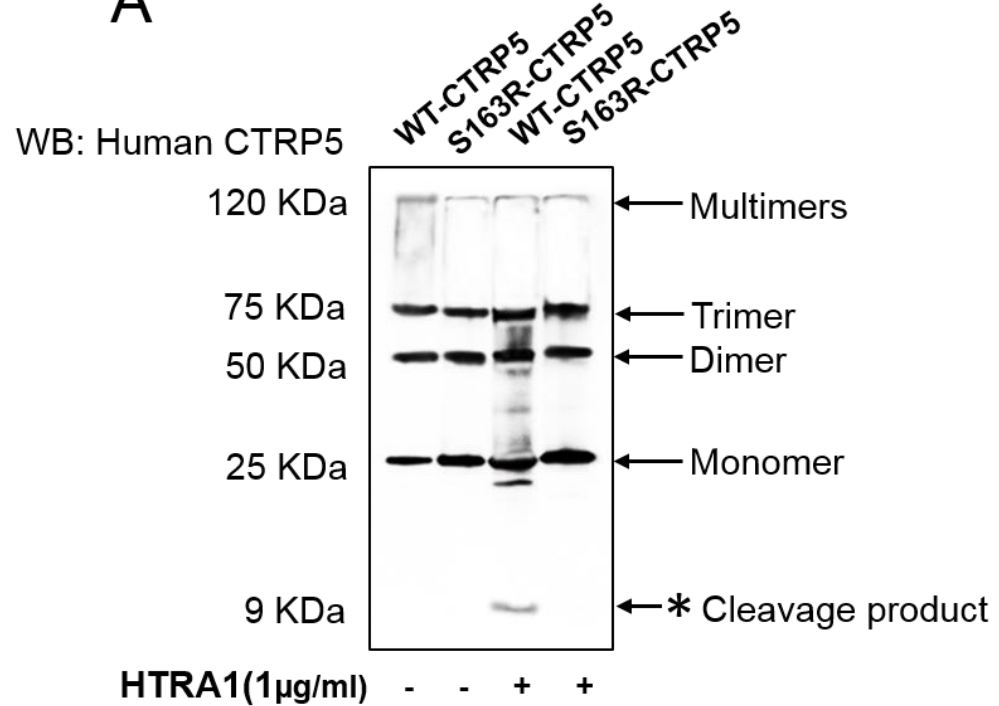
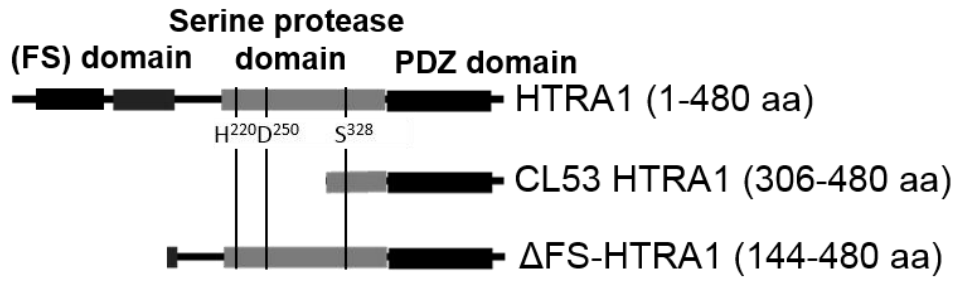


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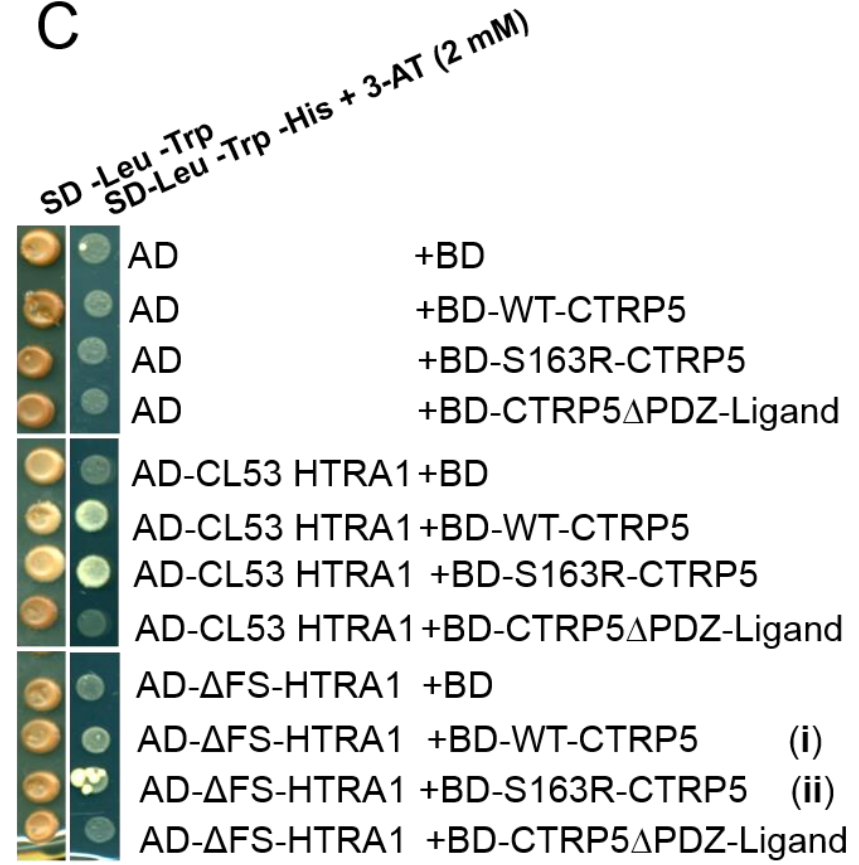
A



B



C



D

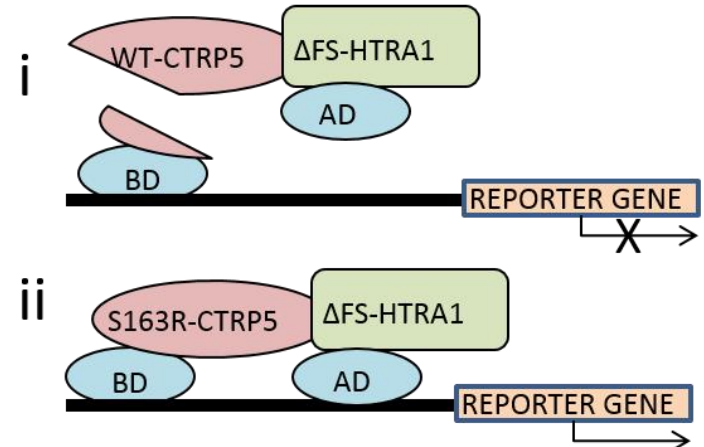


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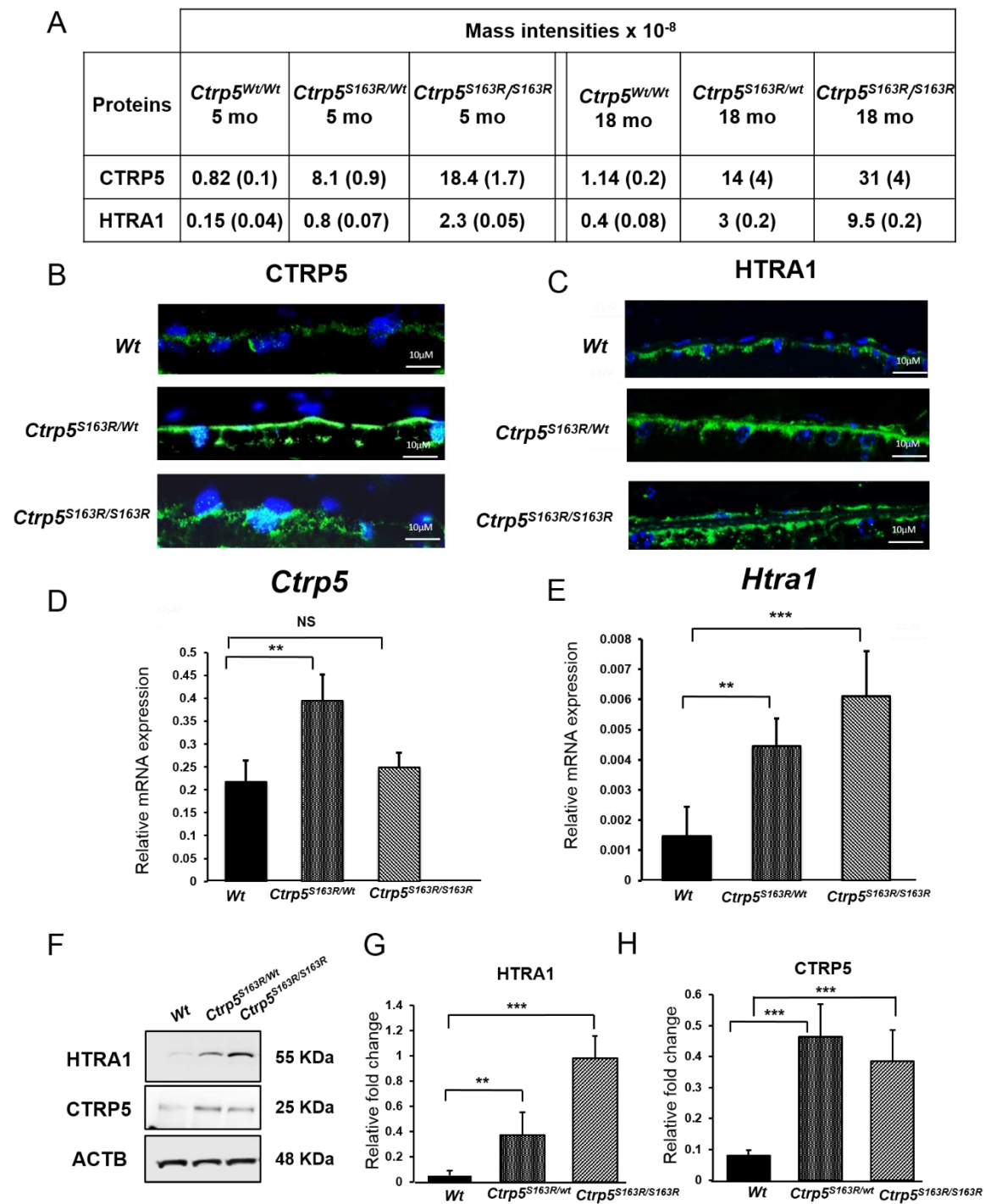
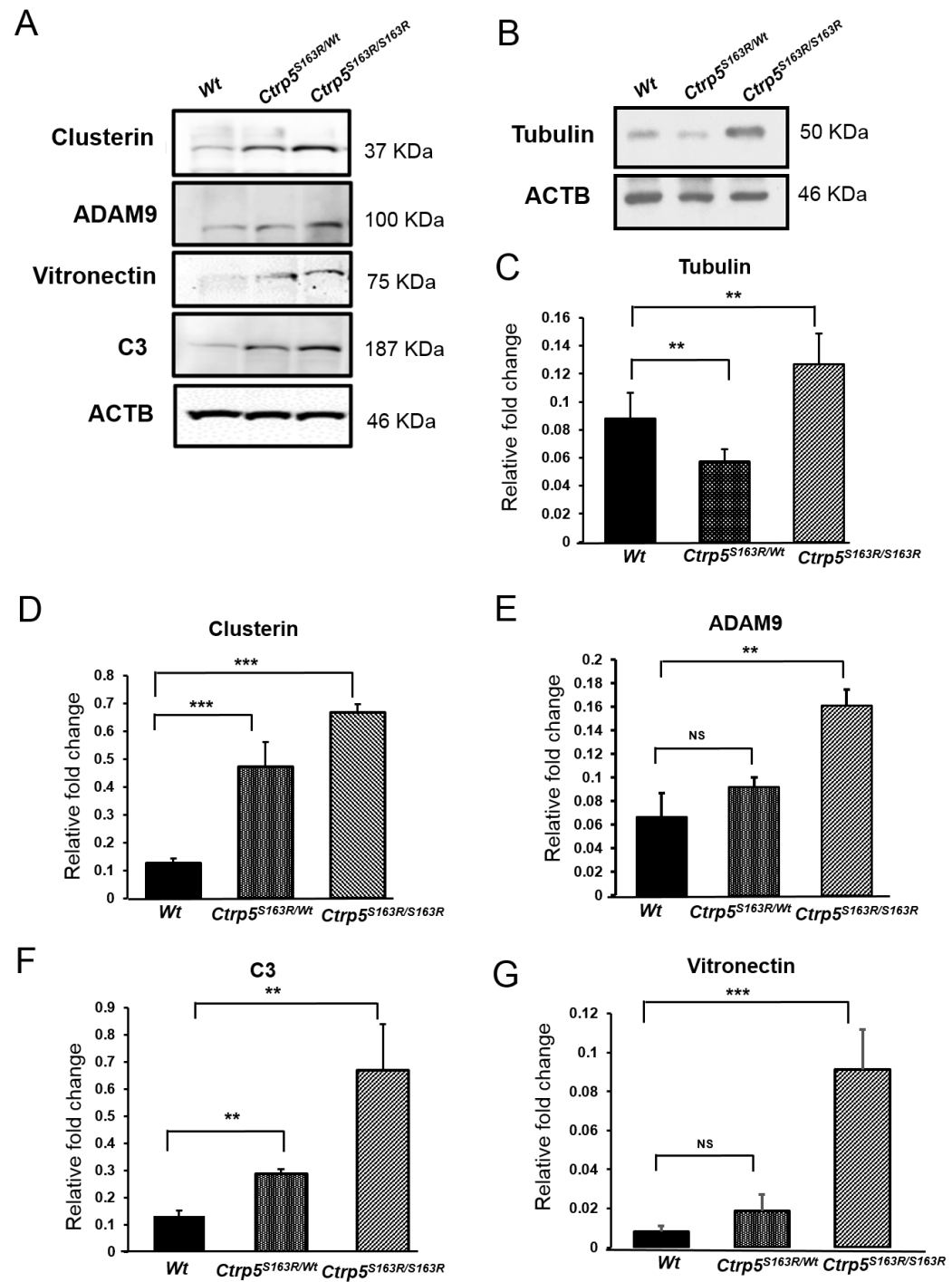
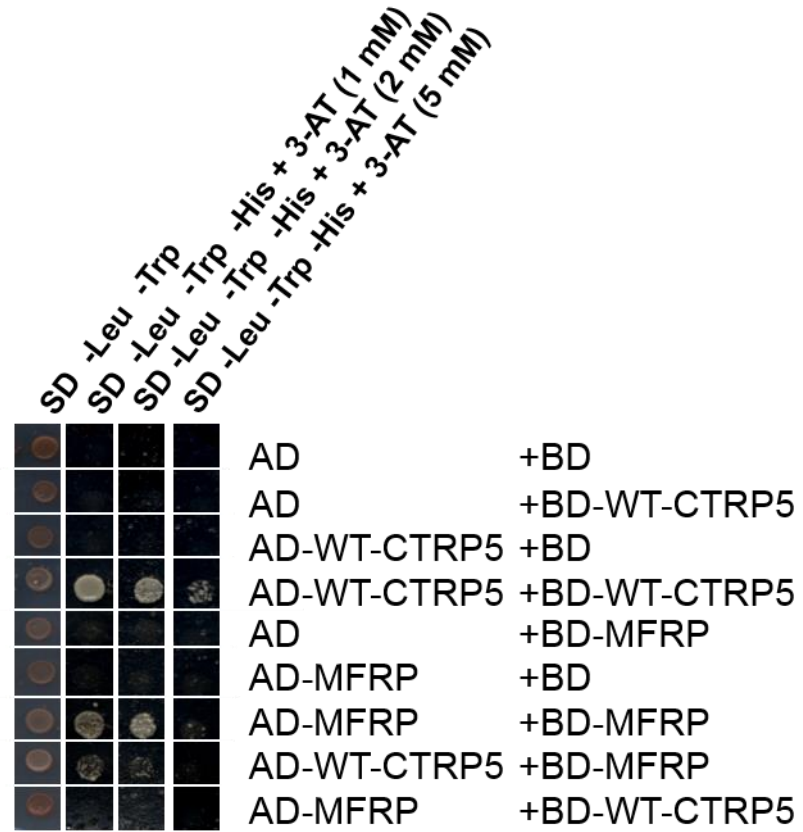


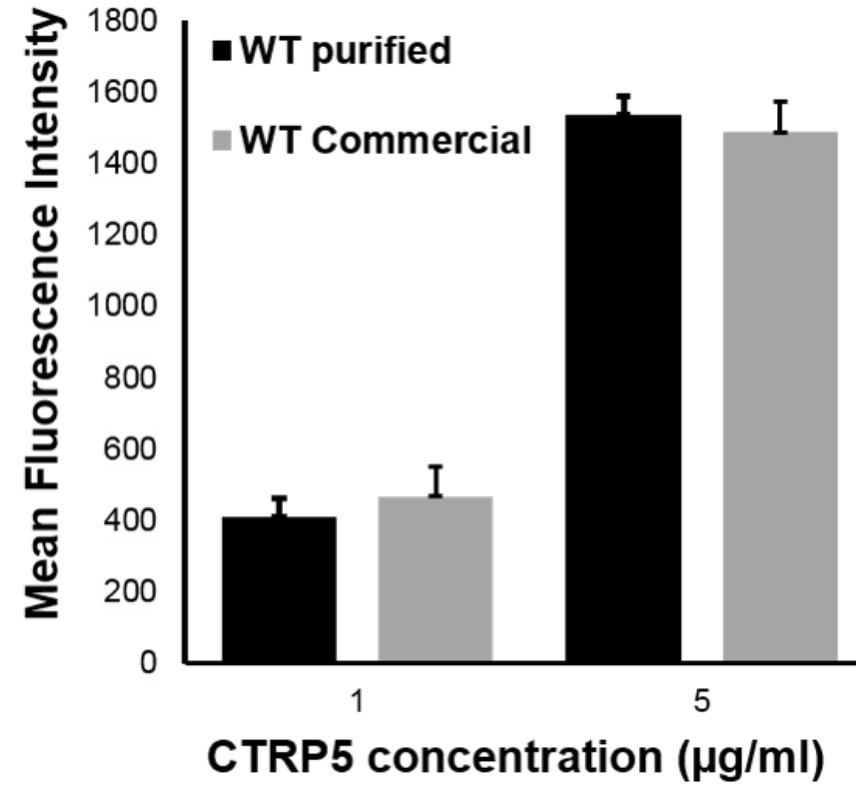
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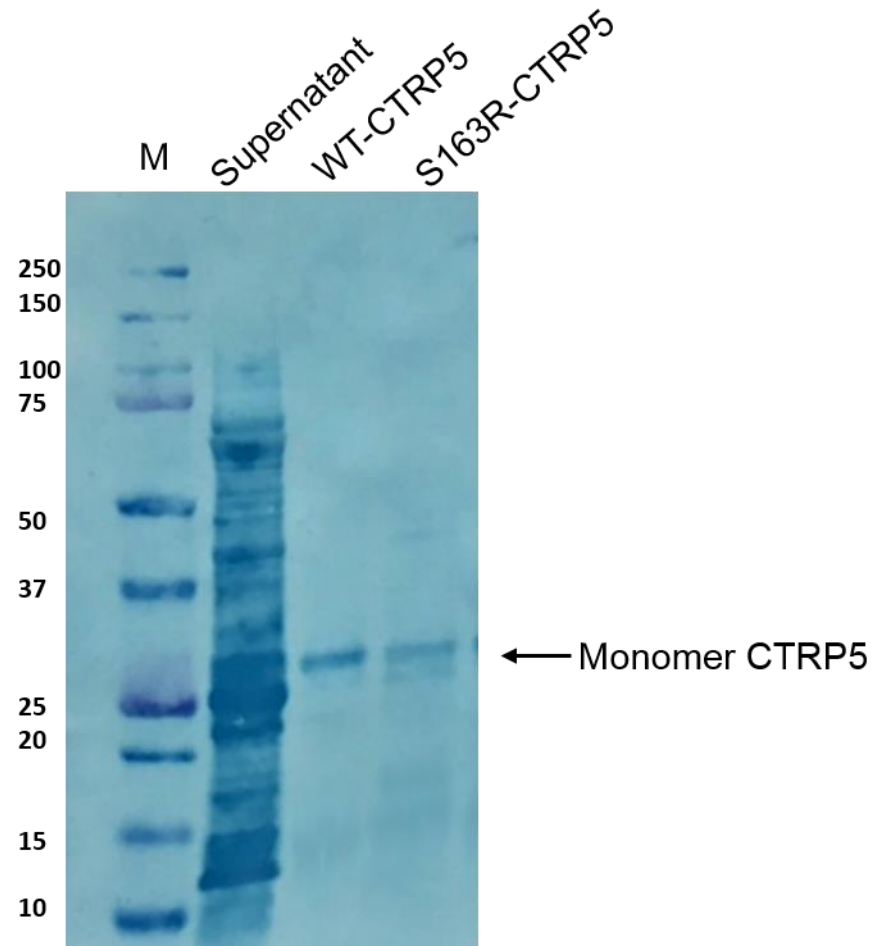
Supplementary Figure S1:



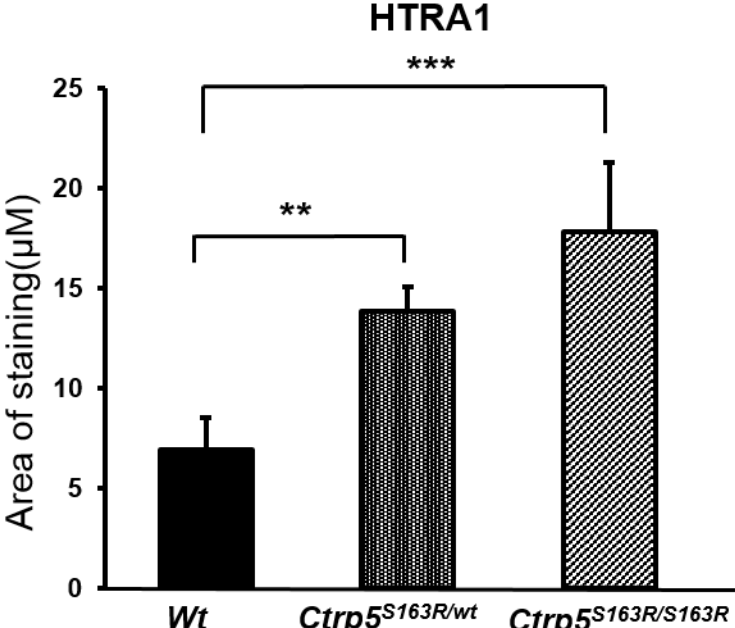
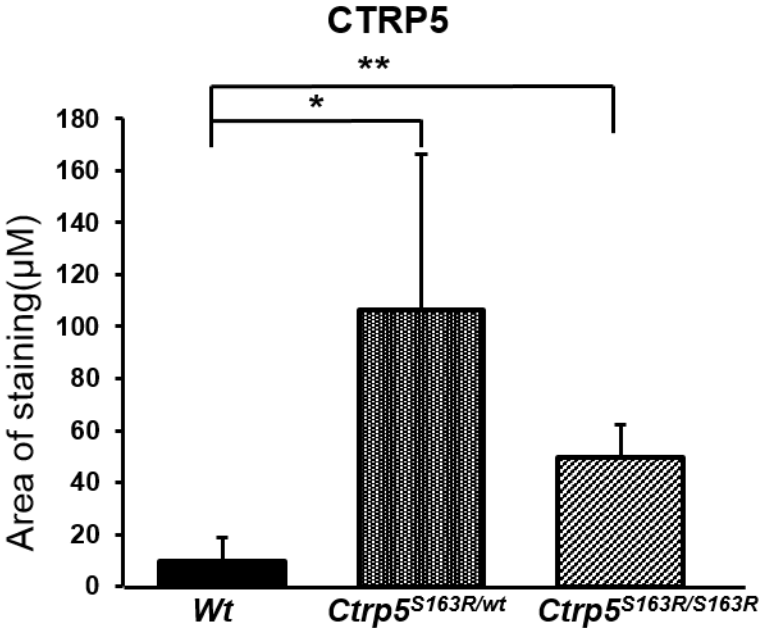
Supplementary Figure S2:



Supplementary Figure S3:

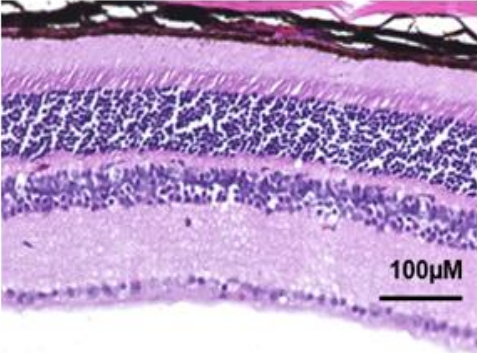


Supplementary Figure S4:

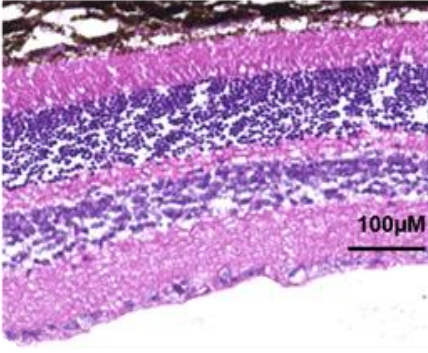


Supplementary Figure S5:

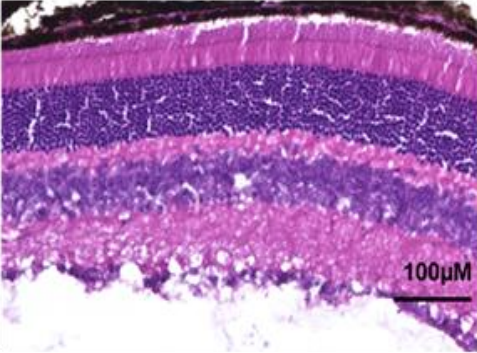
Wt



Ctrp5^{S163R/Wt}



Ctrp5^{S163R/S163R}



Supplementary table S1:

Saccharomyces cerevisiae strains					
Strain	Genotype				Reference
AH109	MATa, trp1-901, leu2-3, 112, ura3-52, his3-200, gal4Δ, gal80Δ, LYS2::GAL1 _{UAS} -GAL1 _{TATA} -HIS3, GAL2 _{UAS} -GAL2 _{TATA} -ADE2, URA3::MEL1 _{UAS} -MEL1 _{TATA} -lacZ				TaKaRa
Y2HGold	MATa, trp1-901, leu2-3, 112, ura3-52, his3-200, gal4Δ, gal80Δ, LYS2::GAL1 _{UAS} -GAL1 _{TATA} -HIS3, GAL2 _{UAS} -Gal2 _{TATA} -ADE2 URA3::MEL1 _{UAS} -MEL1 _{TATA} AUR1-C MEL1				TaKaRa
Plasmids for Y2H screening					
Plasmid name	AD-fusion protein	BD-fusion protein	Background	Selectable marker	Reference
pKZR042	WT-CTRP5 (1-243 aa)		pDEST-AD	Amp/Leu	this study
pKZR043		WT-CTRP5 (1-243 aa)	pDEST-BD	Kan/Trp	this study
pKZR044		WT-CTRP5 (1-243 aa)	pGBKT7	Kan/Trp	this study
pKZR045		S163R-CTRP5 (1-243 aa)	pGBKT7	Kan/Trp	this study
pKZR046	CL53 HTRA1 (306-480 aa)		pGADT7-RecAB	Amp/Leu	TaKaRa (Universal Human Normalized Mate & Plate™ Library)
pKZR047		WT-CTRP5 ΔPDZ-Ligand (1-238 aa)	pGBKT7	Kan/Trp	this study
pKZR048		MFRP	pDEST-BD	Kan/Trp	this study
pKZR049	MFRP		pDEST-AD	Amp/Leu	this study
pKZR050	ΔFS-HTRA1 (144-480 aa)		pGADT7	Amp/Leu	this study
Plasmids for protein expression in E.coli					
Plasmid name	Protein	Back ground	Selectable marker	Reference	
pDEST14-C1QTNF5	WT-CTRP5-His	pDEST14	Amp	Stanton et al 2017	
pDEST14-C1QTNF5-S163R	S163R-CTRP5-His	pDEST14	Amp	Stanton et al 2017	

Supplementary table S2:

Mass intensities x 10 ⁻⁸							
Peptide	Sequence	<i>Ctrp5</i> ^{Wt/Wt} 5 mo	<i>Ctrp5</i> ^{S163R/Wt} 5 mo	<i>Ctrp5</i> ^{S163R/S163R} 5 mo	<i>Ctrp5</i> ^{Wt/Wt} 18 mo	<i>Ctrp5</i> ^{S163R/Wt} 18 mo	<i>Ctrp5</i> ^{S163R/S163R} 18mo
128-142	VLLNEQGHYDPTTGK	1.3	4.9	8.2	1.4	10.0	21.0
162-170	ASLQFDLVK	0.5	0.6	0	0.4	1.2	0
164-170	LQFDLVK	0.1	1.8	2.1	0	2.1	6.5