Supplementary Material

Oligonucleotides and cloning procedures

Oligo	Sequence							
MG1	GGC CGC GGG CGG CAT CGA GGG CAG GGG CGG CGG CGG CTG GTC CAA CCC							
	ACA ATT CGA GAA GCC CGG GTA ATA AC							
MG2	CAT GGT TAT TAC CCG GGC TTC TCG AAT TGT GGG TGG GAC CAG CCG CCG							
	CCG CCG CCC CTG CCC TCG ATG CCG CCC GC							
MG3	CCG <u>GAT ATC</u> ATG ACA ACA GCA GCC AGG CC							
MG4	AAG GAA AAA A <u>GC GGC CGC</u> TTT AAT ATA TTT CTC CAT GAA CTT TTT GTG							
MG5	CCG <u>GAT ATC</u> ATG CCT CGA ATT ATG ATC AAG							
MG6	AAG GAA AAA A <u>GC GGC CGC</u> GAA TTT TGA CTT TAA AGT CTC TTT CTC							
MG7	CCG <u>GAT ATC</u> ATG GAC GTG GGC GAA CTT CTG							
MG8	CTT CCC GAT AGC GTC CGC GTT CTC GAG							
MG9	CTC GAG AAC GCG GAC GCT ATC GGG AAG							
MG10	ATA AGA AT <u>G CGG CCG C</u> GA AGT TCT CCA GCA AGC CCA G							
MG11	CCG GAT ATC ATG TCC CTA ATC TGC TCC ATC TCT AAC							
MG12	AAG GAA AAA AGC GGC CGC CAG GCT GTA GAA CTT GAG GCT TCT GTC							
MG13	CCG <u>GAT ATC</u> ATG GTC GAG GAG GTA CAG AAA C							
MG14	AAG GAA AAA A <u>GC GGC CGC</u> AAA TCT CTT TCT CTT GAT AAT TTC TG							
MG15	CCG <u>GAT ATC</u> TCC AAG GGA CCT GCA GTT G							
MG16	AAG GAA AAA A <u>GC GGC CGC</u> ATC AAC CTC TTC AAT GGT GGG C							
MG17	CCG <u>GAT ATC</u> ATG GCG GGC ACA GGT TTG GTG							
MG18	AAG GAA AAA A <u>GC GGC CGC</u> GAA GTC TTG CCG GAT GTT TTC TTT G							
IL1	TAC <u>GCT AGC</u> ATG ACA ACA GCA GCC AGG CC							
IL2	CTA GT <u>G GAT CC</u> C TAT TTA ATA TAT TTC TCC ATG							
IL3	TAC <u>GCT AGC</u> ATG GCG GGC ACA GGT TTG G							
IL4	CTA GT <u>G GAT CC</u> C TAG AAG TCT TGC CGG ATG TTT TC							
M7-F	GGG GTA CCT AAT ACG ACT CAC TAT AGG GAG ACG GAA TTC GAG CTC GCC							
	C							
M7-R	CGC GGA TCC CCA CTG GAA AGA CC							

To generate FLAG/HA-tagged AD002 and SPF27, cDNAs encoding these proteins were cloned into a modified pIRESneo plasmid (Clontech) containing a N-terminal FLAG/HA tag (2) using PCR based techniques. The AD002 and SPF27 cDNAs were cloned using Nhe I and BamH I restriction sites, with IL1/IL2 and IL3/IL4 primer pairs. In order to introduce a StrepII purification tag (4), oligonucleotides MG1 and

MG2 were hybridized and cloned via Not I and Nco I cleavage sites into the pEU3-NII vector (Toyobo) (3), generating pEU3-NII-StrepII. The cDNAs encoding all seven hPrp19/CDC5L complex proteins were cloned into pEU3-NII-StrepII via EcoRV and Not I cleavage sites using primers MG3-MG18.



Supplementary Figure 1

Schematic illustration of plasmids used for the stable transfection of HeLa cells. The plasmids contain the FLAG/HA-tagged AD002 or SPF27 genes under the control of a CMV promotor. In addition, the plasmids contain ampicillin and neomycine resistance markers for selection in bacteria and mammalian cells, respectively. IVS – intervening sequence; IRES – internal ribosome entry site.



CDC5L, PRL1, hPrp19, and SPF27 form a salt-stable subcomplex. Purified hPrp19/CDC5L complexes were incubated with 0.4 M NaSCN (A) or 300 mM NaCl (B) for 30 min on ice. Subsequently, the complexes were fractionated on a linear 5 to 20% glycerol gradient containing the same NaSCN or NaCl concentration. Proteins across the gradient were analyzed by SDS-PAGE and stained with Coomassie. The position of the proteins is indicated on the left and the molecular mass (kDa) of marker proteins is indicated on the right.

Supplementary Figure 3



Schematic overview of domains in the hPrp19/CDC5L complex proteins. The total number of amino acids (in parenthesis) and the position of domains predicted by the SMART 6 program (1) are indicated. The WD40 domains of hPrp19 and PRL1 both consist of 7 WD40 repeats. CC – Coiled Coil domain; SANT (also cMyb) – <u>S</u>witching-defective protein 3 (Swi3), <u>A</u>daptor 2 (Ada2), <u>N</u>uclear receptor corepressor (N-CoR), <u>T</u>ranscription factor (TF)IIIB.



Limited proteolysis with subtilisin reveals the architecture of the hPrp19/CDC5L complex core. Affinity-selected complexes were incubated for 30 min on ice with 0, 30, 125, or 250 nM of the protease subtilisin. The proteolysed fragments were then fractionated by size via gel filtration and analysed by SDS-PAGE followed by mass spectrometry in order to define those fragments resistant to protease digestion. (A) Gel filtration profile after proteolysis with 0 to 250 nM subtilisin (as indicated). (B) SDS-PAGE analysis of subtilisin digestion products co-purifying during gel filtration. Proteins from pairwise pooled fractions were separated on a 15% polyacrylamide-SDS gel, stained with coomassie and analyzed by mass spectrometry. The protein residues remaining after proteolysis, as determined by mass spectrometry, are indicated in parentheses.

Supplementary Figure 5

		hPrp19	full-length	ı				CDC5	482-802		
10 MSLICSISNE VPH	20 EHPCVSPV	30 SNHVYERRLI	40 EKYIAENGTD	50 PINNOPLSEE	60 OLIDIKVAHP	10 MPRIMIKGGV	20 WRNTEDEILK	30 AAVMKYGKNO	40 WSRIASLLHR	50 KSAKOCKARW	YEWLDPSI
70	8 <u>0</u>	90	100	110	120	70	80	90	100	110	1
130	AILKALQD 140	EWDAVMLHSF 150	TLRQQLQTTR 160	QELSHALYQH 170	DAACRVIARL 180	TEWSREEEEK 130	LLHLAKLMPT 140	QWRTIAPIIG 150	RTAAQCLEHY 160	EFLLDKAAQR 170	DNEEETTD 1
rkevtaarea Lat	TLKPQAGL	IVPQAVPSSQ	PSVVGAGEPM	DLGELVGMTP	EIIQKLODKA	RKLKPGEIDF	NPETKPARPD	PIDMDEDELE	MLSEARARLA	NTQGKKAKRK	AREKQLEE
TVLTTERKKR GK7	TVPEELVK	PEELSKYRQV	ASHVGLHSAS	IPGILALDLC	PSDTNKILTG	RLAALQKRRE	LRAAGIEIQK	KRKRKRGVDY	NAEIPFEKKP	ALGFYDTSEE	NYQALDAD
250 RADKNYVYFD KS	260	270 KGHTKKVTSV	280 VEHPSODLVE	290 SASPDATTRI	300 WSVPNASCVO	250 KLBOODLDGE	260	270 KKDKOHLKRK	280 KESDLPSATL	0TSGVSEFTK	KRSKLVLP
31 <u>0</u>	320	330	340	350	360	310	320	330	340	350	3
VRAHESAVT GLS 370	SLHATGDY 380	LLSSSDDQYW 390	AFSDIQTGRV 400	LTKVTDETSG 410	CSLTCAOFHP 420	QISDAELQEV 370	VKVGQASEIA 380	RQTAEESGIT 390	NSASSTLLSE 400	YNVTNNSVAL 410	RTFRTFAS
GLIFGTGTM DSC	QIKIWDLK	ERTNVANFPG	HSGPITSIAF	SENGYYLATA	ADDSSVKLWD	RILQEAQNLM	ALTNVDTPLK	GGLNTPLHES	DFSGVTPQRQ	VVQTPNTVLS	TPFRTPSN
LRKLKNFKTL QLI	DNNFEVKS	LIFDQSGTYL	ALGGTDVQIY	ICKQWTEILH	FTEHSGLTTG	EGLTPRSGTT	PKPVINSTPG	RTPLRDKLNI	NPEDGMADYS	DPSYVKQMER	ESREHLRL
490 VAFGHHAKFT AS	500 TGMDRSLK	FYSL				490	500 EIVLPENAEK	510 ELEEREIDDT	520	530 RKOAIRDAER	5 VKEMKRMH
						550	560	570	580	590	6
		hPrn1	19			VQKDLPRPSE 610	VNETILRPLN 620	VEPPLTDLQK 630	SEELIKKEMI 640	TMLHYDLLHH 650	PYEPSGNK
10	20		1-148	50		KTVGFGTNNS	EHITYLEHNP	YEKFSKEELK	KAQDVLVQEM	EVVKQGMSHG	ELSSEAYN
MSLICSISNE VPF	EHPCVSPV	SNHVYERRLI	EKYIAENGTD	PINNQPLSEE	QLIDIKVAHP	WEECYSQVLY	LPGQSRYTRA	NLASKKDRIE	SLEKRLEINR	GHMTTEAKRA	AKMEKKMK
70	80	90	100	110	120	730	740	750	760	770	7
130	140	150	160	170	180	790	800	5	TT	SALFALLECS	
FKEVTAAREA LAT 190	TLKPQAGL 200	IVPQAVPSSQ 210	PSVVGAGEPM 220	DLGELVGMTP 230	EIIQKLQDKA 240	EKELQHRYAD	LLLEKETLKS	KF			
TVLTTERKKR GKT	TVPEELVK	PEELSKYRQV	ASHVGLHSAS	IPGILALDLC	PSDTNKILTG						
3ADKNVVVFD KS	SEQILATL	KGHTKKVTSV	VFHPSQDLVF	SASPDATIRI	WSVPNASCVQ			0005			
310	320	330	340	350	360			CDC5	-373-802		
37 <u>0</u>	38 <u>0</u>	390	40 <u>0</u>	41 <u>0</u>	42 <u>0</u>	10	20	30	40	50	
JGLIFGTGTM DSC 430	QIKIWDLK : 440	ERTNVANFPG 450	HSGPITSIAF 460	SENGYYLATA 470	ADDSSVKLWD 480	MPRIMIKGGV 70	WRNTEDEILK	AAVMKYGKNQ	WSRIASLLHR	KSAKQCKARW	YEWLDPSI
LRKLKNFKTL QLI	DNNFEVKS	LIFDQSGTYL	ALGGTDVQIY	ICKQWTEILH	FTEHSGLTTG	TEWSREEEEK	LLHLAKLMPT	QWRTIAPIIG	RTAAQCLEHY	EFLLDKAAQR	DNEEETTD
490 VAFGHHAKFI AST	TGMDRSLK	FYSL				130 RKLKPGEIDP	140 NDETKDARDD	150 PIDMDEDELE	160 MISEARARIA	170 NTOCKKAKRK	1 AREKOLEE
						190	200	210	220	230	2
		hPrp19	9145-504			RLAALQKRRE 250	LRAAGIEIQK 260	KRKRKRGVDY 270	NAEIPFERRP 280	ALGFYDTSEE 290	NYQALDAD 3
10	20	•	140 004	50	60	KLRQQDLDGE	LRSEKEGRDR	KKDKQHLKRK	KESDLPSAIL	QTSGVSEFTK 350	KRSKLVLP
MSLICSISNE VPF	EHPCVSPV	SNHVYERRLI	EKYIAENGTD	PINNQPLSEE	QLIDIKVAHP	QISDAELQEV	VKVGQASEIA	RQTAEESGIT	NSASSTLLSE	YNVTNNSVAL	RTPRTPAS
70 TRPKPPSATS TP	ATLKALOD	90 EWDAVMLHSE	100 TLBOOLOTTE	OFLSHALYOH	DAACEVIARI	370 RILOEAONLM	380 ALTNVDTPLK	GGLNTPLHES	400 DFSGVTPORO	410 VVOTPNTVLS	4 TPFRTPSN
130	140	15 <u>0</u>	160	170	180	430	440	450	460	470	4
ISCOUTAAREA LAT	TLKPQAGL 200	1VPQAVPSSQ 210	PSVVGAGEPM 220	DLGELVGMTP 230	ETIQKLQDKA 240	EGLTPRSGTT 490	500	S10	S20	530	ESKEHLKL 5
TVLTTERKKR GKT	TVPEELVK	PEELSKYRQV	ASHVGLHSAS	IPGILALDLC	PSDTNKILTG	LGLPAPKNDF	EIVLPENAEK 560	ELEEREIDDT 570	YIEDAADVDA 580	RKQAIRDAER 590	VKEMKRMH
SADKNVVVFD KSS	SEQILATE	KGHTKKVTSV	VFHPSQDLVF	SASPDATIRI	WSVPNASCVQ	VQKDLPRPSE	VNETILRPLN	VEPPLTDLQK	SEELIKKEMI	TMLHYDLLHH	PYEPSGNK
VVRAHESAVT GLS	SLHATGDY	LLSSSDDQYW	340 AFSDIQTGRV	150 LTKVTDETSG	CSLTCAQFHP	KTVGFGTNNS	EHITYLEHNP	YEKFSKEELK	KAQDVLVQEM	EVVKQGMSHG	ELSSEAYN
37 <u>0</u>	38 <u>0</u>	39 <u>0</u>	400	410	420	670	680	690	700	CUNTERANDA	7
430	440	450	46 <u>0</u>	470	480	730	740	750	760	770	7
A90	DNNFEVKS	LIFDQSGTYL	ALGGTDVQIY	ICKQWTEILH	FTEHSGLTTG	LGGYQSRAMG 790	LMKQLNDLWD 800	QIEQAHLELR	TFEELKKHED	SAIPRRLECL	KEDVQRQQ
VAFGHHAKFI AST	TGMDRSLK	FYSL				EKELQHRYAD	LLLEKETLKS	KF			
		PRL	.11 02								
1 <u>0</u> 2 <u>0</u> 3 <u>0</u> 4 <u>0</u> 5 <u>0</u> 6 <u>0</u>								CDC	5L ₁₋₂₃₅		
AVEEVOKHSV HTI 70	LVFRSLKR 80	THDMFVADNG 90	KPVPLDEESH 100	KRKMAIKLRN 110	EYGPVLHMPT 120	10	20	3 <u>0</u>	4 <u>0</u>	5 <u>0</u>	
SKENLKEKGP QNF	ATDSYVHK	QYPANQGQEV	EYFVAGTHPY 160	PPGPGVALTA	DTKIQRMPSE	MPRIMIKGGV 70	WRNTEDEILK 80	AAVMKYGKNQ 90	WSRIASLLHR 100	KSAKQCKARW 110	YEWLDPSI 1
1 211	140	150	PGASDRPOPT	AMNSIVMETG	NTKNSALMAK	TEWSREEEEK	LLHLAKLMPT	QWRTIAPIIG	RTAAQCLEHY	EFLLDKAAQR	DNEEETTD
SAAQSLAVAL PLQ	QTKADANR	TAPSGSEIRH			240	130	140	150	160	170	1
SAAQSLAVAL PLQ 190 CAPTMPKPOW HPP	QTKADANR 200 PWKLYRVI	210 SGHLGWVRCT	220 AVEPGNOWEV	230 TGSADRTIKT	WDLASGKLKT.	RKLKPGEIDP	NPETKPARPD	PIDMDEDELE	MLSEARARLA	NTQGKKAKRK	AREKQLEE
130 SAAQSLAVAL PLQ 190 KAPTMPKPQW HPE 250	QTKADANR 200 PWKLYRVI 260	SGHLGWVRCI 270	220 AVEPGNQWFV 280	230 TGSADRTIKI 290	WDLASGKLKL 300	RKLKPGEIDP 190	NPETKPARPD 200	PIDMDEDELE 210 KRKRKRCUDY	MLSEARARLA 220	NTQGKKAKRK 230	AREKQLEE 2
130 SAAQSLAVAL PL(190 KAPTMPKPQW HPI 250 3LTGHISTVR GVI 310	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320	210 SGHLGWVRCI 270 LFSCGEDKQV 330	220 AVEPGNQWFV 280 KCWDLEYNKV 340	230 TGSADRTIKI 290 IRHYHGHLSA 350	WDLASGKLKL 300 VYGLDLHPTI 360	RKLKPGEIDP 190 RLAALQKRRE 250	NPETKPARPD 200 LRAAGIEIQK 260	PIDMDEDELE 210 KRKRKRGVDY 270	MLSEARARLA 220 NAEIPFEKKP 280	NTQGKKAKRK 230 ALGFYDTSEE 290	AREKQLEE 2 NYQALDAD 3
130 SAAQSLAVAL PL(190 KAPTMPKPQW HPE 250 SLTGHISTVR GVJ 310 VLVTCSRDS TAF 370	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380	TAPSGSEYRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA	230 TGSADRTIKI 290 IRHYHGHLSA 350 AEPQIITGSH	WDLASGKLKL 300 VYGLDLHPTI 360 DTTIRLWDLV	RKLKPGEIDP 190 RLAALQKRRE 250 KLRQQDLDGE 310	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320	PIDMDEDELE 210 KRKRKRGVDY 270 KKDKQHLKRK 330	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAIL 340	NTQGKKAKRK 230 ALGFYDTSEE 290 QTSGVSEFTK 350	AREKQLEE 2 NYQALDAD 3 KRSKLVLP 3
130 SAAQSLAVAL PL(190 KAPTMPKPQW HPI 250 SLTGHISTVR GVI 310 SVLVTCSRDS TAF 370 AGKTRVTLTN HKF	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL	TAPSGSETRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 SPDNIKQWKF	230 TGSADRTIKI 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS	WDLASGKLKL 300 VYGLDLHPTI 360 DTTIRLWDLV 420 GHNAIINTLT	RKLKPGEIDP 190 RLAALQKRRE 250 KLRQQDLDGE 310 QISDAELQEV	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA	PIDMDEDELE 210 KRKRKRGVDY 270 KKDKQHLKRK 330 RQTAEESGIT	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAIL 340 NSASSTLLSE	NTQGKKAKRK 230 ALGFYDTSEE 290 QTSGVSEFTK 350 YNVTNNSVAL	AREKQLEE. 2 NYQALDAD 3 KRSKLVLP. 3 RTPRTPAS
130 SAAQSLAVAI PL(190 HPI 250 SLIGHISTVR GVI 310 DVLVTCSRDS TAF 370 4GKTRVTLIN HKF 430 NSDGULVSG ADD	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL 440 NGTMHLWD	TAPSGSETRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG 450 WRTGYNFORV	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 SPDNIKQWKF 460 HAAVOPGSID	230 TGSADRTIKI 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS 470 SESGIFACAF	WDLASGKLKL 300 VYGLDLHPTI 360 DTTIRLWDLV 420 GHNAIINTLT 480 DOSESRLTA	RRLKPGEIDP 190 RLAALQKRRE 250 KLRQQDLDGE 310 QISDAELQEV 370 RILQEAQNIM	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA 380 ALTNVDTPLK	PIDMDEDELE 210 KRKRKRGVDY 270 KKDKQHLKRK 330 RQTAEESGIT 390 GGLNTPLHES	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAIL 340 NSASSTLLSE 400 DFSGVTPQRQ	NTQGKKAKRK 230 ALGFYDTSEE 290 QTSGVSEFTK 350 YNVTNNSVAL 410 VVQTPNTVLS	AREKQLEE 2 NYQALDAD 3 KRSKLVLP 3 RTPRTPAS 4 TPFRTPSN
130 130 190 190 190 190 190 190 190 19	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL 440 NGTMHLWD 500	TAPSGSETRH 210 SGHLGWVRCT 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG 450 WRTGYNFORV 510	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 SPDNIKQWKF 460 HAAVOPGSLD	230 TGSADRTIKI 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS 470 SESGIFACAF	WDLASGKLKL 300 VYGLDLHPTI 360 DTTIRLWDLV 420 GHNAIINTLT 480 DOSESRLLTA	RKLKFGEIDP 190 RLAALQKRRE 250 KLRQDLDGE 310 QISDAELQEV 370 RILQEAQNIM 430 FCITPDCOM	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA 380 ALTNVDTPLK 440 DEEDUINGTO	PIDMDEDELE 210 KRKRKRGVDY 270 KKDKQHLKRK 330 RQTAEESGIT 390 GGLNTPLHES 450 PTPLPDLWT	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAIL 340 NSASSTLLSE 400 DFSGVTPQRQ 460 NPEDGMDYZZ	NTQGKKAKRK 230 ALGFYDTSEE 290 QTSGVSEFTK 350 YNVTNNSVAL 410 VVQTPNTVLS 470 DSSVUVOTT	AREKQLEE. 2 NYQALDAD 3 KRSKLVLP. 3 RTPRTPAS: 4 TPFRTPSN 4 FSEPHILE.
130 SAAQSLAVAL PL4 190 KAPTMPKPQW HPJ 250 SLTGHLSTVR GVJ 310 DVLVTCSRDS TAF 370 AGKTRVTLTN HKF 430 /NSDGVLVSG ADP 490 EADKTIKVYR EDI	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL 440 NGTMHLWD 500 DTATEETH	TAPSGEFIRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG 450 WRTGYNFORV 510 PVSWKPEIIK	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 SPDNIKQWKF 460 HAAVOPGSLD RKRF	230 TGSADRTIKT 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS 470 SESGIFACAF	WDLASGKLKL 300 VYGLDLHPTI 360 DTTIRLWDLV 420 GHNAIINTLT 480 DOSESRLLTA	RRLAFGEIDP 190 RLAALQKRRE 250 KLRQQDLDGE 310 QISDAELQEV 370 RILQEAQNIM 420 EGLTPRSGTT 490	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA 380 ALTNVDTPLK 440 PKPVINSTPG 500	PIDMDEDELE 210 KRKRKRGVDY 270 KKDKQHLKRK 330 GQTAEESGIT 390 GGLNTPLHES 450 RTPLRDKLNT 510	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAII 340 NSASSTLLSE 400 DFSGVTPQRQ 460 NPEDGMADYS 520	NTQGKKAKRK 230 ALGFYDTSEE 290 QTSGVSEFTK 350 YNVTNNSVAL 410 VVQTPNTVLS 470 DPSYVKQMER 530	AREKQLEE 2 NYQALDAD 3 KRSKLVLP 3 RTPRTPAS 4 TPFRTPSN 4 ESREHLRL 5
LIJU SAAQSLAVAL PL4 190 250 SLTGHISTVR GVJ 310 DVLVTCSRDS TAF 370 AGKTRVTLTN HK 430 VNSDGVLVSG ADA 490 EADKTIKVYR EDI	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL 440 NGTMHLWD 500 DTATEETH	TAPSGEIRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG 450 WRTGYNFORV 510 PVSWKPEIIK	220 AVEPGNQWFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 SPDNIKQWKF 460 HAAVOPGSLD RKRF	230 TGSADRTIKI 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS 470 SESGIFACAF	WDLASGKIKL 300 VYGLDLHPTI 360 DTTIRLWDLV GHNAIINTLT 480 DOSESRLLTA	RKLRPGEIDP 190 RLAALQXRE 250 KLRQQDLDGE 310 QISDALQEV 370 RILQEAQNIM 430 EGLTPPSGTT 490 LGLPAPKNDP	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA 380 ALTNVDTPLK 440 PKPVINSTPG 500 EIVLPENAEK	PIDMDEDELĒ 210 KRRKRGVDY X70 KKDKQHLKRK 330 GQINTPLHES 450 RTPLRDRINT 510 ELEEREIDDT	MLSEARARLA 220 NAEIPFEKKP 280 KESDLPSAIL NSASSTLLSE 400 DFSGVTPORQ 460 NPEDGMADYS 520 YIEDAADVDA	NTQGKKAKRĀ 230 ALGPYDTSEĒ 290 QTSGVSEFTK 350 YNVTNNSVAL 410 VVQTPNTVLS 470 DPSYVKQMĒ RKQAIRDAĒR	AREKQLEE 2 NYQALDAD 3 KRSKLVLP. 3 RTPRTPAS: 4 TPFRTPSN 4 ESREHLRL 5 VKEMKRMH
130 130 130 130 130 130 130 131 131 131	QTKADANR 200 PWKLYRVI 260 IVSTRSPY 320 RIWDVRTK 380 KSVRAVVL 440 NGTMHLWD 500 DTATEETH	TAPSOBETRH 210 SGHLGWVRCI 270 LFSCGEDKQV 330 ASVHTLSGHT 390 HPRHYTFASG 450 WRTGYNFORV 510 PVSWKPEIIK SPF2	220 AVEPGNQMFV 280 KCWDLEYNKV 340 NAVATVRCQA 400 HAAVOPGSLD RKRF 77-225	230 TGSADRTIKT 290 IRHYHGHLSA 350 AEPQIITGSH 410 PDGSFIQNLS 470 SESGIFACAF	WDLASGKIKI 300 VYGLDHPTI 360 DTTIRIMDLY GHNAIINTLT 480 DOSESRLLTA	RKLKPGEIDP 190 RLAALQKRE 250 KLRQQDLDCG 310 QISDAELQEV 370 RILQEAQNLM EGLTPRSGT 430 EGLTPRSGT 490 LGLPAPRNDF 550 VQKULRPSE	NPETKPARPD 200 LRAAGIEIQK 260 LRSEKEGRDR 320 VKVGQASEIA 380 ALTNVOTPLK 440 PKPVINSTPG 500 EIVLPENAEK 500 VNETILRPLN	PIDMDEDELE 210 200 270 270 KKKKQHLKRK 330 RQTAEESGIT 390 GGLNTLHES 450 8TPLRDKLNI 510 ELEEREIDDT 510 VEPPLTDLQK	MLSEARARLÄ 220 NAEIPFEKKP 280 KESDLPSAIL 340 NSASSTLLSE 400 DFSGVTPORQ 460 NPEDGMADVS 520 YIEDAADVDA 580 SEELIKKEMI	NTQGKKAKRR 230 290 QTGGVSEFTK 350 YNVTNNSVAL 410 VVQTPNTVIS 470 DPSYVKQMER 530 RKQAIRDAER 590 TMLHYDLLHH	AREKQLEE 2 NYQALDAD 3 KRSKLVLP 3 RTPRTPAS 4 TPFRTPSN 4 ESREHLRL 5 VKEMKRMH 6 PYEPSGNK
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Exhaustive mass spectrometric analyses of hPrp19/CDC5L complex proteins after limited proteolysis and subsequent trypsin digestion. The peptides identified via MALDI-MS/MS are highlighted red. The presence of the N-terminal peptide of CDC5L (482-802), indicated with a grey box, was verified by N-terminal Edman sequencing.

Supplementary references

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