

Table S6. Sequences of the CSN subunit models used. The Phyre models for CSN1 and CSN7 are based on the crystal structures of their respective *Arabidopsis thaliana* homologs (PDB codes 4LCT and 3CHM, respectively).

Protein	Sequence	Boundaries	Model
Human CSN1	SLDLEQYAAASYGLMRIERLQFIADHCPTLRVEALKMALSFVORTFNVDMEYIEHRKLSEATREPPALDTAWVEAT RKALKLEKLDLTKNYKNSIKESIRRGHDDLGDHYLDCGDLNALKCYSRARDYCTSAKHVINMCLNVIKVS LQNWSHVLSYVSKAESTPEIAEQRGERSQTAQLTKLKAAGLAELAAKYKQAACKLLASFDHCDPELLSPS NVAIYGGCLCALATFDROELORNVSSSSFKLFLELPQVRDIIFKFYESKYASCLKMLDEMDNLLDMLAPHVRTL YTQIRNRALIQYFSPYVSADMRMAAFNTTVALEDEL TOLILEGLISARVDSHKL YARDVDQRSTTFEKSLLMG KEFQRRAKAMMLRAAVLRNQIHVKSPPREGSQGELTPANSQSRMSTNM	41-491 Δ104-121	Phyre model
Human CSN2	MSDMEDDFMCDDEEDYDLEYSEDSNSEPNVDLENQYNSKALKEDDPKAALSSFQKVLLEGEKGEWGFALKQ MIKINFKLNFPEMNMRYKOLLTYIRSAVTRNYSEKSINSILDYISTSKQMDLLQEFYETTLEALKDAKNDRLWFKTN TKLGLKYLEREYGLKQILRQLHQSCQTDGDDDLKKGDTQLLEIYALQMYTAQKNNKKLKALYEQSLHIKSAIPH PLIMGVIRECGGKMHLEGEFEKAHTDFFAEAFKNYDESGSPRRTTCLKYLVLNMLMKSGINPFDQSEAKPKNDP EILAMTNLVSAYQNNDDTEFEKILKTNHSNIMDDPFIREHIEELLRNIRTOVLIKLIKPYTRIHIPFISKELNIDVADVESLL VQCILDNTIHGRIDQVNQLLELDHQKRGARYTALDKWTNQLNSLNQAVVSKLA	1-443	Phyre model
Human CSN3	MASALEQFVNSVRQLSAGQGMTOQLCELINKSGELLAKNLSHLDTVLGALDVQEHSLGVLAVLFVKFSMPSPDFET LFSQVQLFISTCNGEHIRYATDTFAGLCHQLTNALVERKOPLRGIGILKQAIDKMQMNTNQLTSIHADLCQLCLLAKC FKPALPYLDVDMMDICKENGAYDAKHFLCYYYGGMIYTGKKNFERALYFYEQAITTPAMAVSHIMLESYKKYILVS LILLGKVOQLPKYTSQIVGRFIKPLSNAYHELAQVYSTNNPSELNRLVNKNMGLVKQCLSSLYKKNIQRLTKTFLTL SLQDMASRVQLSGPQEAKEYVLHMIEDGEIFASINQKDEKYNNPAMLNHDQEMLKCIELDERLKAMDQEITVNPQ FVQKSMGSEQEDDSGNKPSSYS	1-423 Δ282-289 Δ356-364	Phyre model
Human CSN4	MAAAVRQDLAQLMNSSGSHKDLAGKYRQILEKAIQLSGAEQLEALKAFVEAMVNVNSLVISROLLTDFCTHLPNL PDSTAKEIYHFTLEKIOPRVISFEEQVASIROHLASIYEKEEDWRNAAQVLVGIPLTGQKQYNVDYKLETYLIARLY LEDDDDPVQAEAYINRASLLQNESTNEQLQIHYKVCYARVLDYRRKFIEAAQRYNELSYKTIVHESERLEALKHALHC TILASAGQQRSMRLATLTKDERCQQLAAYGILEKMYLDRIIRGNQLQOEFAAMLMPHQKATTADGSSILDRAVIEHNL LSASKLYNNITFEELGALLEIPAAKAEKIASQMITEGRMNGFIDQIDGIVHFTREALPTWQKIQSLCFQVNNLLEKIS QTAPEWTAQAMEAQMAQ	1-406	Phyre model
Human CSN5	AASGSGMAQKTWELANNNMQEAQSIDEIYKDYKQKQOEILAAKPWTKDHHYFKYCKISALALLKMMVHARS VMGLMLGKVDGETMIIMDSFALPVEGTETRVNAQAAAYEYMAAYIENAKQVGRLENAIGWYHSHPGYGCWLSGID VSTQMLNQQFQEPFVAVVIDPRTISAGKVNLFAGRTYKGYKPPDKQYALEVSYFKSSSSLLTNADYTTGQVFD LSEKLEQSEAOQLGRGSFMLGLETHDRKSEDKLAKATRDSCKTIEAIHGLMSQVIKDKLFN	2-229 Δ198-218 Δ232-251	X-ray structure + Phyre model
Human CSN6	SVSVALHPLVILNISDHWIRMRSQEGRPVQVIGALIGKQEGRNIEVMNSFELLSHTVEEKIIDKEYYYTKEEQKQVF KELEFLGWYTTGGPPDPSDIHVHKQVCEIIESPLFLKLNPMTKHTDLPVSVFESVIDIINGEATMLFAELTYTLATEEA ERIGVDHVARMTAHLIAQHSIAIKMLHSRVKLILEYVKASEAGEVPFNHEILREAYALCHCLPVLSTDKFKTDFYDQCN DVGLMAYLGTITKTCNTMNQFVNKFNVLYDRQGIGRRMR	38-323 Δ209-219	X-ray structure + Phyre model
Human CSN7b	MAGEQKPSNNLEQFILLAKGTSGSALTALISQVLEAPGVYVFGELLELANVQELAEAGANAAYLQLLNLFAYGTYPD YIANKESPELSTAQQNKLKHLTIVSLASRMKICIPYVLLKDLNMLNRELEDLIEAVYTDIIQGLDQRNQLLEVDFC IGRDIRKKDINNIVKTLHEWCDGCEAVLLGIEQQVLRANQYKENHNRTQQQVEAEVTNIKKTLKATASSAQEME QLAERECPHAEQROPTKKMSKVGLVSSRH	1-264	Phyre model
Human CSN8	MAESAFSFKLLDQCENQELEAPGGIATPPVYGQLLALYLLHNDMNNARYLWKRI PPAIKSANSELGGIWSVGQRIWQRDFPGIYTTINAHQWSETVQPIMEALRDATRRR AFALVSQAYTSIADDFAAFVGLPVVEAVKGILEQGWQADSTTRMVLPRKPVAGAL DVSFNKFIQQLARL	6-200 Δ182-194	Phyre model