Data collection								
Data set	Se1 peak	Se1 inflection	Se1 remote	Se2 peak	Se2 inflection	Se2 remote		
Data Collection								
Wavelength (Å)	0.9791	0.9793	0.9641	0.9791	0.9792	0.9641		
Resolution (Å)	50-2.70	50-2.70	50-2.70	50-2.10	50-2.10	50-2.10		
Outer shell (Å)	2.80-2.70	2.80-2.70	2.80-2.70	2.18-2.10	2.18-2.10	2.18-2.10		
Unique reflections	28,053	28,202	28,381	58,588	58,671	58,571		
Redundancy	6.5	7.0	7.0	6.4	5.1	4.9		
I/σ (outer shell)	12.6 (4.2)	12.2 (3.6)	10.9 (2.7)	11.0 (2.8)	9.4 (2.1)	8.9 (1.8)		
Completeness (%) (outer shell)	99.9 (100.0)	99.9 (100.0)	99.9 (100.0)	99.3 (95.4)	98.8 (91.3)	98.6 (90.2)		
R _{sym} (outer shell)	0.102 (0.302)	0.097 (0.370)	0.108 (0.513)	0.100 (0.376)	0.093 (0.426)	0.093 (0.479)		
Figure of Merit				0.776				
(50-2.7 Å)								
<u>Refinement</u>								
Resolution (Å)				50-2.1				
Reflections (work/free	2)			55,430/2,931				
Data completeness (we	ork + free)			98.8%				
No. of atoms (waters)				7,191 (133)				
R-work				0.212				
R-free				0.259				
RMSD bond lengths (A	Å)			0.0084				
RMSD bond angles (°))			1.52				
RMSD B-factors over	bonds			4.5				
Average B-factor ($Å^2$)		36.8						
Ramachandran Plot								
within favored (%	6)			97.4				
within allowed (%	6)			99.2				
outliers (%)				0.8				

Supplementary Table 1. Statistics of data collection and structure refinement of subcomplex I.

 $R_{sym} = \Sigma_h \Sigma_i |I_{h,i} - I_h| / \Sigma_h \Sigma_i I_{h,i}$, where I_h is the mean intensity of the *i* observations of symmetry related reflections of *h*. $R = \sum |F_{obs} - F_{calc}| / \sum F_{obs}$, where $F_{obs} = F_P$, and F_{calc} is the calculated protein structure factor from the atomic model (R_{free} was calculated with 5% of the reflections). R.m.s.d. in bond lengths and angles are the deviations from ideal values, and the r.m.s.d. deviation in B factors is calculated between bonded atoms. Ramachandran plots were calculated using the program Molprobity, which uses a tougher standard than Procheck.

Data Collection				
Data set	PAN nucleotidase	Core Particle		
Wavelength (Å)	1.10	1.08		
Resolution (Å)	50-3.10	50-4.10		
Outer shell (Å)	3.21-3.10	4.25-4.10		
Unique reflections	22,762	54,076		
Redundancy	6.6	4.8		
I/σ (outer shell)	19.7 (3.1)	9.5 (3.5)		
Completeness (%) (outer shell)	99.8 (100.0)	99.8 (100.0)		
R _{sym} (outer shell)	0.084 (0.523)	0.126 (0.488)		
Refinement				
Resolution (Å)	50-3.1	50-4.1		
Reflections (work/free)	19,605/1,092	51,010/2,737		
Completeness (%, work+free)	95.8	99.8		
No. of atoms	6,162	93,324		
R-work	0.221	0.265		
R-free	0.277	0.321		
RMSD bond lengths (Å)	0.011	0.009		
RMSD bond angles (°)	1.43	1.26		
RMSD B-factors over bonds	1.0	n/a		
Average B-factor ($Å^2$)	101.1	145.0		
Ramachandran Plot				
Within favored (%)	89.3	72.5		
Within allowed (%)	98.3	93.3		

Supplementary Table 2. Summary of data collection and structure refinement for the nucleotidase domain and the CP.

 $R_{sym} = \Sigma_h \Sigma_i |I_{h,i} - I_h| / \Sigma_h \Sigma_i I_{h,i}$, where I_h is the mean intensity of the *i* observations of symmetry related reflections of *h*. $R = \sum |F_{obs} - F_{calc}| / \sum F_{obs}$, where $F_{obs} = F_P$, and F_{calc} is the calculated protein structure factor from the atomic model (R_{free} was calculated with 5% of the reflections). R.m.s.d. in bond lengths and angles are the deviations from ideal values, and the r.m.s.d. deviation in B factors is calculated between bonded atoms. Ramachandran plots were calculated using the program Molprobity, which uses a tougher standard than Procheck.



Supplementary Figure 1 The PAN regulatory particle consists of two

subcomplexes. The PAN regulatory particle was eluted from gel filtration as a large complex, with an apparent molecular mass in excess of 500-kDa (red chromatogram). Limited proteolysis of the PAN regulatory particle generates two subcomplexes: I and II. Subcomplex I contains amino acids 74-150 and is stable on gel filtration (green chromatogram). Subcomplex II contains residues 155-430 and appears to dissociate on gel filtration (blue chromatogram). Boxed bands show coomassie-stained SDS-PAGE gel of the fractions from the corresponding gel filtration runs on the left. Gel filtration was performed using a Superdex 200 column (10/30, GE Healthcare). The injection volume was 0.5 ml for each gel filtration run. Concentrations of the protein samples prior to injection were: 10 mg/ml for full-length PAN and PAN (74-150), and 20 mg/ml for PAN (155-430).



Supplementary Figure 2 The interdimer interface within subcomplex I. (A) Schematic representation of the interdimer interface between molecules B and C. Compared to the A-B interface, the interface between molecules B and C is considerably smaller, involving 820 Å² surface area. Formation of subcomplex I involves three interfaces of the A-B type and three interfaces of the B-C type. Together, these interactions involve 42 H-bonds and 9100 Å² surface area in subcomplex I of the PAN regulatory complex. (B) A stereo view of the interdimer interface. Side chains from molecules B and C are colored blue and magenta, respectively. H-bonds are represented by red dashed lines. There are 4 backbone H-bonds and a number of van der Waals contacts.



Supplementary Figure 3 Schematic representation of the three molecules of the PAN nucleotidase domain in each asymmetric unit. These three molecules are colored green, magenta, and cyan. The bound ADP molecules are colored red. Two perpendicular views are shown.



		Cis/Tra	ans Pro	5	999			R134	
						-	::	1	
ScRpt1	APSHLWD.	IMGURQRL	GEEHPL(VARCI	KII	eN ges de tittinnNSGN SNSNSNQQS TD an Eddeda k y	VINLKQIAKF	VVGLGERVSPTD-IEEGMRVGV	137
SpRpt1 CaRpt1	APISFWD	JAAD RORM	BEOPLO	VARCI	KII KIT	NBOSA EKNAM	VINLKQIAKE	VVSLGERVSPTD-IEEGMRVGC	146
K1Rpt1	APSHLWD	IVGO RORL	S EQPL	VARCI	KIII	A BEPORS CNALOG DADGE GEARAAAAAAAAAAAAAA	VINLKQIAKF	VVGLGERVSPTD-IEEGMRVGV	184
PSRpt1 DhRpt1	APPHLND	VMGD KORM	SEEOPL	VARCI	K I I	ATTP - A QAGA LQNA DNK S KY ATNPNPOAGLLONA DNK S KY	VINIKQIAKF	VVGLGERVSPTD-IEEGMRVGV VVGLGERVSPTD-IEEGMRVGV	155
Y1Rpt1	APHHLMD'	LOWD KORM	SEENPL	VARCI	KII	TAEDPGKSKV	VINVKQIAKF	VVSLGERVSPTD-IEEGMRVGV	145
DrRpt1	APPALNDI	LAADKOTL	QSEQPL	VARCI	KII	ADSEDPKY	IINVKQFAKF	VVDLSDQVAPTD-IEEGMRVGV	142
XtRpt1 AtRpt1	APPALNDI	LAAL KOTL	QSEQPL(VARCE	KIIN	ADS EDPKM	IINVKQFAKF VINVKOIAKF	VVDLSDQVAPTD - IEEGMRVGV	142
CeRpt1	APPALND	TAADKQAM	OEOPL	VARCI	KIII	SDKHDPRY	LINVKQFAKF	VVDLADSVAPTD-IEEGMRVGV	144
DmRpt1 MmRpt1	APPALNDI	LAADKQIL	OSEOPL	VARC	KIIN	A	IINVKQFAKF IINVKQFAKF	VVDLADSVAPTD-IEEGMRVGV	142
RnRpt1	APPALNDI	LAADKOTL	QSEQPL	VARCI	KIIN	ADSEDPKY	I INVKQFAKF	VVDLSDQVAPTD-IEEGMRVGV	142
ScRpt2	KQE	SEKKOLEE	IRGNPLS	GIGTLE	BII	DDHA	IVTEPTMPDY	TVSILSFVDKEL-LEPGCSVLL	149
SpRpt2 CaRpt2	RQ	ZERNRVDE	LRGTPMS	IGTLE		DDHA DDHA	IVS - TAGPEN	VSIMSFVDKDM-LEPGCSVLL	159
K1Rpt2	KQE	SEKKOLDD	IRGTPLS	IGTLE	EIVI	DDHA	IVTSPTTPD	YVSILSFVDKEL-LEPGCSVLL	146
DhRpt2	KQAI	SEREKVDE	LRGIPM	IGTLE	BII	DDHA DDHA	IVS STACSE IVS STACSE	TVSIMSFVDKGL-LEPSCSVLL	146
Y1Rpt2	SKVAI	SERSKUDT	LRGSPM	VENLE	BII	DDHA DDHA	IVSSTS GPEY	YVSIMSFVDKDL-LEPGCSVLL	148
DrRpt2	KQE	BERSKUDD	LRGTPMS	VGTLE	RIII	DNHA	IVSTSVESEN	YVSILSFVDKDL-LEPGCSVLL	152
AtRpt2	KAE	ZERSKVDD	LRGTPMS	VGTLE VGNLE	BLI	DNHA ENHA	IVS IS VOSEH IVS SS VOPEN	YVGILSFVDKDL-LEPGCSVLL YVGILSFVDKDQ-LEPGCSILM	152
CeRpt2	RQE	SERAK VDE	LRGTPM	VGSLE	BII	DQHA	IVSTNVGSER	IVN IMS FVD KEQ-LEPGCSVLL	155
MmRpt2	KQE	EERSKVDD	LRGTPM	VGTLE	BII	DNHA DNHA	IVS TE VOS EN	VSILSFVDKDQ-LEPGCSVLL	151
RnRpt2 HsRpt2	KQE	REPSKUDD	LRGTPMS	VGTLE	BII	DNHA DNHA	IVSTSVGSEN	YVSILSFVDKDL-LEPGCSVLL	152
ScRpt3	EL KI	RAQUEVKR	IOSVPL	IGOPI	RPI	QNTQ	IVSSTTEMST	VVRILSTLDREL-LKPSMSVAL	139
SpRpt3 CaRpt3	ELII	RACEEVKR	IKSVPL	ICOPI	EPI	QNTA ENTG	IVEST TESN	VVRILSTLOREL-LKPSASVAL	101
K1Rpt3	EL LI	RAQEEVKR	IOSVPL	I I GOFL	EPII	ENTO	IVS ST TOMS	VVRILSTLDREL-LKPSTSVAL	139
DhRpt3	EL VI	RAQUEVER	IKSVPL	IGOFI	EPI	EN10 ENTG	IVSSITCSNI	VVRILSTLOREL-LKPSSSVAL	121
V1Rpt3 DdRpt3	EL VI	ADDEEVER	ISVPL	IGOLI	EPII	QQTG 8	IVAST TOSNY	CVPILSTLEREL-LKPSSSVAL	115
DrRpt3	EFL	HAQLEVKR	IOSIPL	/ IGOPI	EAVI	QNTA	IVESTTESNY	YVRILSTIDREL-LKPNASVAL	132
XtRpt3 AtRpt3	EFL	HAQEEVKR RAOEEVKR	IOSVPL	IGOPI	EAVI EMVI	QNTA ONIMG	IVEST TESN	VRILSTIDREL-LKPNASVAL VVRILSTINREL-LKPSASVAL	134
CeRpt3	ELL	AQUEVER	IOSVPL	IGOFL	HAV	QNHA	IVCST TCSNY	YVRVLSILDREL-LKPGCSVAL	129
MmRpt3	EFL	HAQHEVKR	ISIPL	IGOPI	RAVI	QNIG	IVESTTESNY	YVRILSTIDREL-LKPNASVAL	132
RnRpt3 HsRpt3	EFL	HAOREVKR	IOSIPL	I I I I I I I I I I I I I I I I I I I	RAVI	QNTA 0	IVEST TESNY	YVRILSTIDREL-LKPNASVAL	132
ScRpt4	EKLTDI	KTENDIKA	LOSICO	IGEVM	KELS	EEKY	IVKASS GPRY	IVGVRNSVDRSK-LKKGVRVTL	149
CaRpt4	DKKUDI	KTENDIKA	LOSVGO	IGEVI	KOL	8ERF DERF	IVKASSOPRI	IVGCRNTIKKEN-LKNGVRVSL	139
K1Rpt4	EAEYE	ATEQDIKA	LOSICOL	IGEV	KELS	EEKY	IVKASSGPRI	IVGVRNSVDRSK-LKKGVRVTL	145
DhRpt4	DSDYDI	KTENDIKA	LOSVGO	IGEVI	KOL	DERP	IVKASSGPRY	IVGCRNTIKKES - LKNGVRVSL	126
Y1Rpt4 DdRpt4	ERKFDI KKDFOI	KTEDDIKA KTEDHIKT	LOSVEQI	IGEVI	REL	EERF EERF	IVKASNOPR	IVGCRSSIKKEK-LLQGVRVSL VVRCANYODKAHLLVPGARVTL	121
DrRpt4	TKQVE	KSENDLKA	LOSVGQI	VGEVL	KQLI	EEKF	IVKATNGPRY	VVGCRRQLDKSK-LKPGTRVAL	100
AtRpt4	KKEPN	KTEDDLKS	LOSVGO	IGEVI	RPL	NERL	IVKASSGPRY	VVGCRSKVDKEK-LTSGTRVVL	106
CeRpt4 DmRpt4	TKQFDI TKLADI	(SENDIKS KSENDIKA		VGEVI	KOLS	EEKF	IVKATNOPRY	VVGCRRSINKEE-LKQGTRVSL	117
MmRpt4	TKQUE	KSENDLKA	LOSVOO	VGEVI	KOL 1	EEKP	IVKATNOPR	VVGCRROLDKSK-LKPGTRVAL	100
HsRpt4	TKOTE	IS ENDLKA		VGEVI	KOLI	EEKb R	TVKALNOPR	VVGCRRQLDKSK-LKPGTRVAL	114
ScRpt5	VMLEKIKI	ONKEKIKN	NROLPH	VANV	EVMI	MNEIEDKERSESTTOGGNVNLDNTAVGKAA	VVKTS SROTV	FLPMVGLVDPDK-LKPNDLVGV	148
CaRpt5	VMLERIK	DNOEKINN	NKQLPI	VGNVV	LLA	LDADKRASECGANIDIDAARAGKSA	VIKTS TROTI	FLPMIGLVDPSK-LKPNDLIGV	167
PSRpt5	VMLERIKI	DNOEKINN	NKOLPYI	VANV	ELL	LDAE	VIKTSTROTI	FLPLIGLVDPAK-LKPNDLIGV	146
DhRpt5	VMLERIK	DNORK INN	NKOLPTI	VGNV	ELLI	LSAEKEASECGANVULDATRSGKSA	VIKTS TROTI	FLPLIGLVDPAN - LKPNDLIGV	140
DdRpt5	SIQKRIK	ENNUKLQV	NTQLPHI	VANV	BII	MVLDGBTQPSKCV	VVKAS TROTI	FLAYPGIVDVDK-LRPGDLVGI	135
DrRpt5 XtRpt5	AMKDKIKI	ENSEKIKV	NKTLPH	VSNVI	RLL	VDPNDQEEDGANIDLDSQRKGKCA VDPNDOEEDGANIDLDSORKGKCA	VIKTS TROTY	FLPVIGLVDAEK-LKPGDLVGV	118
AtRpt5	SYKEKIKI	ENQ. KIKL	NKQL <mark>P</mark> II	VGNIV	BIL	MNPEDDAEEDGANIDLDSÖRKGKCV	VLKTE TRQTI	PLPVVGLVDPDS - LKPGDLVGV	139
DmRpt5	AQNEKIKI	DNTEKIKV	NKTLPI	VSNVI	RLL	VDPQRBEDDGSVTVLDNQRKCA	VIKTSTRQAT	FLPVIGLVDAEK-LKPGDLVGV	142
MmRpt5 PoPot5	AMKDKIKI	ENSEKIKU	NKTLPII	VSNVI	FLL		VIKTS TROTY	FLPVIGLVDAEK-LKPGDLVGV	156
HSRpt5	AMKDETE	INSEKTAN	NETLEN	USNU	RLL	VILDNI	VINTETROT	PLPVICLUBARK - L.KPCDL.VCV	153
ScRpt6	N DKVRI N ARVRI	LLREEIOL	LOEPGS	VGEVI	KINS	КККУ ПККУ	LVKVQPECKI	VVDISPDIEIKE-IKPNIRVAL	115
CaRpt6	NNKVR	LKDELKL	LOEPGS	VGEV	KVM	ГККУ	LVKIHPECKP	IVNVTKDIOVKK-LTPSIRVCL	111
PsRpt6	NNKVR	LKDELRL	LOEPGS	VGEV	KVM	ГККЛ ККА	LVKIHPEGKY	IVNVTKDILIKK-LTPSIRVCL	112
DhRpt6 Y1Rpt6	NNKVR NTKVR)LKDELRL LLKDELHV	DEPGS	VGEVI	K VMC	ККХУ ГККХ	LVKVHPECKY	IVNISKDIDIKK-LTPSLRVCL	111
DdRpt6	NNRVRI	ALKEELQL	LINPOS	VAEV	KLM	кŇКУ	LVKVNPEGKF	VVDIDPTVDIAK-LTPSTRAAL	112
XtRpt6	NAKVRI	LLREELOL	LOEOGS	VGEV	RAM	K	LVKVHPEGKP	VVDVDKNIDIND-VTPNCRVAL	116
AtRpt6	NSRVRI	MLR ELQL	LOEPGS	VGEV	KVM	KNKV	LVKVHPECKT	VVDIDKSIDITK-LTPSTRVAL	128
DmRpt6	NAKVRI	MLRBELQL	LQEQGS	VGEV	KPM	KKKA	LVKVHPECKF	VVDLDKNIDIND-VTPNCRVAL	115
MmRpt6 RnRpt6	NAKVRI NAKVRI	LLREELQL	DECCS	VGEV	RAM	K	LVKVHPECKP	VVDVDKNIDIND-VTPNCRVAL VVDVDKNIDIND-VTPNCRVAL	116
HsRpt6	NAKVRI	LLREELQL	LOEQGS	VGEV	RAM	кккл	LVKVHPECKP	VVDVDKNI DIND-VTPNCEVAL	116

		_							
MIPAN	NOOTLTWDVLPEN	KDY RA KAMEVOR PNVR	DIGGLEKOMO	BIREVVELPLKHP	ELPEKVGIEPPI	GILLYGPPOTC	KTLLAKA VA TETNA	FIRVVGBELVKKPIGE	247
ScRpt1 SpRpt1	DRSKINIELPLPPR DRNKIAIOLPLPPK	IDPSVTMMTVEEKPEVTYS IDPSVTMMOVEEKPEVTYS	SDVGGCKDOIE	KLREVVELPLLSP RLREVVELPLLSP	RFATLGI DPPI	KGILLYGPPGTG	KTLCARAVANRTDA KTLCARAVANRTDA	FIRVIGSELVOKTVGE	296 256
CaRpt1	DRHKTEIOLPLPPR	IDPSVTMMTVEEKPDVTTS	DVGGCKEOIE	KLREVVELPLLSP	REVELGIDEP	KGILL YGPPOTG	KTLCARAVANETDA	FIRVIGSELVOFIVCE	263
PsRpt1	DROK EIQLPLPPR	IDPSVTMMTVEEKPDVTYS	DVGGCKEQIE	KLREVVELPLLSP	RFVKLGIDPP	KGILLIGPPOTG	KTLCA BAVANETDA	FIRVIGERLVOKIVGE	265
DhRpt1 V1Rpt1	DROKYELQLPLPPR DRSKYOLOLPLPPR	IDPSVTMMTVERKPOVTYS		KLREVVELPLLSP	RFVKLGIDPP	GILL GPPGTG	KTLCARAVANETDA	FIRVIGSELVOKYVCE	265
DdRpt1	DRNKTQIQIPLPPK	IDASVTMMQVEBKPDITT	UV GGCKEOIE	KLREVVEMPLLHP	KFVNLGIDPP	KGVLMT GPPGTG	KTLCARA VANETDA	FVRVIGSELVOKTVGE	247
DrRpt1 XtRpt1	DRNK YOIH IPLPPK	IDPTVTMMOVEEKPDVTYS IDPTVTMMOVEEKPDVTYS	DVGGCKECIE	KLREVVETPLLEP	REVNLGIEPPI	KGVLLPGPPGTG	KTLCARA VANRTDAG	FIRVIGSELVOKIVGE	252 252
AtRpt1 CePpt1	DRNKYQIQIPLPPK	IDPSVTMMTVEEKPOVTI		KMR HVVEL PMLHP	KPVKLGIDPP	GVLC GPPGTG	KTLLARAVANETDAC	FIRVIGERLVOKTVCE	245
DmRpt1	DRNK QIHIPLPPK	IDPTVTMMQVEDKPDVTY	DVGGCKEQIE	KLREVVETPLLHP	KFVNLGIEPP	KGVLLPGPPGTG	KTLCA HA VANRTDAG	FIRVIGSELVOKYVGE	254
MmRpt1 RnRpt1	DRNK QIHIPLPPK DRNK OIHIPLPPK	IDPTVTMMOVEEKPOVTYS	DVGGCKEOIE	KLREVVETPLLHP	RFVNLGI EPP	KGVLLPGPPGTG	KTLCARAVANETDAG	FIRVIGERLVOKTVGE	252 252
HsRpt1	DRNK YOIH IPLPPK	IDPTVTMMOVERKPDVTYS	DVGGCKEOIE	KLREVVETPLLEP	REVNLGIEPPI	KGVLLFGPPGTG	KTLCA RAVANET DAG	FIRVIGSELVOKYVGE	252
SpRpt2	HHKAMS IVGLLLD	TDPMINVMKLDKAPTES 1	DIGGLESOIO	EIKEAVELPLTHP	ELYEEMGIKPP	KGVILYGAPGTG	KTLLAKA VANQTSA	FLRVVGSELIOKYLGD	268
CaRpt2 K1Rpt2	HHKTVAVVGVLODO HHKTMSVVGVLODO	ADPMVS VMKLDKS PTES D ADPMVS VMKMDKS PTEN IS	DIGGLESOIO	EIKENVELPLTHP	EEMGIKPPI	KGVIL GAPGIG	KTLLAKA VANQTSA	FLRIVGSELIOKILGD	263 256
PsRpt2	HHKTVSVVGVLOD	ADPMVS VMKLDKS PTES 13	DI GGLESOIO	EIKEAVELPLTHP	ELTEEMGIKPP	GVIL GAPGTG	KTLLA KA VANOTSA	FLR IVGSELIOKYLGD	256
Y1Rpt2	HHKTVSVVGVLOD	ADPMVS VMKLDKAPTES I	DIGGLESOIO	EIKESVELPLTHP	ELTEEMGIKPPI	KOVIL YGAPOTG	KTLLAKA VANOTSA	FLRIVGSELIOKYLGD	259
DdRpt2 DrRpt2	NNKTESVVGVIDGE NHKVHAVIGVLMDD	TUPLVTVMKVEKAPTES (S	DIGGLEAOVO	EIKESVELPLTHP	EENGIKPPI	GVIL GEPCIC	KTLLAKA VANQTSA KTLLAKA VANQTSA	FLRVVGSELIOKYLGD	261 262
XtRpt2	NHKVHAVI GVLMDD	TOPLVTVMKVEKAPOETUS	DI GGLENOIO	EIKESVELPLTHP	ETTEEMGI KPP)	KGVIL GPPGTG	KTLLAKAVANOTSA	FLRVVGSELIOKYLGD	262
CeRpt2	NHKNHAVIGVLSD	TDPMVS VMKLEKAPQETTS	DVGGLDQQIQ	EIKEAVELPLTHP	ETYEEMGIRPPI	KGVILIGCPGTG	KTLLAKAVANQTSA	FLRIVGSELIOKYLGD	265
DmRpt2 MmRpt2	NHKVHAVVGVLSDO	TOPMVTVMKLEKAPOET () TOPLVTVMKVEKAPOET ()	DIGGLDTQIQ DIGGLDNOIO	EIKESVELPLTHP	EEMGIKPP	GVIL GPPGIG	KTLLAKA VANOTSA	FLRVVGSELICKYLGD	261
RnRpt2	NHKVHAVI GVLMDD	TOPLVTVMKVEKAPOETV3	DIGGLINOIO	EIKESVELPLTHP	EEMGIKPP	KGVILYGPPOTG	KTLLA KAVANOTSA	FLRVVGSELIOKYLGD	262
ScRpt3	HRHENALVDILPPD	SISSIS VMGENEK POVTO	DVGGLDMOKO	BIREAVELPLVQA	EPIGICIPPI	ROVLLYGPPOTG	KTMLVKAVANSTKA	FIRVNGSEFVHKILGE	262
SpRpt3 CaRpt3	QRHSNALVDILPPS HRHSNALVDILPPS	AUSSISML RPDER PDVS 73 AUSSIS IVGEDOK PDVT 73	DVGGLDVOKO	EVREAVEL PLTQG	ROIGIDPPI	RGVLLYGPPGTG	KTMLVKAVANSTAAN KTMLVKAVANSTAA	FIRVVGSEFVORLGE	211 232
K1Rpt3	HRHENALVDILPPD	SISSIS IMAANEKPUVTI	DVGGLDMOKO	BIREAVELPLVQA	DLXQQIGIDPPI	REVILLIGPPOT	KTMLVKAVANATEA	FIRVNGSEFVHKYLCE	249
DhRpt3	HRHSNALVDTLPPE	ADSSISIVGDEOKPOVID	DVGGLDMOKO	RIREAVELPLIQGI	DLISQIGIDPPI	RGVLL GPPGTG	KTMLV KA VANSE TAS	FIRINGSEFVORTLGE	237
Y1Rpt3 DdRpt3	HRHSNALVDILPPR ORHSNALVDILPPR	AUSSIAML RPDEK PUVSIA	DVGGLDIOKQ	EIREAVELPLTOF	KOIGIDPPI	RGVLLFGPPGTG	KTMLVKAVANNTTA	FIRVVGSRFVQFILGE	225
DrRpt3	HKHENALVDVLPPE	ADSSIMMLTEDOKPDVLTS	DIGGMDIOKO	EVREAVELPLTHE	LYKOIGIDPPI	IGVLMI GPPGCG	KTMLAKA VAHHT TAS	FIRVVGSEFVOKILGE	242
AtRpt3	HRHSNALVDVLPPE	AUSSISLLSQSEKPDVS 1	DIGGCDICKO	BIREAVELPLTH	KOIGIDPPI	RGVLLYGPPGCG	KTMLA KA VANHT TAS	FIRVVGSEFVQKYLGE	232
CeRpt3 DmRpt3	HKYSNALVDVLPPE HKHSNALVDVLPPE	ADSSIGNL RPDEK PDIST ADSSISNLOPDEK PDVST	DIGGLIDMOKO	EVREAVELPLTHC	I QOIGIDPPI	RGVLMTGPPGCG	KTMLAKAVAANTAAN KTMLAKAVAHHTTAS	FIRVVGSEFVQKYLCE	239 237
MmRpt3	HKHSNALVDVLPPE	ALSSIMML TSDOKPDVM		EVREAVELPLTHP	KOIGIDPPI	RGVLMT GPPGCG	KTMLAKAVAHHTTA	FIRVVGSEFVOKTLGE	242
HsRpt3	HKHSNALVDVLPPE	ALSSIMML TEDOKPOVMI	DIGGMDICKO	EVREAVELPLTHE	KÖIGIDPPI	ROVIMYGPPGCG	KTMLA KA VA HHTTA	FIRVVGSEFVQKYLCE	242
ScRpt4 SpRpt4	DMTTLTIMR ILPRE	VDPLVYNMSIEDPGDISP3	GIGGLIEGIR GVGGLNEGIR	BLREVIELPLKNP	LP LRVGI KPP	KGVLL GPPGTG	KTLLARA VAATIGAN	FLEVVSSAIVDEIGE	258
CaRpt4 K1Rpt4	DMTTLT IMR ILPRE	VDPLVYNMTTFEPGEISF1 TDPLVYNMTTFEOGEISF1	GIGGLTEOIR	BLREVIELPLKNP	ELFTRVGI KPP	COVLL GPPGTG	KTLLAKAVAATIGAN	FIFSPASAIVDEYICE	249 255
PsRpt4	DMTTLT IMR ILPRE	VDPLVYNMTTFEPGEISF1	GIGGLTEOIR	ELREVI ELPLKNP	ELFHRVGI KPP)	GVLLYGPPOT	KTLLA KA VAATI GAN	FIFSPASA IVDEYIGE	237
Y1Rpt4	DMTTLT IMR ILPRE	VDPLVYNMTTFEPGELTFS	GIGGLNEOIR	ELREVIEL PLKNP	LFLRVGIKSP	KGVLL GPPGIG	KTLLA KA VAATIGAN	FIFSPASAIVDEVICE	236
DdRpt4 DrRpt4	DLTTLTILKILPR DMTTLTIMRMLPR	VDPIIFNMTAESPGSVSI VDPLVYNMSHEDPGSVSI	EIGGLSNOIR	ELREVVELPLMIP	LFIRVGIKAP	CULTGPPGTG	KTLLARA IASNLEAN	FLKVVSEA IVDKYIGE	214 210
XtRpt4	DMTTLT IMR ILPR	VDPLVYNMSHEDPGNVSY	EIGGLSEOIR	ELREVI ELPLINP	LFORVGI IPP)	GCLL GPPGTG	KTLLA RA VASQLDC	IFL KVVSSSIVDKYIGE	210
CeRpt4	DMTTLT IMRQLPRE	VDPLVYKMSHEDPGNIS	DVGGLAEOIR	BLREVVELPLINP	LPKRVGI TPP	KGCLLPGPPGTG	KTLLA RA VASQLDC	IFLKVVSSAIILKIIGE	216
DmRpt4 MmRpt4	DMTTLT IMRYLPRE	VDPLVYNMSHEDPGDVTYS	CALGGLTDOIR	ELREVIELPLLNPI	ELF LRVGI TPPI	GCLL GPPGTG	KTLLARA VASQLDAN	FLKVVSSA IVDKYIGE	211 210
RnRpt4	DMTTLT IMR YLPRE	VDPLVYNMSHEDPONVSYS	EIGGLSEOIR	ELREVIELPLINP	LFORVGI IPP	KGCLL GPPGTG	KTLLARA VASQLDCA	FLEVVSSSIVIETICE	224
ScRpt5	NKDS LLLDTLPS	FUSRV KAMEVDEKPTETYS		ELVEAIVLPMKRA	KFKDMGIRAP	KGALMYGPPOTG	KTLLARACAAQTNA	FLELAAFOLVOMIGE	258
SpRpt5 CaRpt5	NKDSTLIIDKLPS NKDSTLVLDTLPS	Y SRVKAMEVDEK PTERMS	DIGGLSKOIE	ELIEAVULPMQQA	KPRKLGVKPP KPKNLGIKPP	KGCLMFGPPGTG	KTLLARACAAQENAI	FLYLAAPOLVOMFIGD	262 277
K1Rpt5	NKDSYLILDTLPSE	FOSRVKAMEVDEKPTETYS	DVGGLDKOIE	REVEAIVLPMKQG	KFKDMGIKAP	KGALMY GPPOTG	KTLLARACAAQTNA	FLKLAAPOLVOM IGE	256
DhRpt5	NKDS ILILD TLPSE	TISRVKAMEVDEKPTED	DIGGLDKOIE	BLIBAVVLPMKQA	KEKNLGIKPPI	GALM GPPGTG	KTLLARACAAQS GA	FLYLAAPOLVOMFIGD	250
DdRpt5	NKDSTILLDTLPPE	TOSRVKAMEIDEKPTEETS	DIGGLDKOIO	ELVEAVVLPMTHK	RFESIGIKPPI	KOVIMIGPPOTG	KTLLARACAAO INS	WLKLAGPOLVOMFIGD	237
DrRpt5	NKDS IL ILETLPTE	YDSRVKAMEVDERPTEONS		BLVRA IVLPMNHK	KFENLGIOPPI	CULMY GPPCTC	KTLLARACAAQTKA	FLKLAGPOLVOMPIGD	228
AtRpt5	NKDS ILILDILPSE	YD SRVKAMEVDEKPTEDY	IDI GGLEKOIO	ELVEAIVLPMTHK	RFEKLGVRPPI	GVLL GPPGTG	KTLMA RA CAAQTNAT	FLELAGPOLVOMFIGD	248
DmRpt5	NKDSILILEKLPAR NKDSILILETLPAR	TDARVKAMEVDERPTEQUS YDARVKAMEVDERPTEQUS		ELIEAVVLPMTHK	KFKNLGIHPPI	KGVLLYGPPGTG	KTLLARACAAOTKSI	FLKLAGPOLVOMFIGD	254
MmRpt5	NKDS ILILETLPT	YLSRVKAMEVDERPTEONS	DIGGLOKOIO	BLVEAIVLPMNHK	KPENLGI OPP	CULM GPPGTG	KTLLABACAAOTKA	FLKLAGPOLVOMFIGD	266
HsRpt5	NKDSYLILETLPT	YL SRVKAMEVDERPTEO	DIGGLOKOIO	BEVEAIVL PMNHK	KFENLGIOPPI	GVLMY GPPGT	KTLLARACAAOTKA	FLKLAGPOLVOMFIGD	263
SCRPt6 SpRpt6	RND <mark>S TOLIK ILP</mark> NK	VDPLVSLMMVEKIPDSTI	EMVGGLIKOIK EMVGGLEKQIK	BIKEVIELPVKHP	ELFESLGIAQPI ELFESLGIPQPI	KGILL GPPGTG	KTLLARA VAHHTDCH	FIRVSGAELVORTIGE	225
CaRpt6 K1Rpt6	KPDBHDLYKILPTK	VDPLVSLMMVEKVPDSTYI	MVGGLDKOIK	RIKEVIELPVKEP	LFESLGIAOP	GVILYGPPGTG	KTLLARAVAHHTECH	FIRVSCRELVORYICE	221
PsRpt6	KSD <mark>SY</mark> DLHKILPNK	VDPLVSLMMVEKVPDSTY	MVGGLDKQIK	EIKEVIELPVKHP	LFESLGIAOPI	KGVILIGPPGIG	KILLARA VAHHIECH	FIRVSCSELVOKYICE	222
VIRpt6	RSD <mark>S TLEOILPNK</mark>	VDPLVSLMMVEKVPDSTVI	MVGGLDKOIK MVGGLDOOIK	BIKEVIELPVKHP	ELFESLGIAOPI	KGVIL GPPGTG	KTLLARAVAHHTECH	FIRVSGSBLVOKTIGE	221 223
DdRpt6	KHES TLHR ILPNK	IDPLVSLMKVEKIPDSTY	MVGGLDKOIK	RIKEVIELPIKHP	LPESLGIAOP	GVLL GPPGTG	KTLLARAVAHHTDC	FIRVSGSELVOETIGE	222
XtRpt6	RND <mark>S Y</mark> TLHK ILPNK	VDPLVSLMMVEKVPDSTI	EMI GGLDKOIK	BIKEVIELPVKHP	HFEALGIAOPI	GVLL GPPGTG	KTLLARA VAHHTDC	FIRVSGBELVOKFIGE	221
CeRpt6	RAD <mark>S YALHKLLP</mark> NK	VDPLVSLMMVEKVPDSTVI	EMV GGLDKOIK	EIKEVIELPVKHP	ELFDALGIAOPI	KGVLLFGPPGTG	KTLLARAVAHHTEC	FIRVSGSBLVOKFIGE	238
DmRpt6	RNES TLAKILPNK	VDPLVSLMMVEKVPDSTI		RIKEVIELPVKHP	LE DALGIAOPI	GVLL GPPGTG	KTLLARAVAHHTEC	FIRVSCERLVOKFICE	225
RnRpt6	RND <mark>S TTLEK ILP</mark> NK	VDPLVSLMMVEKVPDSTT	EMI GGLDKOIK	EIKEVIELPVKHP	LFEALGIAOP	GVLL GPPGTG	KTLLARA VAHHTDC	FIRVSGSELVOKPIGE	226
HSKPt6	KNUS TIMK INPNK	WELVELOPVERVEDSTOP	STAR BELEVEL	THEY TRUPY KHP	DE RADGIA QPI	KOV LL TGPPGTG	CLARR VAHHT DC	LIKASCARTACKLICE	226

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MjPAN ScRpt1	GASLVK DIPKL	AREKAPSI I PI DE	IDA IAAKRIDALIG-GORE	VOR IMOLICARMO	FEA-RGDVKIIGATNR	PETERPART RPGREDR	I IEVP-APDEKGRLEILKI KVERS-LPDLEGRANIERI	352
SpRpt1	GARMVRELFEM	ARTKKACIIFFDE	IDAIGGARFDD GAG - CONE	VORTMLELITOLDO	FDP-RGNIKVLFATNR	PNTLDEALMRPGRIDE	KVEFG-LPDLEGRAHILRI	361
CaRpt1	GARMVRELPEM.	ARTKKACIIFFD	VDAIGGARFDDGAG-GDNH	VORTMLELITOLDO	FDP-RGNIKVMFATNR	PNTLEPALLEPGRIDE	KVEPS - LEDLEGRANIPRI	369
PsRpt1	GARMVRELPEM	ARTKKACIIFPDE	VDAIOGAR PDD GAG - GDNE	VORTMLELITOLDO	PDP-RGNIKVMFATNR	PNTLDPALLRPGRIDE	KVEFS-LPDLEGRANIFRI	370
DhRpti	GARMVRELFEM.	ARTKKACIVFFDE	IDAIGGARFDD GAG - GDNE	VORTMLELITOLDO	FDP-RGNIKVMFATNR	PNTLDPALLRPGRIDE	KVEFS - LPDLEGRANIFRI	370
DdRpt1	GARMVRDLFOM	ARSKKACIIFFDR	VDAIGGARFEDGAG-GENH	VORTMURLINGUDG	FDP-RGNIKVLMATNR	PDTLDPALLEPGRLDR	KVEFG-LPDLEGRAHIFTI	352
DrRpt1	GARMVRELFEM.	ARTKKACLIFFDE	IDAIGGARFDDGAG-CDNE	VORTMLELINQLDO	FOP-RGNIKVLMA TNR	POTLOPALMRPGRLDR	KIEFS - LPDLEGRTHIFKI	357
AtRpt1	GARMVRELPOM	ARSKKACIVFFD	VDAIGGARFDDGVG-GDNH	VORTMLE IVNOLDO	FDA-RGNIKVLMATNR	PDTLBPALLRPGRLDR	KVEFG-LPDLESRTQIPKI	357
CeRpt1	GARMVRELFEM.	ARTKKACLIFFDE	IDAVGGARFOD GQG - CONH	VORTMLELINOLDO	FDP-RGNIKVLMATNR	PUTLEPALMRPGRLDR	KVEFA-LPDLAGRAHILKI	359
MmRpt1	GARMVRELFEM	ARTKKACLIFFDE	IDAIGGARFDD GAG - GDNH	VORTMLELINOLDO	FDP-RGNIKVLMA TNR	POTLDPALMRPORLDR	KIEFS-LPDLEGETHIFKI	357
RnRpt1	GARMVRELFEM.	ARTKKACLIFFD	IDAIGGARFDDGAG-GENH	VORTMLELINGLOG	FUP-RONIKVLMATNR	POTLEPALMRPGRLDR	KIEFS - LPDLEGRTHIFKI	357
ScRpt2	GPRLCROIPKV.	AGENAPSIVFIDE	IDAIGTERTDSNEG-GERE	IORTMLELLNOLDO	FDD-RGDVKVIMATNK	I STLDPAL I RPGR I DR	KILFE-NPDLSTKKKILGI	364
SpRpt2	GPRLVROLFNA.	A EE HS PS IVFIDE	IDAIGTERYDAQSG - ABRE	IORTMLELLNQLDG	FDT QRDIKVIMATNR	ISDLOPAL I RPGR I DR	KILFE-NPDEATKRKIFTI	374
K1Rpt2	GPRLCROIFKV.	AAENAPSIVFIDE	IDAIGTERYESNEG-GEER	TORTMLELLNOLDO	FDD-RODVKVIMATNK	IESLOPALI RPORIDE	KILFE-NPD ITTKRKIVGI	361
PsRpt2	GPRLCROIFOI.	AGE HAPS IVFIDE	IDAIGTKRYES TEG-GERE	IORTMLELLNOLDO	FDD-RGDIKVIMA TNK	I ESLOPAL I RPGR I DR	KILFE-NPDANTKKKILTI	361
Y1Rpt2	GPRLCROIF OI	AARHAPSIVFIDE	IDAIGTERYRS TEG-GERE	VORTMLELLNOLDO	FDD-RGDVKVIMATNK	IES LOPAL I RPGR I DR	KILFE-NPDSTTKRKIMGI	363
DdRpt2 DrPpt2	GPKLVRELFRV.	ADECAPSIVEIDE	IDAVGTERYDSQSG - GERE	TORTMLELLNOLDO	FDA - RTDVKVIMATNR	IETLOPALIRPGRIDE	KIEFP-LPDIKTKRKIFEI	366
XtRpt2	GPKLVRELFRV.	AEEHAPSIVFIDE	IDAIGTERYDSNSG-GERE	IORTMLELLNOLDO	FDS-RGDVKVIMATNR	IETLDPALIRPGRIDR	KIEFP-LPDEKTKKRIFOI	367
AtRpt2 CeRpt2	GPKLVRELPRV.	ADDLS PEIVPIDE	IDAVGTKRYDA HSG - GERE	TOPTML BLLNOL DO	FDS-RGDVKVILATNR	I BELDPALL RPGR I DR	KIRFP-LPDIKTRRRIPOI	370
DmRpt2	GPKLVRELFRV.	A E HAPS IVFIDE	IDAVGTKRYDSNSG - GERE	IORTMLELLNOLDO	FDS-RCDVKVIMATNR	IETLDPALIRPGRIDR	KIEFP-LPDEKTKRRIFTI	366
MmRpt2 RnRpt2	GPKLVRELFRV.	A EE HAPS IVFIDE	IDAIGTERYDSNEG-GERE	IORTMLELLNOLDO	FDS-RGDVKVIMATNR	I RTLEPAL I RPGR I DR	KIEFP-LPDEKTKKRIFQI	367
HsRpt2	GPKLVRBLFRV.	AEBHAPS IVFIDE	IDAIGTERYDSNSG-GERE	IORTMLELLNOLDO	FDS-RGDVKVIMATNR	I BTLDPALI RPGRIDR	KIEPP-LPDEKTKKRIFOI	367
ScRpt3 SpRpt3	GPRMVRDVFRL GPRMVRDVFRM	ARENAPSIIFIDE	VDSIATERFDA QTG - SDRH TDAIATERFDA OTG - ADRH	VORILIELLTOMDO	FDQ-STNVKVIMATNR	ADTLEPALLEPGRLER	KIEFPELRORRERRLIPGT KIEFPETRORRORRLVFOT	355
CaRpt3	GPRMVR DVFRL.	ARENSPAILFIDE	IDAIATEPDA QTG - ADRE	VORILLELLNOMD	FDQ-TSTVKVIMATNR	ADTLOPALLEPGELDE	KIRFPSLKDRRERRLIPST	338
PSRpt3	GPRMVRDVFRL	ARENSPAILFIDE	IDA IATKEFDA OTG-ADRE	VORILLELLNOMDO	FDQ-TSTVKVIMATNR	ADTLDPALLRPGRLDR	KIEFPSLKDRRERRLIPST	337
DhRpt3	GPHMVR DVFRL.	ARENSPAIIFILE	IDAIATERFDA QTG - ADRE	VORILLELNOMDO	FIQ-NSTVKVIMATNR	HDTLDPALLRPGRLDR	KIEPPSLKDRRERRLIPST	343
DdRpt3	GPRLVR DVFRL	ARENSPALIFIDE	IDAIATERFDA OTG-ADRH	VORILMELLNOMDO	FUV-SVNVKVIMATNR	DTLBPALLRPGRLDR	KIEFP-LPORROKRLIFOV	331
DrRpt3	GPRMVR DVFRL	AKENAPAIIFIDE	IDAIATERFDA OTG - ADRE	VORILLELLNOMDO	FDQ-NVNVKVIMATNR	ADTLDPALLCPGRLDR	KIEFP-LPDRRQKRLVFST	347
AtRpt3	GPRMVRDVFRL	AFENAPALIFIDE	VDAIATARPDA OTG - ADRH	VORILMELLNOMDO	FDQ-TVNVKVIMATNR	ADTLEPALLEPORLER ADTLEPALLEPORLER	KIRFP-LPDRRQKRLVPQV	349
CeRpt3	GPEMVE DVFRL.	AFENSPEIIFIDE	IDAIATERFDA OTG-ADRE	VORILLELLNOMDO	FDQ-STNVKVIMATNR	OTLOPALL RPGRLDR	KIEFP-LPDRROKRLVFST	343
MmRpt3	GPRMVRDVFRL	AFENAPAIIPIDE	IDAIATKRFDA OTG-ADRE	VORILLELLNOMDO	FDQ-NVNVKVIMATNR	ADTLDPALLRPGRLDR	KIRFP-LPDRRQKRLIFST	342
RnRpt3	GPRMVR DVFRL	AFENAPAIIPIDE	IDAIATERFDA QTG - ADRE	VORILLELINOM	FDQ-NVNVKVIMATNR	ADTLEPALLEPORLDR	KIRPP-LPDRRQKRLIPST	347
ScRpt4	SARIIREMFAL	AKEHEPCIIFMDE	VDAIGGREPSE CTS -ADRE	IORTLMELLTOMD	FDN-LOOTKIIMATNR	PUTLOPALLRPGRLDR	KVEIP-LPNHAGHLEIFKI	363
SpRpt4	SARIIREMPGY.	AKEHEPCVIFMDE	IDAIGGRRESE GTS - ADRE	I ORTLMELLNOMDO	FDY-LOOTKIIMA THR	POTLOPALLRPGRLDR	KIEIP-LPNEVGRMEILKI	314
K1Rpt4	SARIIREMPAT	AKEHEPCIIFMDE	IDAIGGRRPSE GTS - ADRE	IORTLMELLTOMDO	FDN-LCOTKVIMA INR	PDTLDPALLRPGRLDR	KIEIS-LPNRAGRLEIPKI	360
PsRpt4	SARLIREMPAN.	AREHEPCI IFMDE	VDAIGGRRESE GTS - ADRE	I ORTLMELLNOMDO	FDT-LEOTKVIMATNR	POTLOPALLRAGRLDR	KIEIG-LPNEAGRLEIPKI	342
Y1Rpt4	SARLIREMPGY	AKEHEPCIIFMDE	VDAIGGREPSEGTS-SDRE	IORTLMELLNOMDO	FDY-LOKTEVIMA TNR	PUTLEPALLRAGREDR	KIRIP-LPNHAGRLEVPKI	336
DdRpt4 DrRpt4	SARLIREMPOL	ARDHOPCVIFMDE	IDAIGGRRFSEGTS-ADRE	TORTIMELLNONDO	FDT-LSKVKIIMATNR FDT-LHRVKMIMATNR	POVLOPALLRPGRLDR	KIEIP-LPNEAGEVDVLKI KIHIE-LPNEOARLDILKI	319
XtRpt4	SARLIREMENT	ARDHOPCIIFMDE	IDAIGGRRFSEGTS-ADRE	IORTLMELLNOMDO	FDT-LHRVKMIMATNR	POTLOPALLRPGRLDR	KIHIE-LPNRQARLDILKI	315
CeRpt4	SARLIREMPNY	ARDHOPCIVFMDE	IDAIGGREPSE GTS - ADRE	IORTLMELLNOLDO	FDS-LGKVKVIMATNR	PDTLDPALLRPGRLDR	KIEIG-LPNEOSRLEILKI	321
DmRpt4	SARLIREMPNY.	ARDHOPCIIFMDE	IDAIGGRRPSE GTS - ADRE	IORTLMELLNOMDO	FDS-LGOVEMIMATNR	PDTLDPALLRPGRLDR	KIEIP-LPNEQARLEILKI	316
RnRpt4	SARLIREMPNY	ARDHOPCIIFMD	IDAIGGREFSEGTS-ADRE	ICRILMELLNOMDO	FDT-LHRVKMIMATNR	PUTLOPALLEPGRLDR	KIHID-LPNBQARLDILKI	329
HsRpt4	SARLIREMENT.	ARDHOPCIIFMDE	IDAIGGRRFSEGTS-ADRE	IORTLMELLNOMDO	FDT-LHRVKMIMA TNR	PUTLEPALLRPGRLDR	KIHID-LPNBQARLDILKI	315
SpRpt5	GALLVE DA FAL.	AKEKSPALIPIDE	LDAIGTERFDS EKA - GDRE	VORTMLELLNOLDO	FSS-DDRVKVIAA TNR	VDTLDPALLESGRLDR	KLEFP-LPNHEARVGILRI	367
CaRpt5 K1Rpt5	GAELVEDAFAL.	AKEKAPTIIPIDE	LDAIGTERFDS DES - GDRE	VORTMLELLNOLDO	FGS-DDRVKVLAATNR	VOTLEPALLES GELDE	KIRFP-LPSHEARESVLKI KIRFP-LPTHDARAOLLOI	382
PsRpt5	GARLVEDAFAL	AFEKAPTIIFIDE	LDAIGTERFDS DES - GDRE	VORTMERLENQEDO	FDS-DDRVKVLAATNR	VDTLDPALLRSGRLDR	KIEFP-LPSHEARESVLKI	355
VIRpt5	GALLVEDAFAL	AFEKAPTIIFIDE	LDAIGTERFDS DES - GDRE	VORTMLELINGLO	PGS - DDRVK VLAATNR	VDVLDPALLES GRLDR	KIEFP-LPSHEARESVLKI	355
DdRpt5	GAKLVE DA FAL.	AFEKGPTIIFIDE	LDAIGTERFDS EVS - GDRE	VORTMLELLNOLDO	FSS -DANIKVIAA THR	IDILDPALLES GRLDR	KIEPP-LPNHEARAHILOI	350
XtRpt5	GAELVEDAFAL	AKEKAPSIIFIDE	LDAIGTERPDS EKA - GDRE	VORTMLELLNOLD	FOP-NTOVEVIAATNE	VDILDPALLESCELDE	KIEFP-MPNHEARARIMOI	353
AtRpt5	GANLVEDAFQL	AKEKAPCIIPIDE	IDAIGTERFDS EVS - GDRE	VORTMLELLNOLDO	FSS -DERIKVIAATNR	ADILDPALMES GRLDR	KIEFP-HPTHEARARILOI	353
DmRpt5	GAKLVRDAFAL	AKEKAPALIFIDE	LDAIGTERFDSEKA - GDRE	VORTMERLENGE	FSS-TADIKVIAATNR	VDILDPALLRSGRLDR	KIEFP-HPNHEARARIMQI	357
MmRpt5	GAYLVE DA PAL	AFEKAPSIIPIDE	LDAIGTKRFDS EKA - GDRE	VORTMERLENGED	POP-NTOVEVIAATNE	VDILDPALLES GRLDP	KIEFP-MPNHEARARIMOI	371
HsRpt5	GAKLVRDA FAL.	AKEKAPSIIFIDE	LDAIGTERFDSEKA - GDRE	VORTMLELLNOLDO	FOP-NTOVEVIAA THR	VUILOPALLESGELDE	KIEFP-MPNHEARARIMQI	369
ScRpt6	GSEMVRELFVM.	AREHAPSIIFMDE		VORTMLELLNQLDO	FRA-TKNIKIIMAINR	IDIL DPALL RPGR I DR	KIEPP-PPSVAARAELLRI	330
CaRpt6	GSRMVRELFVM.	ARBHAPSIIFMDE	IDSIGSSRVEGSSGGDSE	VORTMLELLNOLDO	FRS-SKDIKIIMATNR	LDILDPALL RPGR I DR	KIRFP-APTVAARTDILKI	326
KIRpt6 PsRpt6	GERMVRELFVM.	ARBHAPSIIPMDE		VORTMERLINGLOG	FET-SKNIKIIMATNE	DILDPALL RPGRIDE	KIEFP-PPTVAARTELLRI	329
DhRpt6	GERMVRELFIM	AREHAPSIIPMDE	IDSICSSRVEGSSGCDSE	VORTMLELLNOLDO	FEN-SKDIKIIMATNR	LDILDPALL RPGR I DR	KIEFP-APTITARTDILKI	326
DdRpt6	GERMVRELFIM	AREHAPSIIFMDE	IDS ICSARTES GOGGGGGGS SE	VORTMLELLNOLDO	FES-SKNIKIIMATNR	IDILDPALLRPGR IDR	KIEPP-NPGDAGRLDILKI	331
DrRpt6	GARMVRELFVM.	AREHAPSIIFMDE	IDSIGSSRLEG GSG-GDSE	VORTMLELLNOLDO	FEA -TKNIKVIMA TNR	IDILDSALL RPGR IDR	KIEFP-PPNHEARLDILKI	331
AtRpt6	GSRMVRELFVM	AREHAPSIIFMDE	IDSIGSARMES GEGNGLSE	VORTMLELLNOLDO	FRA-SNKIKVLMATNR	IDILDOALL RPGR IDR	KIEFP-NPNEESPFDILKI	344
CeRpt6	GARMVRELFVM.	AREHAPSIIFMDE	IDSIGSSRVEG SEG-GDSE	VORTMLELLNOLDO	FEA - TKNIKVIMA TNR	IDILDPALL RPGR IDR	KIEFP-APDEKARADILKI	341
MmRpt6	GARMVRELFVM	AREHAPSIIFMDE	IDSICSSRLBGGSG-GDSE	VORTMLELLNOLDO	FRA-TKNIKVIMATNR	IDILDSALL RPGR IDR	KIEFP-PPNHEARLDILKI	331
RnRpt6	GARMVRELFVM.	AREHAPSIIFMDE		VORTMERLENGEDO	FEA -TKNIKVIMATNR	IDILDSALL RPGR IDR	KIEFP-PPNEEARLDILKI	331



Supplementary Figure 4 Sequence alignment of Rpt subunits from 16 representative species. Sc: Saccharomyces cerevisiae; Sp: Schizosaccharomyces pombe; Ca: Candida albicans; Kl: Kluyveromyces lactis; Ps: Pichia stipitis; Dh: Debaryomyces hansenii; Yl: Yarrowia lipolytica; Dd: Dictyostelium discoideum; Dr: Danio rerio (zebrafish); Xt: Xenopus tropicalis; At: Arabidopsis thaliana; Ce: Caenorhabditis elegans; Dm: Drosophila melanogaster; Mm: Mus musculus; Rn: Rattus norvegicus; Hs: Homo sapiens.



Supplementary Figure 5 Subcomplex I in one asymmetric unit. Two copies of subcomplex I in each asymmetric unit form a cage-shaped structure. Two perpendicular views are shown here. Six CC-OB domains within the same subcomplex I are labeled A through F.



Supplementary Figure 6 The interface between two molecules of subcomplex I. (A) Molecules A and B of subcomplex I interact with molecules A' and B' of an adjacent subcomplex I. Two copies of subcomplex I associate with each other through their respective coiled coils. The coiled coil from molecules A and B interacts with the coiled coil in molecules A' and B' as well as the β domain of molecule A'. (B) A stereo view of the interface. Side chains from molecules A and B are colored green and blue, respectively. Side chains from molecules A' and B' are colored pink and purple, respectively. H-bonds are represented by red dashed lines.