SUPPORTING INFORMATION

Nucleobase Recognition By Truncated α -Hemolysin Pores

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Table S1. Sequences of the oligonucleotides used in this study. B represents the 3' biotin-TEG tag and linker (Figure S1).

Oligonucleotide name	Oligonucleotide sequence $(5' \rightarrow 3')$
poly(dC) ₄₀	СССССССССССССССССССССССССССССССССССССС
poly(dC) ^{A7}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A8}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A9}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A10}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A11}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A12}	ССССССССССССССССССССССССССССССССССССС
poly(dC) ^{A13}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A14}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A15}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A16}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A17}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A18}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A19}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{A20}	ССССССССССССССССССССССССССССССССССССС
poly(dC) ^{T14}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{G14}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{T16}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{G16}	ССССССССССССССССССССССССССССССССССССС
poly(dC) ^{T18}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
poly(dC) ^{G18}	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

Table S2. Residual currents ($I_{RES\%}$) for poly(dC) and oligonucleotides that contain a single adenine nucleobase for the α HL TBM $\Delta 2$ and TBM $\Delta 4$ proteins. The position of a single adenine (A_x) nucleobase (nucleobase position between 7-20) is numbered relative to the 3' biotin tag. The $I_{RES\%}$ values are the mean values (± sd) from n ≥ 3 experiments. $\Delta I_{RES\%}$ is defined as the difference in residual current between an A_x oligonucleotide and poly(dC) ($I_{RES\%}$ ^{Ax oligo} - $I_{RES\%}$ ^{pC}). The mean of the $\Delta I_{RES\%}$ values from individual experiments and the associated error (± sd) are given. The data were collected by using the voltage protocol described in Experimental Methods. Briefly, +160 mV was applied for 900 ms to drive the negatively charged DNA into the pore, followed by -140 mV for 50 ms, to eject the immobilized DNA and a final step to 0 mV for 50 ms.

Position		ΤΒΜΔ2		Position		ΤΒΜΔ4			
of adenine	I _{RES} ^{Ax} (%)	I _{RES} ^{pC} (%)	∆I _{RES} (%)	of adenine	I _{RES} ^{Ax} (%)	I _{RES} ^{pC} (%)	∆I _{RES} (%)		
7	35.2 ± 0.2	35.2 ± 0.2	0.0 ± 0.0	7	31.3 ± 0.1	31.3 ± 0.1	0.0 ± 0.0		
8	35.4 ± 0.4	35.2 ± 0.3	+0.2 ± 0.1	8	30.9 ± 1.5	30.8 ± 1.4	+0.1 ± 0.1		
9	34.9 ± 0.6	35.3 ± 0.6	-0.5 ± 0.0	9	30.2 ± 1.0	30.8 ± 1.0	-0.6 ± 0.0		
10	34.2 ± 0.4	35.0 ± 0.5	-0.8 ± 0.1	10	29.3 ± 2.7	29.8 ± 2.9	-0.4 ± 0.2		
11	34.9 ± 0.4	35.2 ± 0.4	-0.3 ± 0.1	11	29.3 ± 2.2	29.1 ± 2.2	+0.2 ± 0.1		
12	35.1 ± 0.5	35.1 ± 0.5	0.0 ± 0.0	12	30.5 ± 3.0	30.0 ± 2.9	+0.5 ± 0.1		
13	35.2 ± 1.1	34.6 ± 1.2	+0.5 ± 0.1	13	31.5 ± 2.3	30.8 ± 2.3	+0.7 ± 0.0		
14	35.9 ± 0.4	35.3 ± 0.4	+0.6 ± 0.0	14	30.7 ± 1.6	30.7 ± 1.7	-0.1 ± 0.1		
15	35.5 ± 0.7	35.5 ± 0.7	+0.0 ± 0.0	15	29.2 ± 1.6	30.5 ± 1.6	-1.4 ± 0.0		
16	33.5 ± 0.3	34.7 ± 0.4	−1.3 ± 0.1	16	29.2 ± 1.3	30.5 ± 1.3	-1.3 ± 0.0		
17	33.9 ± 0.3	35.2 ± 0.3	−1.4 ± 0.0	17	30.7 ± 1.7	31.3 ± 1.8	-0.6 ± 0.1		
18	34.0 ± 0.4	34.5 ± 0.4	-0.5 ± 0.1	18	31.3 ± 1.5	31.3 ± 1.5	0.0 ± 0.0		
19	34.1 ± 0.9	34.1 ± 0.9	0.0 ± 0.0	19	31.9 ± 1.7	31.9 ± 1.7	0.0 ± 0.0		
20	34.4 ± 1.5	34.4 ± 1.5	0.0 ± 0.0	20	31.4 ± 0.1	31.4 ± 0.1	-0.1 ± 0.1		

Table S3. Residual currents ($I_{RES\%}$) for poly(dC) and oligonucleotides that contain a single adenine nucleobase for the TBM Δ 6 and TBM Δ 6/M113G pores. The position of a single adenine (A_x) nucleobase (nucleobase position between 7-20) is numbered relative to the 3' biotin tag. The $I_{RES\%}$ values are the mean values (± sd) from n ≥ 3 experiments. $\Delta I_{RES\%}$ is defined as the difference in residual current between an A_x oligonucleotide and poly(dC) ($I_{RES\%}$ ^{Ax oligo} - $I_{RES\%}$ ^{pC}). The mean of the $\Delta I_{RES\%}$ values from individual experiments and the associated error (± sd) are given. The data were collected by using the voltage protocol described in Experimental Methods. Briefly, +160 mV was applied for 900 ms to drive the negatively charged DNA into the pore, followed by -140 mV for 50 ms, to eject the immobilized DNA and a final step to 0 mV for 50 ms.

Position	sition TBM∆6				TE	3M∆6/M11	3G
ot adenine	I _{RES} ^{Ax} (%)	I _{RES} ^{pC} (%)	∆I _{RES} (%)	of adenine	I _{RES} ^{Ax} (%)	I _{RES} ^{pC} (%)	∆I _{RES} (%)
7	21.3 ± 1.4	21.3 ± 1.4	0.0 ± 0.0	7	23.5 ± 0.5	23.5 ± 0.5	0.0 ± 0.0
8	21.3 ± 1.8	21.3 ± 1.8	0.0 ± 0.0	8	25.5 ± 2.0	25.5 ± 2.0	0.0 ± 0.0
9	22.2 ± 1.0	22.6 ± 1.1	-0.4 ± 0.1	9	24.6 ± 1.3	24.6 ± 1.3	0.0 ± 0.0
10	21.6 ± 0.3	21.6 ± 0.3	0.0 ± 0.0	10	24.1 ± 0.2	23.7 ± 0.3	+0.4 ± 0.1
11	22.8 ± 1.3	23.7 ± 1.2	+0.9 ± 0.1	11	26.0 ± 1.4	24.6 ± 1.3	+1.4 ± 0.1
12	23.0 ± 0.5	21.9 ± 0.6	+1.1 ± 0.0	12	25.0 ± 0.2	23.7 ± 0.2	+1.3 ± 0.1
13	22.1 ± 0.6	22.1 ± 0.6	0.0 ± 0.0	13	25.9 ± 1.8	25.9 ± 1.8	0.0 ± 0.0
14	20.8 ± 0.2	22.1 ± 0.2	-1.3 ± 0.0	14	23.1 ± 1.0	24.4 ± 1.0	-1.3 ± 0.0
15	21.0 ± 0.1	21.8 ± 0.1	-0.9 ± 0.1	15	22.8 ± 0.2	23.7 ± 0.2	-0.9 ± 0.1
16	21.5 ± 0.1	21.5 ± 0.1	0.0 ± 0.0	16	25.5 ± 1.9	25.8 ± 1.9	-0.3 ± 0.1
17	23.0 ± 1.4	23.0 ± 1.4	0.0 ± 0.0	17	25.2 ± 1.8	25.2 ± 1.8	0.0 ± 0.0
18	22.2 ± 0.1	22.2 ± 0.1	0.0 ± 0.0	18	23.5 ± 0.4	23.5 ± 0.4	0.0 ± 0.0

Table S4. Residual currents (I_{RES%}) for poly(dC) and oligonucleotides that contain a single substituted base at position 18 (αHL NN), 16 (TBMΔ2 and TBMΔ4) or 13 (TBMΔ6 and TBMΔ6/M113G) blocking pores. I_{RES%}, $\Delta I_{RES%}^{OVERALL}$ and δ values are shown for $n \ge 3$ experiments. $\Delta I_{RES%}^{OVERALL}$ is defined as the difference in residual current between the two most widely dispersed current peaks. The δ value is the product of the successive differences between the peaks. If any two peaks overlap, then the δ value is equal to zero. Mean values (± s.d.) are given.

		Residual C		Residual Differen	Current ce (%)	
NN	C ₁₈	T ₁₈	A ₁₈	G ₁₈	$\Delta I_{\text{RES}}^{\text{OVERALL}}$ (%)	δ
	36.9 ± 0.5	36.4 ± 0.5	36.0 ± 0.5	35.7 ± 0.5	1.2 ± 0.0	0.07 ± 0.00
Δ2	C ₁₆	T ₁₆	A ₁₆	G ₁₆	$\Delta I_{RES}^{OVERALL}$ (%)	δ
	35.7 ± 0.1	34.2 ± 0.1	34.2 ± 0.1	35.0 ± 0.1	1.5 ± 0.1	0.00 ± 0.00
Δ4	C ₁₆	T ₁₆	A ₁₆	G ₁₆	$\Delta I_{\text{RES}}^{\text{OVERALL}}$ (%)	δ
	31.4 ± 2.8	30.0 ± 2.7	30.0 ± 2.7	30.0 ± 2.7	1.4 ± 0.1	0.00 ± 0.00
Δ6	C ₁₃	T ₁₃	A ₁₃	G ₁₃	$\Delta I_{\text{Res}}^{\text{OVERALL}}$ (%)	δ
	22.9 ± 1.4	20.9 ± 1.3	21.6 ± 1.3	22.2 ± 1.3	2.0 ± 0.2	0.29 ± 0.06
Δ6/M113G	C ₁₃	T ₁₃	A ₁₃	G ₁₃	$\Delta I_{\text{Res}}^{\text{OVERALL}}$ (%)	δ
	24.2 ± 0.3	22.4 ± 0.3	22.8 ± 0.3	23.7 ± 0.3	1.8 ± 0.1	0.19 ± 0.03

Table S5. Kinetic parameters for the interaction of $am_7\beta$ CD with the homoheptameric TBM Δ 6 and TBM Δ 6/M113N mutant pores. $k_{on} = 1/\tau_{on}[am_7\beta$ CD], where τ_{on} is the mean inter-event interval. $k_{off} = 1/\tau_{off}$, where τ_{off} is the mean dwell time of $am_7\beta$ CD in the pore. $K_D = k_{off}/k_{on}$. Values are shown for $n \ge 3$ experiments. Mean values (± s.d.) are given.

		at +120 mV, 4 (added t	0 μM am ₇ βCD to <i>trans</i>)
	k _{on} (M⁻¹s⁻¹)	k _{off} (s⁻¹)	K _D (mM)
ΤΒΜΔ6	33000 ±1000	4600 ±300	143 ±8
TBMΔ6/M113N	21200 ±1000	2200 ±200	104 ±4

Table S6. Kinetic parameters for dNMP and rNMP identification. Comparison of the kinetic parameters of mononucleotide binding to am₇βCD within the TBMΔ6, TBMΔ6/M113F and TBMΔ6/M113N αHL pores, at pH 6.0 (+120 mV). Mean τ_{off}, k_{off}, I_{RES%}, ΔI_{RES%}, ΔI_{RES%}, ^{OVERALL} and δ values are shown for n ≥ 3 experiments. Values of k_{off} were determined by using k_{off} = 1/τ_{off}, where τ_{off} is the mean dwell time of each NMP in the pore. I_O and I_{RES%} values are mean values (±s.d.) taken from Gaussian fits to event histograms. I_{RES%} = (I_{RES}/I_O) x 100. ΔI_{RES%} ^{OVERALL} is defined as the difference in residual current between the two most widely dispersed current peaks. The δ value is the product of the successive differences between the peaks. If any two peaks overlap, then the δ value is equal to zero. Mean values (± s.d.) are given.

		40 μM am ₇ βCD (<i>trans</i>) at +120 mV (n = ≥3)								
		ΤΒΜΔ6		TBN	/Δ6/M1 ⁻	13F	TBN	MΔ6/M1 ⁻	13N	
Mononucleotide	τ_{off}	$\mathbf{k}_{\mathrm{off}}$	I _{RES}	τ_{off}	k _{off}	I _{RES}	τ_{off}	k _{off}	I_{RES}	
	(ms)	(s⁻¹)	(%)	(ms)	(s ⁻¹)	(%)	(ms)	(S ⁻¹)	(%)	
dGMP	15.0	69.0	44.2	18.0	54.0	19.9	8.0	121.0	22.8	
	±1.0	±1.0	±0.3	±1.0	±2.0	±2.0	±1.0	±1.0	±0.4	
dAMP	14.0	73.0	45.3	17.0	60.0	22.5	6.0	164.0	25.2	
	±1.0	±2.0	±0.3	±1.0	±2.0	±1.8	±2.0	±2.0	±0.8	
dCMP	10.0	98.0	46.8	15.0	65.0	25.9	14.0	72.0	25.6	
	± 2.0	±1.0	±0.3	±1.0	±1.0	±1.8	±1.0	±2.0	±0.5	
dTMP	11.0	90.0	46.3	21.0	47.0	21.5	17.0	58.0	23.1	
	±1.0	±2.0	±0.4	±1.0	±1.0	±2.4	±2.0	±2.0	±0.4	
$\Delta I_{RES}^{OVERALL}(\%)$		2.6 ±0.4	ŀ	6	6.0 ±1.4			2.8 ±0.6		
δ		0.5 ±0.1			5.4 ±0.4			0.3 ±0.1		
										
rGMP	16.0	61.0	41.6	7.0	152.0	14.9	15.0	68.0	30.4	
	±1.0	±1.0	+0.6	±2 0	±1 0	±1 2	+3 0	120	+0.3	
			10.0	±2.0	±1.0	II.Z	10.0	±2.0	10.0	
rΔMP	14.0	70.0	43.2	±2.0 14.0	1.0 70.0	±1.2	9.0	±2.0 108.7	29.5	
rAMP	14.0 ±1.0	70.0 ±2.0	±0.0 43.2 ±0.4	14.0 ±1.0	±1.0 70.0 ±2.0	±1.2 17.1 ±1.5	9.0 ±2.0	±2.0 108.7 ±2.0	29.5 ±0.3	
rAMP	14.0 ±1.0 19.0	70.0 ±2.0 52.0	43.2 ±0.4 43.9	14.0 ±1.0 9.0	111.0 <u>±1.0</u> ±2.0	17.1 ±1.5 17.9	9.0 ±2.0 18.0	±2.0 108.7 ±2.0 55.2	29.5 ±0.3 28.2	
rAMP	14.0 ±1.0 19.0 ±1.0	70.0 ±2.0 52.0 ±2.0	$ \begin{array}{r} 43.2 \\ \pm 0.4 \\ 43.9 \\ \pm 0.7 \\ \end{array} $	14.0 ±1.0 9.0 ±1.0	11.0 70.0 ±2.0 111.0 ±1.0	±1.2 17.1 ±1.5 17.9 ±1.2	9.0 ±2.0 18.0 ±1.0	±2.0 108.7 ±2.0 55.2 ±2.0	29.5 ±0.3 28.2 ±0.4	
rAMP rCMP	14.0 ±1.0 19.0 ±1.0 12.0	70.0 ±2.0 52.0 ±2.0 85.0	$ \begin{array}{r} 10.0 \\ 43.2 \\ \pm 0.4 \\ 43.9 \\ \pm 0.7 \\ 44.1 \\ \end{array} $	$\frac{\pm 2.0}{14.0}$ ± 1.0 9.0 ± 1.0 6.0	11.0 70.0 ±2.0 111.0 ±1.0 167.0	17.1 ±1.5 17.9 ±1.2 20.4	9.0 ±2.0 18.0 ±1.0 10.0	± 2.0 108.7 ± 2.0 55.2 ± 2.0 96.2	29.5 ±0.3 28.2 ±0.4 27.9	
rAMP rCMP rUMP	14.0 ±1.0 ±1.0 ±1.0 ±1.0 ±1.0	70.0 ±2.0 52.0 ±2.0 85.0 ±1.0	$ \begin{array}{r} 10.0 \\ 43.2 \\ \pm 0.4 \\ 43.9 \\ \pm 0.7 \\ 44.1 \\ \pm 0.6 \\ \end{array} $	± 2.0 14.0 ± 1.0 9.0 ± 1.0 6.0 ± 1.0	± 1.0 70.0 ± 2.0 111.0 ± 1.0 167.0 ± 2.0	± 1.2 17.1 ± 1.5 17.9 ± 1.2 20.4 ± 1.4	$ \begin{array}{r} 13.0 \\ 9.0 \\ \pm 2.0 \\ 18.0 \\ \pm 1.0 \\ 10.0 \\ \pm 2.0 \\ \end{array} $	± 2.0 108.7 ± 2.0 55.2 ± 2.0 96.2 ± 3.0	$ \begin{array}{r} 10.0 \\ 29.5 \\ \pm 0.3 \\ 28.2 \\ \pm 0.4 \\ 27.9 \\ \pm 0.6 \\ \end{array} $	
rAMP rCMP rUMP ΔI _{RES} ^{OVERALL} (%)	$ \begin{array}{r} 14.0 \\ \pm 1.0 \\ 19.0 \\ \pm 1.0 \\ 12.0 \\ \pm 1.0 \\ \end{array} $	$70.0 \\ \pm 2.0 \\ 52.0 \\ \pm 2.0 \\ 85.0 \\ \pm 1.0 \\ 2.3 \pm 0.6 \\ $	$ \begin{array}{r} 10.0 \\ 43.2 \\ \pm 0.4 \\ 43.9 \\ \pm 0.7 \\ 44.1 \\ \pm 0.6 \\ \end{array} $	± 2.0 14.0 ± 1.0 9.0 ± 1.0 6.0 ± 1.0	± 1.0 70.0 ± 2.0 111.0 ± 1.0 167.0 ± 2.0 5.5 ± 1.2	± 1.2 17.1 ± 1.5 17.9 ± 1.2 20.4 ± 1.4	$ \begin{array}{r} 13.0 \\ 9.0 \\ \pm 2.0 \\ 18.0 \\ \pm 1.0 \\ 10.0 \\ \pm 2.0 \\ \end{array} $	± 2.0 108.7 ± 2.0 55.2 ± 2.0 96.2 ± 3.0 2.5 ± 0.3	$ \begin{array}{r} 10.0 \\ 29.5 \\ \pm 0.3 \\ 28.2 \\ \pm 0.4 \\ 27.9 \\ \pm 0.6 \\ \end{array} $	

Table S7. Voltage dependences of the residual currents ($I_{RES\%}$), dwell times (τ_{off}) and dissociation rate constants ($k_{off} = 1/\tau_{off}$) for dNMP bound to the TBM Δ 6/M113F•am₇ β CD α HL pore. Mean τ_{off} , k_{off} , $I_{RES\%}$ are shown for $n \ge 3$ experiments. Values of k_{off} were determined by using $k_{off} = 1/\tau_{off}$, where τ_{off} is the mean dwell time of each NMP in the pore. I_O and $I_{RES\%}$ values are mean values (±s.d.) taken from Gaussian fits to event histograms. $I_{RES\%} = (I_{RES}/I_O) \times 100$.

Nucleotide	Potential	τ_{off}	k_{off} = 1/ τ_{off}	I _{RES}	Nucleotide	Potential	τ_{off}	$k_{off} = 1/\tau_{off}$	I _{RES}
Nucleotide	mV	ms	s⁻¹	(%)	nucleotide	mV	ms	s⁻¹	(%)
dGMP	100	16.0 ±1.0	63.0 ±1.0	15.3 ±1.2	dCMP	100	13.0 ±1.0	77.0 ±2.0	23.2 ±1.3
	120	18.0 ± 1.0	54.0 ±2.0	19.9 ±2.0		120	15.0 ±2.0	65.0 ±1.0	25.9 ±1.8
	140	23.0 ±2.0	43.0 ±1.0	21.6 ±1.6		140	17.0 ±1.0	59.0 ±1.0	27.4 ±1.4
	160	27.0 ±2.0	37.0 ±1.0	24.6 ±1.6		160	18.0 ±1.0	56.0 ±1.0	29.1 ±1.6
	180	32.0 ±2.0	31.0 ±1.0	27.5 ±2.2		180	21.0 ±2.0	48.0 ±1.0	31.3 ±1.5
	200	30.0 ±2.0	33.0 ±1.0	31.1 ±1.4		200	24.0 ±2.0	42.0 ±2.0	33.1 ±1.4
dAMP	100	16.0 ±1.0	63.0 ±1.0	20.4 ±0.8	dTMP	100	19.0 ±1.0	53.0 ±1.0	19.8 ±1.6
	120	17.0 ±1.0	60.0 ±2.0	22.5 ±1.8		120	21.0 ±1.0	47.0 ±1.0	21.5 ±2.4
	140	21.0 ±2.0	48.0 ±1.0	48.0 29.7 ±1.0 ±1.6		140	27.0 ±1.0	37.0 ±2.0	24.6 ±1.6
	160	29.0 ±2.0	34.0 ±2.0	32.4 ±1.6		160	31.0 ±1.0	32.0 ±1.0	27.3 ±1.3
	180	28.0 ±2.0	36.0 ±2.0	34.1 ±0.8		180	29.0 ±1.0	34.0 ±1.0	29.8 ±1.4
	200	33.0 ±1.0	30.0 ±1.0	35.8 ±1.9		200	32.0 ±1.0	31.0 ±2.0	32.3 ±1.8

Table S8. Voltage dependences of the residual currents ($I_{RES\%}$), dwell times (τ_{off}) and dissociation rate constants ($k_{off} = 1/\tau_{off}$) for rNMP bound to the TBM $\Delta 6/M113F \cdot am_7\beta$ CD pore. Mean τ_{off} , k_{off} , $I_{RES\%}$ are shown for $n \ge 3$ experiments. Values of k_{off} were determined by using $k_{off} = 1/\tau_{off}$, where τ_{off} is the mean dwell time of each NMP in the pore. I_O and $I_{RES\%}$ values are mean values (±s.d.) taken from Gaussian fits to event histograms. $I_{RES\%} = (I_{RES}/I_O) \times 100$.

Nucleotide	Potential	τ_{off}	k_{off} = 1/ τ_{off}	I _{RES}	Nucleotide	Potential	τ_{off}	k_{off} = 1/ τ_{off}	I _{RES}
Nucleotide	mV	ms	s⁻¹	(%)	Nucleotide	mV	ms	s⁻¹	(%)
rGMP	100	6.0 ±1.0	167.0 ±2.0	9.3 ±1.2	rCMP	100	8.0 ±1.0	125.0 ±1.0	15.4 ±1.2
	120	7.0 ±2.0	152.0 ±1.0	14.9 ±1.2		120	9.0 ±1.0	111.0 ±1.0	17.9 ±1.2
	140	12.0 ±1.0	83.0 ±1.0	19.3 ±2.0		140	13.0 ±1.0	77.0 ±2.0	23.3 ±1.4
	160	13.0 ±2.0	77.0 ±1.0	22.7 ±2.0		160	17.0 ±2.0	59.0 ±1.0	27.6 ±1.6
	180	16.0 ±2.0	63.0 ±2.0	29.2 ±2.0		180	21.0 ±1.0	48.0 ±1.0	31.1 ±1.2
	200	17.0 ±2.0	59.0 ±1.0	31.1 ±1.4		200	20.0 ±1.0	50.0 ±1.0	34.8 ±2.0
rAMP	100	13.0 ±1.0	77.0 ±2.0	14.6 ±1.2	rUMP	100	5.0 ±1.0	200.0 ±1.0	19.2 ±2.0
	120	14.0 ±1.0	70.0 ±2.0	17.1 ±1.5		120	6.0 ±1.0	167.0 ±2.0	20.4 ±1.4
	140	16.0 ±2.0	62.0 ±1.0	19.6 ±1.4		140	10.0 ±1.0	100.0 ±1.0	24.4 ±2.0
	160	17.0 ±1.0	59.0 ±1.0	23.5 ±1.2		160	13.0 ±2.0	77.0 ±2.0	29.6 ±1.8
	180	20.0 ±1.0	50.0 ±1.0	28.6 ±2.0		180	17.0 ±1.0	59.0 ±2.0	32.3 ±2.0
	200	22.0 ±2.0	45.0 ±2.0	32.3 ±1.6		200	21.0 ±2.0	48.0 ±1.0	35.8 ±1.6

Figure S1. The structure of the biotin-TEG linker used to biotinylate the 3' end of the DNA oligonucleotides. The structure was produced with ChemBioDraw Ultra 12.0. The length of the linker, from the biotin to the 3'-phosphate of the first DNA base is ~3 nm, as measured by using Pymol.



Figure S2. Current-voltage (IV) curves for α HL NN, TBM Δ 6, TBM Δ 6/M113G, TBM Δ 6/M113F and TBM Δ 6/M113N. The mean current levels for individual pores (± s.d.) were determined (n ≥ 3) in 1 M KCI, 25 mM Tris.HCI, pH 8.0, containing 0.1 mM EDTA, over a range of applied potentials: TBM Δ 6 (navy) and (A) α HL NN (yellow); (B) TBM Δ 6/M113G (purple); (C) TBM Δ 6/M113F (red); (D) TBM Δ 6/M113N (green).



Figure S3. Representative single-channel recordings with the α HL TBM Δ 6, Δ 6/M113N and Δ 6/M113F pores, showing CD adapter binding (40 μ M am₇ β CD, *trans*). In the case of TBM Δ 6/M113F, the am₇ β CD remains bound for >1.5 h. The traces were recorded in 1 M KCl, 25 mM Tris.HCl, at pH 6.0.



Figure S5. (A) Variation of residual currents ($I_{RES\%}$) with applied potential for each dNMP detected with the TBM $\Delta6/M113F \cdot am_7\beta$ CD pore. (B) Variation of k_{off} with applied potential for each dNMP detected with the TBM $\Delta6/M113F \cdot am_7\beta$ CD pore. Number of experiments: $n \ge 3$. The data are tabulated in **Table S7.**



Figure S6. (A) Variation of residual currents ($I_{RES\%}$) with applied potential for each rNMP detected with the TBM Δ 6/M113F•am₇ β CD pore. (B) Variation of k_{off} with applied potential for each rNMP detected with the TBM Δ 6/M113F•am₇ β CD pore. Number of experiments: n ≥ 3. The data are tabulated in **Table S8.**



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Figure S7. Typical current traces for the TBM Δ 6 pore when blocked with immobilized poly(dC)₄₀ or poly(dC)^{A15} oligonucleotides.

