

Supplementary Figure S1A

In Vitro Acetylated Pol δ

73 exclusive unique peptides, 114 exclusive unique spectra, 197 total spectra, 880/1107 amino acids (79% coverage)

9 exclusive unique peptides, 11 exclusive unique spectra, 22 total spectra, 87/107 amino acids (81% coverage)

1 MGRKRLITDS YPVVKRR EGP AGHSKGELAP ELGEEPQPRD EEEAELELLR QFDLAWQYGP CTGITRLQRW CRAKQMGLEP PPEVWQVLKT
91HPGDPRFQCS LWHLYPL

Immunoprecipitated Pol δ from HEK293T Cells

42 exclusive unique peptides, 50 exclusive unique spectra, 138 total spectra, 634/1107 amino acids (57% coverage)

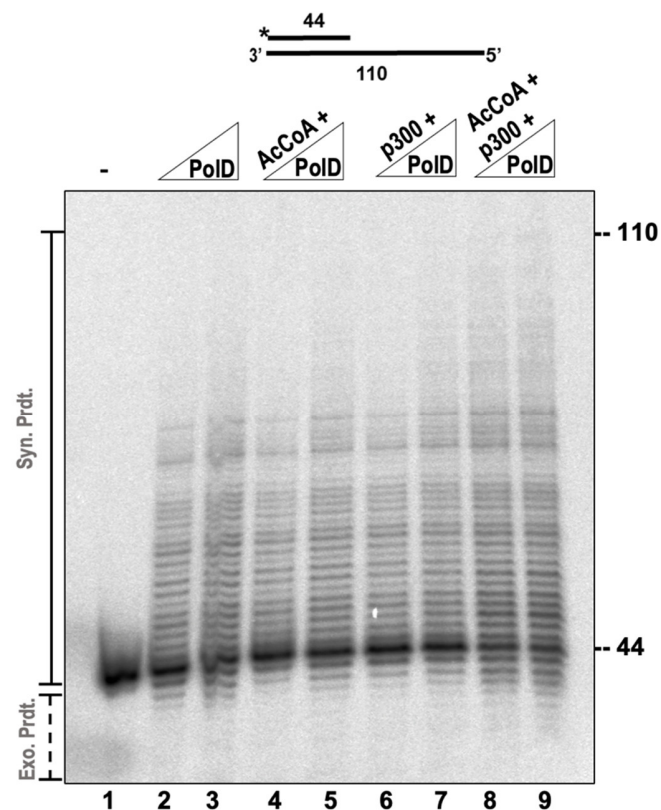
91	MDGKKRPPGPG	PGVVPKKRARG	GUGDDDDADPR	PSQFEEDLAL	MEEMEAHRL	QEQEELLESQ	VLEGVADGGV	PPSALDPRWL	RPTPPDALDP
97	TEPLIFFOOLE	IDHYVVGPAQP	VGPPGPPPSRG	SVPVLRFAVG	TDEGFSVCCH	IHGFAFPYFT	PAPPGFGPEH	MGDLORELNL	AISRDSPGGR
187	ELTGPAVLVA	ELCSRESFMFG	YHGSDGSPSPFL	RITVALPRLV	APARRLLEQG	IRVAVGLGTPS	FADPYEGLDF	EIRFMWDTDF	VGCNWLPLPA
271	GKYALRLKEK	ATKQCLEADV	LHGSDVVSHPP	EGVPQRITAPL	RVLSPDIECA	GRKGIPEPE	RDRVIQICSL	GLRWGEPEFI	LRALALTLPK
381	APILGAKVQS	YEKEEDLLQA	WSTFIRIMDP	DVPTGYNIQN	FDLPYLISRA	QTLKVQTFPF	LGRVAGLCSN	IRDSSFQSKQ	TGRDRTKVVS
451	MVGRVQMDML	QVLLREYKLR	SYTLNNAVSFH	FLGGEQKEDVQ	HSITLTLQNG	NDQTRRLAV	YCLDKDAYLPL	RLLERLMVLV	NAVEMAVRTG
547	VPLSYLLSLRG	QGVKKVVSQLL	RQAMHEGLLM	PVVKSEGGED	VTGATVIIEPL	KGYDVPDIAT	LDFFSLYPSI	MLAHNLCTYT	LLRPGTAQKL
621	GLTDEQFIRI	PTGDEFEVKT	VRKGLLPQIL	ENLLSARKRA	KAELEAKETDP	LRRQVLDGRQ	LALKVNSAVS	YGFTGAQGVK	LPCLIEISQV
737	TGFGRRQMIK	TQOLVESKYTS	VENGYSSTSAK	VYVGDTDSVQ	CRFGVSSVAE	AMALGREAAD	VWSGFFSPSI	RLFEFGVYFP	YLLISKKRYA
811	GLLFSSRPDR	HDRMDCKGLGE	AVRRDNCPLV	ANLVTASLRR	LLIDRDPEGA	VAHAQDVISD	LLCNRIDISQ	LVITKELTRA	ASDYAGKQAH
901	VELAERMRKA	DGGSAPSLGD	RVPVYVISA	KGVAAVMKSE	PLDFVLVLESH	PIDTQYYLEK	QLAKPLRLIF	EPILGEGRAE	AVLLRGDHTR
991	CKTVLTGKVG	GLLFAFAKRRN	CCIGCRPTVLS	HQGAIVEFCFO	PRESELYQKE	VSHNLALEER	FSRLWTQCQR	CQGSLEDHVI	CTSRDPCIFY
1081	MRKKVRKDL	DEQELLRRRG	PPGPEAW						

10 exclusive unique peptides, 13 exclusive unique spectra, 24 total spectra, 87/107 amino acids (81% coverage)

1 MGRKRLITDS YPVVKRR EGP AGHSK GELAP ELGEEPQPRD EEEAELELLR QFDLAWQYGP CTGITRLQRW CRAK QMGLEP PPEVWQVLKT
91 HPGDPR FQCS LWHLYPL

Peptide sequences detected by mass spectrometric analysis are highlighted in yellow. Lysine residues detected have a +42 dalton change were identified as acetylated residues and have been highlighted in green. Oxidized methionine residues served as dynamic modification controls (also highlighted in green). Supplementary Figure 1A displays the sequence obtained from *in vitro* acetylated Pol d and Figure 1B displays the sequence obtained from endogenous polymerase that was immunoprecipitated from HEK293T cells. Coverage obtained is also indicated above the sequence.

Supplementary Figure S2



Supplementary Figure S2: Synthesis Activity of Pol Delta

The synthesis activity of pol δ was assayed using the 5nM substrate (U1:T1) in the presence of varying concentration (20, 50 nM) of either pol δ , pol δ + AcCoA, pol δ + p300 (HAT domain) and acetylated pol δ (pol δ +AcCoA+p300) as described in Materials and Methods. The substrate is depicted above the gel image and the asterisk denotes the location of the radiolabel. Exonuclease products (Exo.Prdt.), and synthesis products (Syn. Prdt.) are indicated adjacent to the gel image. Nucleotide sizes are also indicated.