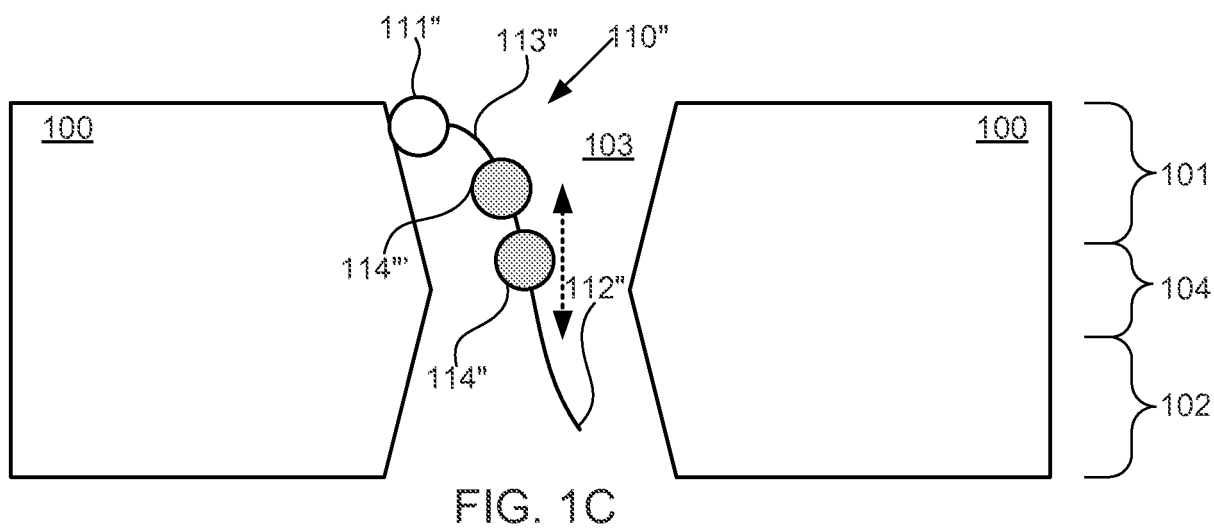
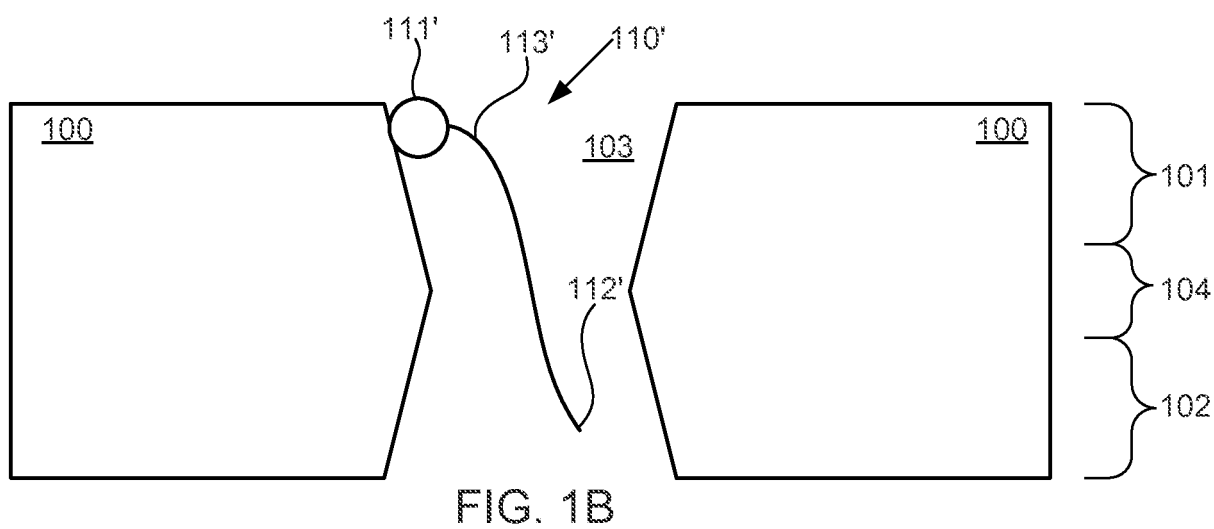
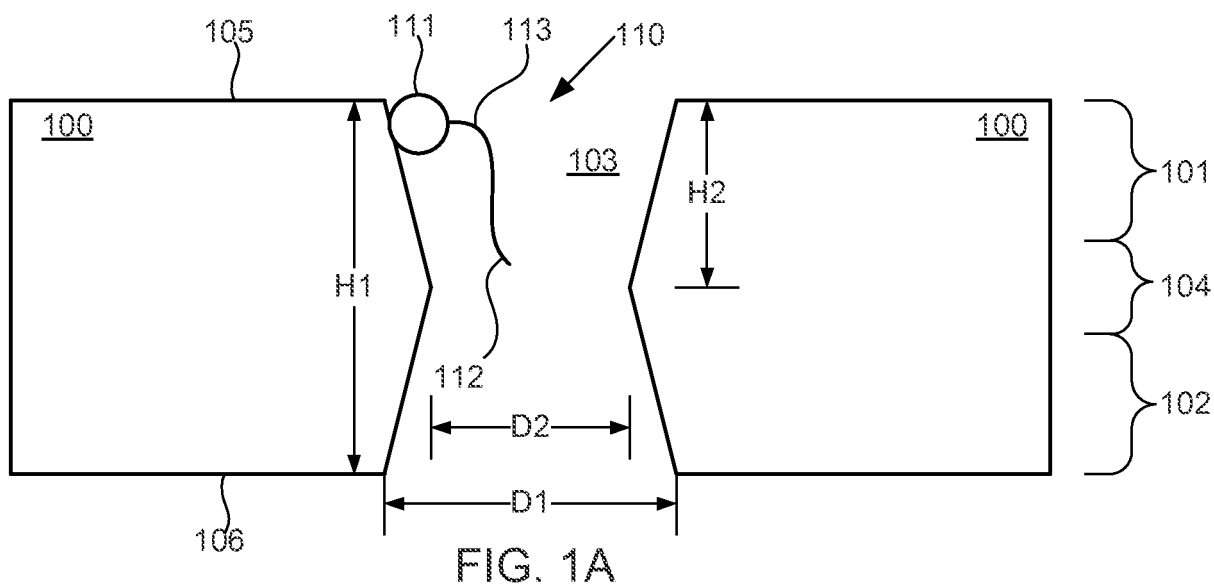
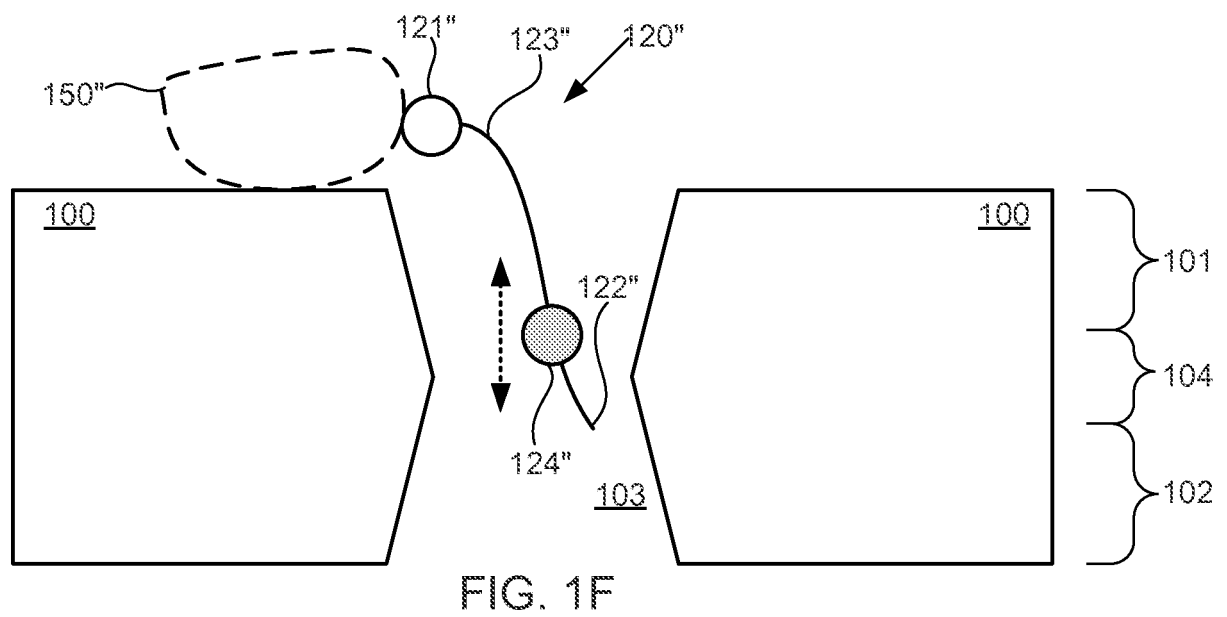
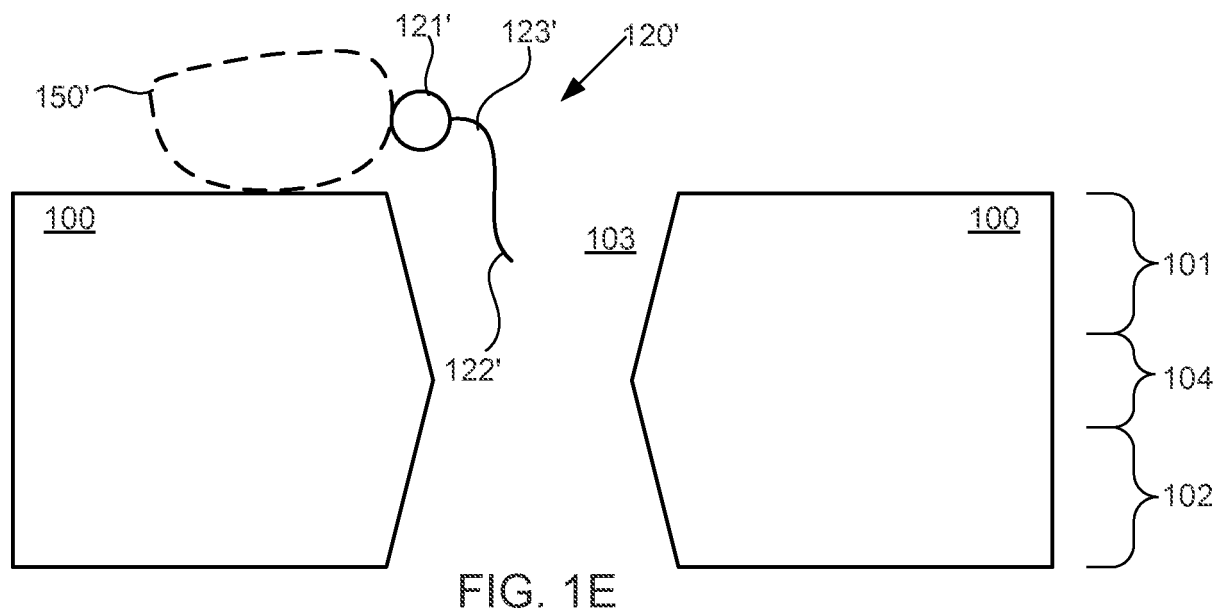
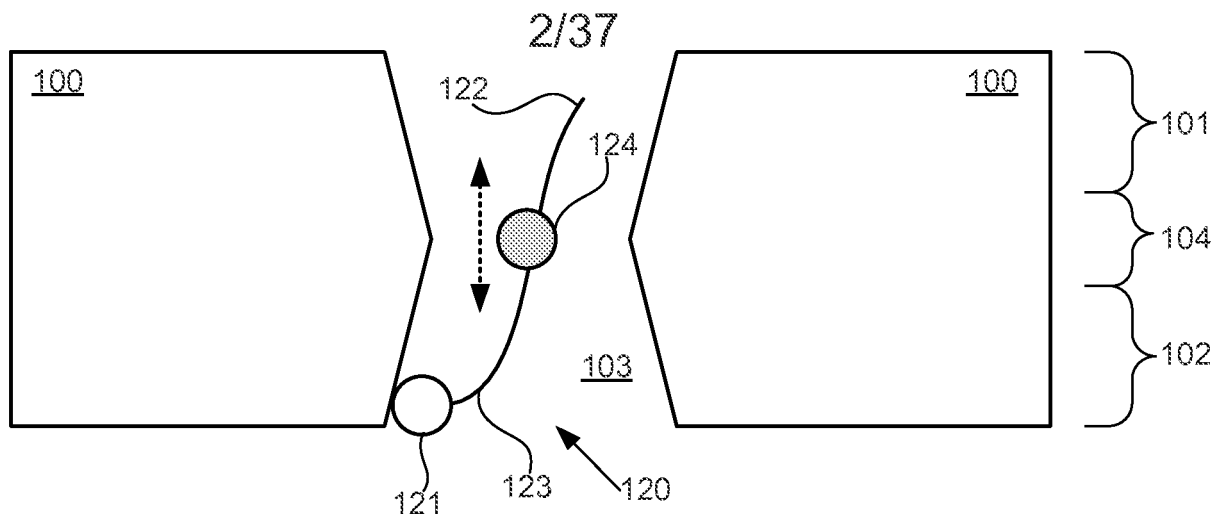
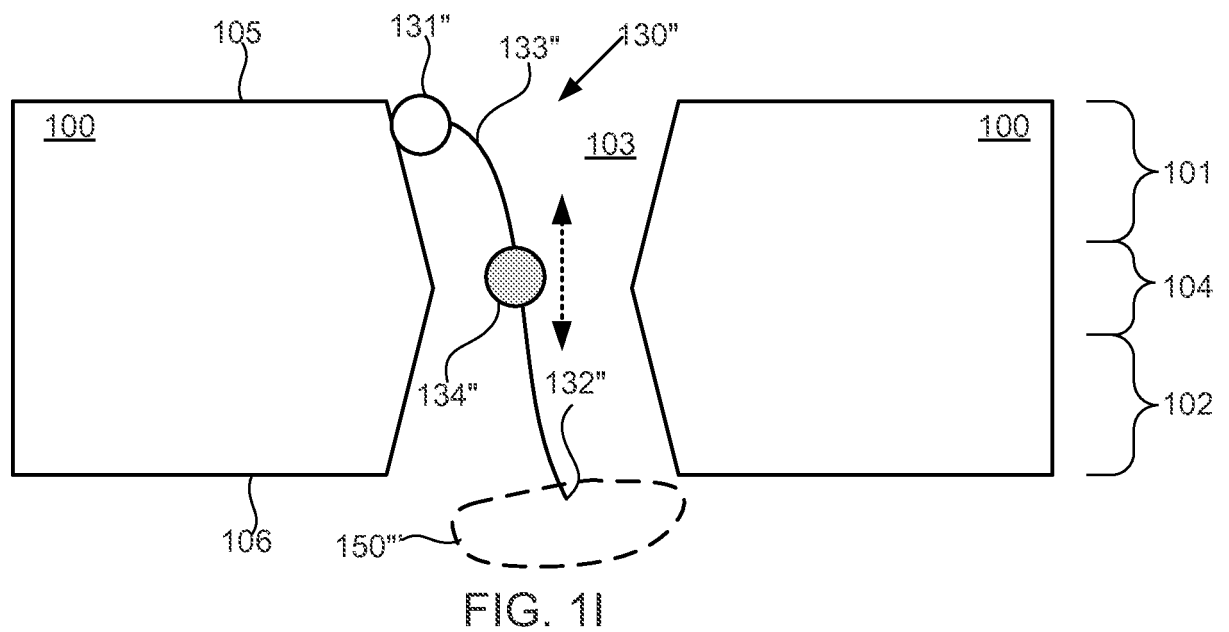
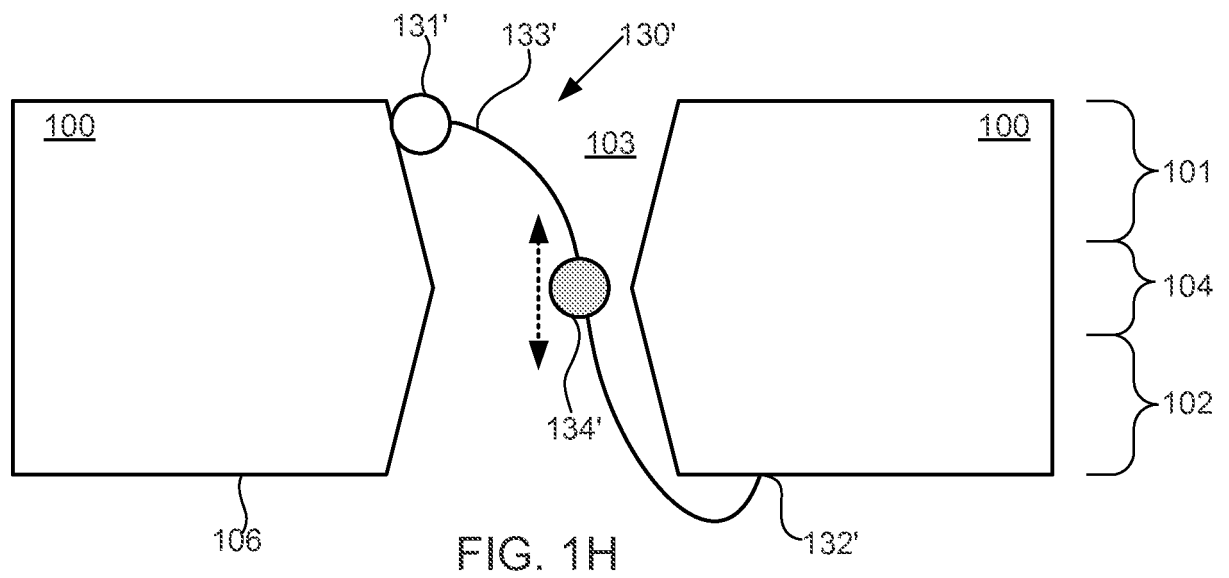
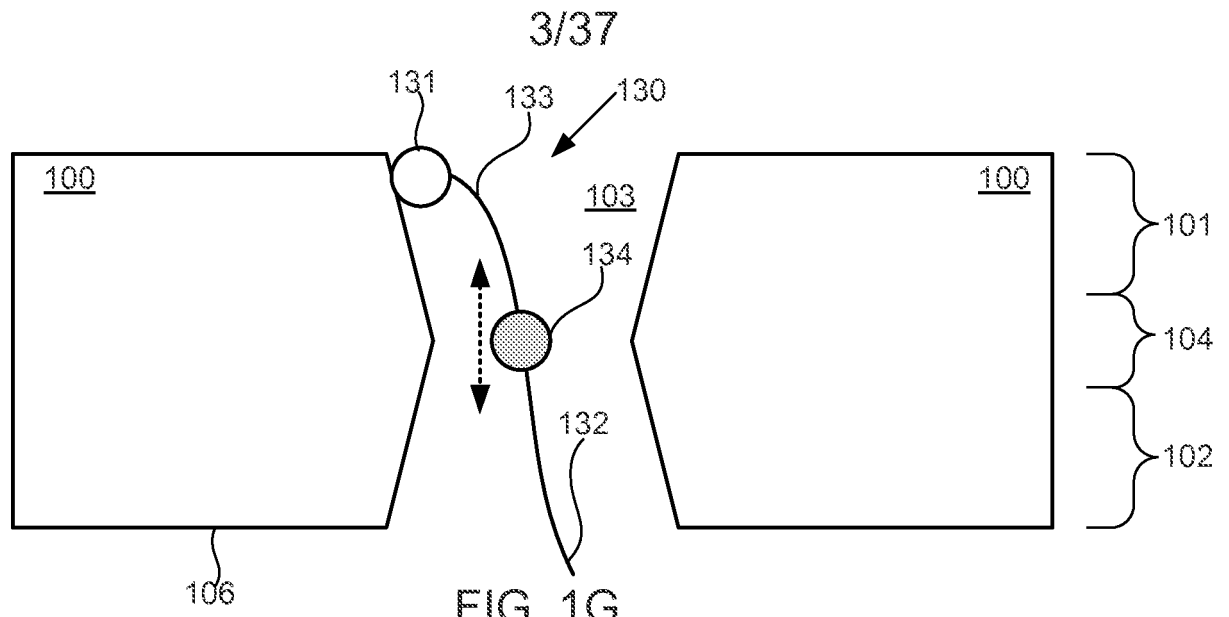


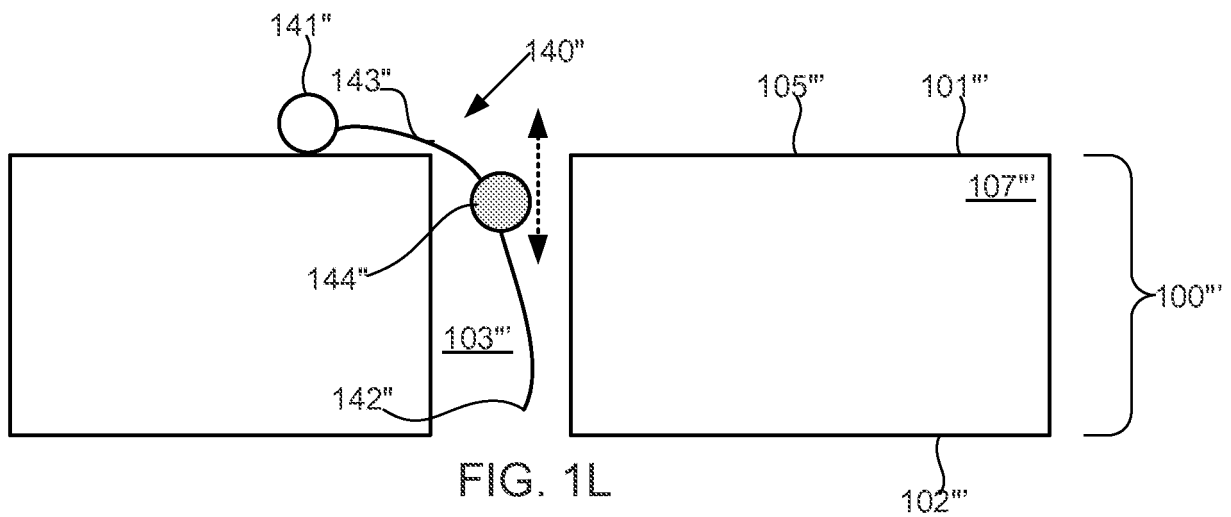
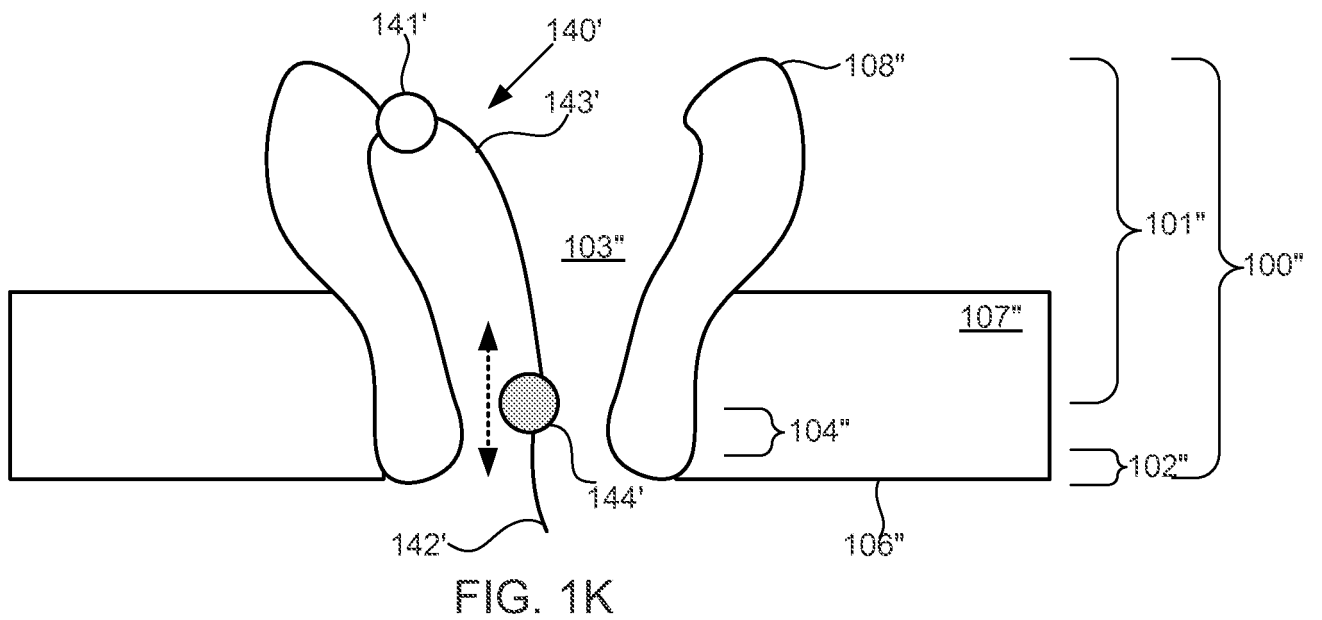
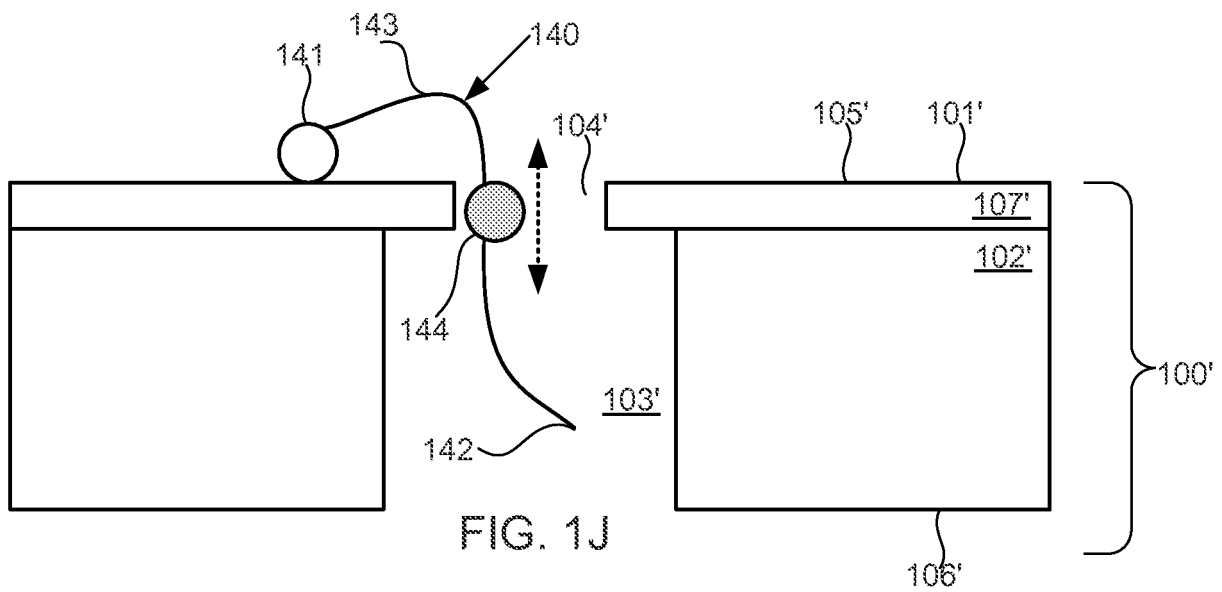
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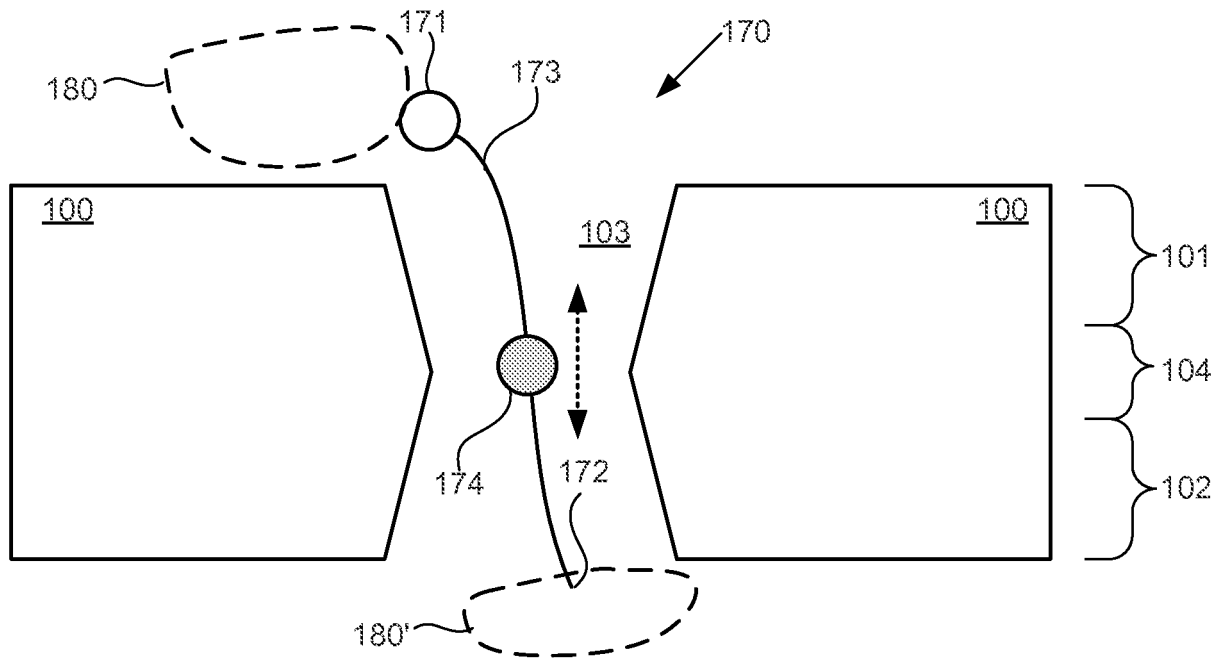
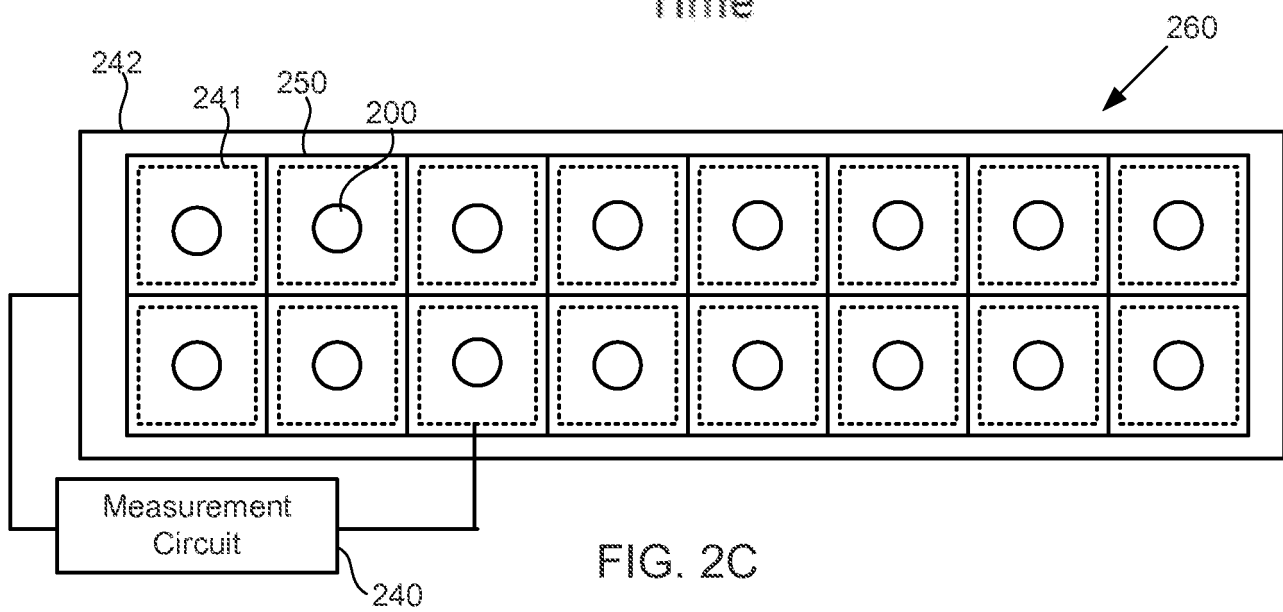
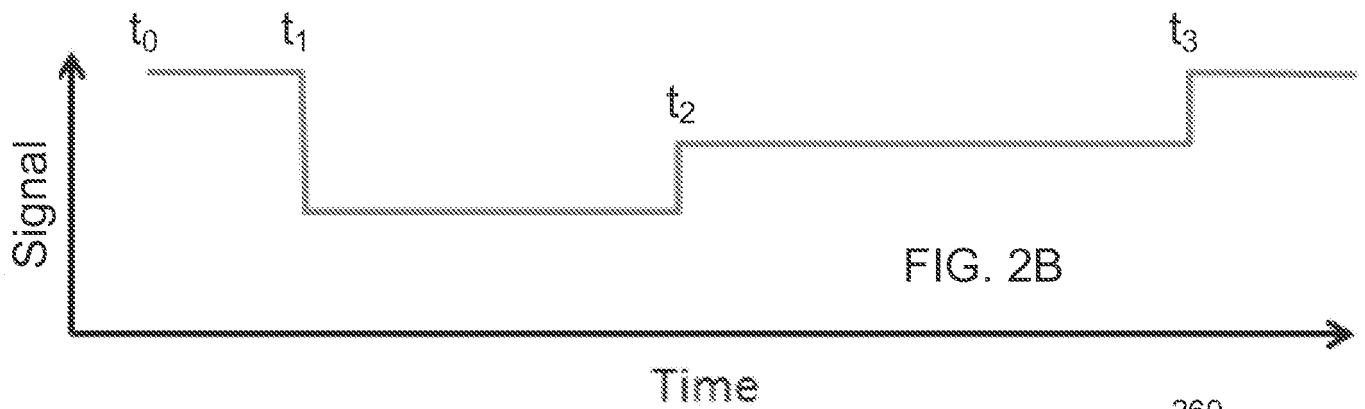
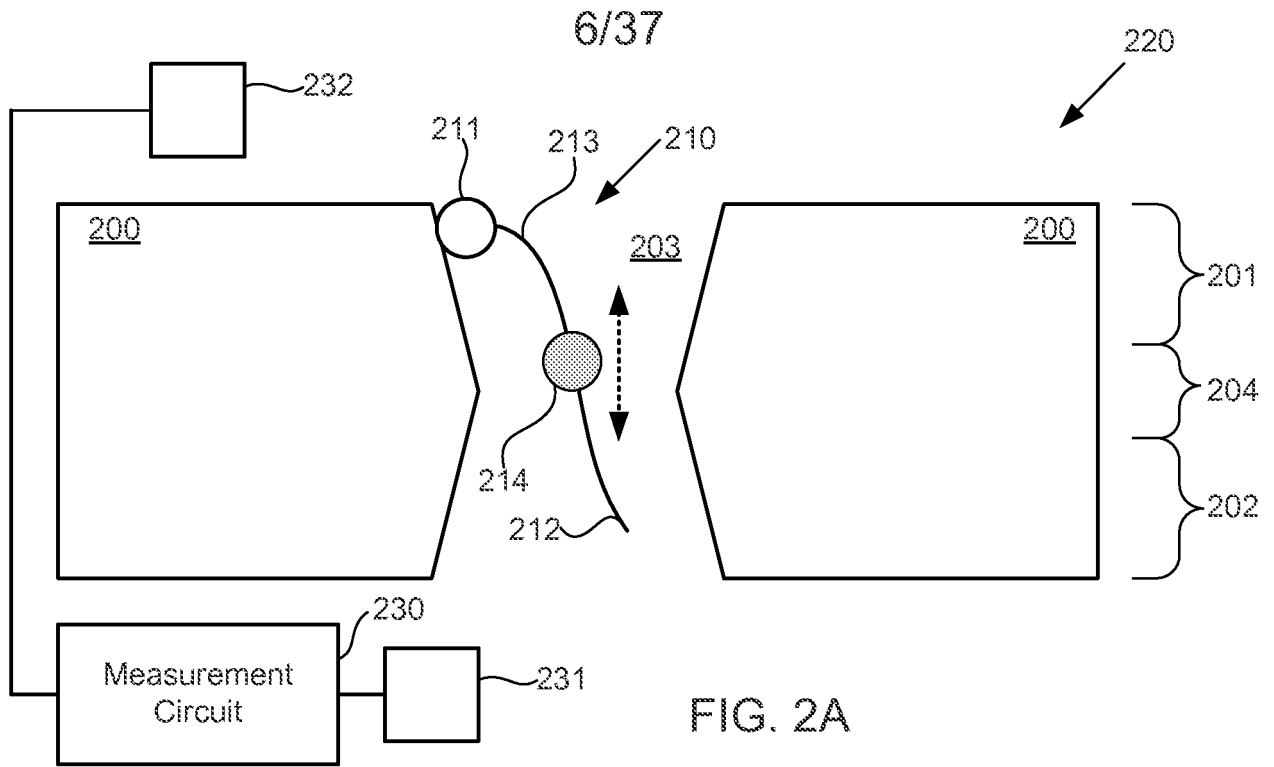


FIG. 1M



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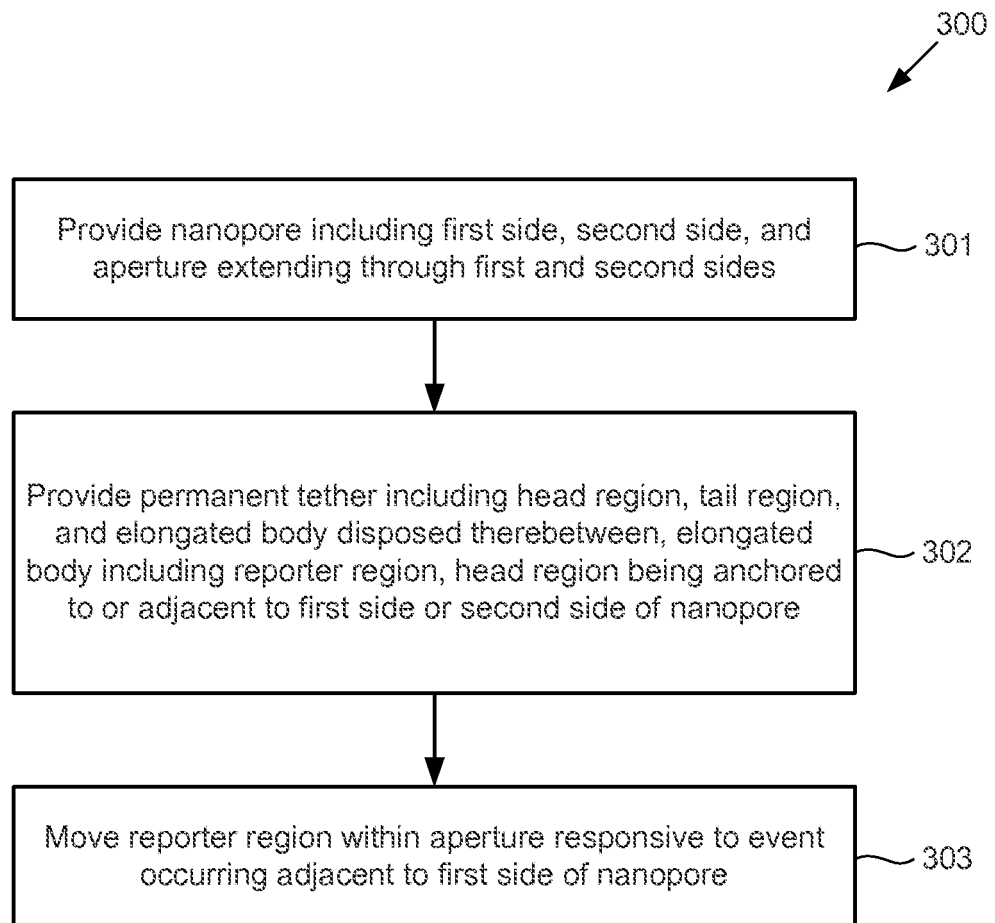


FIG. 3A

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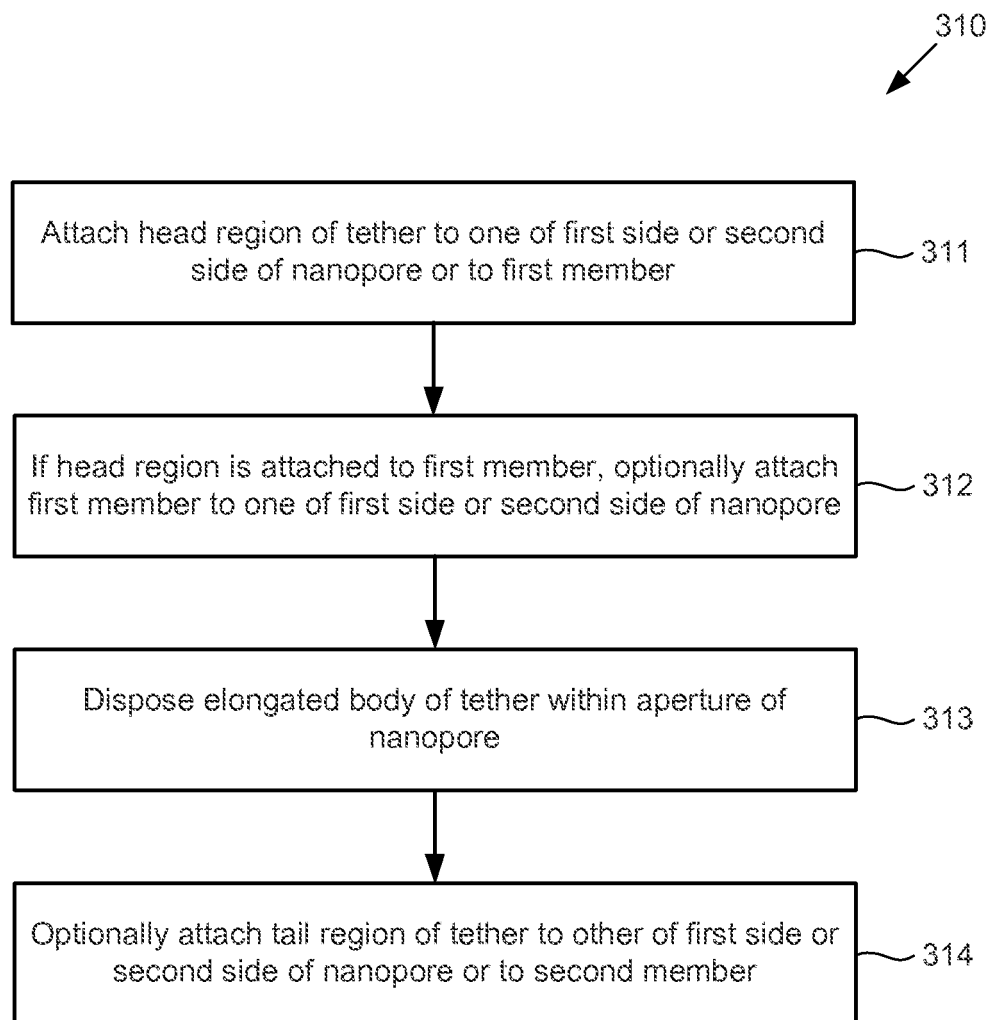


FIG. 3B

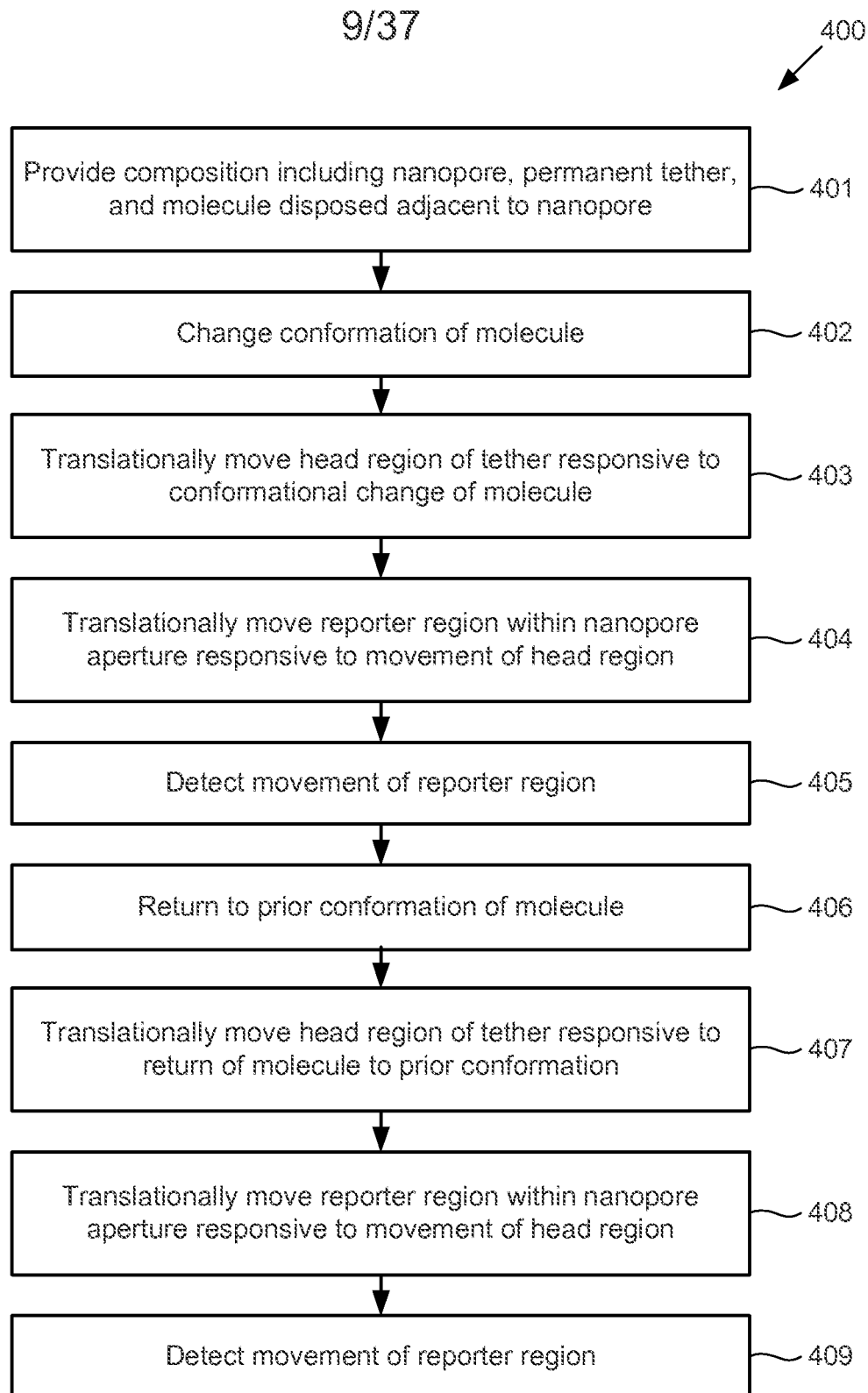


FIG. 4A

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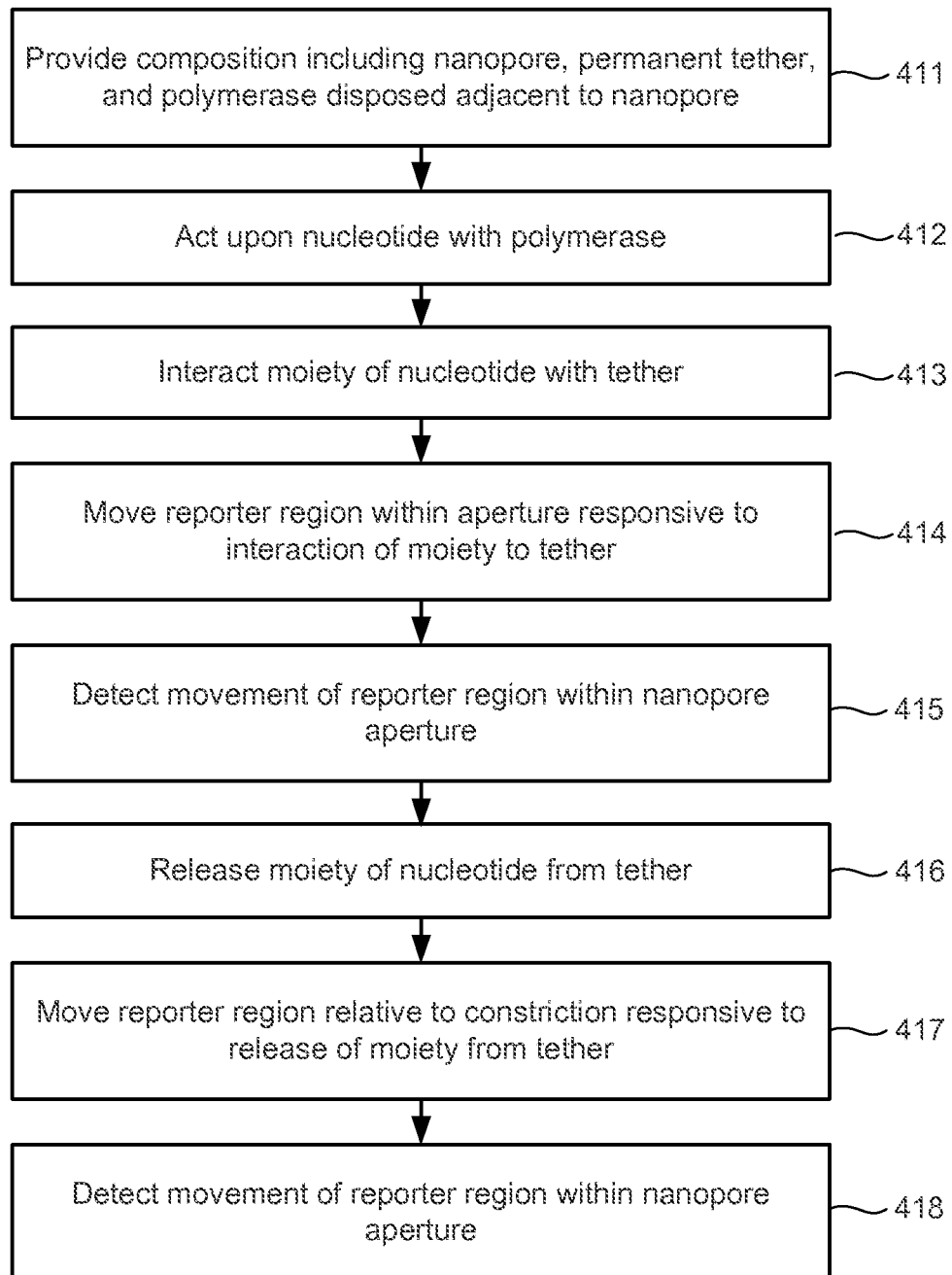


FIG. 4B

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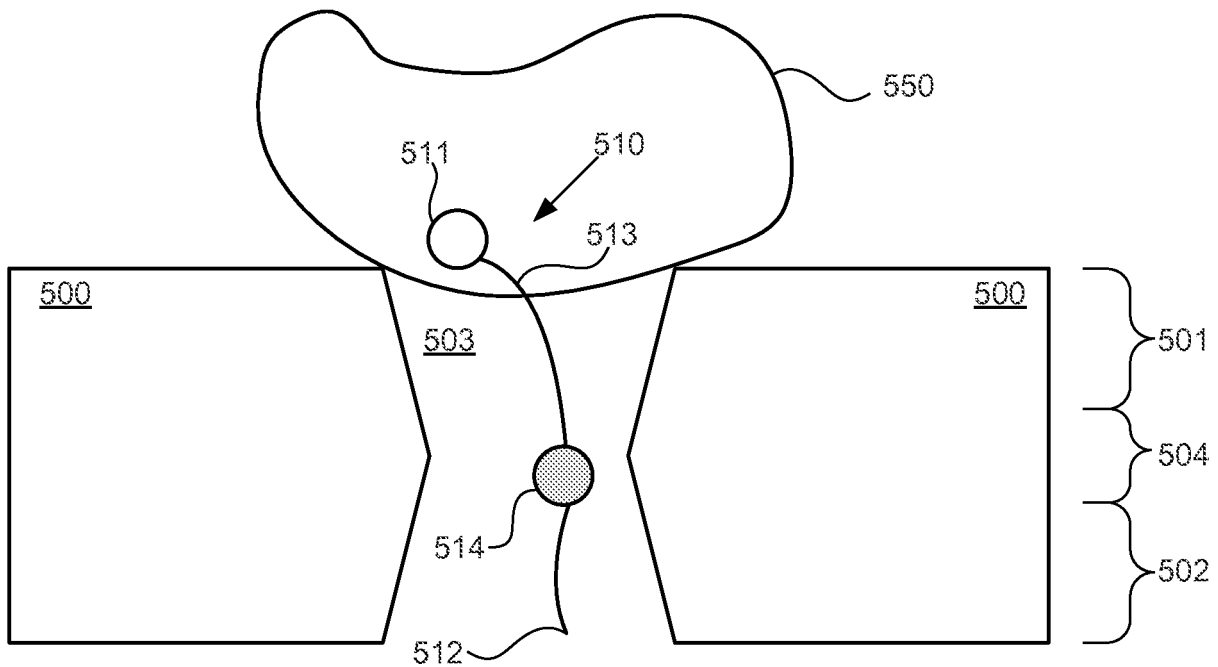


FIG. 5A

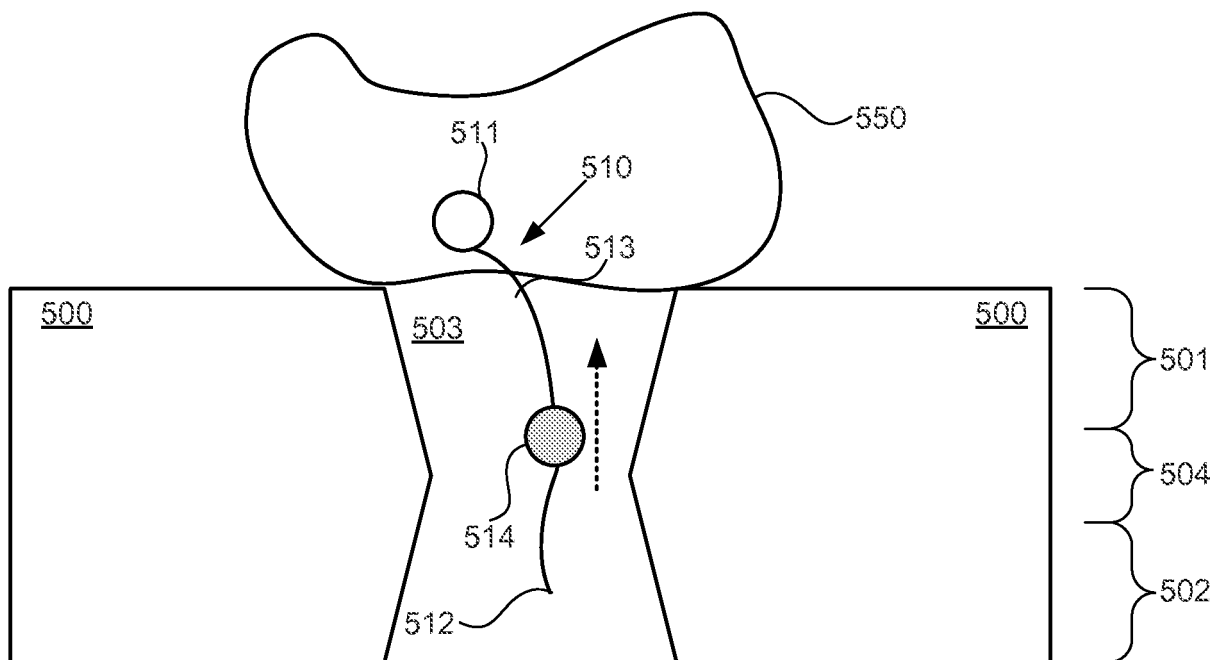


FIG. 5B

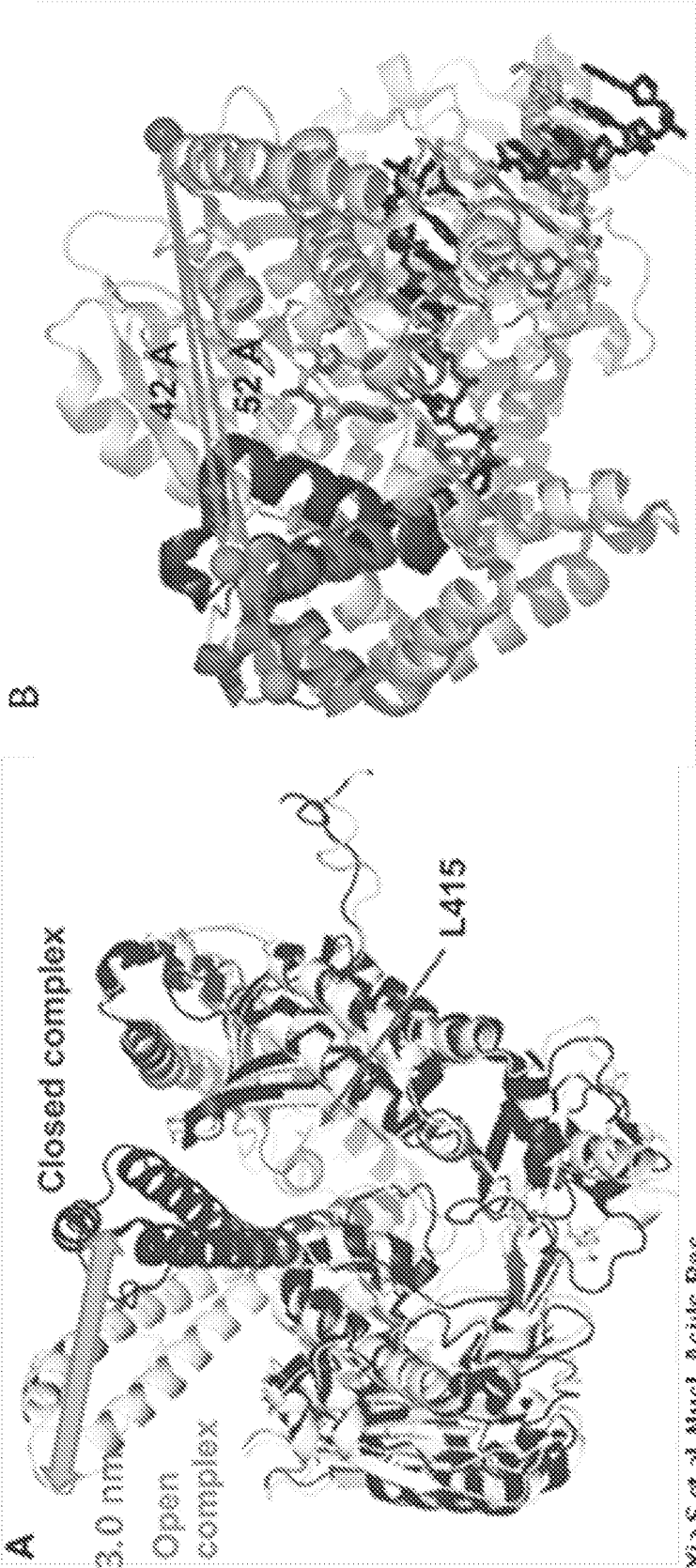


FIG. 6B

FIG. 6A

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2013;naa. gk4674

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Open State

Closed State

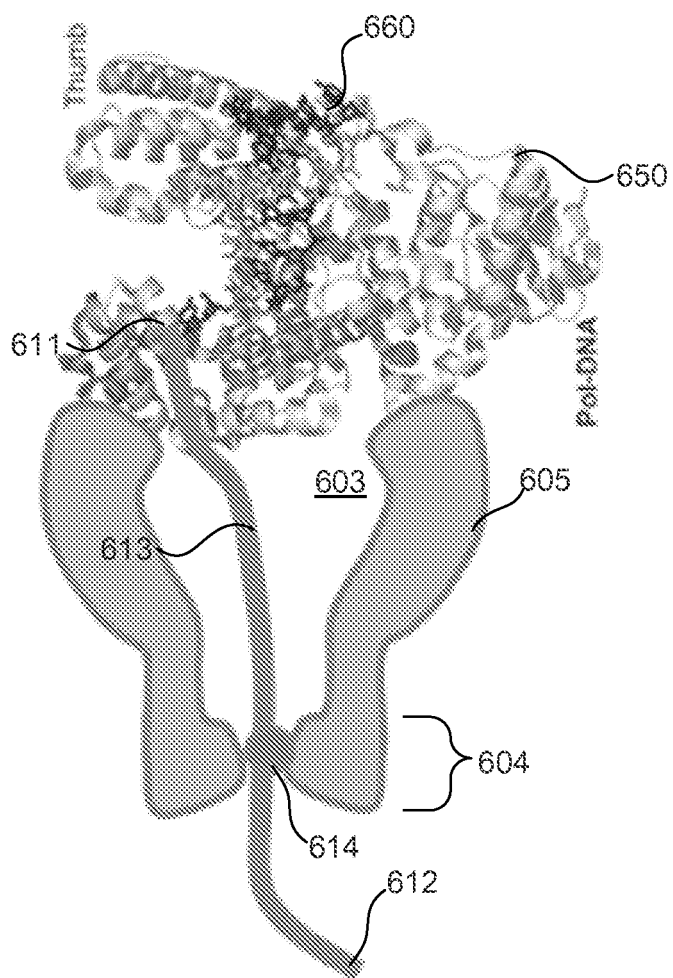


FIG. 6C

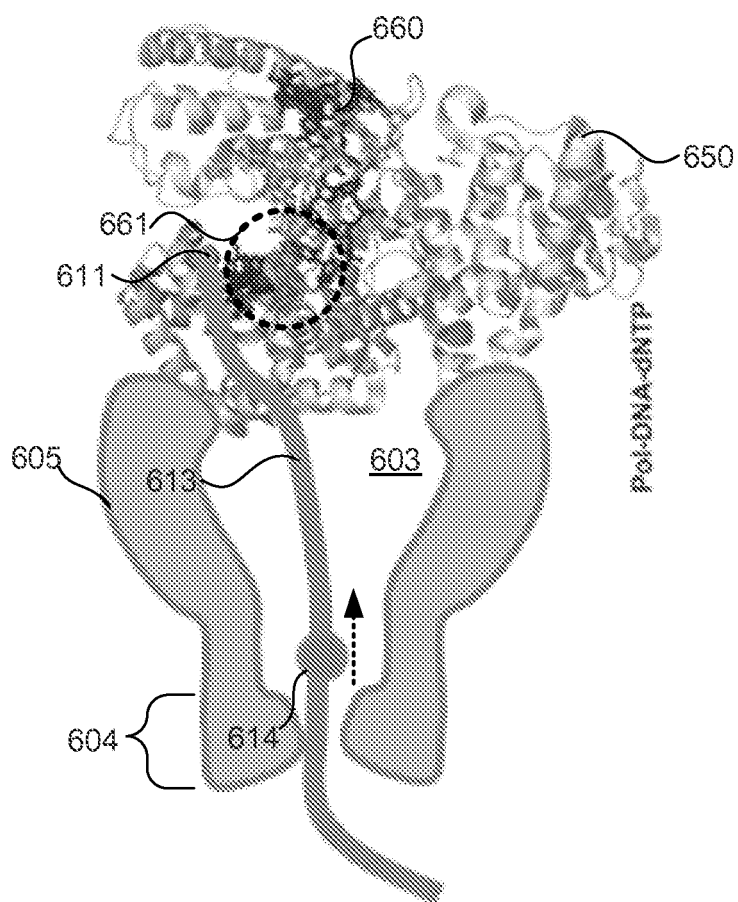
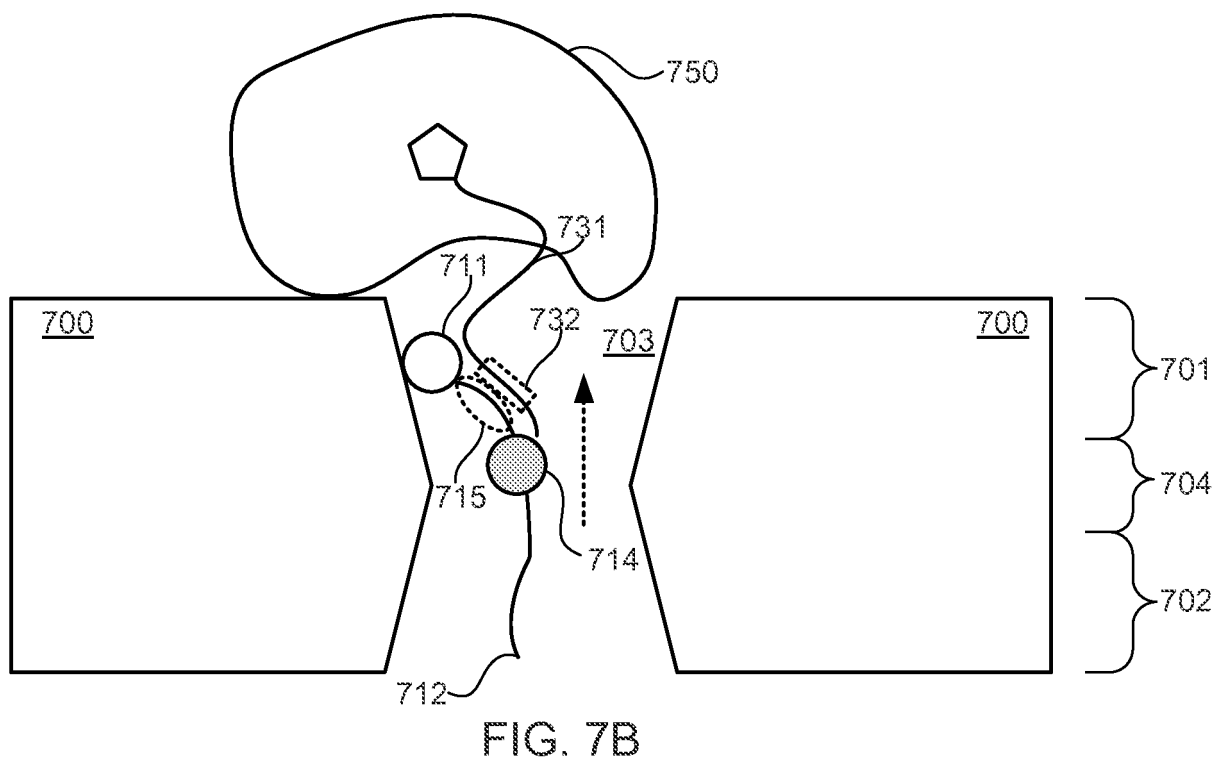
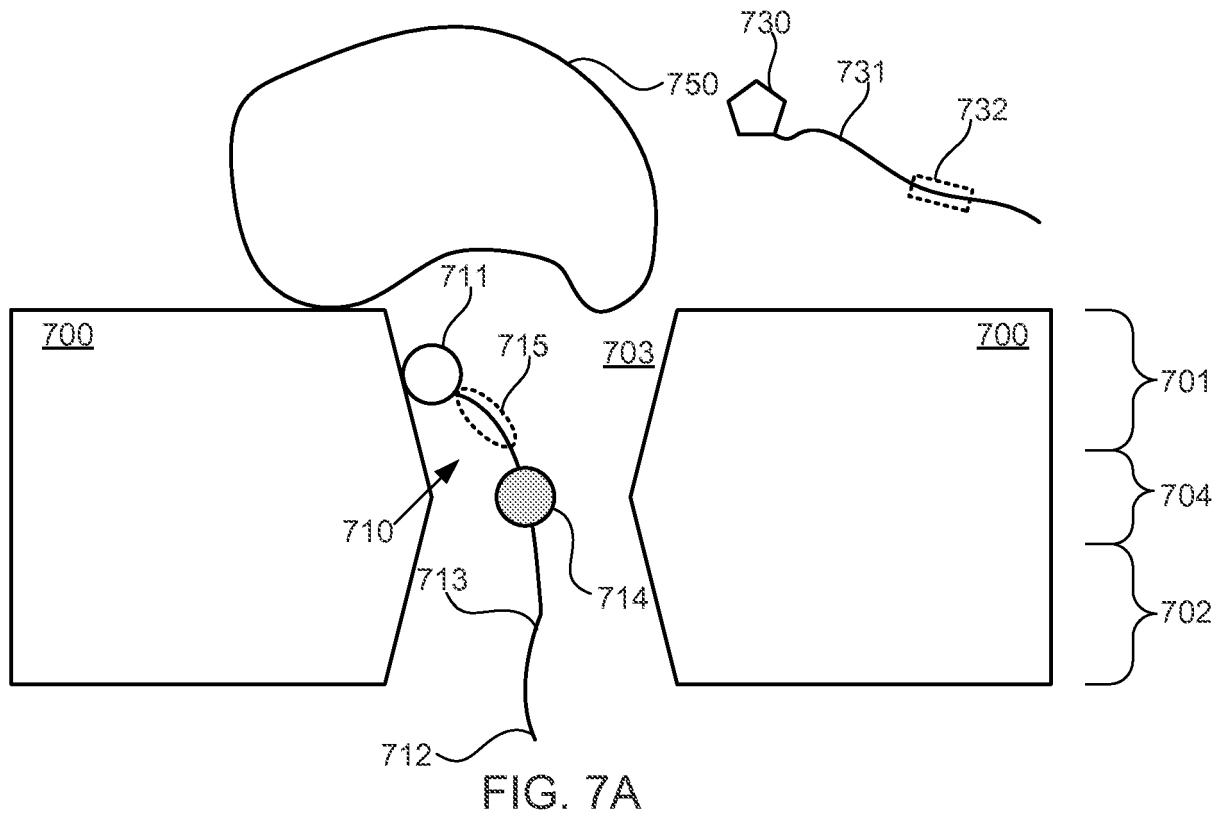


FIG. 6D

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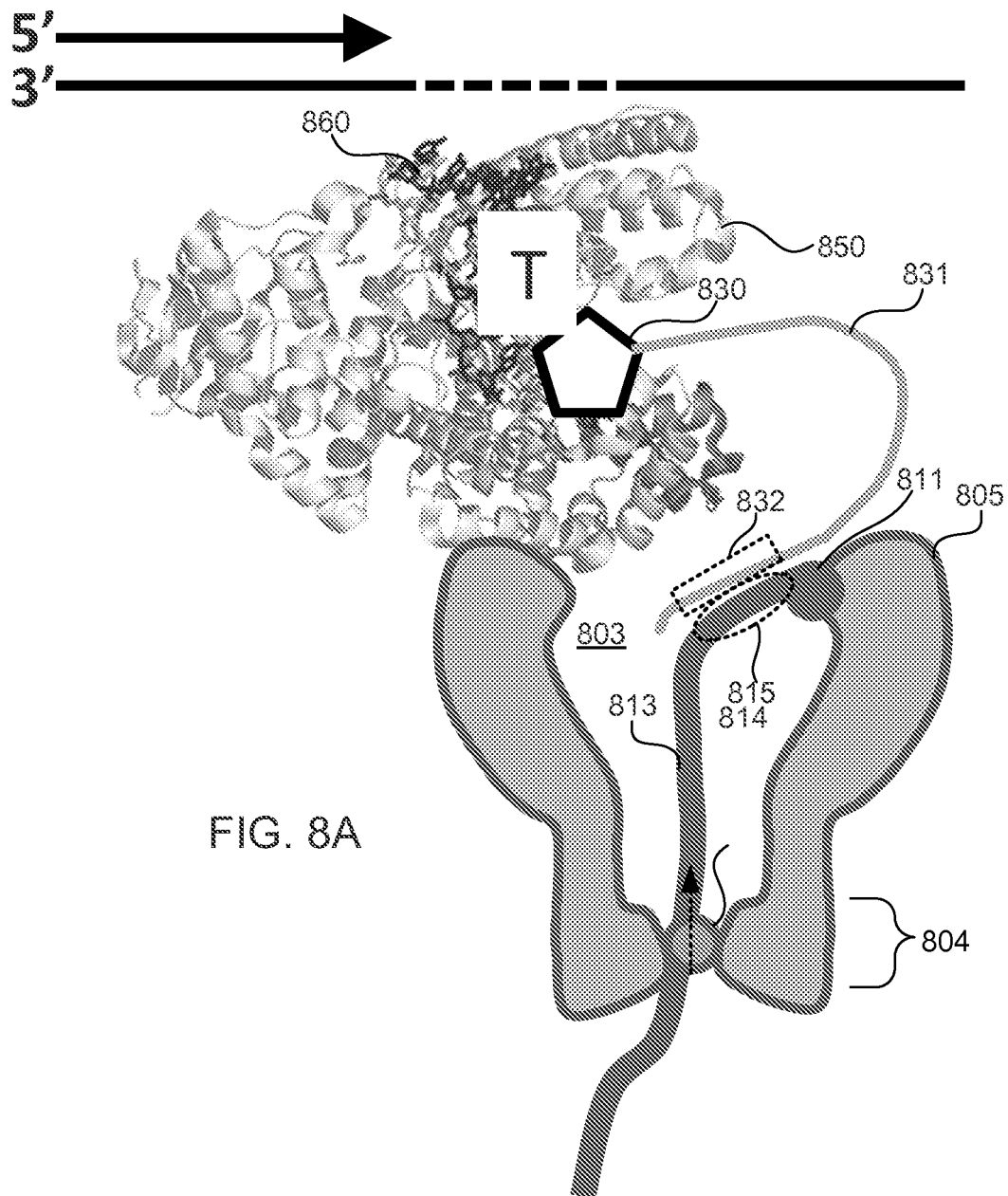


FIG. 8A

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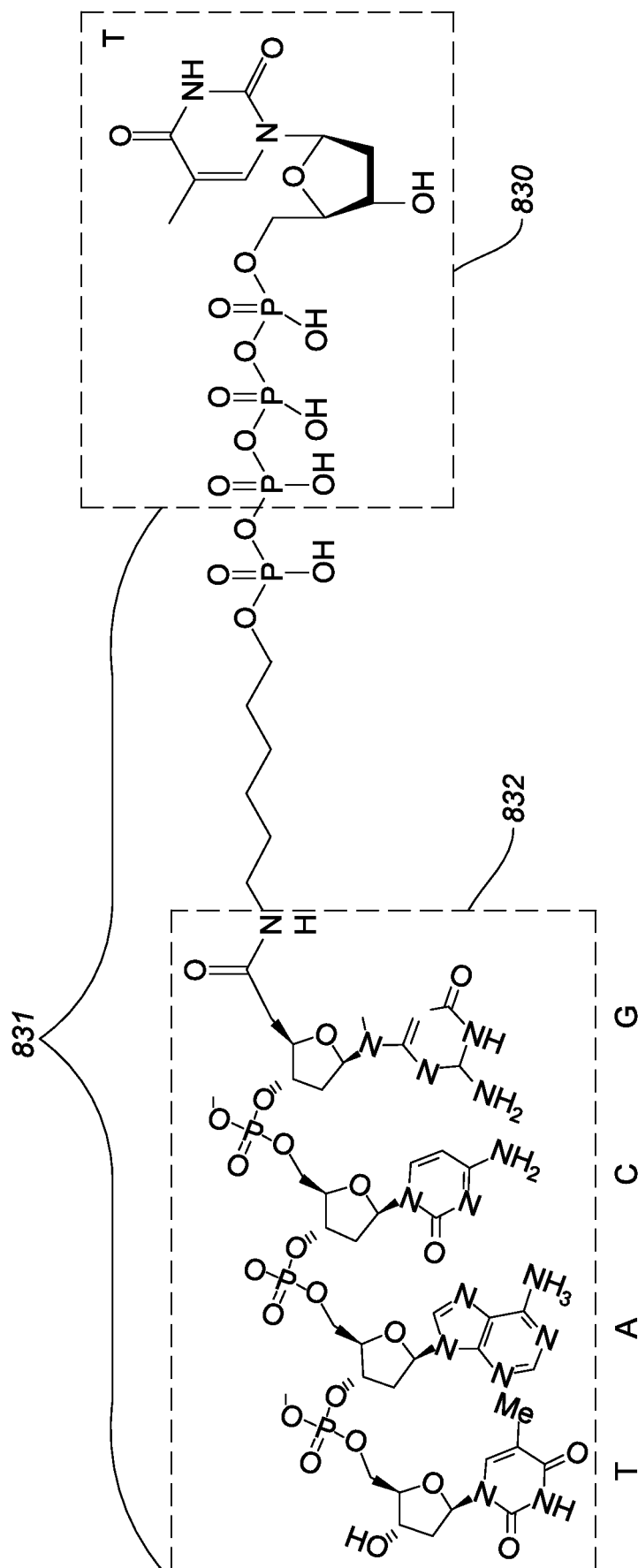


FIG. 8B

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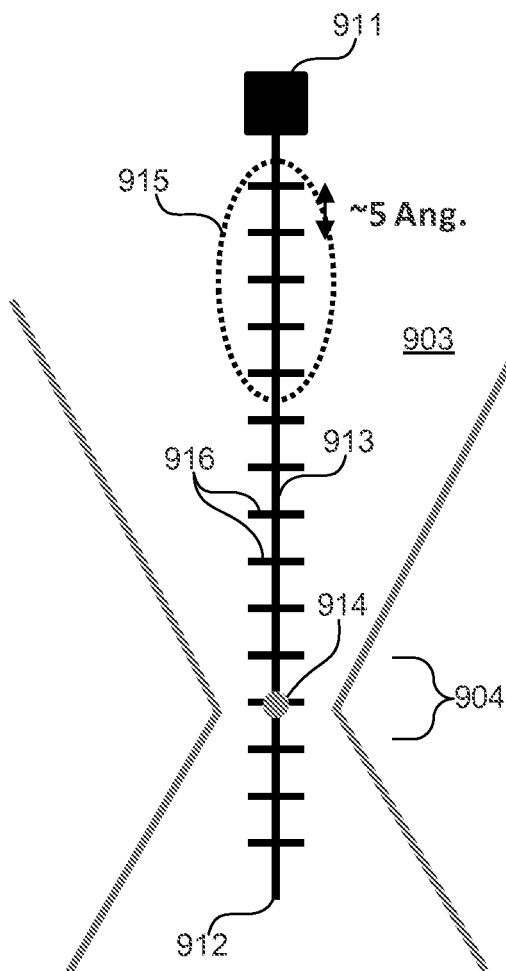


FIG. 9A

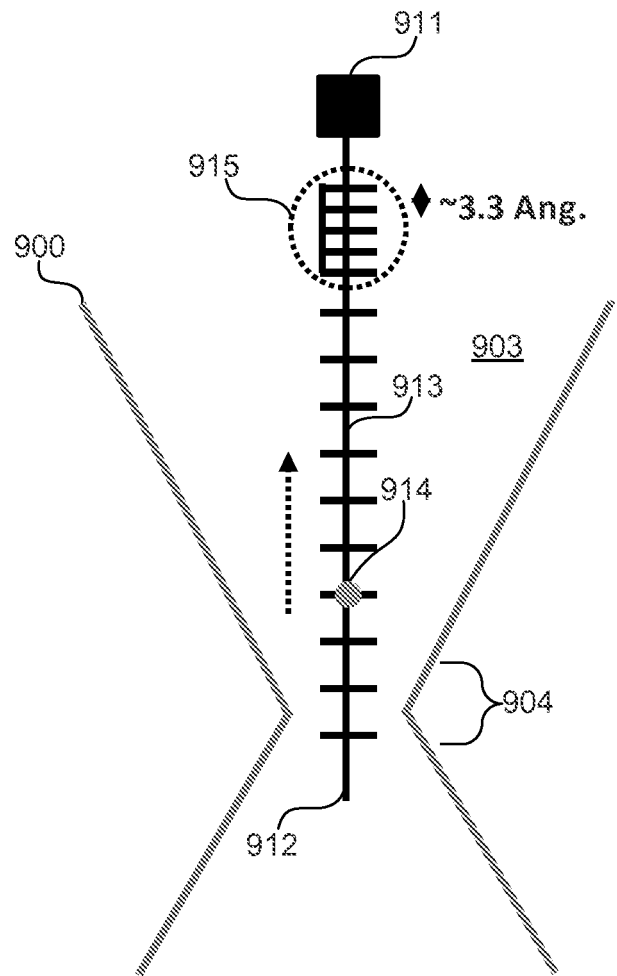


FIG. 9B

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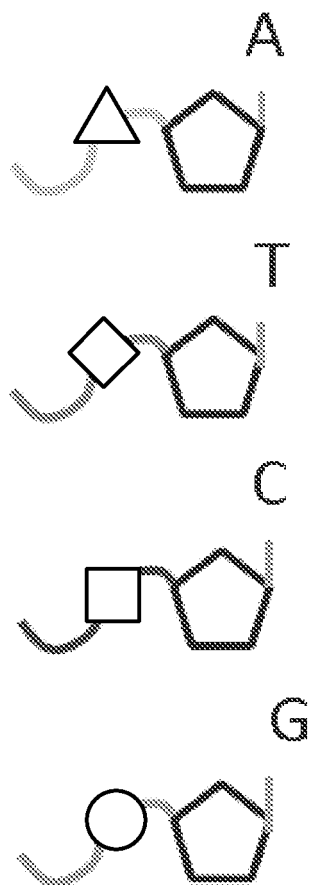


FIG. 10A

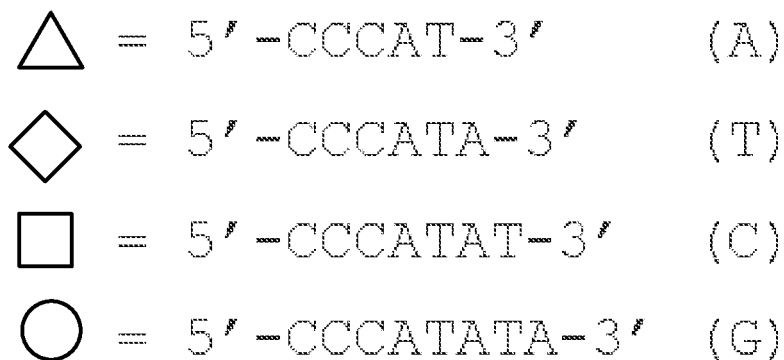


FIG. 10B

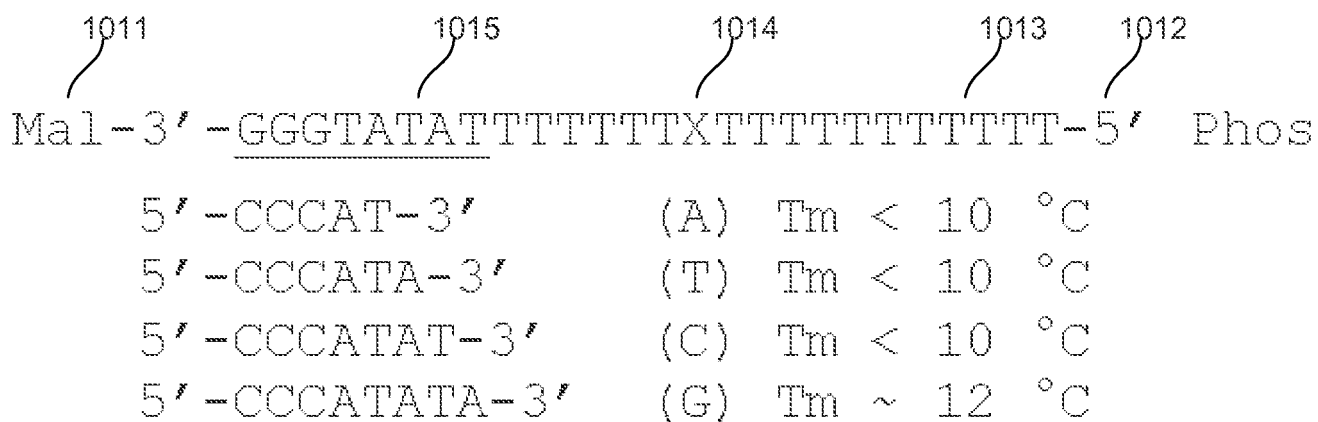


FIG. 10C

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See Fig. 11(continued)

Tether sequence: 5' Phos-TTTTTTTTTTTTNTTTTTTTTATATGAGG-3' (maleimide)

A		B	
Tag Sequence:	5' -CCCAT-3'	5' -CCCAT-3'	
Best match # base pairs:	5	6	
Best delta G (kcal/mole):	-9.57	-10.53	
Hyb:	5' -TTTTTTTTTTTTTTTATATGAGG 3' - TACCC (1A)	5' -TTTTTTTTTTTTTTTATATGAGG 3' - ATACCC (2A)	
Tag Sequence:	5' -CCCAT-3'	5' -CCCAT-3'	
Second-best match # base pairs:	2	3	
Best delta G (kcal/mole):	-3.07	>-3.20	
Hyb:	5' -TTTTTTTTTTTTTTTATATGAGG 3' - TACCC (1B)	5' -TTTTTTTTTTTTTTTATATGAGG 3' - ATACCC (2B)	

FIG. 11

C		D	
5' -CCCATAT-3'		5' -CCCATATA-3'	
7		8	
-12.00		-12.96	
5' -TTTTTTTTTTTNTTTTTTATATGGG TATACCC (3A) 3' -		5' -TTTTTTTTTTTNTTTTTTATATGGG ATATACCC (4A) 3' -	
5' -CCCATAT-3'		5' -CCCATATA-3'	
3		3	
>-3.20		>-3.20	
5' -TTTTTTTTTTTNTTTTTTATATGGG TATACCC (3B) 3' -		5' -TTTTTTTTTTTNTTTTTTATATGGG : ATATACCC (4B) 3' -	

See Fig. 11

FIG. 11(continued)

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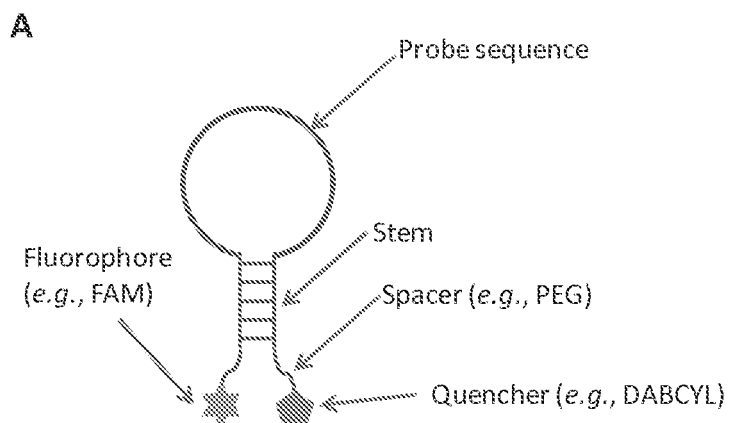
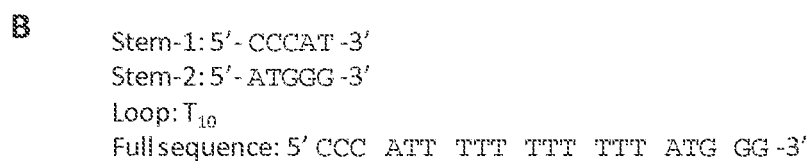


FIG. 12



Mfold (from IDT DNA) used to predict stem melting temperature with the following parameters:

- Temp: 25 °C
- Na⁺ concentration: 50 mM
- Mg²⁺ concentration: 2 mM
- Suboptimality: 50%

The most stable predicted structure is shown in (C)

- Delta G (kcal/mole): -2.54
- Delta H (kcal/mole): -34
- Delta S (cal/K⁻¹mole⁻¹): -105.53
- T_m: 49 °C

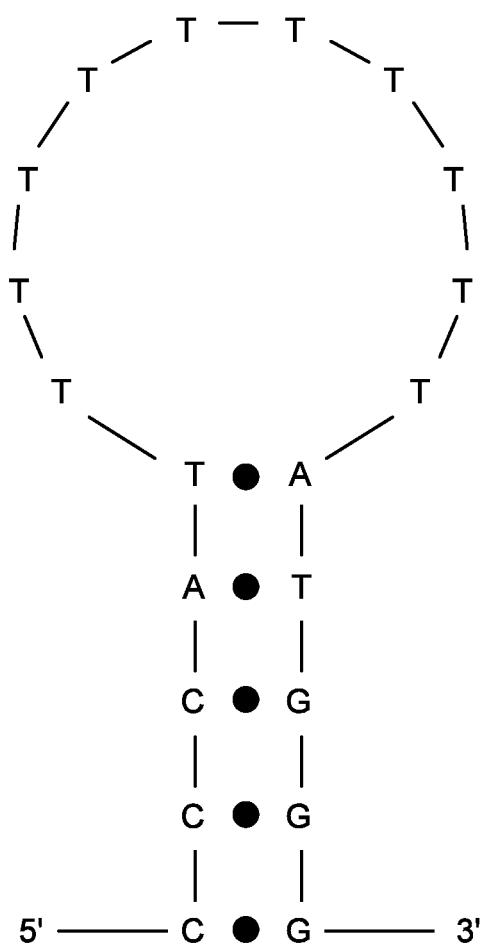
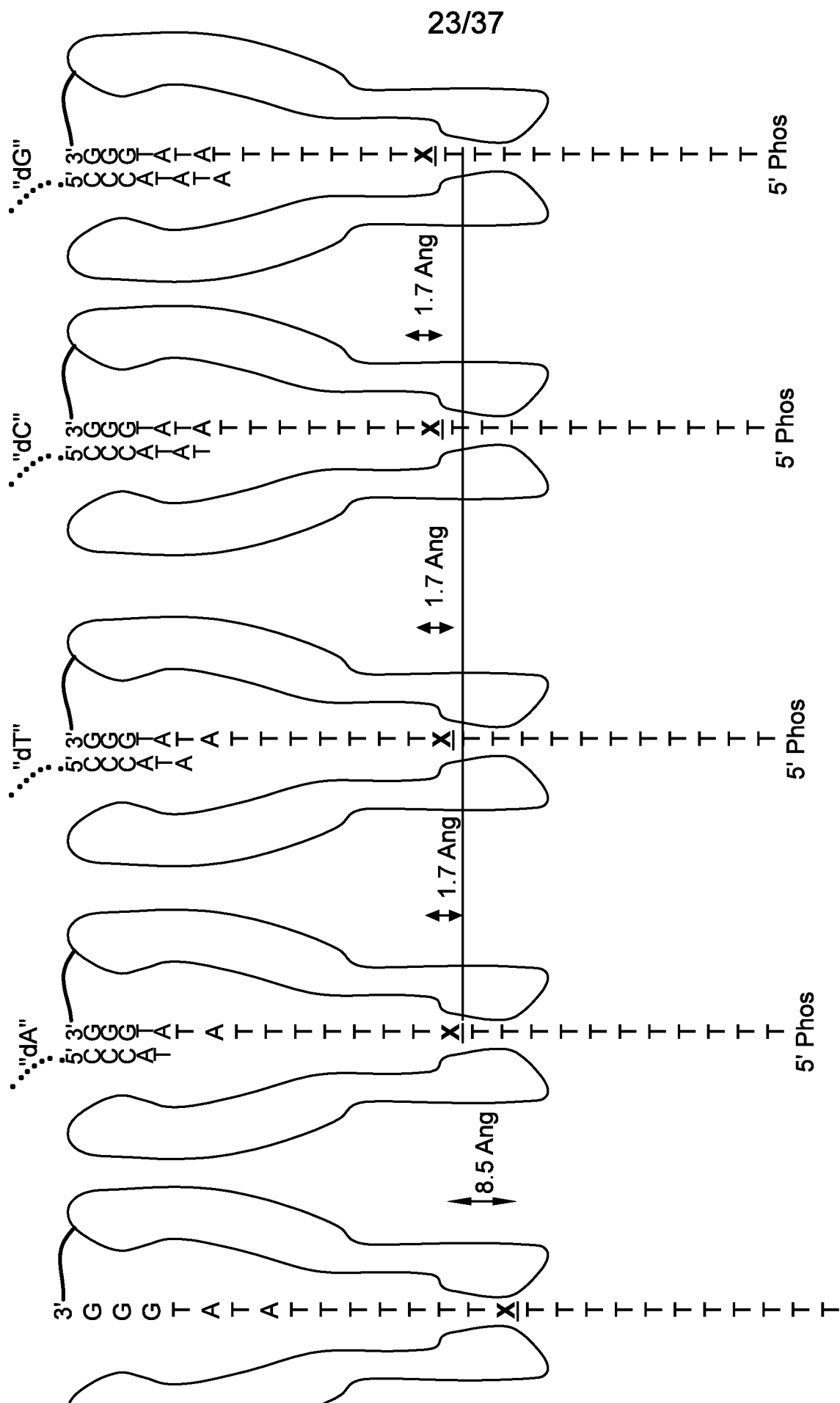


FIG. 12C



5' Phos

FIG. 13A

FIG. 13B

FIG. 13C

FIG. 13D

FIG. 13E

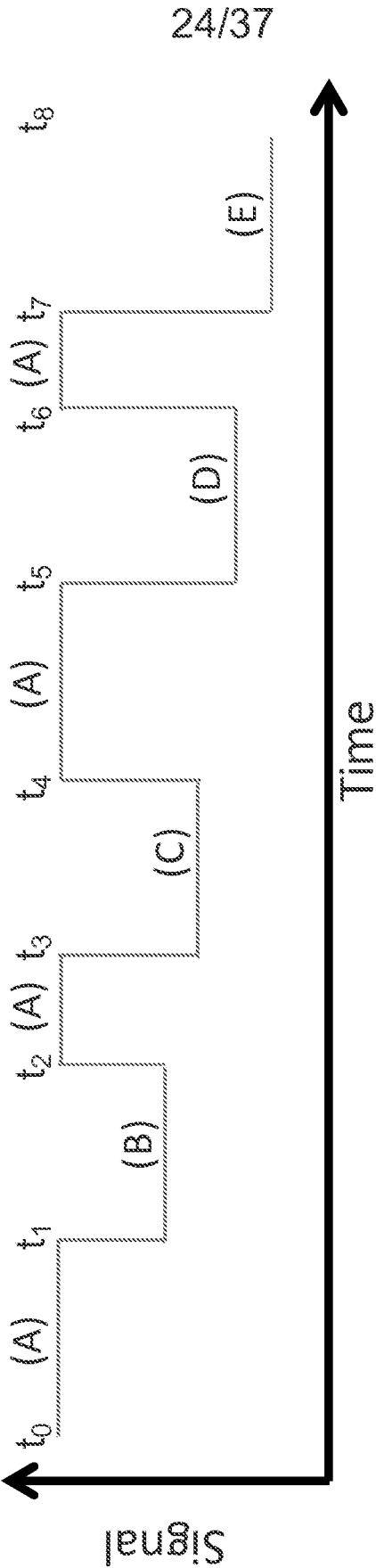


FIG. 14

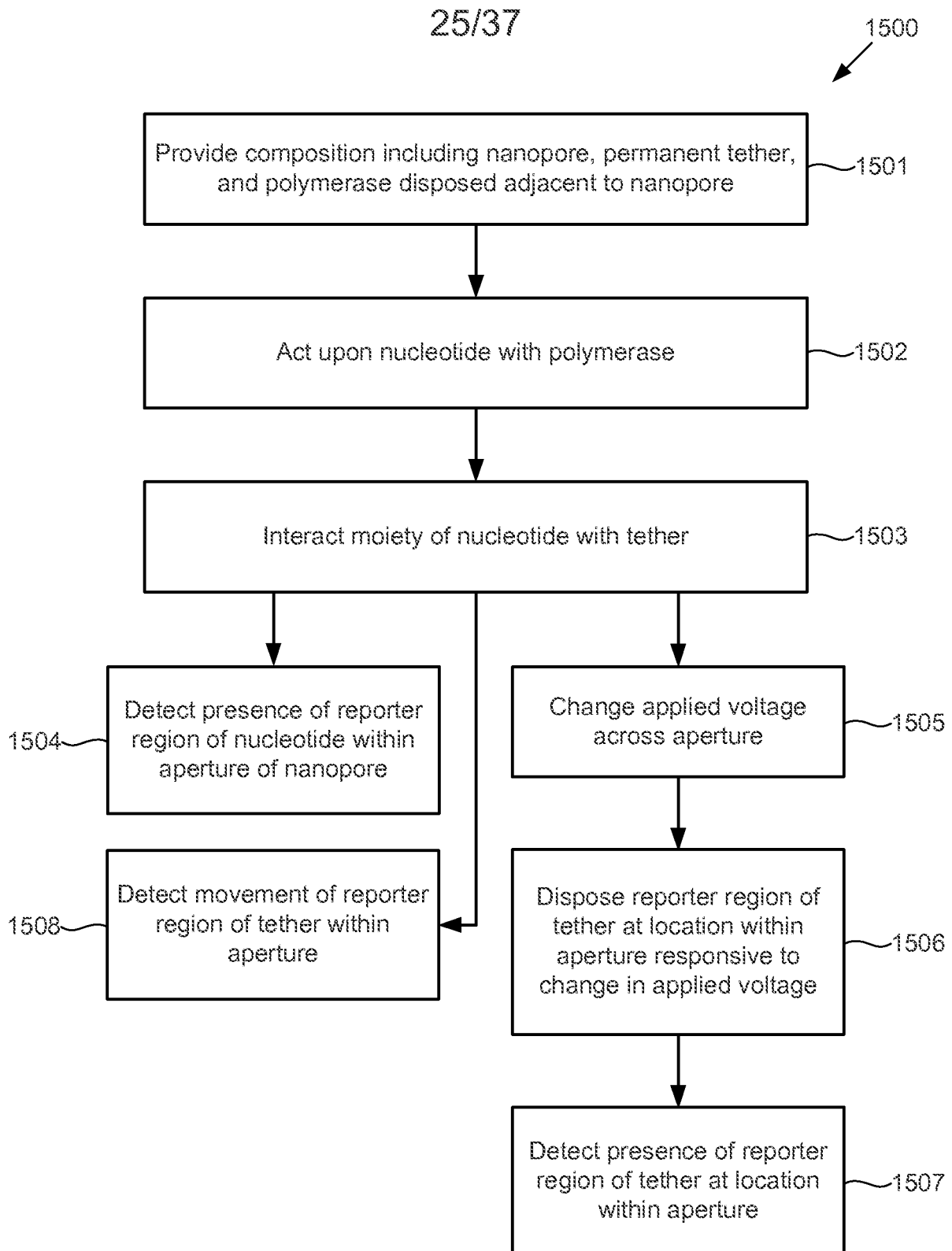


FIG. 15

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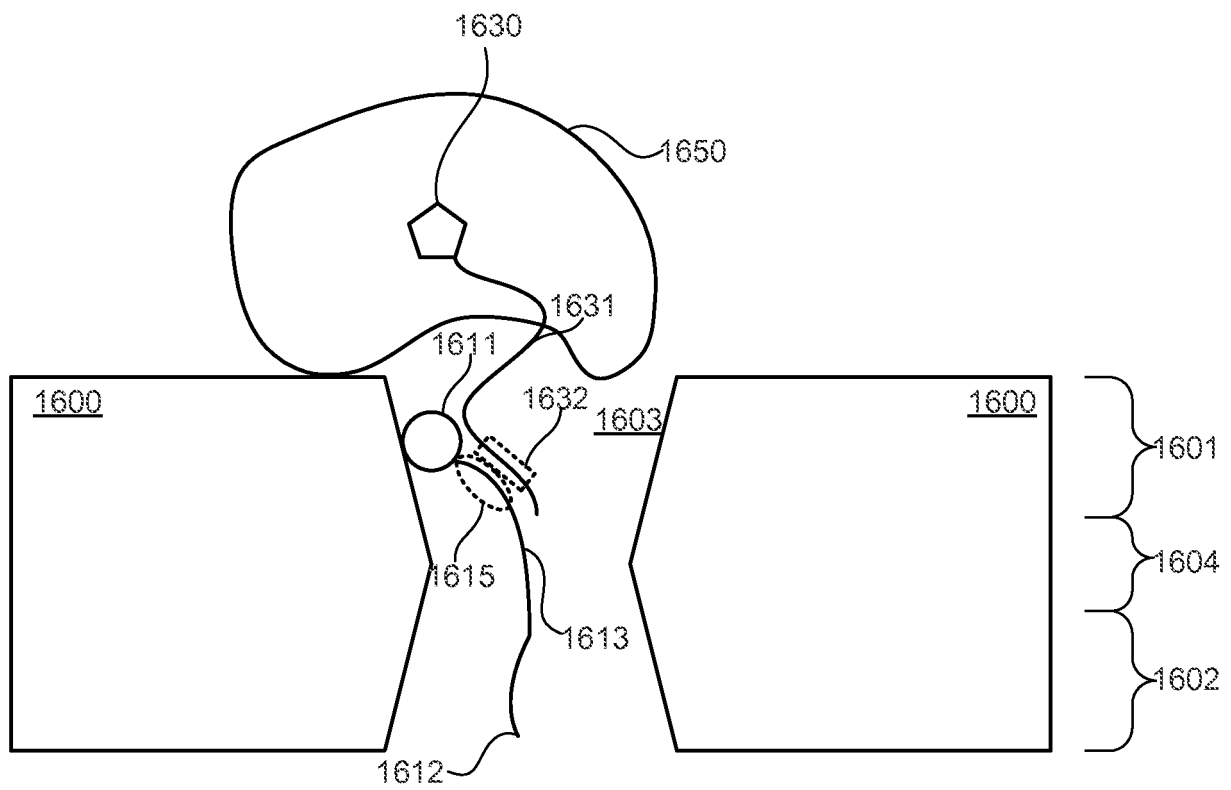


FIG. 16

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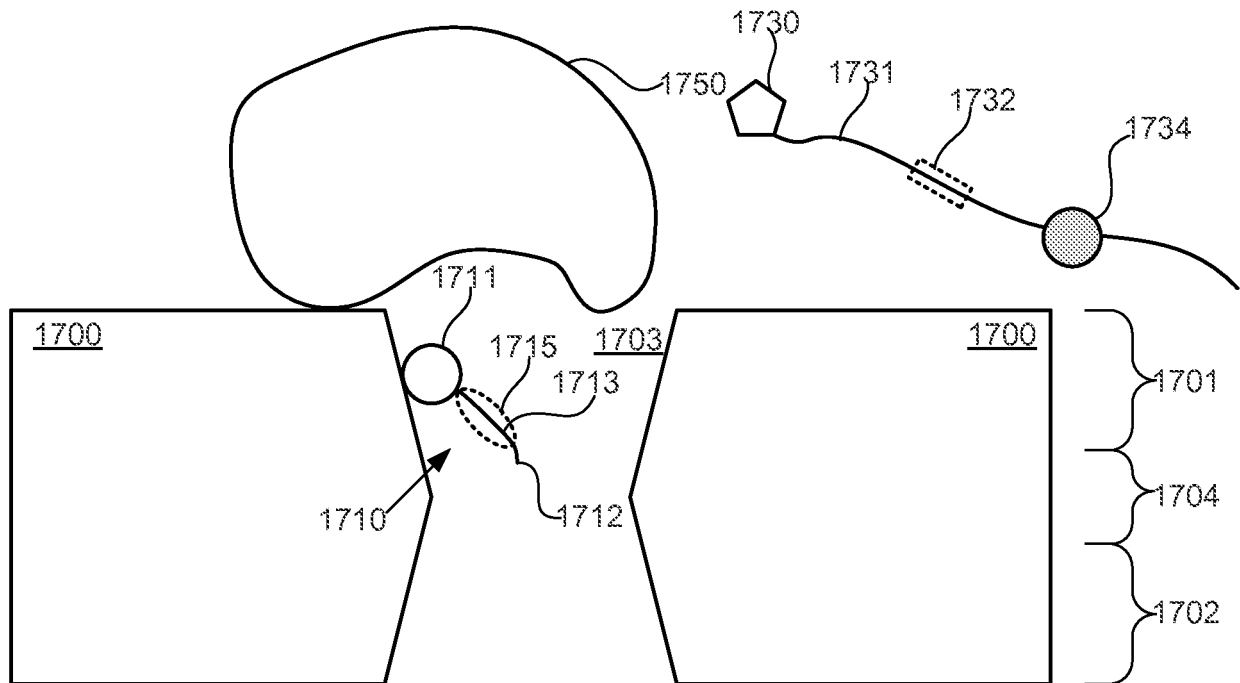


FIG. 17A

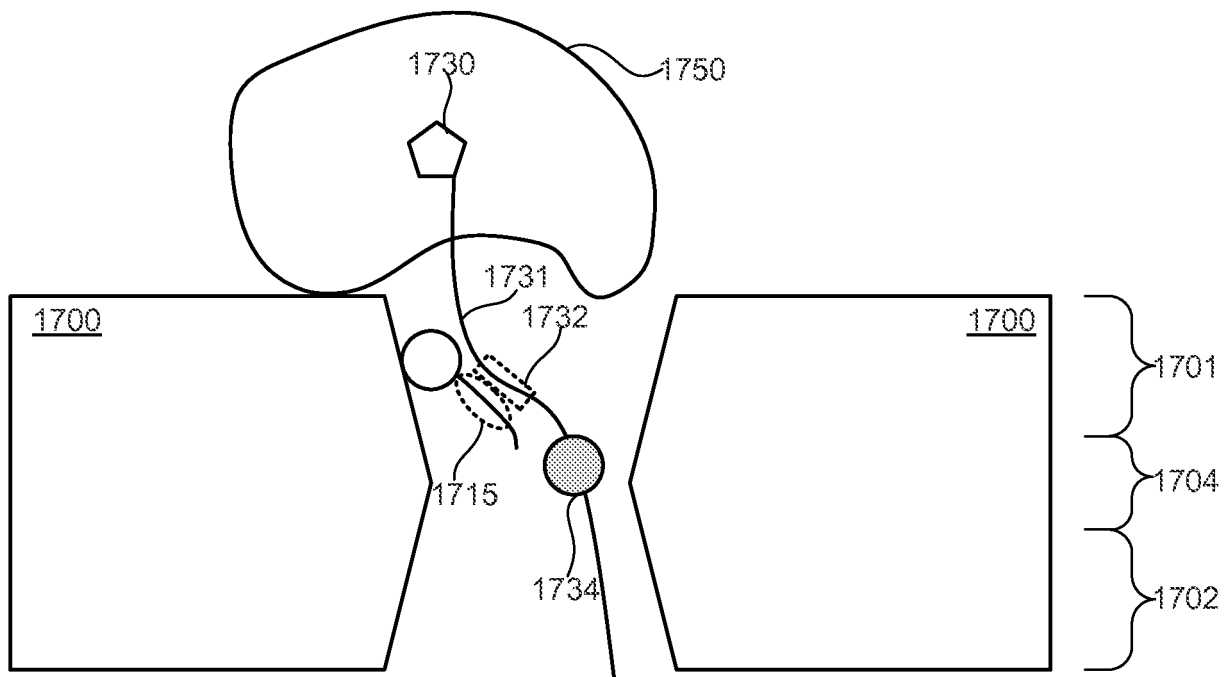


FIG. 17B

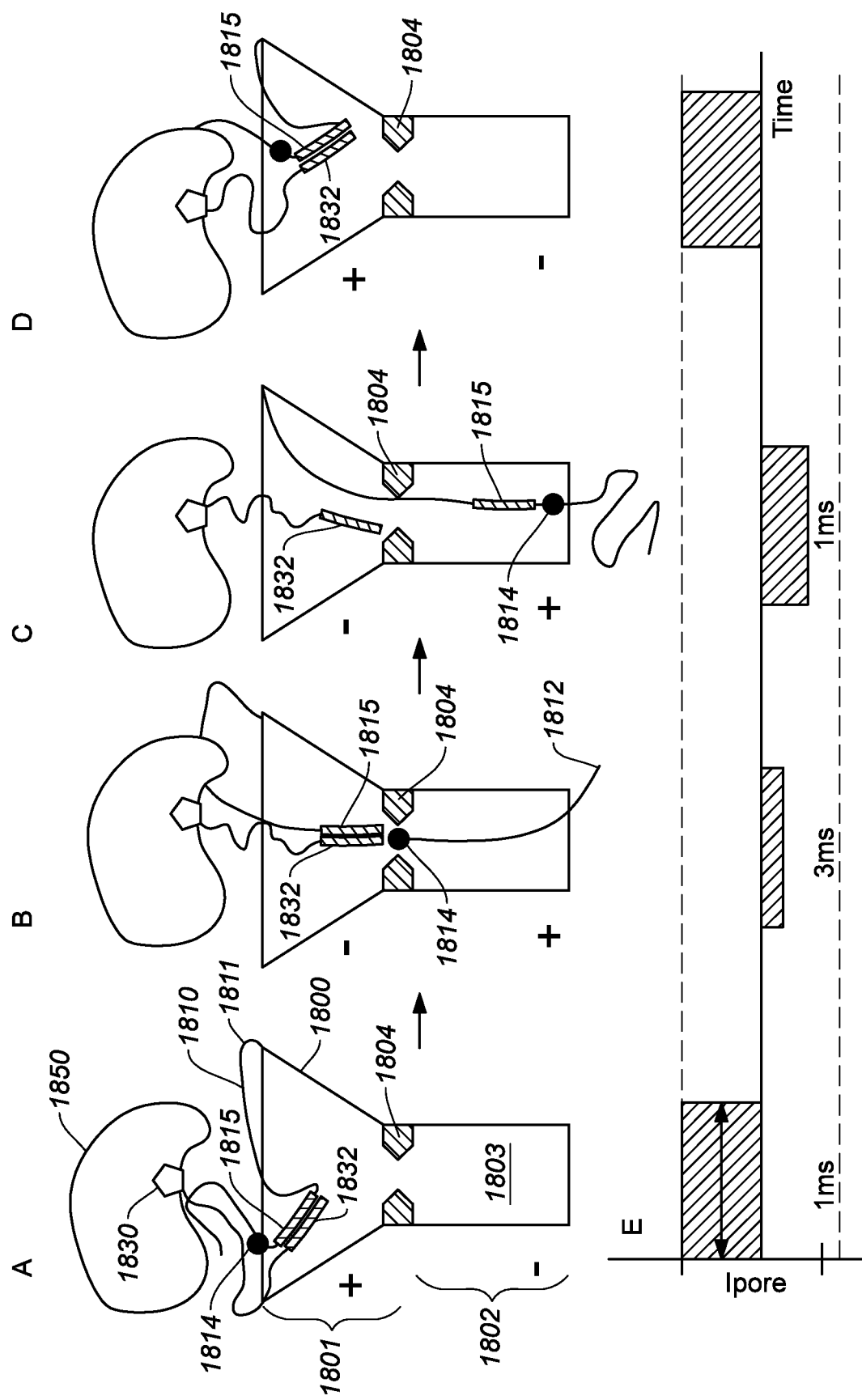


FIG. 18

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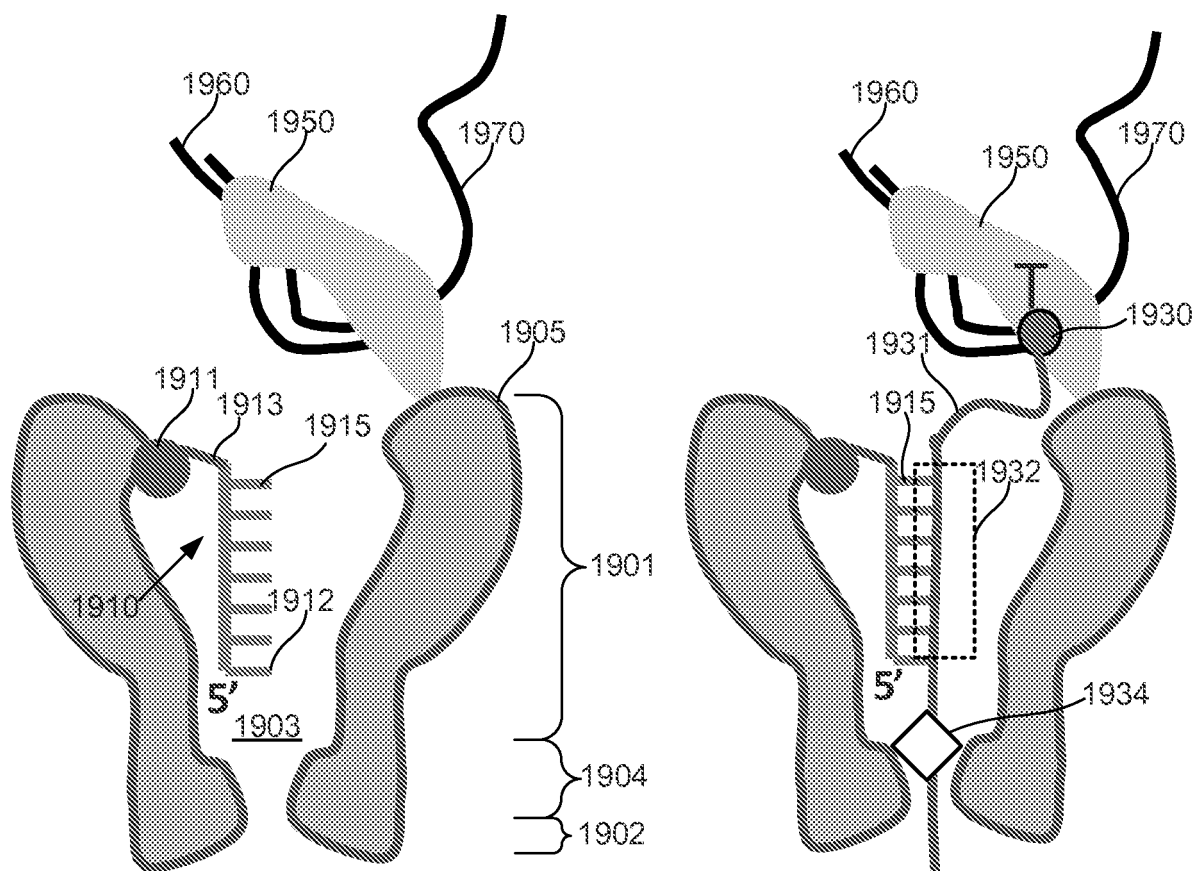


FIG. 19A

FIG. 19B

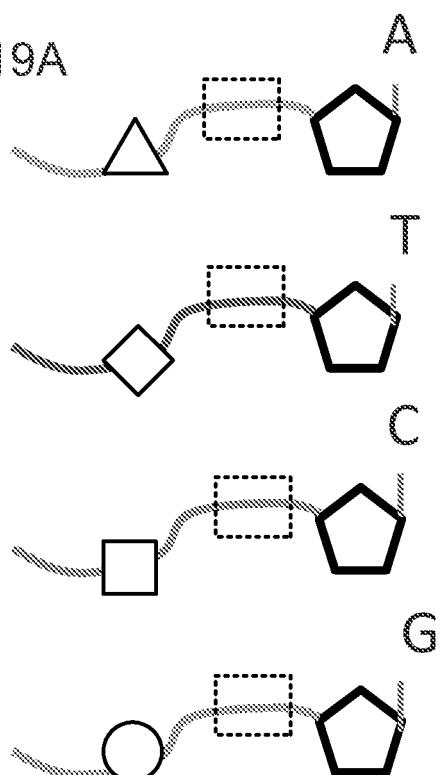


FIG. 19C

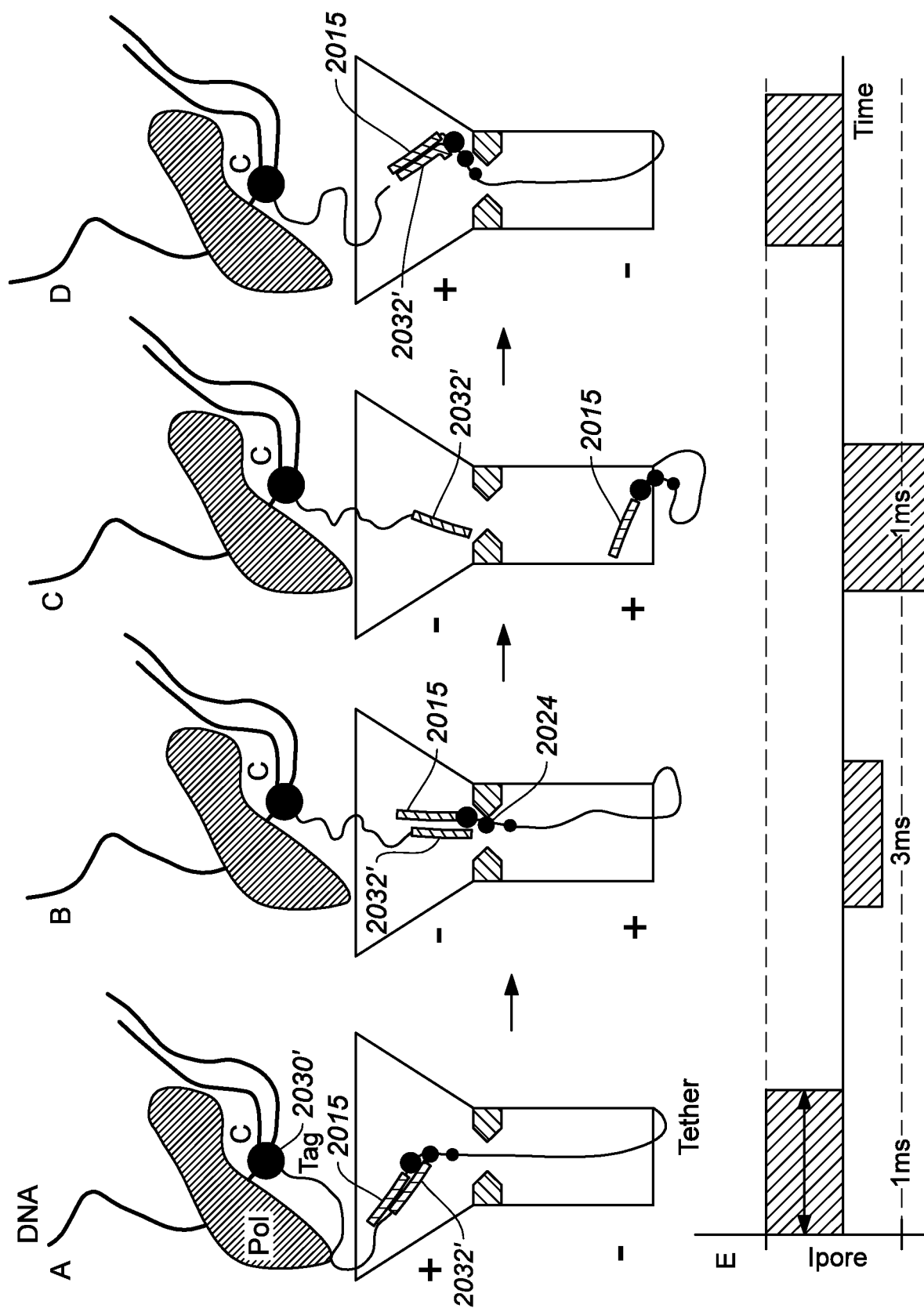
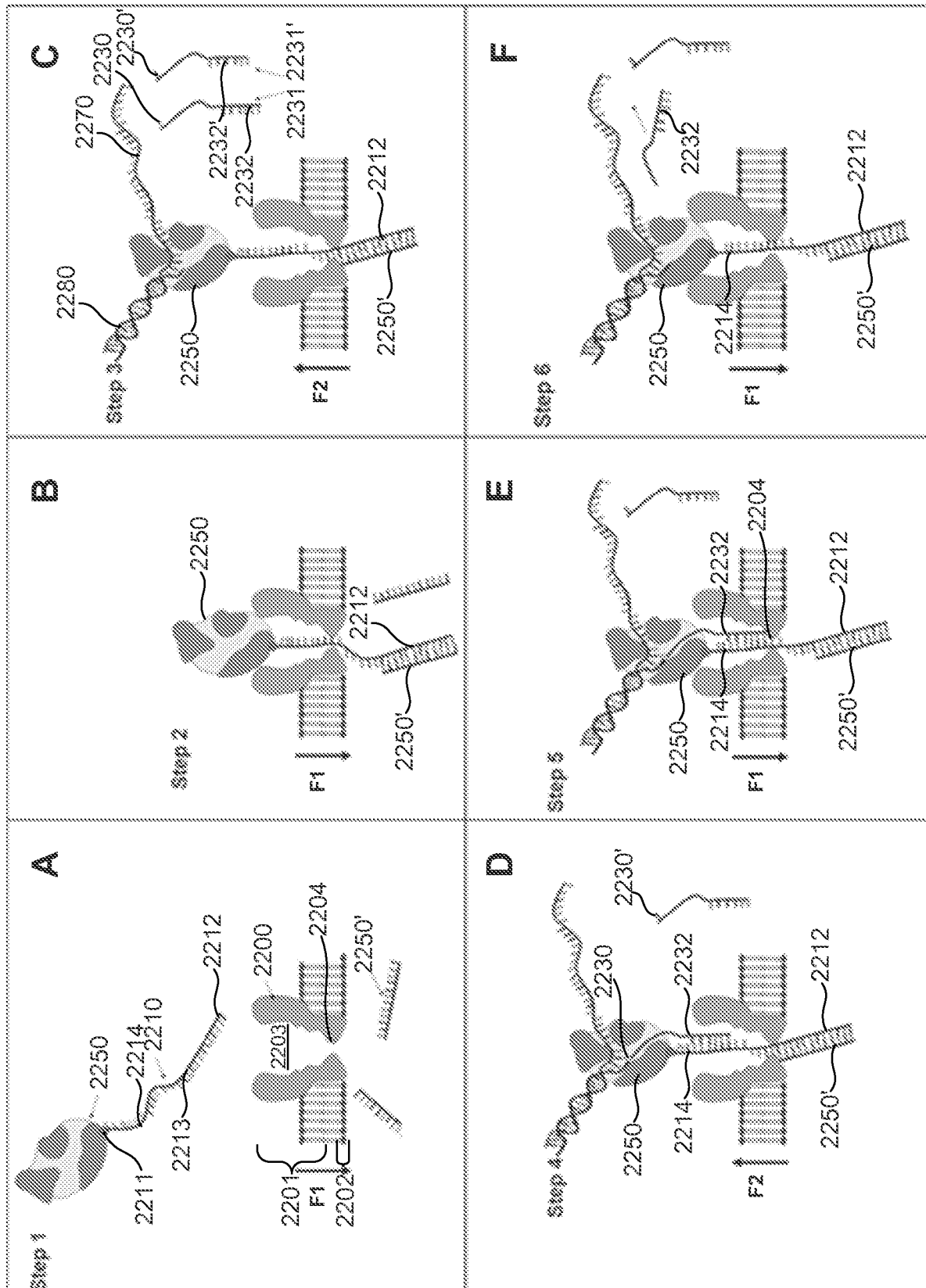


FIG. 21



22
G^K
1000000
F

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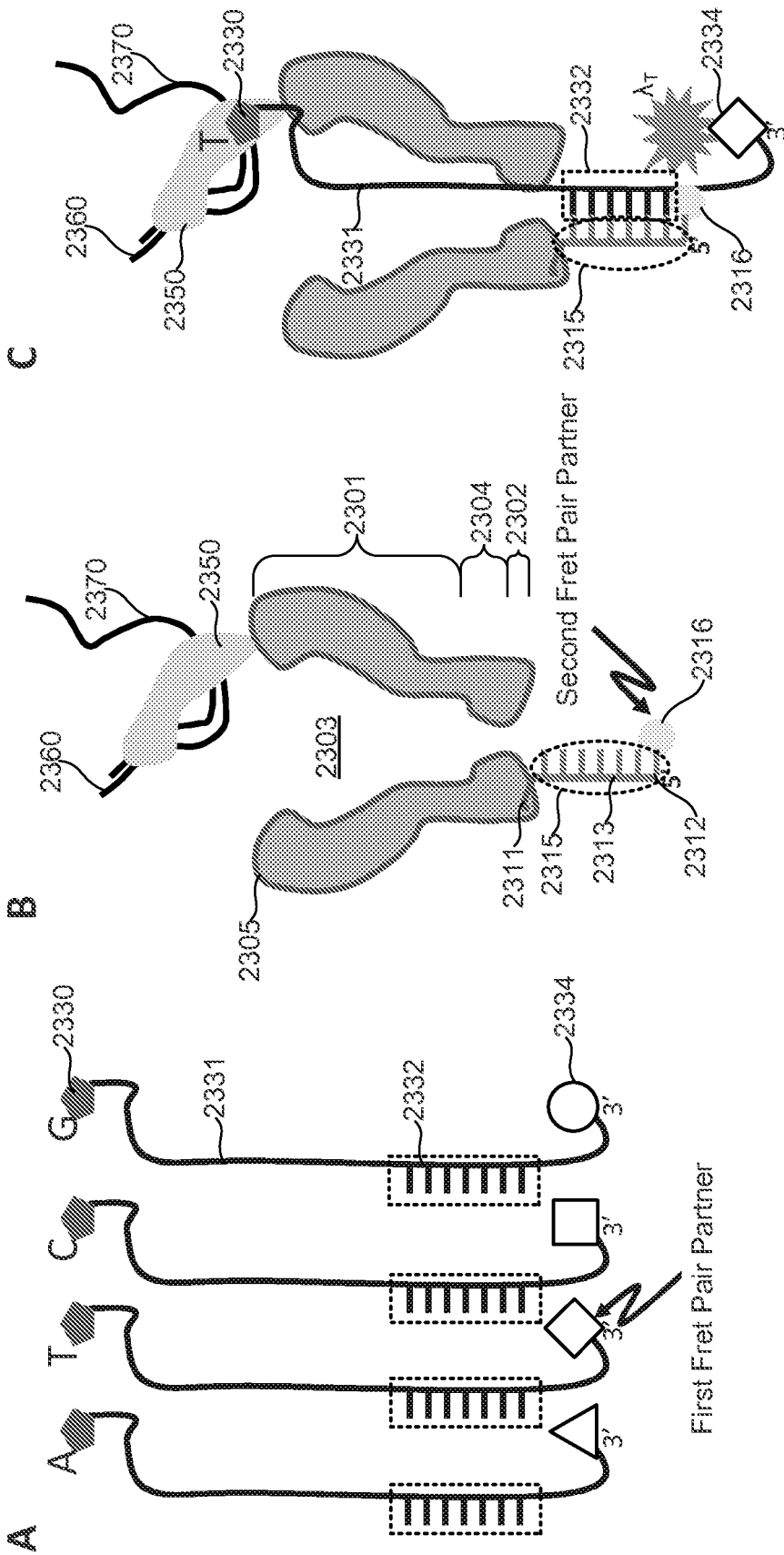


FIG. 23

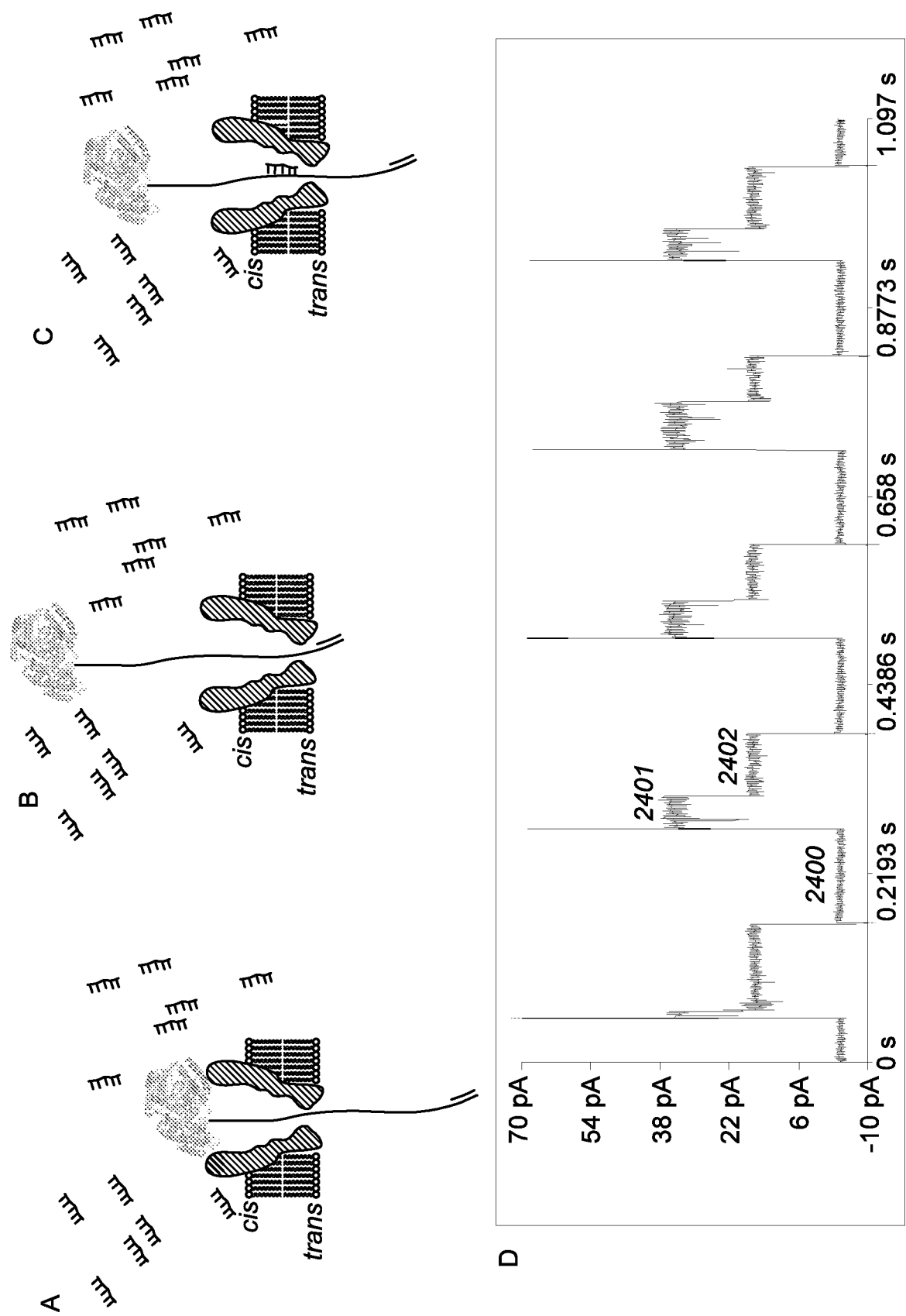


FIG. 24

	Reaction Parameters	Tag Dwell Time (usec)
Reaction Scheme	$\begin{array}{ccccccc} ED_n + dNTP & \xrightleftharpoons{K_1} & ED_n dNTP & \xrightleftharpoons[k_2]{k_2} & FD_n dNTP & \xrightleftharpoons[k_3]{k_3} & FD_{n+1} PP_i \xrightarrow{fast} ED_{n+1} + PP_i \\ \text{open} & & \text{open} & & \text{closed} & & \text{closed} \quad \text{open} \end{array}$	$1/(k_2 + k_3)$
Perfect Match Nucleotide	$\begin{array}{ccccccc} ED_n + dNTP & \xrightleftharpoons{28 \mu M} & ED_n dNTP & \xrightleftharpoons[1.6 \text{ s}^{-1}]{660 \text{ s}^{-1}} & FD_n dNTP & \xrightleftharpoons[360 \text{ s}^{-1}]{360 \text{ s}^{-1}} & FD_{n+1} PP_i \xrightarrow{fast} ED_{n+1} + PP_i \\ \text{open} & & \text{open} & & \text{closed} & & \text{closed} \quad \text{open} \end{array}$	2760
Mismatch Nucleotide	$\begin{array}{ccccccc} ED_n + dNTP & \xrightleftharpoons{200 \mu M} & ED_n dNTP & \xrightleftharpoons[420 \text{ s}^{-1}]{220 \text{ s}^{-1}} & GD_n dNTP & \xrightleftharpoons[0.3 \text{ s}^{-1}]{0.3 \text{ s}^{-1}} & GD_{n+1} PP_i \xrightarrow{fast} ED_{n+1} + PP_i \\ \text{open} & & \text{open} & & \text{mismatch} & & \text{mismatch} \quad \text{open} \end{array}$	2380

FIG. 25

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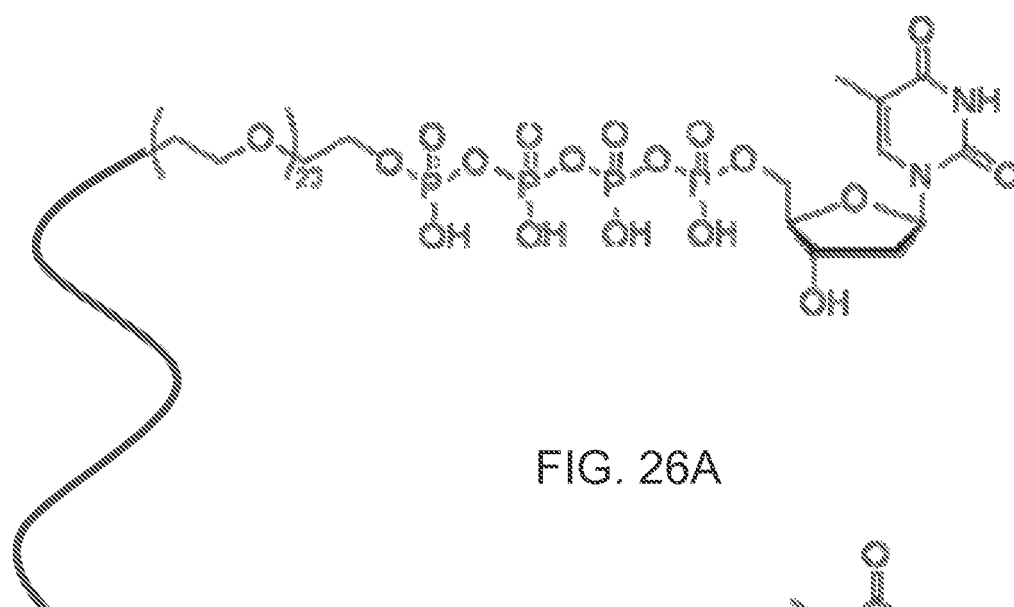


FIG. 26A

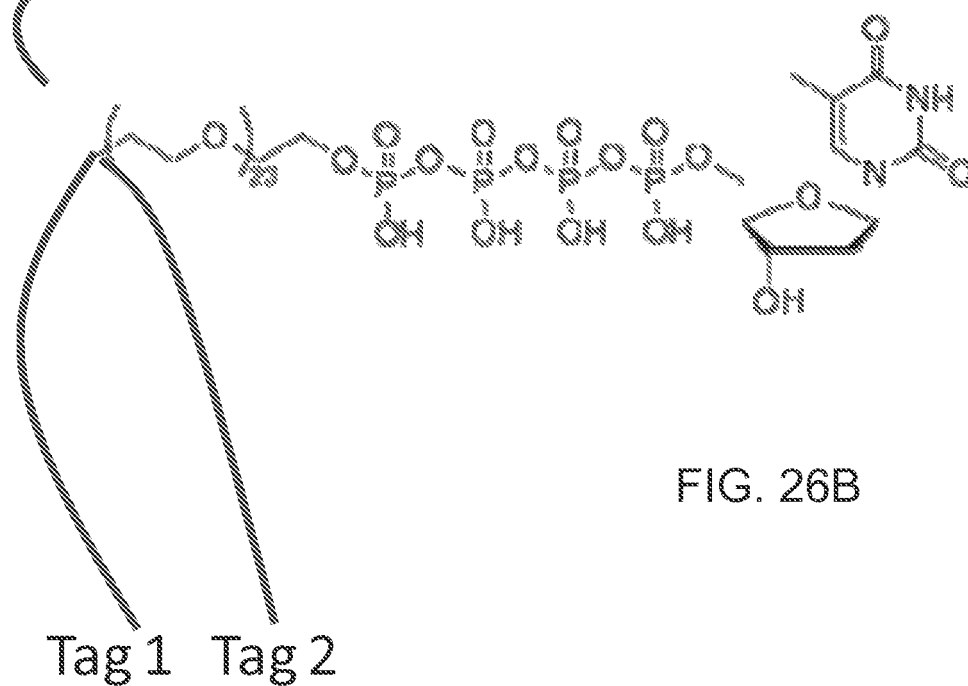


FIG. 26B

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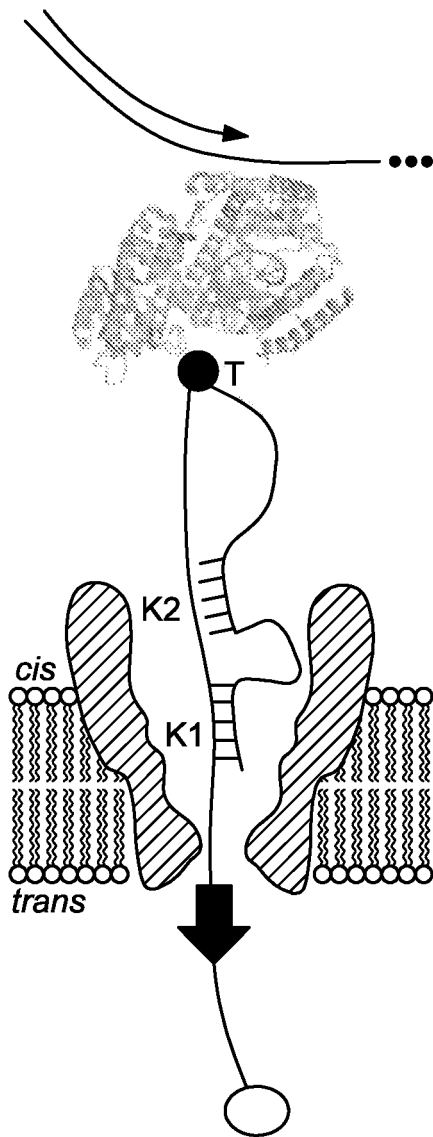


FIG. 26C

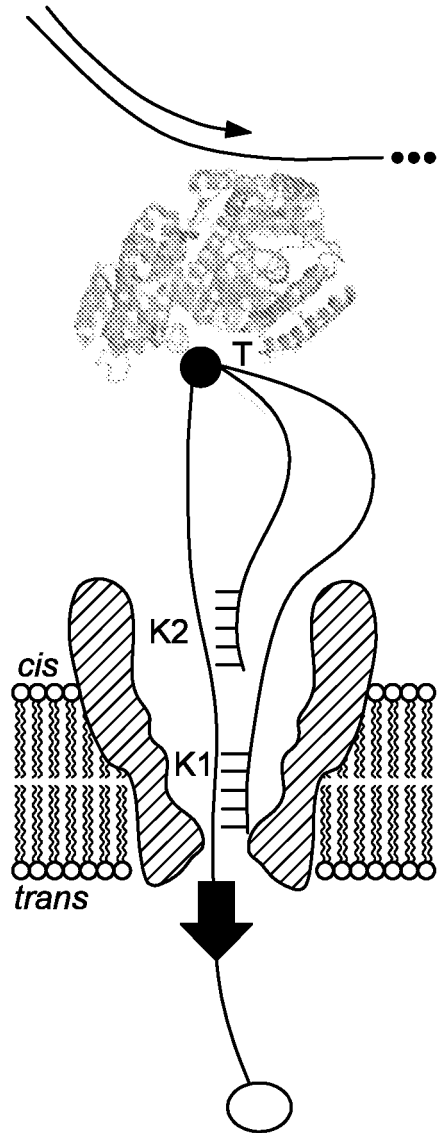


FIG. 26D