

# Supporting Information

## **A flow extension tethered particle motion assay for single-molecule proteolysis**

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**Table S1. Relationship between DNA substrate binding density and trajectory mobility**

<i>[substrate], pM</i>	<i>Total beads per fov, count*</i>	<i>Trackable trajectories per fov, count*</i>	<i>Fully mobile trajectories*</i>
0.2	641 ± 93	298 ± 63	60.3 ± 6.5%
1	1,308 ± 218	418 ± 114	27.9 ± 9.3%
5	2,561 ± 202	1,038 ± 239	3.2 ± 1.4%
25	2,475 ± 409	1,206 ± 346	0.3 ± 0.1%

\*n = 3, reported as mean ± S.E.M.

**Table S2. Peptides, oligonucleotides<sup>a</sup>, oligonucleotide-peptide conjugates<sup>b</sup>, and fluorogenic peptides used in this study.**

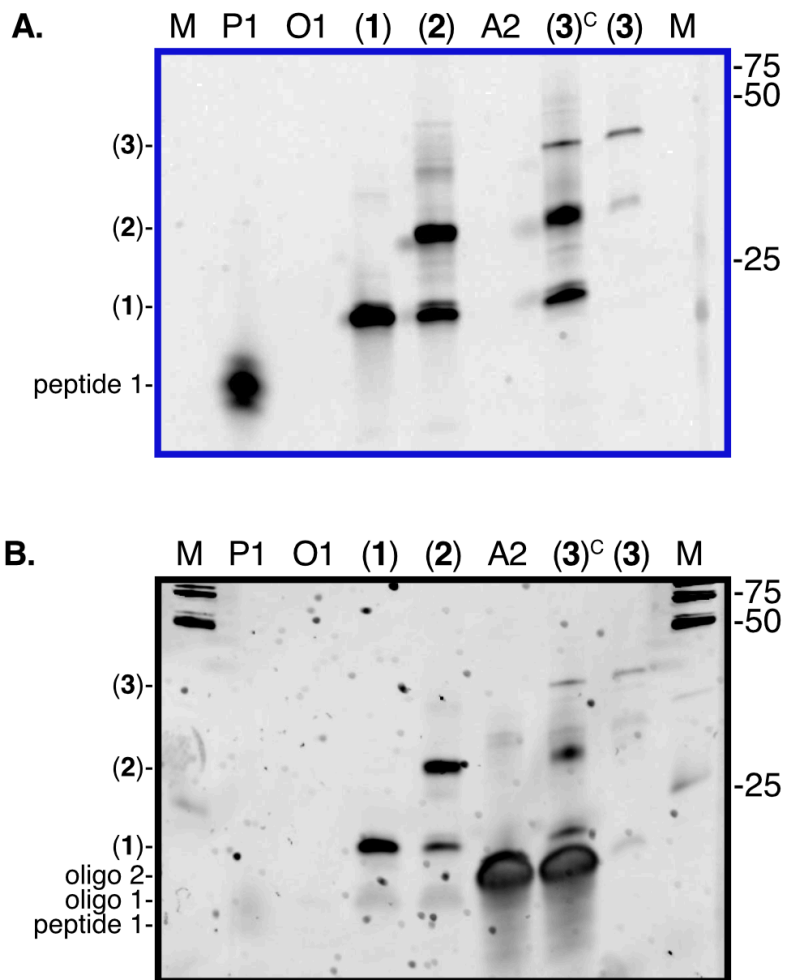
<i>Biopolymer ID</i>	<i>Sequence</i>	<i>Description</i>	<i>Source</i>
peptide 1	H <sub>2</sub> N-GGG[K-(5-FAM)]GC-COOH	Sortase donor peptide with ε-[5-amino-fluorescein (5-FAM)]-Lys (6aa)	Genscript
peptide 2	H <sub>2</sub> N-CNIPYKIEAVQSLPATGGH-COOH	Human Notch1 S2 containing peptide (19aa)	Genscript
peptide 3	H <sub>2</sub> N-CGENLYFQGLPRTGGH-COOH	TEV consensus containing peptide (16 aa)	Genscript
oligo-peptide conjugate 1 (1)	H <sub>2</sub> N-GGG{K-(5-FAM)}G{C-[SMCC-HN-(oligo 1)-3']}-COOH	Polyglycine-oligonucleotide Sortase donor peptide (6 aa-17 nt)	This study
oligo-peptide conjugate 2-N (2)	H <sub>2</sub> N-CNIPYKIEAVQSLPAT-GGG[K-(5-FAM)]G{C-[SMCC-HN-(oligo 1)-3']}-COOH	Notch1 S2 oligo-peptide conjugate, intermediate (20 nt-23 aa-17 nt)	This study
oligo-peptide conjugate 2-T (2)	H <sub>2</sub> N-CGENLYFQGLPRT-GGG{K-(5-FAM)}G{C-[SMCC-HN-(oligo 1)-3']}-COOH	TEV oligo-peptide conjugate, intermediate (20 nt-19 aa-17 nt)	This study
oligo-peptide-conjugate 3-N (3)	H <sub>2</sub> N-{{3'-(oligo 2)-NH-SMCC}-C}-NIPYKIEAVQSLPAT-GGG{K-(5-FAM)}G{C-	Notch1 S2 double oligo-peptide conjugate (20 nt-23 aa-17 nt)	This study

	(SMCC-HN-(oligo 1)-3')- COOH		
oligo-peptide conjugate 3-T (3)	H <sub>2</sub> N-{{3':(oligo 2)-NH- SMCC]-Cys}- GENLYFQGLPRTGGG[K-(5- FAM)]G{C-[SMCC-HN- (oligo 1)-3']}-COOH	TEV double oligo-peptide conjugate (20 nt-19 aa-17 nt)	This study
oligonucleotide 1	/5AmMC6/GTAAAACGACG GCCAGT	5'-amino-oligonucleotide, from M13F sequencing primer (17 nt)	IDT
activated oligonucleotide 1	4-(N-maleimidomethyl)- cyclohexane-1-amide-HN-5'- (oligo 1)	5'-maleimide-oligonucleotide 1 (17 nt)	This study
oligonucleotide 2	/5AmMC6/G*TCAGAGGTG GCGAAACCC	5'-amino-oligonucleotide, derived from pUC19 vector <i>ori</i> (19 nt) * indicates phosphoramidite bond	IDT
activated oligonucleotide 2	4-(N-maleimidomethyl)- cyclohexane-1-amide-HN-5'- (oligo 2)	5'-maleimide-oligonucleotide 2 (20 nt)	This study
oligonucleotide 3	CTAGACTGGCCGTCGTTT TAC	5' XbaI overhang-containing bridging oligonucleotide, contains the reverse- complement to M13F primer (oligo 1) (21 nt)	IDT

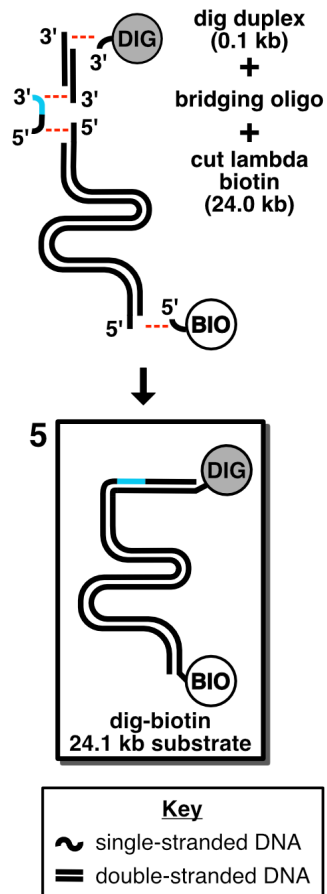
oligonucleotide 4	/5DigN/CAGGGTCGGAAC AGGAGAGC	5'-digoxigenin- oligonucleotide from the pUC19 <i>ori</i> , HPLC purified (20 nt)	IDT
oligonucleotide 5	GCTTAATTAACGACAGGA CTATAAAGATAACCAGGCGT TTCCCCCTGGAAGCTCCC TCGTGCGCTCTCCTGTTC CGACCCTG	Forward strand of the 100 bp duplex from pUC19 <i>ori</i> , with 3' overhang complimentary to dig-oligonucleotide 4, contains a unique PacI site (81 nt)	IDT
oligonucleotide 6	GCACGAGGGAGCTTCCAG GGGGAACGCCTGGTATC TTTATAGTCCTGTCGTAA TTAAGCGTTTCGCCACC TCTGAC	Reverse strand of the 100 bp duplex from pUC19 <i>ori</i> with 3' overhang complimentary to oligonucleotides 2 and 8, contains a unique PacI site (80 nt)	IDT
oligonucleotide 7	GGGCGGCGACCT/3BioTE G/	3'-biotin-oligonucleotide from $\lambda$ phage cohesive site, cosR (12 nt)	IDT
oligonucleotide 8	CTAGGTCAGAGGTGGCGA AACCC	5' XbaI overhang-containing bridging oligonucleotide from pUC19 vector <i>ori</i> , for the all-DNA substrate (23 nt)	IDT

<sup>a</sup> Listed 5' to 3'. Purified by desalting except where HPLC purification is indicated.

<sup>b</sup> SMCC: the portion of crosslinker remaining after Sulfo-SMCC reaction with an amino oligo (R<sub>1</sub>) and cysteine (C) containing peptide (R<sub>2</sub>).



**Figure S1. SDS-PAGE analysis of the double oligo-peptide conjugate intermediate for TEV cleavage.** 15% TBE-Urea PAGE analysis showing: (A) in gel fluorescence of an unstained gel to detect the fluorescein label, and (B) in gel UV excitation fluorescence, of a SybrSafe stained gel to enable DNA detection. Abbreviations above lanes: M, low MW DNA marker (NEB); P1, peptide 1; O1, oligonucleotide 1; (1) oligo-peptide conjugate 1; (2) partially purified oligo-peptide conjugate 2-T; A2, activated oligonucleotide 2; (3)<sup>C</sup> crude double oligo-peptide conjugate 3-T; (3) double oligo-peptide conjugate 3-T.



**Figure S2. Scheme for assembly of DNA-only control substrate.** Product (5) (boxed) is produced by annealing and ligation of a 5' digoxigenin-containing oligonucleotide, a short (100 bp) DNA duplex, a bridging oligonucleotide (oligonucleotide 8, cyan and black), the XbaI-cleaved 24.5 kbp fragment of phage  $\lambda$ , and a terminal biotinylated oligonucleotide.

## Legends for Supporting Movies V1 and V2

**Supporting Movie V1. Flow extension of all-DNA substrate (5) captured at 0.2 pM.** The frame rate is 45 fps. Scale bar is 10 microns. Flow is from left to right. Flow starts at ~8 sec.

**Supporting Movie V2. Single molecule proteolysis of TEV consensus DNA-peptide conjugate (4) with TEV protease.** The frame rate is 45 fps. Scale bar is 10 microns. Flow is from left to right. Flow starts at ~8 sec. Cleavage starts at ~16 sec.