# Supporting Information

## Strübbe et al. 10.1073/pnas.1007916108

### SI Text

**S1: Oligonucleotide Sequences Used for Cloning.** PstI_1-2225_SmaI: Pc-BioI (CTGCAGTCGGCCACTCCTTCACTACC)

Pc-BioCtermII (CCCGGGAGCTACTGGCGACGAATCGC); SmaI_2226-3712_PstI: Pc-BioCtermIII (CCCGGGTGAGCTTCGACCCAAACAATG)

Pc-BioIV (CTGCAGTGGCGCCTTATCATC).

Linker sequence 1 (GAGAATTTGTATTTTCAGGGTATGGCCTCCTCGCTGCGCCAGATCCTGGATTCCCAGAAGATGGAGTGGCGCTCGAACGCCGGCGGCTCCGACTACAAGGACGACGATGACAAGGCTTGA)

Linker sequence 2 (TCAAGCCTTGTCATCGTCGTCCTTGTAGTCGGAGCCGCCGGCGTTCGAGCGCCACTCCATCTTCTGGGAATCCAGGATCTGGCGCAGCGAGGAGGCCATACCCTGAAAATACAAATTCTC)

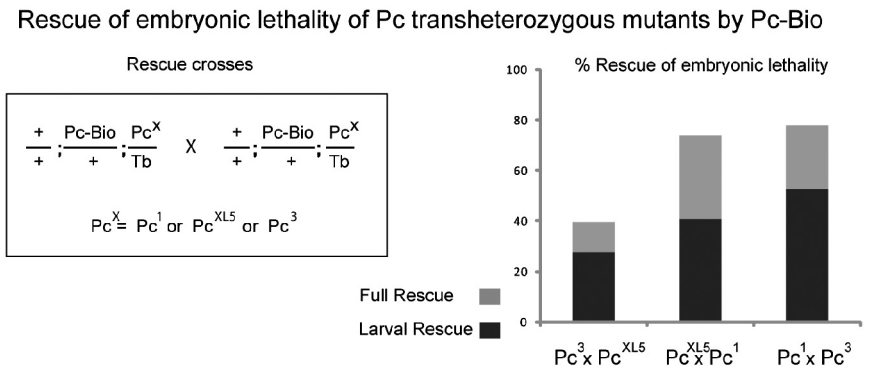
NotI-Flag-BirA (GCGGCCGCATGGCTGACTACAAGGACGACGATGACAAGATGAAGGATAACACCGTGC)

**S2: Mass Spectrometric Analysis of Pc-Bio Pull-downs.** 2 μl of the dissolved peptide mixture was analyzed by LC-MS/MS. The setup of the μRPLC-MS system was as described previously (1). The hybrid LTQ-FT-ICR mass spectrometer was interfaced to a nanoelectrospray ion source (both Thermo Electron) coupled online to a Tempo 1D-plus nanoLC (Applied Biosystems/MDS Sciex). Peptides were separated on an RP-LC column (75 μm× 15 cm) packed in-house with C18 resin (Magic C18 AQ 3 μm; Michrom BioResources) using a linear gradient from 98% solvent A and 2% solvent B (98% acetonitrile, 2% water, 0.15% formic acid) to 30% solvent B over 40 minutes at a flow rate of 0.3 μl/ min. Each survey scan acquired in the ICR-cell at 100,000 FWHM was followed by MS/MS scans of the three most intense precursor ions in the linear ion trap with enabled dynamic exclusion for 20 seconds. Charge state screening was employed to select for ions with at least two charges and to reject ions with undetermined charge state. The normalized collision energy was set to 32%, and one microscan was acquired for each spectrum. Before database searching, the acquired raw files (with Xcalibur 2.0 SR1) were converted to the mzXML data format employing the ReadAW 3.5.1 software (2). MS/MS-spectra were exported as dta files without further processing using the mzXML2other program (2). The MS/MS-spectra were searched using the X!Tandem search tool (3) (Version: X! TANDEM 2 (2007.07.01.2)) against the Flybase protein database (release version 5.7, April 2008) as well as known contaminants such as porcine trypsin and human keratins (Non-Redundant Protein Database, National Cancer Institute Advanced Biomedical Computing Center, 2004, ftp://ftp.ncifcrf.gov/pub/nonredun/; total number of protein sequences searched: 21129). The search was performed with full-tryptic cleavage specificity, mass tolerance of 25 ppm, methionine oxidation as variable modification, and cysteine carbamidomethylation as fixed modification. The database search results were further processed and analyzed using the Trans-Proteomics Pipeline 3.5 (TPP) (4). First, the identified peptides were validated using the PeptideProphet software (5) and then assigned for protein identification using the ProteinProphet program (6). Both software tools employed allow filtering and evaluation of large proteomic datasets with assessment of predictable sensitivity and false positive identification error rates. In this study, only peptides with a PeptideProphet score of ≥0.55 were considered. Moreover, only proteins identified with a minimum of four peptides were accepted as correct calls for further analysis and all of the 22 identified proteins had a ProteinProphet score of ≥0.9. This represents a false error rate of less than 5% on the peptide and less than 1% on the protein level as determined by Peptide- and ProteinProphet, respectively. Protein coverage and number of unique and total peptides found for specifically enriched proteins are displayed in Table S3 together with the peptide sequences identified.

**S3: Analytical Gel Filtration Experiments.** Analytical gel filtration experiments were performed on a Superose 6 HR column (23.56 ml, 1 cm × 30 cm, GE Healthcare) equilibrated with three column volumes of DB-3. After that, 200 μl of nuclear extract (2.5 mg protein) was loaded onto the column, followed by two column volumes of DB-3 for elution. Fractionation was carried out using a linear flow rate of 0.5 mL/ min and the obtained samples were acetone precipitated and dissolved in sample buffer for SDS/PAGE and Western blotting with specific antibodies. The column was calibrated with a selection of molecular weight standards for gel filtration (GE Healthcare).

**S4: Eye Pigment Measurements.** Freshly hatched flies were aged for three days at 29 °C until stored at −20 °C. For quantitative measurements, heads were isolated (30 heads for each sample) and ground in 1.5 mL tubes with a micropestle in 80 μl EPE buffer (30% Ethanol-HCL pH 2). Extraction was allowed to proceed at room temperature for 1 h and followed by sedimentation at 13.000 rpm. Supernatants were collected and the OD at 480 nm was measured with a nanodrop spectrophotometer.


1. Schmidt A, et al. (2008) An integrated, directed mass spectrometric approach for in-depth characterization of complex peptide mixtures. *Mol Cell Proteomics* 7:2138–2150.
2. Pedrioli PG, et al. (2004) A common open representation of mass spectrometry data and its application to proteomics research. *Nat Biotechnol* 22:1459–1466.
3. Craig R, Beavis RC (2004) TANDEM: Matching proteins with tandem mass spectra. *Bioinformatics* 20:1466–1467.
4. Keller A, Eng J, Zhang N, Li XJ, Aebersold R (2005) A uniform proteomics MS/MS analysis platform utilizing open XML file formats. *Mol Syst Biol* 1:2005 0017.
5. Keller A, Nesvizhskii AI, Kolker E, Aebersold R (2002) Empirical statistical model to estimate the accuracy of peptide identifications made by MS/MS and database search. *Anal Chem* 74:5383–5392.
6. Nesvizhskii AI, Keller A, Kolker E, Aebersold R (2003) A statistical model for identifying proteins by tandem mass spectrometry. *Anal Chem* 75:4646–4658.
7. Sato T, Denell RE (1985) Homoeosis in *Drosophila*: Anterior and posterior transformations of Polycomb lethal embryos. *Dev Biol* 110:53–64.
8. Messmer S, Franke A, Paro R (1992) Analysis of the functional role of the Polycomb chromo domain in *Drosophila melanogaster*. *Gene Dev* 6:1241–1254.




| | Pc Alleles x no transgene | | | Pc Alleles x Pc-Bio transgene | | |
|---|---|---|---|---|---|---|
| Mutant | $Pc^3 \times Pc^{XL5}$ | $Pc^{XL5} \times Pc^1$ | $Pc^1 \times Pc^3$ | $Pc^3 \times Pc^{XL5}$ | $Pc^{XL5} \times Pc^1$ | $Pc^1 \times Pc^3$ |
| Total no. of flies | 608 | 323 | 350 | 1397 | 521 | 737 |
| % Larval Rescue | - | - | - | 27.5 | 40.9 | 52.9 |
| % Full Rescue | - | - | - | 12.2 | 32.8 | 24.8 |

**Fig. S1.** Rescue of embryonic lethality of transheterozygous Pc mutants by Pc-Bio. Animals heterozygous for the Pc-Bio transgene were combined with $Pc^1$, $Pc^3$ or $Pc^{XL5}$ alleles (7, 8). Transheterozygous mutants missing an intact copy of endogenous Pc protein were identified by selection of wild-type larvae lacking the tubby (Tb) balancer chromosome. Larval rescue (black bars) was scored by the number of larvae that were able to pupariate and full rescue (gray bars) was attested for hatching flies.

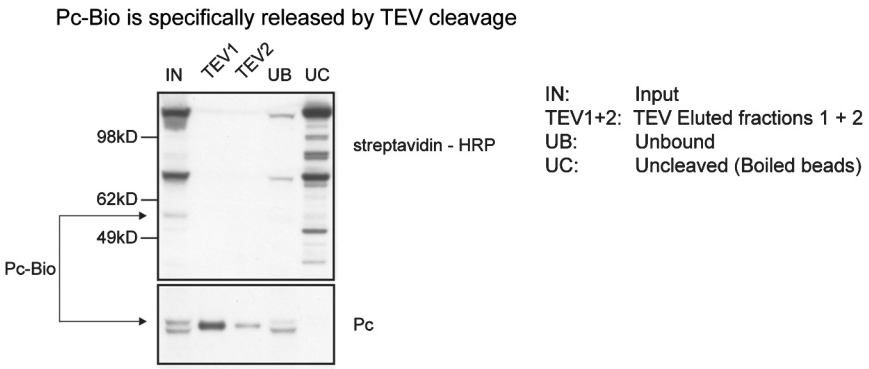



**Fig. S2.** Pc-Bio is specifically released by TEV cleavage. Elution of biotinylated Pc-Bio from streptavidin beads was perfomed in 100 μl using 15 U of AcTEV protease (Invitrogen). Endogenously biotinylated proteins were not eluted and could not be detected in the supernatant (TEV1 + 2 lanes) but became visible after boiling of the beads in sample buffer (lane uncleaved UC).

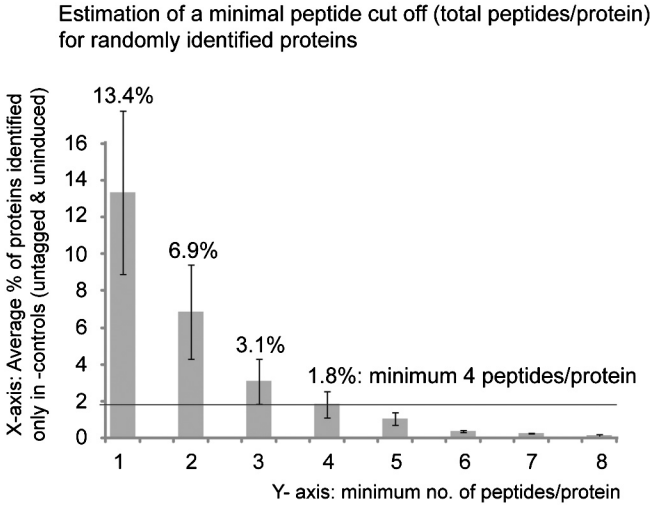



**Fig. S3.** Calculation of a minimal peptide cut off for excluding randomly identified proteins. Peptides specifically found in negative controls (untagged and uninduced) were assumed to be detected at random and their contribution to the sample assessed. If only proteins identified by four peptides minimum are considered, the amount of randomly detected proteins ≤1.8%.

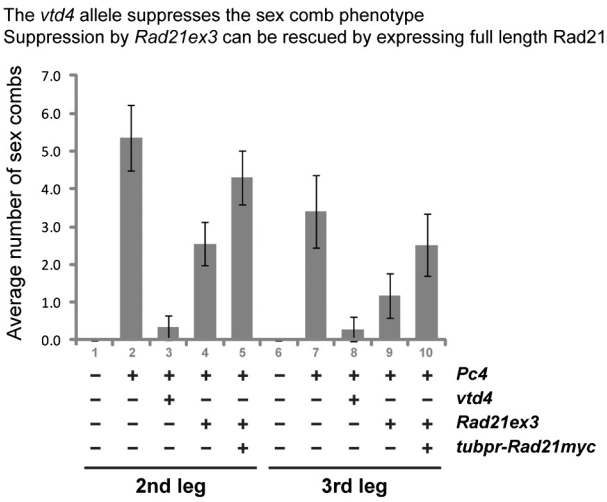



**Fig. S4.** Rad21 alleles suppress extra sex comb phenotype. The Polycomb Pc4 mutant shows extra sex combs on second and third legs (lanes 2 and 7). This phenotype is suppressed in a *vtd4 (verthandi)* mutant background (*Pc4*/*vtd4*; lanes 3 and 8), as has been published previously (1). *vtd4* is a known allele of the *Rad21* locus that can be rescued by transgenic Rad21 (2). Suppression also occurs in the *Rad21ex3* background (lanes 4 and 9) (3) and the extra sex combs phenotype can be rescued by expressing a full-length form of myc-tagged Rad21 (lanes 5 and 10).

1 Schulze S, et al. (2001) Essential genes in proximal 3L heterochromatin of *Drosophila melanogaster*. *Mol Gen Genet* 264:782–789.
2 Hallson G, et al. (2008) The *Drosophila* cohesin subunit Rad21 is a trithorax group (trxG) protein. *Proc Natl Acad Sci USA* 105:12405–12410.
3 Pauli A, et al. (2008) Cell-type-specific TEV protease cleavage reveals cohesin functions in *Drosophila* neurons. *Dev Cell* 14:239–251.

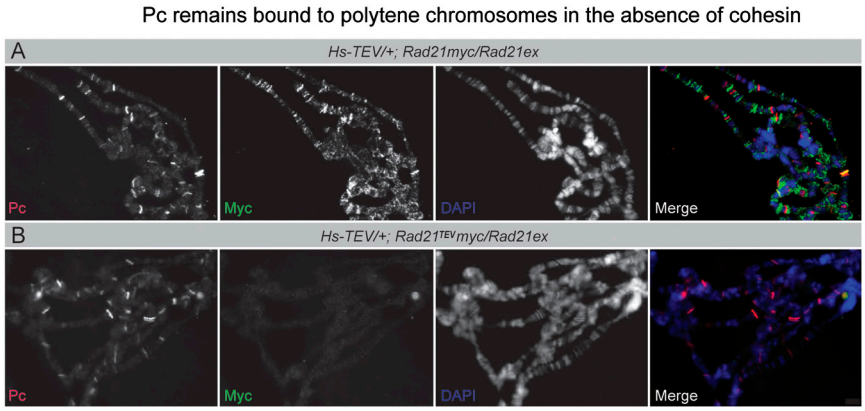



**Fig. S5.** Pc remains bound to polytene chromosomes in the absence of cohesin. Animals expressing TEV cleavable and myc-tagged Rad21$^{TEV}$myc protein in a Rad21 null background (1) were stained with myc and Pc antibodies. (*A*) Coimmunostainings reveal mutual exclusive localization of the two proteins except for one prominent band. (*B*) Rad21 is removed from chromosomes after heat shock induction of TEV protease. Polycomb localization is not altered after loss of Rad21 binding.

1 Pauli A, et al. (2008) Cell-type-specific TEV protease cleavage reveals cohesin functions in *Drosophila* neurons. *Dev Cell* 14:239–251.

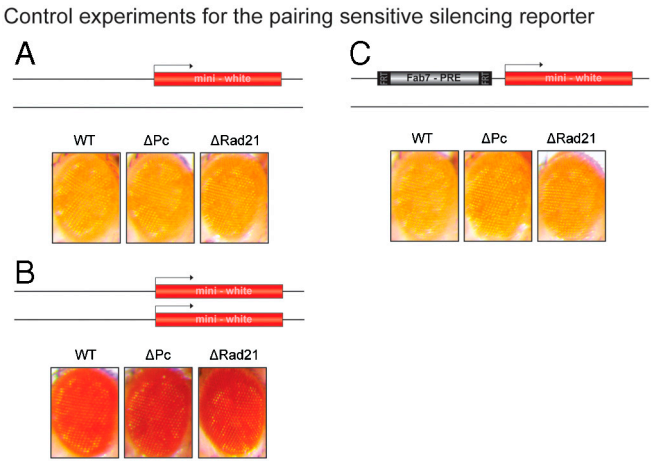



**Fig. S6.** Control experiments for pairing sensitive silencing reporter. The reporter shows PRE-dependent pairing sensitive silencing (PSS). Heterozygous animals with or without a PRE or homozygotes lacking the PRE do not show repression of the miniwhite reporter and do not respond to Pc and Rad21 mutations.

**Table S1. Library of UAS-BirA ligase strains**

| Ligase Name | L4.2 | L4.1 | L4.7 | L4.3 | L4.5 | L4.11 | L4.14 | L6.2 |
|---|---|---|---|---|---|---|---|---|
| Chromosome | X | II | II | III | III | III | III | X |
| Promoter | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp |
| Marker | white | white | white | white | white | white | white | white |
| Epitope Tag | Flag | Flag | Flag | Flag | Flag | Flag | Flag | - |
| Biotinylation competent | n.t. | n.t | n.t | n.t. | n.t. | n.t | n.t | Yes |
| Ligase Name | L6.1 | L11 | L8.1 | L3.8 | L3.24 | L3.6 | L3.10 | L3.16 |
| Chromosome | II | II | III | X | X | II | II | II |
| Promoter | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp | pUASp |
| Marker | white | white | white | eGFP | eGFP | eGFP | eGFP | eGFP |
| Epitope Tag | - | - | - | - | - | - | - | - |
| Biotinylation competent | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| Ligase Name | L3.3 | L3.12 | L3.15 | L5.5 | L5.2 | L5.3 | L5.6 | L5.8b |
| Chromosome | III | III | III | X | II | III | III | III |
| Promoter | pUASp | pUASp | pUASp | pUASt | pUASt | pUASt | pUASt | pUASt |
| Marker | eGFP | eGFP | eGFP | yellow | yellow | yellow | yellow | yellow |
| Epitope Tag | - | - | - | Flag | Flag | Flag | Flag | Flag |
| Biotinylation competent | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |

The table displays different ligase strains, which were generated in the course of this study. Transgene markers used were either white, eGFP, or yellow. Some ligases further feature a Flag-Tag. We tested the expression of the ligase transgenes by glass or *daughterless*-Gal4 induction in *Drosophila* heads and subsequent Western blot of head protein extracts.

**Table S2. List of fly strains used in this study**

| Name | *Genotype* | Source and Notes |
|---|---|---|
| Mutants | | |
| Pc[1] | *w[1118]; ; Pc[1]/TM6B, Tb* | Paro Lab stock collection |
| Pc[3] | *w[1118]; ; Pc[3]/TM6B, Tb* | Paro Lab stock collection |
| Pc[XL5] | *w[1118]; ; Pc[XL5]/TM6B, Tb* | Paro Lab stock collection |
| Pc[4] | *w[1118]; ; Pc(4) p(p) e(s)/TM6B, Hu Sb e Tb ca* | 1 |
| rad21 excision alleles | *+; Rad21[ex3 or ex 8 or ex15 or ex16] ;* | 2 |
| rdx[1] | *cn[1] ; ry[506] P{PZ}mei – P*19 *[03477] rdx[1]/ TM3, ry[RK] Sb [1] Ser[1]* | Bloomington stock no: 11592 |
| rdx[2] | *w[1118]; ; Rdx[2]/TM3* | Kornberg Lab (UCSF) |
| rdx[5], rdx[6] | *w[1118]; ; Rdx[5or6]/TM6B, Tb* | 3 |
| vtd[4] | $Eip74EF^{v4}vtd^{4}/TM3, st^{24}Sb^{1}$ | Bloomington stock no: 5050 |
| ebi [WKS-24] | *w[1118]; ebi[WKS-24]/CyO, P{GMR – p21.Ex}2; +* | Bloomington stock no: 8398 |
| ebi [CCS-6] | *w[1118]; ebi[CCS-6]; +* | Bloomington stock no: 8396 |
| ebi [E90], ebi [E4] | *w[1118]; Ebi[E90 or E4]/Cyo; +* | 4 |
| In vivo biotinylation system | | |
| Pc-Bio (C-term, TEV- Bio- Flag) | *w[1118]; P{Pc – Bio(23), GFP};* | This work |
| BirA ligase | *w[1118]; ; P{BirAL*3.15,*GFP}* | This work (see Table S1) |
| *da*-Gal4 | *w[1118]; ;P{da – Gal*4.*w]* | Paro Lab stock collection, white transgene marker |
| TEV cleavable Rad21 system | | |
| TEV degradable & Myc-tagged Rad21 | *w-; ; Rad21ex, tubPr.-Rad21(3xTEV)myc 10* | 2 |
| Myc-tagged Rad21 | *w-; ; Rad21ex, tubPr.-Rad21myc 10* | 2 |
| Pc-GFP, ΔRad21, hs TEV | *w-; Pc-GFP,hsTEV/CyO; Rad21ex/TM6Bubi-GFP* | Pc-GFP (5) Rad21ex (2) |
| PSS reporter | | |
| pFas (Cre) | *w- ; pFas;* | 6 |
| pFas (Flp; Cre) | *w- ; pFas (Flp) ;* | 6 |


1 Kennison JA, Tamkun JW (1988) Dosage-dependent modifiers of polycomb and antennapedia mutations in *Drosophila*. *Proc Natl Acad Sci USA* 85:8136-8140.

2 Pauli A, et al. (2008) Cell-type-specific TEV protease cleavage reveals cohesin functions in *Drosophila* neurons. *Dev Cell* 14239-251.

3 Kent D, Bush EW, Hooper JE (2006) Roadkill attenuates Hedgehog responses through degradation of *Cubitus interruptus*. *Development* 133:2001-2010.

4 Tsuda L, Nagaraj R, Zipursky SL, Banerjee U (2002) An EGFR/Ebi/Sno pathway promotes delta expression by inactivating Su(H)/SMRTER repression during inductive notch signaling. *Cell* 110:625-637.

5 Dietzel S, Niemann H, Bruckner B, Maurange C, Paro R (1999) The nuclear distribution of Polycomb during *Drosophila melanogaster* development shown with a GFP fusion protein. *Chromosoma* 108:83-94.

6 Schmitt S, Prestel M, Paro R (2005) Intergenic transcription through a polycomb group response element counteracts silencing. *Genes Dev* 19:697-708.

**Table S3. Proteins and peptides identified by mass spectrometry**

| Psc | |
|---|---|
| LPTLAPFVGFNPLQNPAAGK | QAGNLPM[147]SAPPNK |
| TTTTTTPPTTTTTTTAAAAAEATTNADK | AITPPSPSVQQSASPK |
| ENQEQQLAVEVASSK | CEMVINNAKPN |
| LPTLAPFVGFNPLQNPAAGK | PNPFANIPNDVNR |
| QNSVTIIDMSDPER | SEEDPTAAVAASSTATTTSDLATTSR |
| SDTTLQAIVYK | SSPCTPVSSPSEPNIK |
| SVVSNANSSGNNSSK | DVAATPPTETLK |
| VYESPQPLVKPAPR | SPSPLTVPPLTIR |
| SEEDPTAAVAASSTATTTSDLATTSR | YESPQPLVKPAPR |
| DRPEEAALATPEQR | SENTLATTANAALAAATTTTTTATPALATGK |
| LPVTNGNSSGTASPK | IMSPSGVSTLSPR |
| M[147]GPPALPATTPSQGNK | LVNGGQSQPAQQK |
| QNSVTIIDM[147]SDPER | VGFNPLQNPAAGK |
| VGNEVFNDYLQK | IEKPLM[147]PPPAKPPM[147]LAPR |
| VTSGAFSEDPK | GNSSNNYLNLALFNSSK |
| SEEDPTAAVAASSTATTTSDLATTSRPR | SPVNNYIEIVK |
| ATSEDASSNGGASADEEK | PQPLVKPAPR |
| LPDQPQDQVQAAK | FSIDIM[147]YK |
| PGLYER | YLQCPAMCR |
| CEM[147]VINNAKPNIK | PELVDTLRPR |
| LTAAATAPQTK | TDSEPELVDTLR |
| MGPPALPATTPSQGNK | SEPELVDTLRPR |
| NPT[181]PPPPSLPAVGK | S[167]PSPLTVPPLTIR |
| SPQPLVKPAPR | CEM[147]VINNAKPNIK |
| VYESPQPLVKPAPR | LALSQSQK |
| PPLPTVDFK | FVYDKFEIDAQR |
| ESPQPLVKPAPR | QQLFAACSIK |
| VYESPQPLVK | GGNGGSLGGLFPSPPTK |
| YLQCPAM[147]CR | ASRPNPFANIPNDVNR |
| LSPPLPTVDFK | SQLSTLAK |
| TDSEPELVDTLRPR | E[111]IVKPLKPEK |
| TDSEPELVDTLRPR | VKVES[167]PER |
| VTPLKPVLTPTQVDK | PPPPSSPR |
| NPTPPPPSLPAVGK | RVLPLK |
| LVPGLYER | SFALKPIK |
| RYQPILPK | YDKFEIDAQR |
| GNNLDDSILM[147]KPPSCM[147]PPK | C[143]EM[147]VINNAKPNIK |
| FEIDAQR | VEPVSLPEDQK |
| AIT[181]PPS[167]PSVQQSASPK | KLALSQSQK |
| EIVKPLKPEK | |
| Ph-p | |
| YADKDVSDEPPK | GPTATLVPIGSPK |
| VVGHLTTVQQQQQATNLQQVVNAAGNK | HLVNAM[147]GM[147]K |
| LSGIASAPGSDM[147]VACEQCGK | QEFPTHTTSGSGTELK |
| TEIGQVAGQNK | AAVQPPSSTTPNSVSGK |
| M[147]VVM[147]STTGTPITLQNGQTLHAATAAGVDK | GPTATLVPIGS[167]PK |
| SSTPATVSASVEASSSTGEALSNGDASDR | STASSGGGGSIPATPTK |
| VVGHLTTVQQQQQATNLQQVVNAAGNK | IIQEANEPFPVTR |
| SSEVNGTDRPPISSWSVDDVSNFIR | LSGIASAPGSDMVACEQCGK |
| AQQQQAVAQQQQAVAQAQQQQR | QQQQLQLFQK |
| QQQQQQQVGTTNQTQQQQLAVATAQLQQQQQQLTAAALQR | LSTASSGGGGSIPATPTK |
| NQPDGTQGM[147]FIQQQPATQTLQTQQNQIIQCNVTQTPTK | TQLDALAPK |
| M[147]VVMSTTGTPITLQNGQTLHAATAAGVDK | QEFPTHTTSGSGTELK |
| PASSVSTQTAQNQSLLK | ATMQEDIK |
| QIIQCNVTQTPTK | LDEAM[147]AEEK |
| NGIGGVGSGETNGLGTGGIVGVDAM[147]ALVDR | SVALPTLAPLSVVTSGAAPK |
| QSNAAVQPPSSTTPNSVSGK | VIDGFIIQEANEPFPVTR |
| Q[111]EFPTHTTSGSGTELK | LTTVQQQQQATNLQQVVNAAGNK |
| ATM[147]QEDIK | ADKDVSDEPPK |
| QSNAAVQPPSSTTPNSVSGK | LDEAMAEEK |
| YADKDVSDEPPK | VIDGFIIQEANEPFPVTR |
| QLAAATGGVGGDWTQGR | VLTHVIDGFIIQEANEPFPVTR |
| PTHTTSGSGTELK | TVQQQQQATNLQQVVNAAGNK |
| MVVMSTTGTPITLQNGQTLHAATAAGVDK | AAGLQPFGPNQIILR |
| QSNAAVQPPSSTTPNSVSGKEEPK | EVPPPGEAK |
| IGQVAGQNK | Q[111]QQQLQLFQK |
| HTSLTLEK | QSNAAVQPPSSTTPN |
| PPSSTTPNSVSGK | YCSPGCSR |
| HLVNAM[147]GMK | LS[167]ESFPILGASTEVPPMSLP |

| Psc | |
|---|---|
| DKDVSDEPPK | HLVNAMGM[147]K |
| PVRPALATLK | |
| Sce/dRing | |
| DPGHSGTSAASAITSASNAAPSSSANSGASTSATR | KPQEVITDSTEIAVSPR |
| FNQTQSQQALVNSINEGIK | LTLDLGADLPEACR |
| GHSGTSAASAITSASNAAPSSSANSGASTSATR | M[147]QVDDASNPPSVR |
| NASNQM[147]HVHDTASNDSNSNTNSIDR | SEESESDSQMDCR |
| SLHSELM[147]CPICLDM[147]LK | SEESESDSQM[147]DCR |
| DPGHSGTSAASAITSASNAAPSSSANSGASTSATR | KPQEVITDSTEIAVSPR |
| PGHSGTSAASAITSASNAAPSSSANSGASTSATR | AM[147]SVLTSER |
| GGGGGGGGGGNGNGAANVAAPPAPGAPTAVGR | STPSPVPSNSSSSK |
| NASNQM[147]HVHDTASNDSNSNTNSIDR | ANATVDHLSK |
| GGGGGGGGGGNGNGAANVAAPPAPGAPTAVGR | FNQTQSQQALVNSINEGIK |
| S[167]TPSPVPSNSSSSKPK | SLHSELM[147]CPICLDMLK |
| S[167]TPS[167]PVPSNSSSSKPK | PVPSNSSSSKPK |
| Q[111]SQNRPQR | CSDCIVTALR |
| LQSQNRPQR | VNKPM[147]EM[147]YYSWK |
| AAPSSSANSGASTSATR | TANATVDHLSK |
| FCSDCIVTALR | PSPVPSNSSSSKPK |
| MQVDDASNPPSVR | STPSPVPSNSSSSKPK |
| PPAPGAPTAVGR | VAAPPAPGAPTAVGR |
| TTANATVDHLSK | ADPNFDLLISK |
| TWELSLYELQR | SPVPSNSSSSKPK |
| PNFDLLISK | TTANATVDHLSK |
| TPSPVPSNSSSSKPK | YEAIQEK |
| DPGHSGTSAASAITSASN | KPQEVITDSTEIAVS[167]PR |
| FNQTQSQQALVN | EEYEAIQEK |
| LQSQNRPQR | PSNSSSSKPK |
| M[147]TSLDPAPNK | NATVDHLSK |
| PSPVPSNSSSSKPK | DPNFDLLISK |
| Ph-d | |
| VVGHLTTVQQQQQATNLQQVVNAAGNK | SSASSGGGAGFPATPTK |
| VVGHLTTVQQQQQATNLQQVVNAAGNK | QEFPTHTTSGSGTELK |
| M[147]VVM[147]STTGTPITLQNGQTLHAATAAGVDK | LSSASSGGGAGFPATPTK |
| NGIGGVGSGETNGLGTGGIVGVDAM[147]ALVDR | SASSGGGAGFPATPTK |
| SSTPATVSASVEASSSTGEALSNGDASDR | LSGIASAPGSDMVACEQCGK |
| MVVMSTTGTPITLQNGQTLHAATAAGVDK | QQQQLQLFQK |
| NQPDGTQGM[147]FIQQQPATQTLQTQQNQIIQCNVTQTPTK | GPTATLVPIDS[167]PK |
| M[147]VVMSTTGTPITLQNGQTLHAATAAGVDK | LDEAM[147]AEEK |
| Q[111]QQQLQLFQK | YCSPGCSR |
| GPTATLVPIDSPK | AAVQPPSSTIPNSVSGK |
| LSGIASAPGSDM[147]VACEQCGK | Q[111]EFPTHTTSGSGTELK |
| TEIGQVAGQNK | ATM[147]QEDIK |
| LDEAMAEEK | YADKDVSDEPPK |
| TQLDALAPK | ENHLVNAM[147]GM[147]K |
| QEFPTHTTSGSGTELK | YADKDVSDEPPK |
| ATMQEDIK | AAGLQPFGSNQIILR |
| PPGDVKD | QSNAAVQPPSSTIPNSVSGK |
| ENHLVNAMGM[147]K | |
| Su(z)2 | |
| INQDIEPEHSVR | ILLYDNEQTK |
| NIGLKPIEQPLQQSASNPDSK | NQDIEPEHSVR |
| LSQAQAM[147]ASSYAAK | SVTFAEDLESEIDSGSPR |
| SHSLASGELDLQK | LHAEISSQTDGK |
| KSYVDAEDFELK | PGLYQR |
| LDSTSTSEALNR | PPALINLR |
| SYVDAEDFELK | TNPAKPPLSSNNNR |
| YQSTPSSIASAANK | EAEPESPVSNFK |
| INQDIEPEHSVR | NQPAAASTAASISK |
| DLTLPTSPPLPPSLFK | AAALAEEAPPVLSSNAAK |
| PEQEQFLLPR | SPPLSVALSGQR |
| TTTAVALRPEPK | LVPGLYQR |
| SMSLDESHPAK | LSM[147]PLSAGPR |
| SM[147]SLDESHPAK | QDIEPEHSVR |
| AVYCPECK | PAKPPLSSNNNR |
| Q[111]FHDLITCR | AYTPSTTPTAPHTVAGGKPK |
| SEPEQEQFLLPR | LM[147]GPPAALPK |
| SVTFAEDLESEIDSGSPR | EINELNLK |
| YSDYAVSK | PNPSALAFR |
| LHAEISSQTD | NDENNLSR |
| GLTM[147]PPLSPPATSSAR | |
| Pc | |

| Psc | |
|---|---|
| TSPDGPTIKPQPTQQVTPSQQQPFQDQQQAEK | IDHSSSSNSSFTHN |
| EPDPEPESEEDEYTFTENDVDTHQATTSSATHDK | LIDIYEQTNK |
| EKEPDPEPESEEDEYTFTENDVDTHQATTSSATHDK | RLIDIYEQTNK |
| EKEPDPEPES[167]EEDEYTFTENDVDTHQATTSSATHDK | YNTWEPEVNILDR |
| TSPDGPTIKPQPTQQVTPSQQQPFQDQQQAEK | PQPTQQVTPSQQQPFQDQQQAEK |
| E[111]KEPDPEPESEEDEYTFTENDVDTHQATTSSATHDK | KGVVEYR |
| EKEPDPEPESEEDEY[243]TFTENDVDTHQATTSSATHDK | PCNNLAINQK |
| TSPDGPT[181]IKPQPTQQVTPSQQQPFQDQQQAEK | FWLPAK |
| IDHSSSSNSSFTH | IASEAATQLK |
| DNATDDPVDLVYAAEK | PFQDQQQAEK |
| IDHSSSSNSSFTH | IDHSSSSNSSFTHN |
| QQVTPSQQQPFQDQQQAEK | SFVPEPDSNSSSSEDQPLIGTK |
| PVDLVYAAEK | EKEPDPEPESEEDEYTFTENDVDTH |
| IDHSSSSNSSF | QPLTPLSPR |
| NNLAINQK | PLTPLSPR |
| ASEAATQLK | IDIYEQTNK |
| TSPDGPTIKPQPTQQVTPSQQQPF | SESPLTHH |
| SEAATQLK | QPLTPLS[167]PR |
| Smc1 | |
| TALFEEISGSGLLK | YSM[147]VDLESSK |
| FEDEIENESQR | SEQDTLDGETNR |
| NFLVFQGAVENIAM[147]K | FDALALDGTFYQK |
| VQSTNEEFENAR | FM[147]EAIIVDTEK |
| ELVM[147]QQER | QSELATVESQIK |
| SGLISGGSHDLAR | SELDSVNR |
| SVQDEEDALEGLK | HEKMEADR |
| SSQAALEEQNR | VIGGSS[167]EYR |
| AVIGGSSEYR | |
| Smc3/Cap | |
| LDLTIVDLNDEVQGDNK | INQM[147]ATAADSYR |
| LPGEVTFM[147]PLNR | QELM[147]STLSSQDQR |
| STGLDCVTLDGDQVSSK | TEYTSQIAEFEK |
| AYYGPVIENFSCDK | LDNLLINNLFR |
| TIEDRL | TELVSAEK |
| EVENSDAFTGIGIR | EIDQLNDDIR |
| SVLM[147]TEQQQLLR | GSLTGGYFNTSR |
| VLDSFVER | LQTLEEEKEELKEYQK |
| IASLGAVPLVDPSYTR | VSHIDCVTR |
| dSfmbt | |
| GELYSLVLNTK | GNIDPSVIPIQK |
| ISDLIAQLK | TPTDNNTQSVK |
| M[147]NFTFDEYYSDGK | IEPVNRPGLVLK |
| DNNFDDNGSELEPK | LGLNLECVDKDR |
| LVCVATVAR | INDSLQSR |
| PP1-87B | |
| IFCCHGGLSPDLTSM[147]EQIR | ICGDIHGQYYDLLR |
| YSENFFLLR | AHQVVEDGYEFFAK |
| HEFDLICR | IYGFYDECK |
| TFTDCFNCLPVAAIVDEK | |
| Ebi | |
| DLLASGSGDSTAR | PGTGVAGSAGGNK |
| IEPGTGVAGSAGGNK | APSGAVTIR |
| LASTLGQHK | HLASGSFDK |
| Enok | |
| TDVSSLVEQPVK | VVSSVNVVSTAR |
| VQLLEEIER | TDQQLVQVK |
| STPVASSTPEK | |
| Grh | |
| TAVHGSQNSPTTSLVDTSTNGSTR | VVGPNGEQQQIISR |
| IEFDENQIIR | NEAGEHILTR |
| ISTTSINNIYR | |
| Eaf6 | |
| NEGSVVSGM[147]VSGSTNSGGNK | KAETSEQLANLER |
| DLLGTPTSNTK | AETSEQLANLER |
| SSITSM[147]AICNPER | |
| Pho | |
| KGDNVINYNIHENDK | VLTNSLSNNDINTEESGVVDK |
| GNLSQENNISER | NIGYGENQETSK |
| Fs(1)h | |
| NNAAAGNAAGGAAGAAAGAGSVGGVGGAGAAGGGNASK | EELELEPVTAK |
| GGRGAKGS[167]GAGGVGASNNAAAGNAAGGA | GSSSAGAGGGVGGANASAGGAGAR |
| CG1845 | |

| Psc | |
|---|---|
| SLNNSSSPVGINR | LLLAAPASEGIVQK |
| GCILNADAPPLEENAPWAR | EPVDTSEVPDYTDIVK |
| Rdx | |
| VAITDVDHEVLK | DFLLDEANGLLPEDK |
| SSTFSAGANDK | M[147]ADDLLAAADK |
| Rad21 | |
| YLLADCNEAFVK | DSLELSQLTSGNSR |
| AHVFETNIEK | |
| 26–29 kd proteinase | |
| HGPLSVAIDASPK | LYGAVTPVK |
| DEIPDQYDWR | |

This table displays the peptide coverage as well as the number of unique and total peptides found for the 23 proteins, which were specifically enriched in the sample and could be identified by a minimum of four peptides. Below the table, the individual peptides are listed.