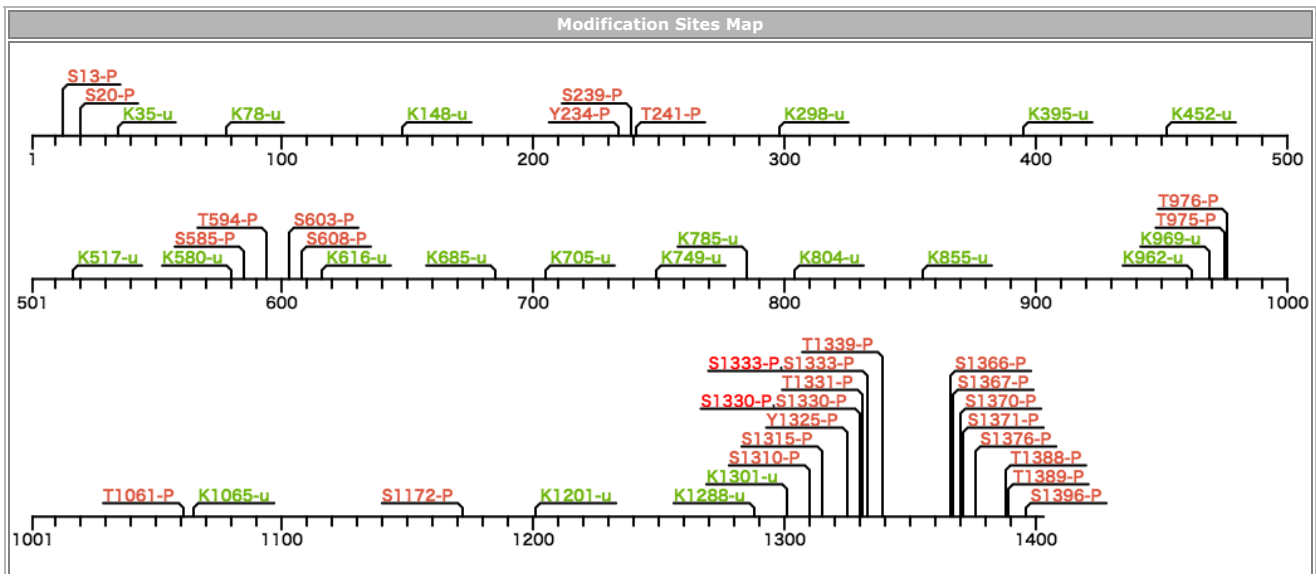


ID	Accession	GeneName	Chr.No.	Description
CND1_HUMAN	Q15021	NCAPD2	12p13.31 6602522..6641121	Condensin complex subunit 1



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
1333	S	P	Lab	140320_Mag_new_.mgf[F017424]
1333	S	P	Lab	140320_Mag_new_.mgf[F017424]
1333	S	P	Lab	140320_Mag_old_.mgf[F017425]
1333	S	P	Lab	140320_tita_C18_.mgf[F017426]
1333	S	P	Lab	140320_tita_SDB_.mgf[F017430]
1333	S	P	Paper	J Proteome Res 2009, 8(10), 4553-4563
1333	S	P	Paper	J Proteome Res 2013, 12(1), 260-271
1333	S	P	Paper	J Proteomics 2011, 75(4), 1343-1356
1333	S	P	Paper	Mol Cell Proteomics 2010, 9(6), 1047-1062
1333	S	P	Paper	Mol Cell Proteomics 2010, 9(6), 1167-1181
1333	S	P	Paper	Mol Cell Proteomics 2011, 10(1), M110.004457
1333	S	P	Paper	Mol Cell Proteomics 2012, 11(9), 651-668
1333	S	P	Paper	Mol Cell Proteomics 2015, 14(6), 1599-1615
1333	S	P	Paper	Proc Natl Acad Sci USA 2008, 105(38), 10762-10767
1333	S	P	Paper	Proc Natl Acad Sci USA 2014, 111(21), E2182-E2190
1333	S	P	Paper	Sci Signal 2009, 2(84), ra46
1333	S	P	Paper	Sci Signal 2011, 4(164), rs3

Protein Sequence	
MAPQMYEFHL PLSPEELLKSGGVNQYVVQE VLSIKHLPPQ LRAFQAQFRA QGPLAMLQHF DTIYSILHHF RSDIPGLKED TLQFLIKVVS RSHQELPAIL DDTTLTSGSDR NAHL NALKMN CYALIRLLES FETMASQTNL VDLDLGGKGGK KARTKAAHG F DWEEERQPIL QLLTQLQLD IRHLWNHSII EEEFVSLVTG CCYRLENPT INHQKRNPRTR EAITHLGG VA LTRYNHMLSA TVKIIQLMH FEHLAPLVVA AVSLWATDYG MKSIVGEIVR EIGQKCPQEL SRDPSGTGFAAFLTELAER VPAILMSSMC ILLDHLDDGEN YMMRNLAVLAA MAEMVLQVLS GDQLEAAARD TRDQFLDTLQ AHGHVDVNSF RSRVLQLFTR IVQQKALPLT RFQAVVALAV GRLADKSVLV CKNAIQLLAS FLANNPFSCK LSDADLAGPL QK ETQKLQEM RAQRRTAAAS AVLDPEEWE AMLPELKSTL QLLQLPQGE EEIPEQIANT ETTEDEVKGR IYQLLAKASYK KAIILTREAT GHFQSEPF S HIDPEESET RLLNILG LIF KGPAASTQEK NPRESSTGNMV TGOITVCKNKP NMSDPEESRG NDELVKQEML VQYLQDAYSF SRKITEAIGI ISKMMYENTT TVVQVEIEFF VMVFQGVQPQ ALFGVRRML P LIWSEKPGVR EAVLNAYRQL YLNPKGDSAR AKAQALIQNL SLLLVDA SVG TIQCLEILC ERFVQKDELKPAVTQLLWERA TEKVACCPLE RCSSVMLLGM MARGKPEIVG SN LDTLVSIG LDEKFPQDYR LAQQVCHAIA NISDRRKPSL GKRHPPFRLP QEHLRFLERL ETVTKGFVHP DPLWIPFKEV AVTLIYQLAE GPEVICAQIL QGCAQALEK LEEKRTS QED PKESPAMLPT FLLMNLSSLA GDVALQQLVH LEQAVSGELC RRRVLRREEQE HKT KDPEKN TSSETTMEEE LGLVGATADD TEALIRGIC EMELLDGKQT LAAFVPLLLK VCNNPGLYSN PDLSSAAASLA LGKFCMISAT FCDSQLRLLF TMLKKSPLI VRSNLMVATG DLAIRFPNLV DPWTPHLYAR LRDPAQVRK TAGLVMTHLI LKDMVKVKGQ VSE MAVLLID PEPQIAALAK NFFNELSHKG NAIYNLLPDI ISRLSDPELG VEEEPFHTIM KQLLSYITKD KQTESLVEKL CQRFRTRTE RQRDLAYCV SQLPLTERGL RKMLDNFD CF GDKLSDESIF SAFLSVVGKL RRGAKPEGKA IIDEFEQLR ACHTRGLDGI KELEIQAGS QRAPSAKKPS TGSRYQPLAS TASNDFVTP EPRTRRRHP NTQQRASKKK PKVVFSSDES SEEDLSAEMT EDETPKKTTP ILRASAARRHR S	

Backcolor of amino acid : Yellow -> site of modification, gray -> in front of processing