

DRAWINGS

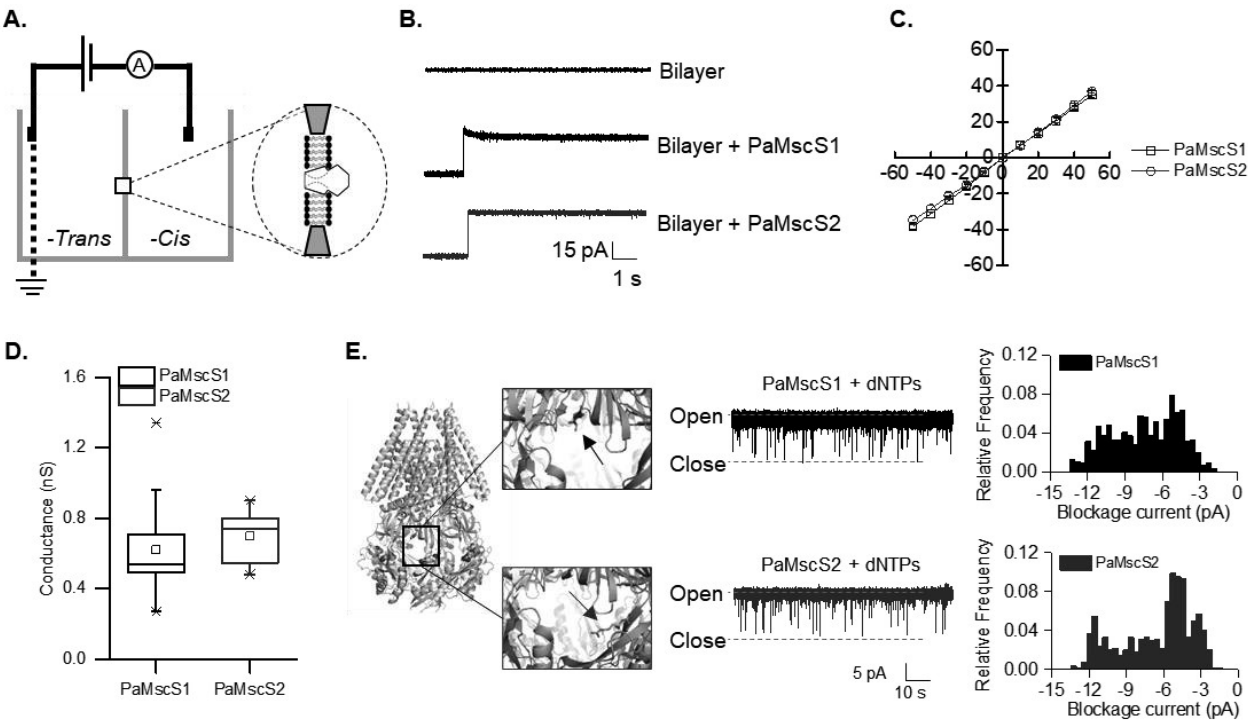


Fig. 1

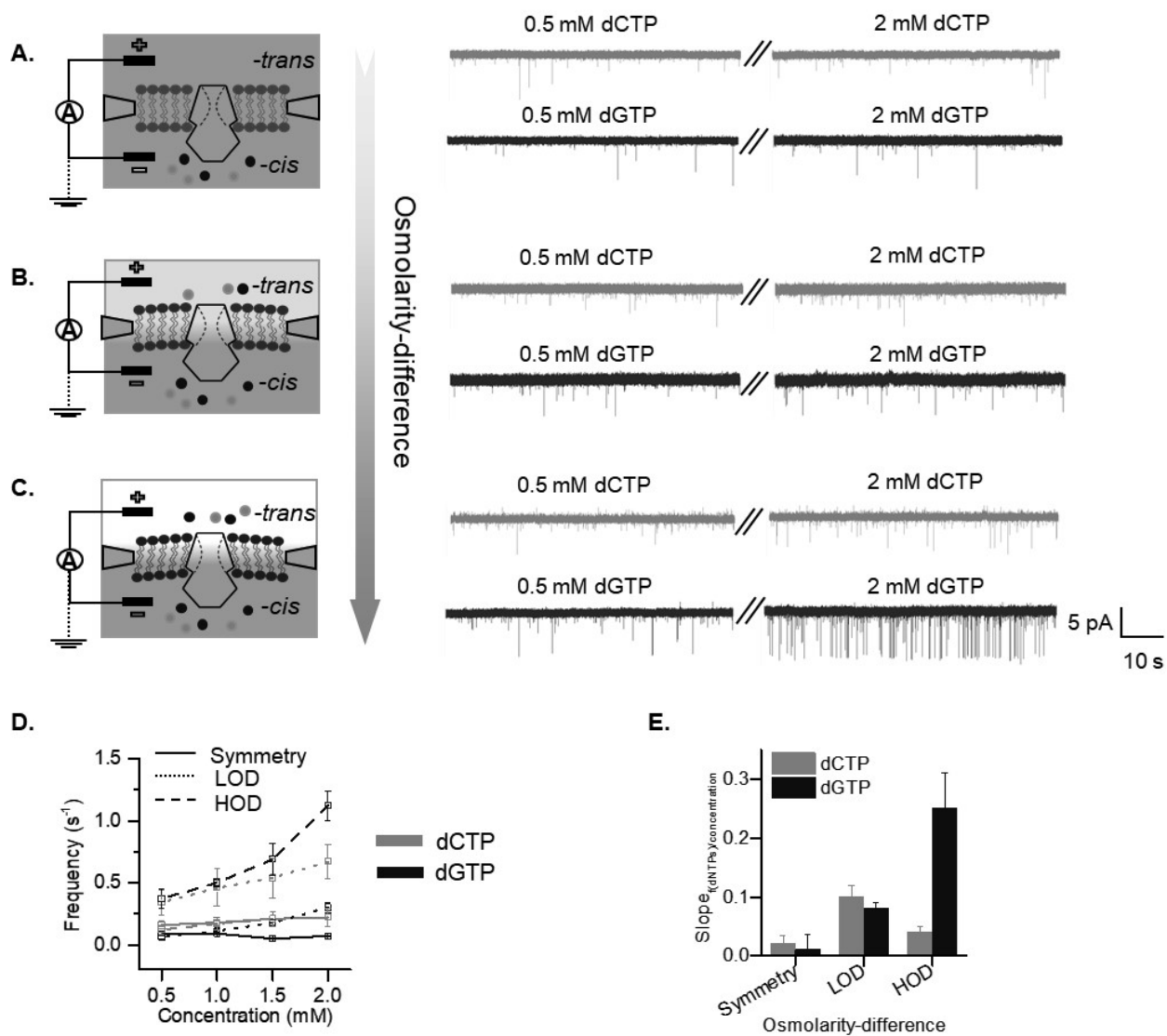


Fig. 2

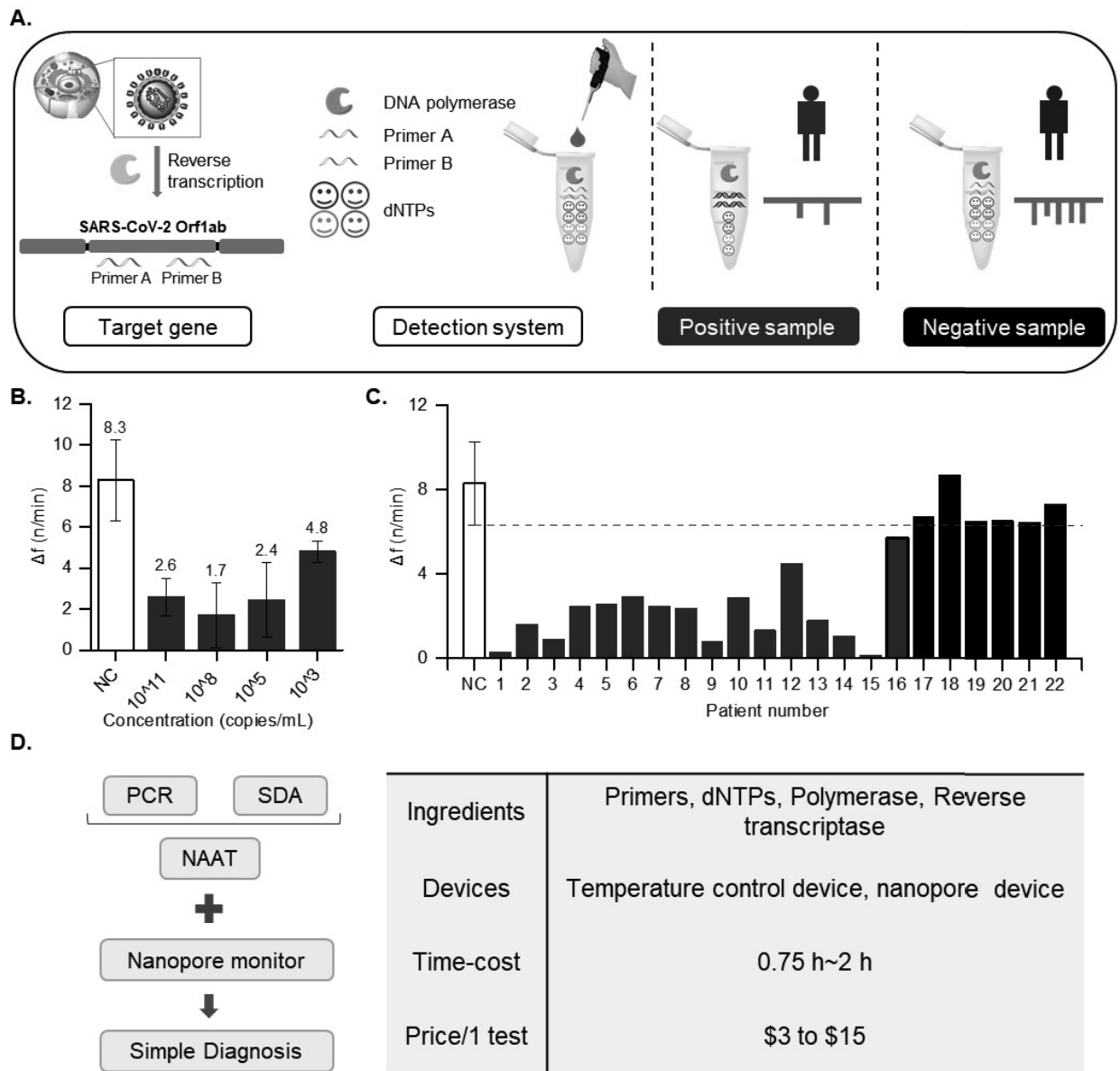


Fig. 3

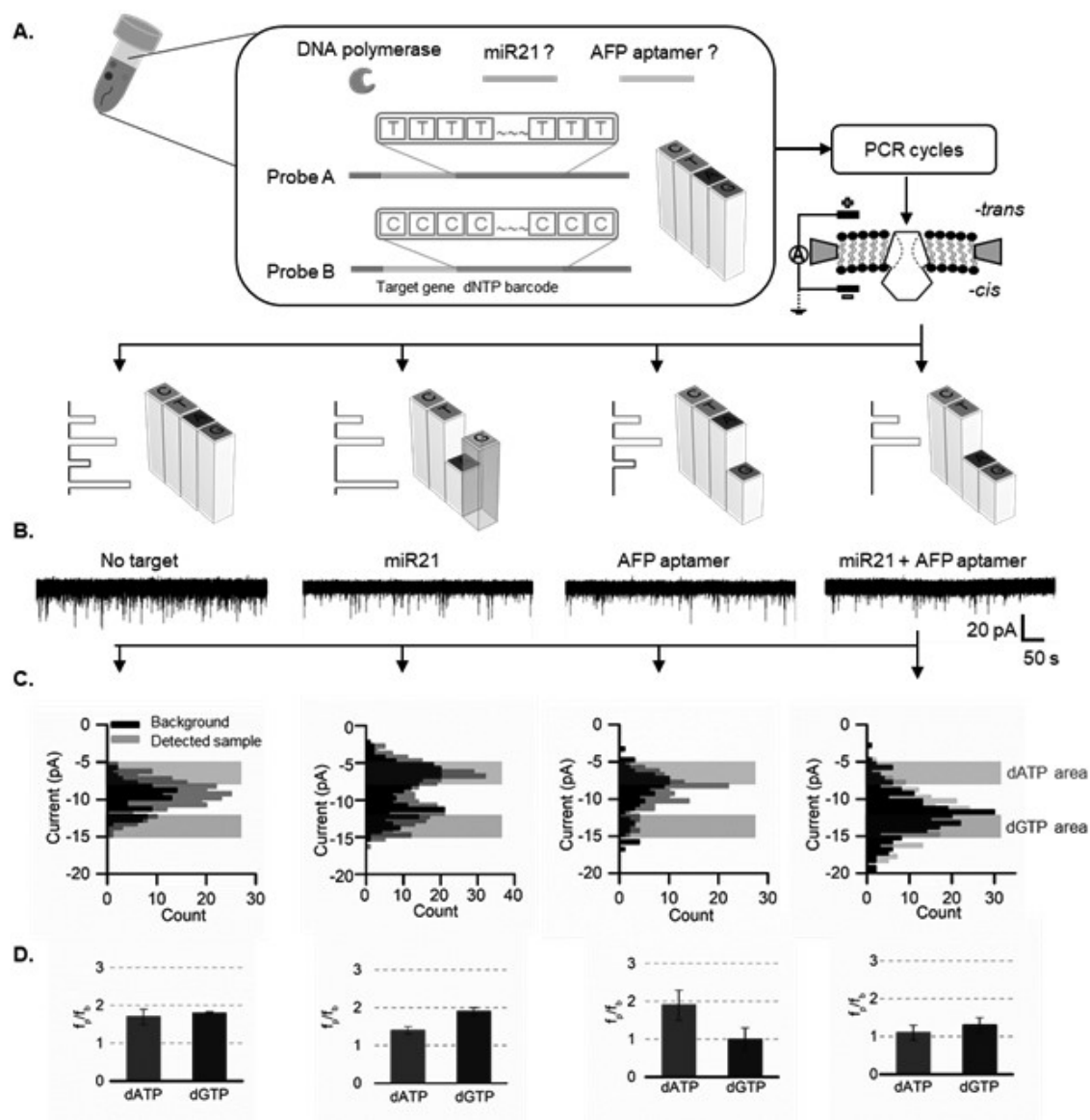


Fig. 4

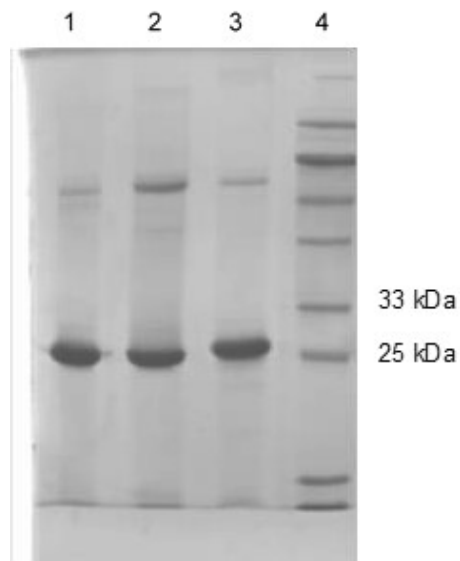


Fig. 5

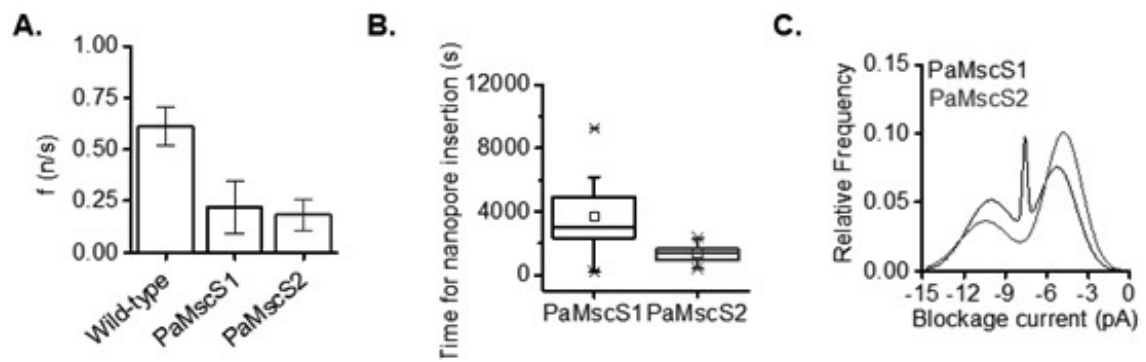


Fig. 6

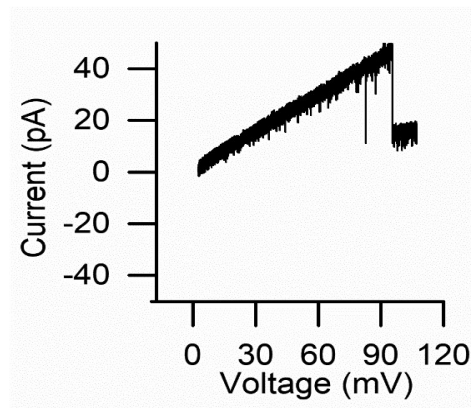


Fig. 7

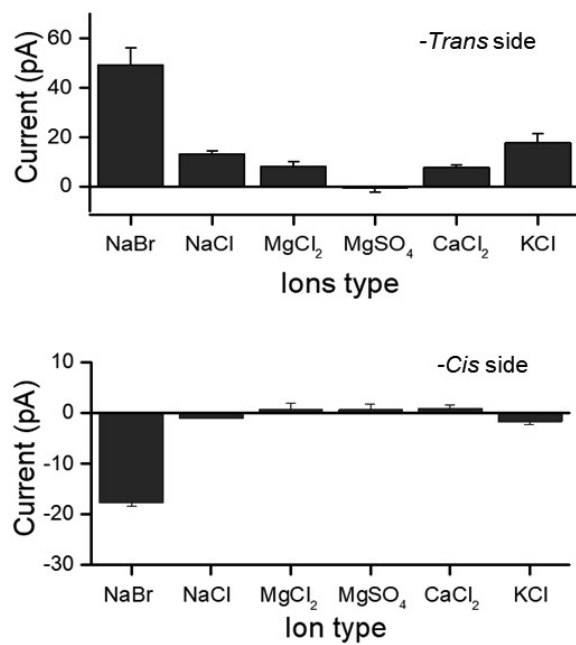


Fig. 8

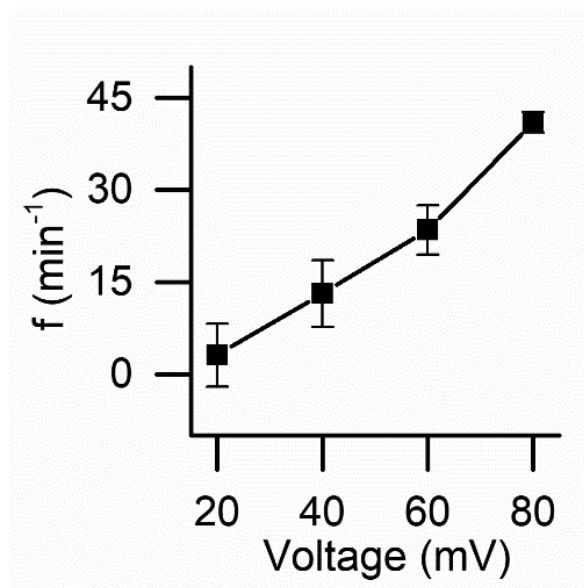


Fig. 9

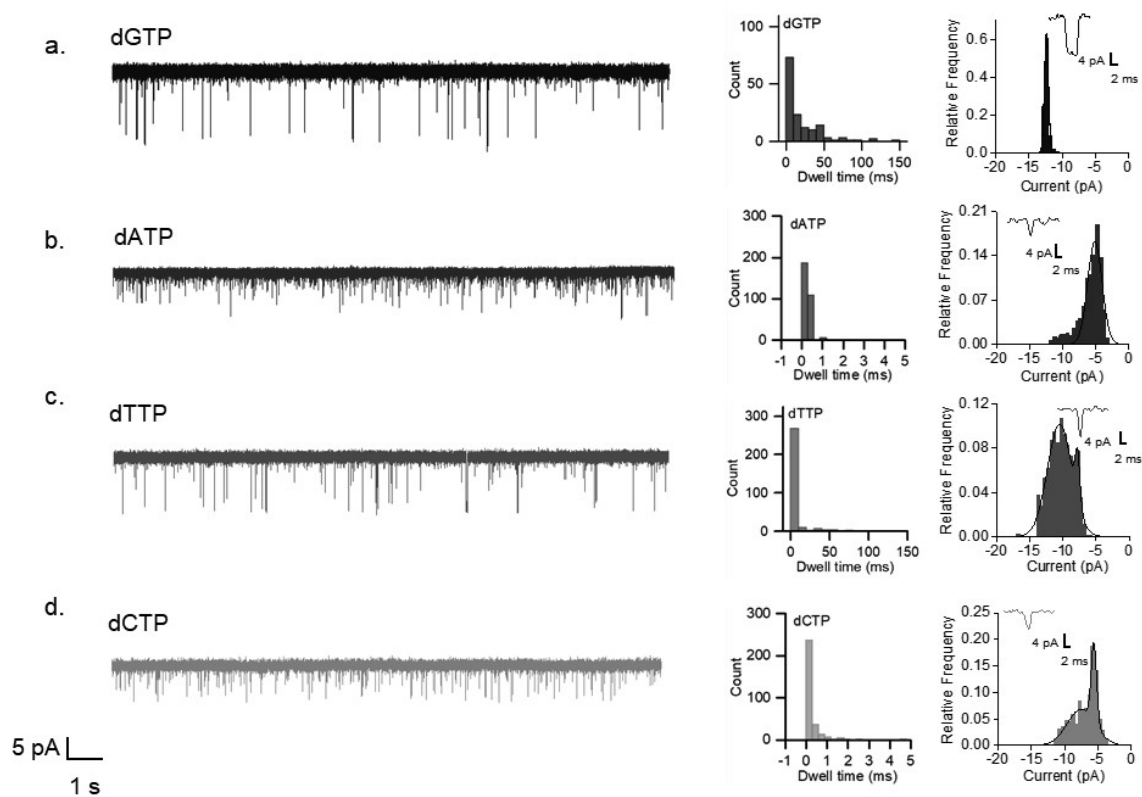


Fig. 10

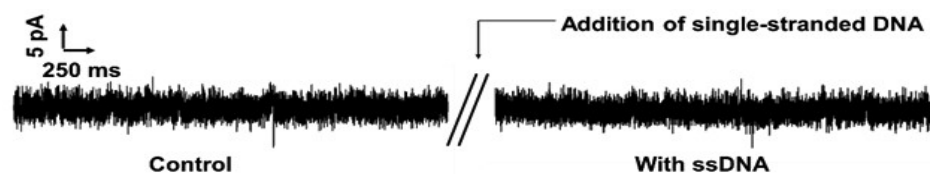


Fig. 11

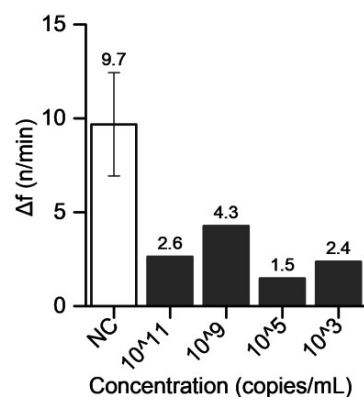


Fig. 12

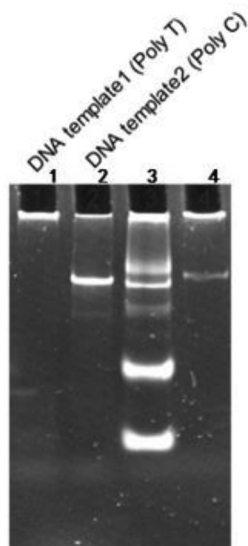


Fig. 13

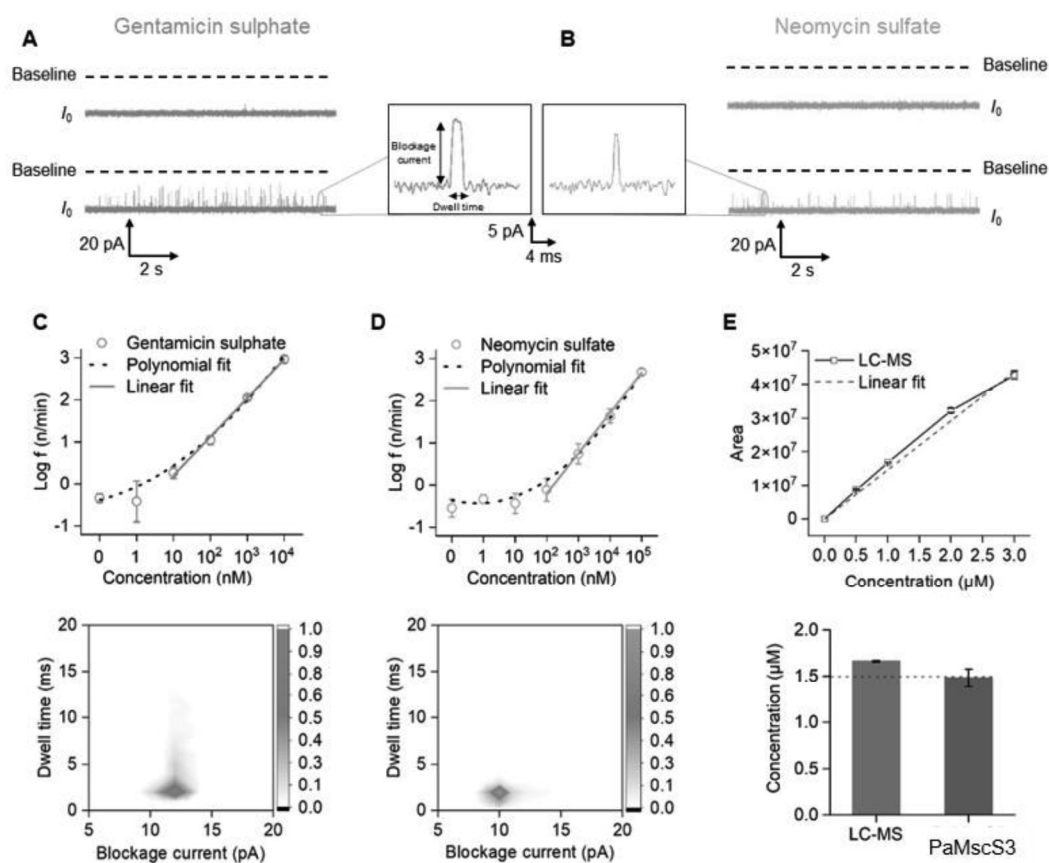


Fig. 14

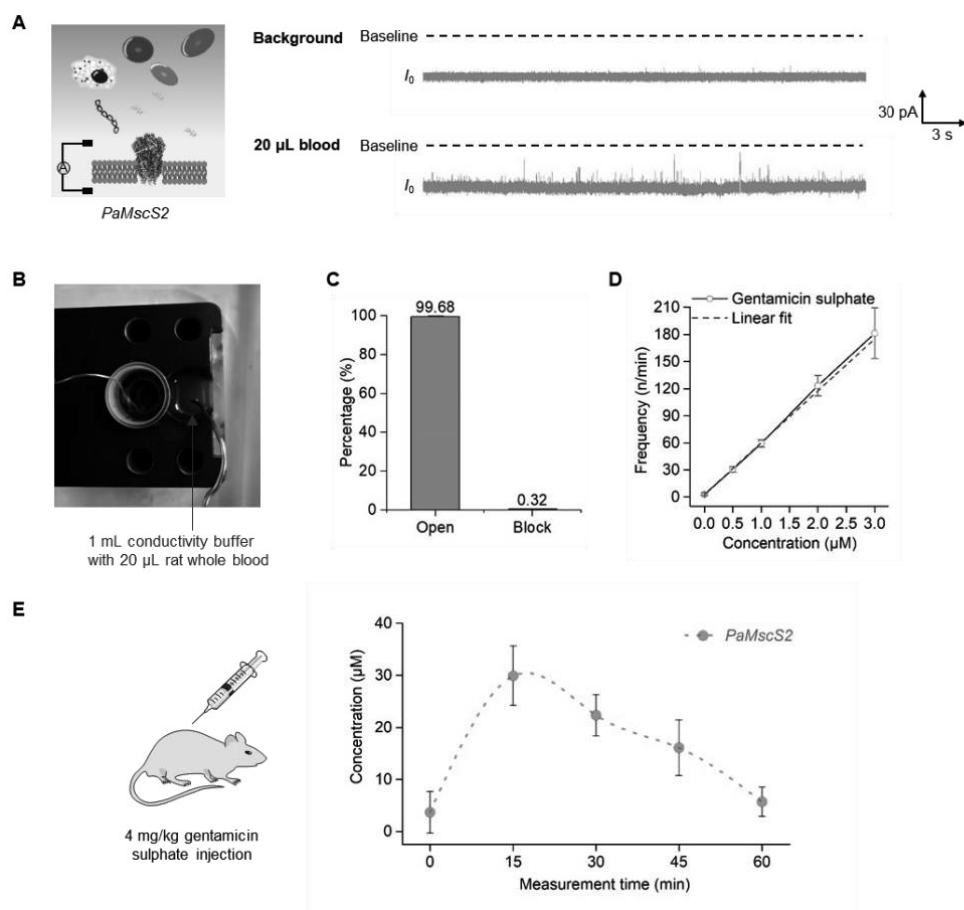


Fig. 15

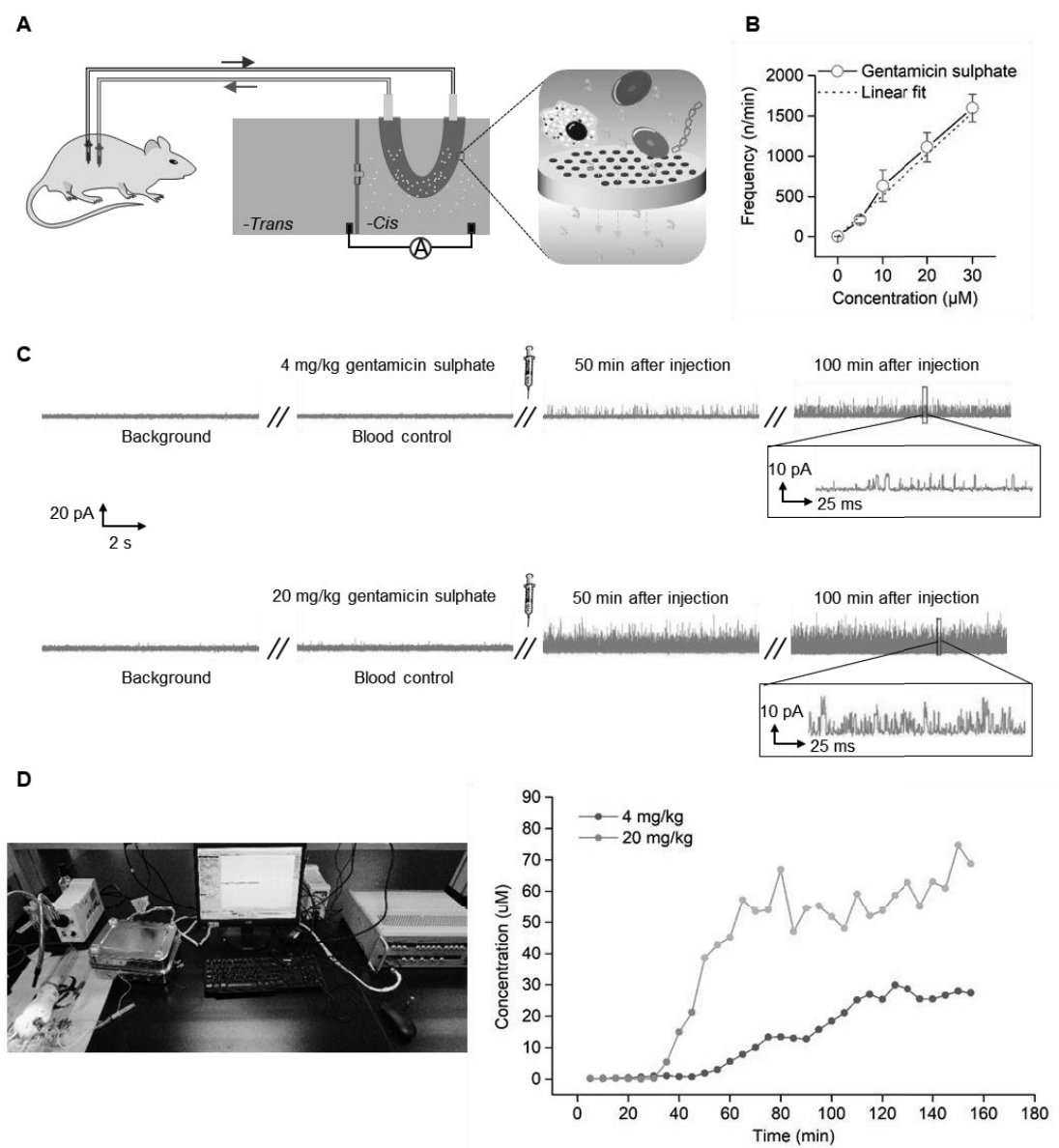


Fig. 16

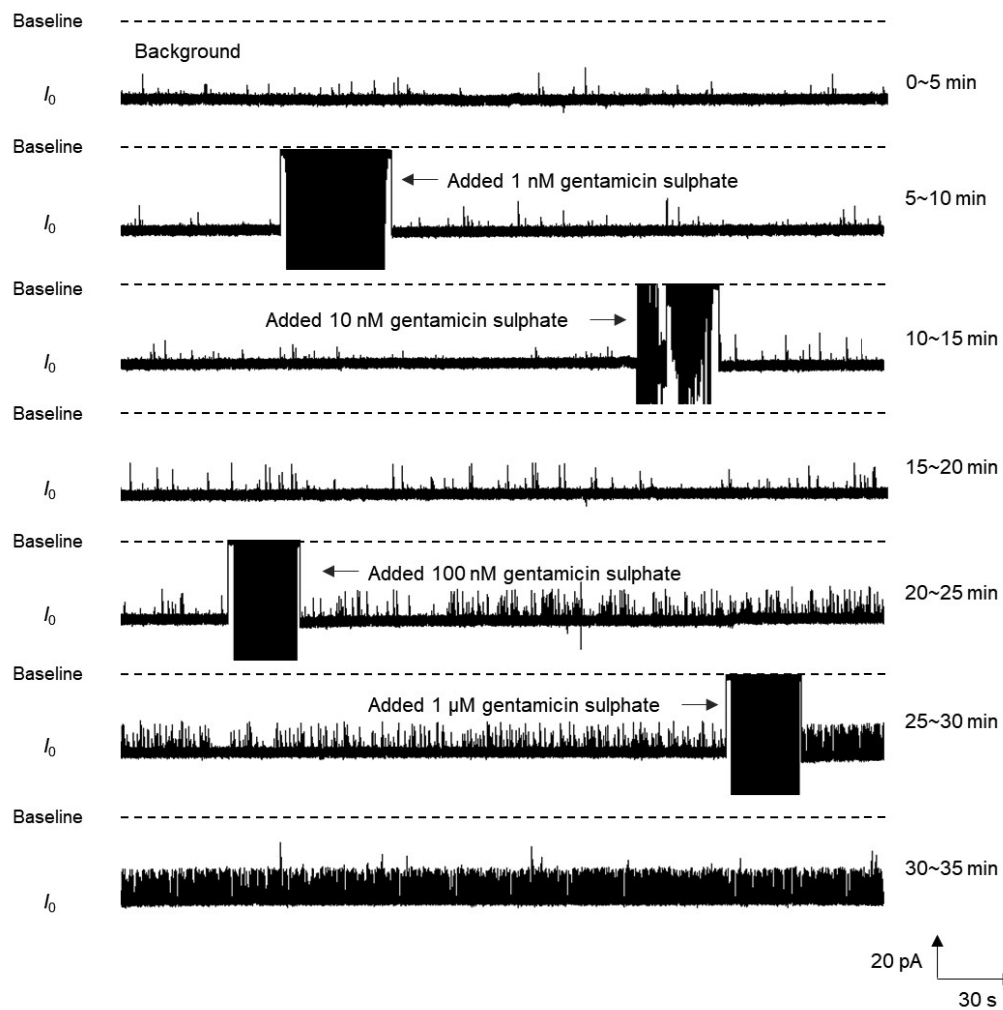


Fig. 17

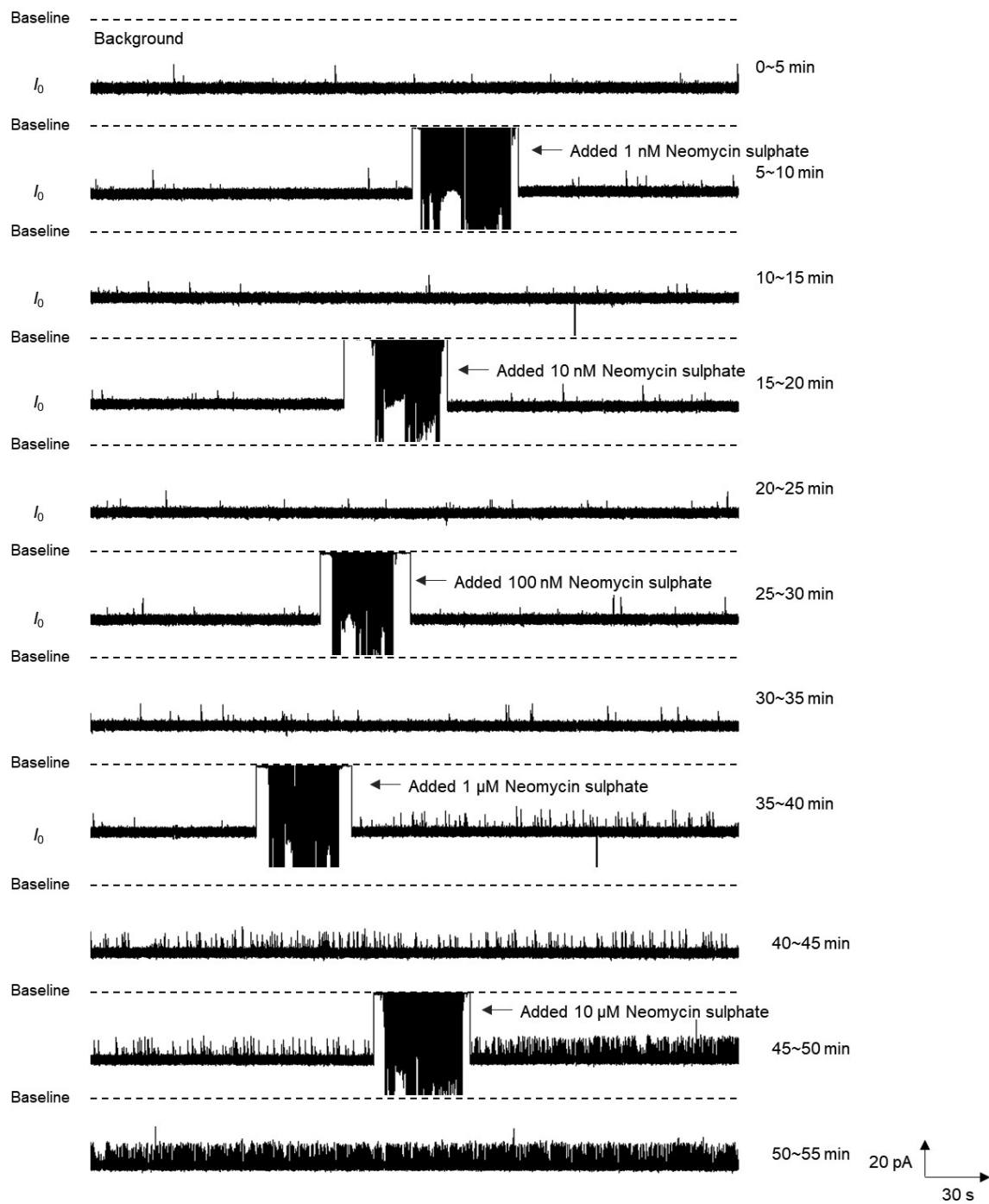


Fig. 18

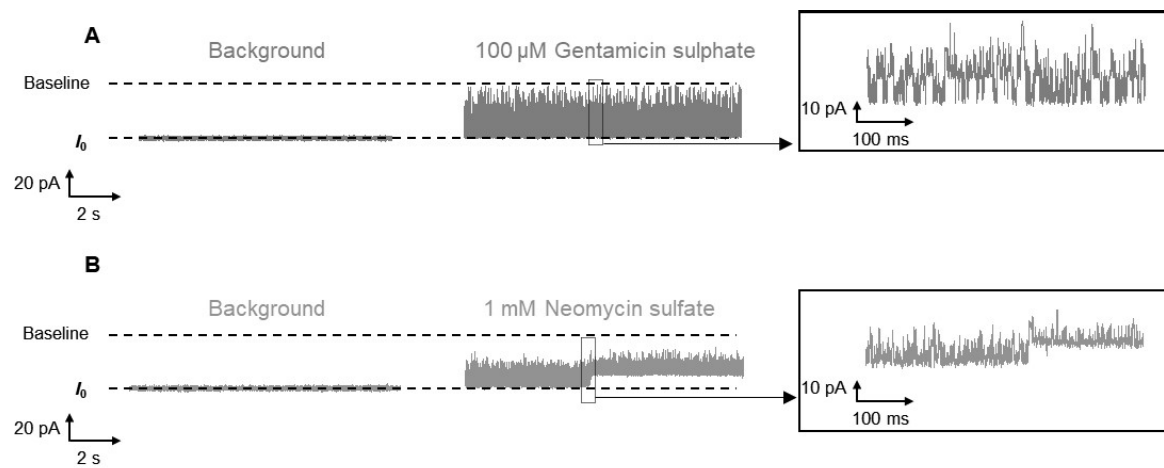


Fig. 19

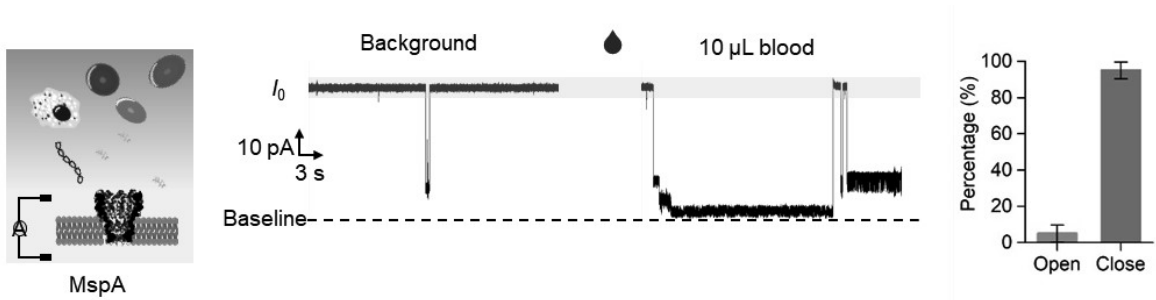


Fig. 20

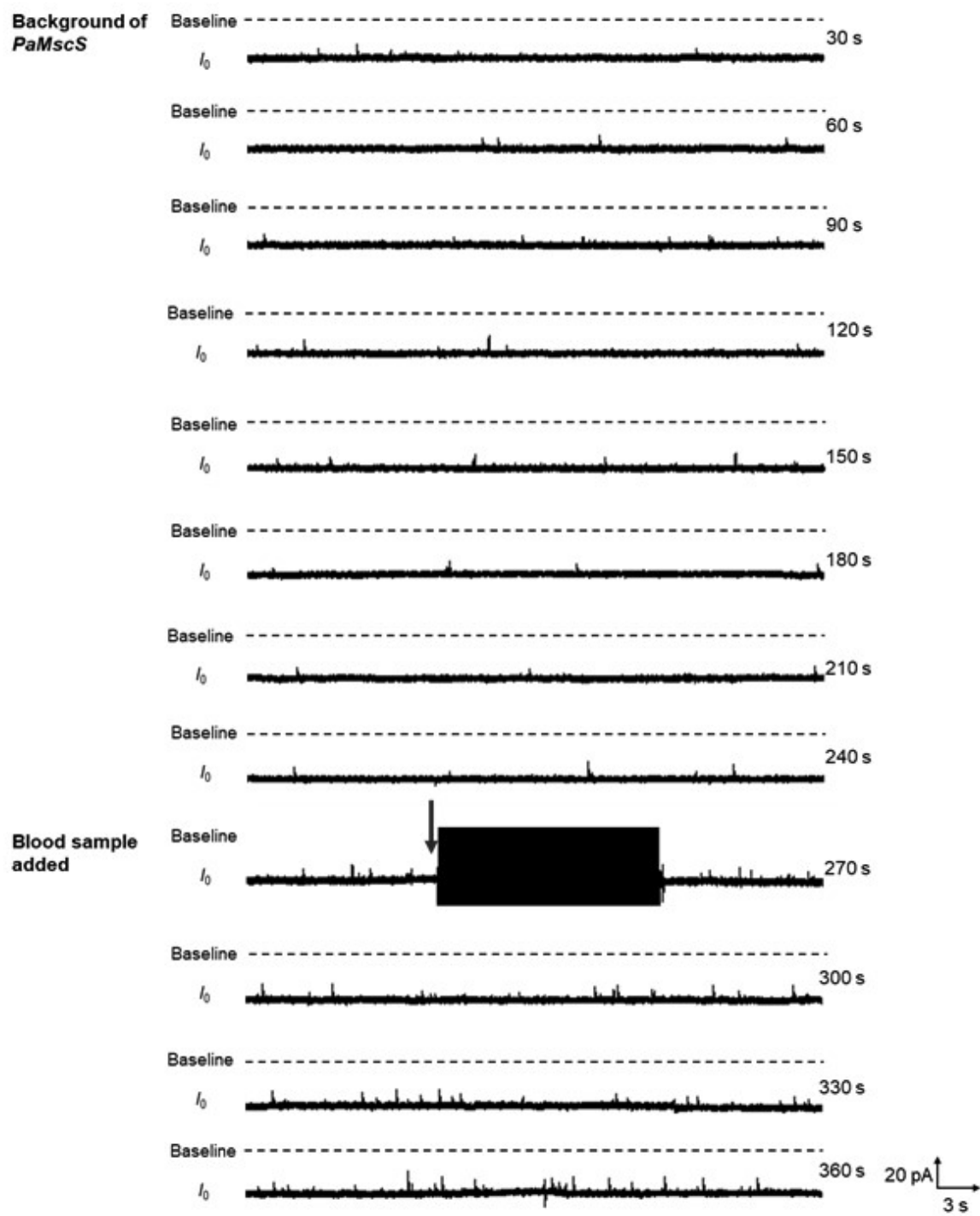


Fig. 21

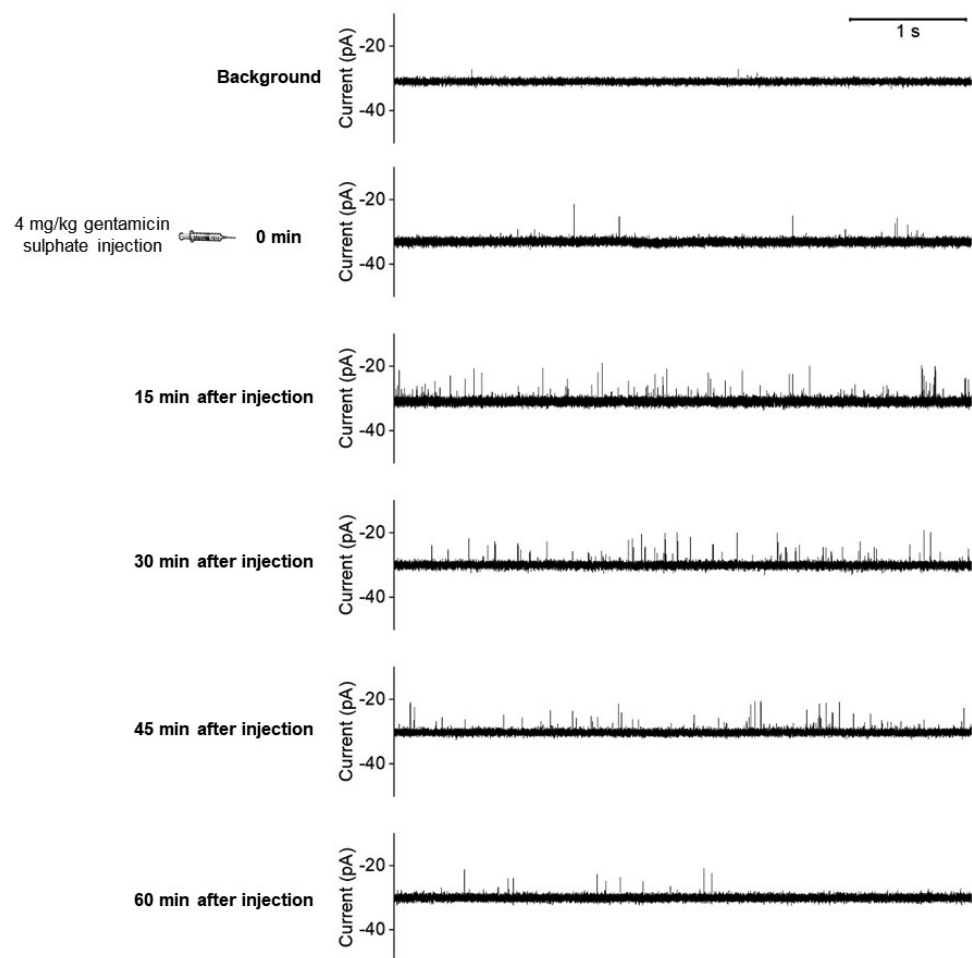


Fig. 22

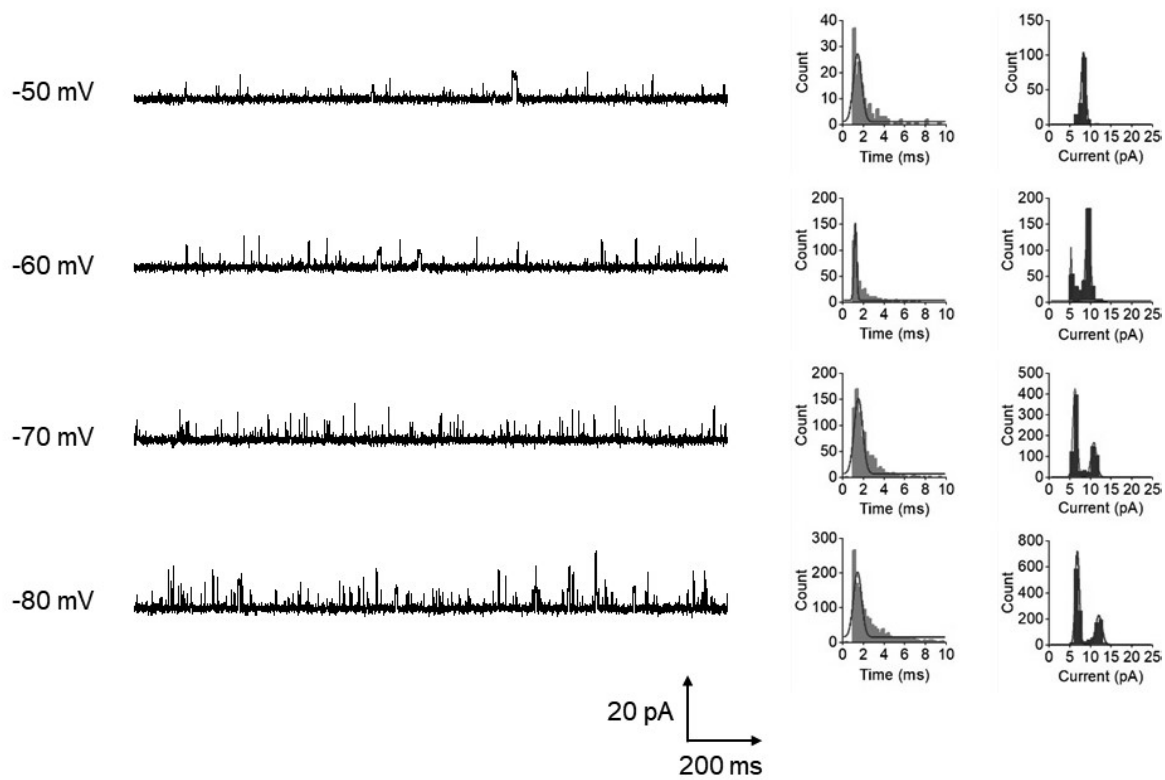


Fig. 23

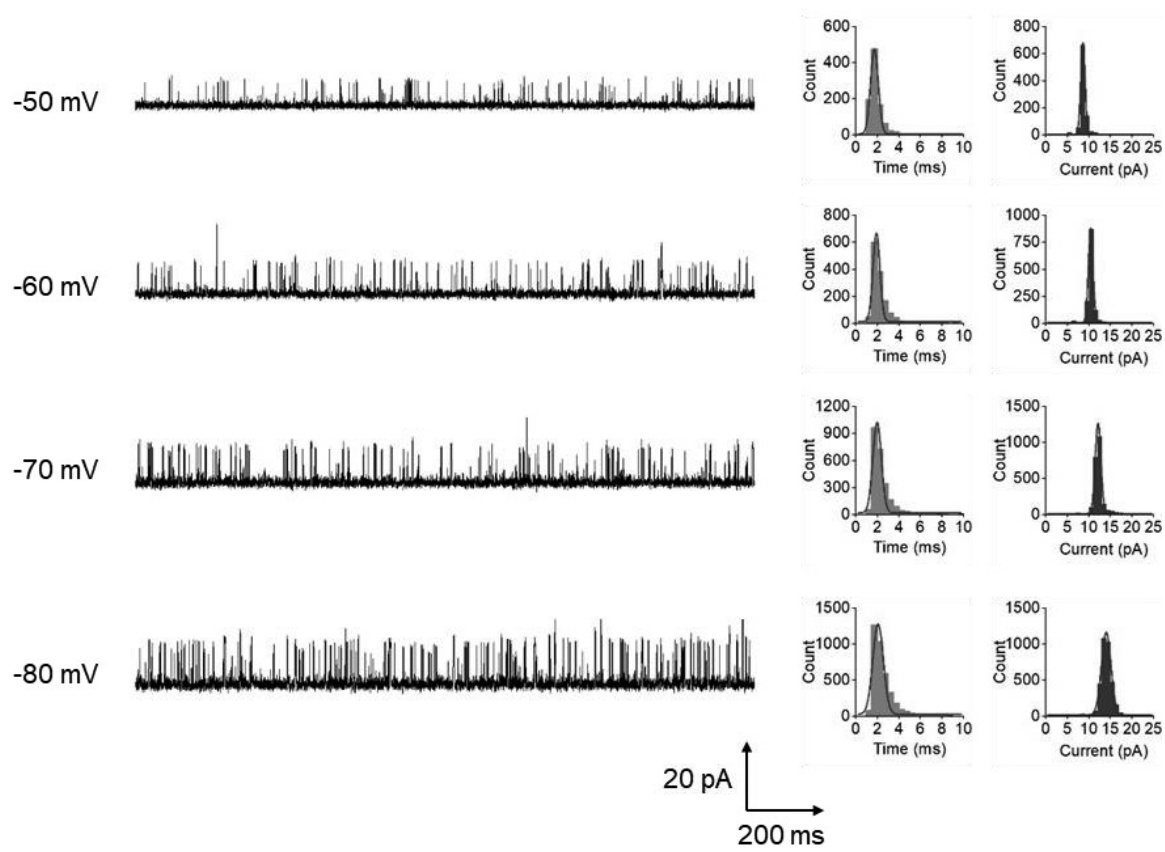


Fig. 24

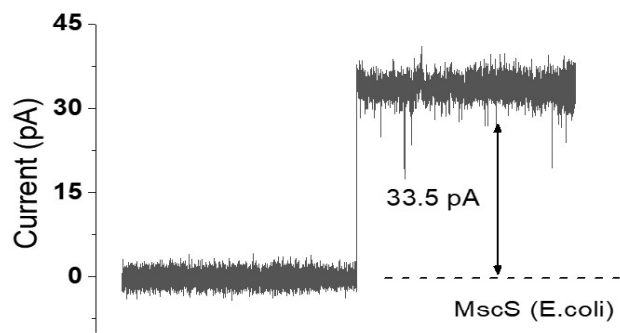


Fig. 25

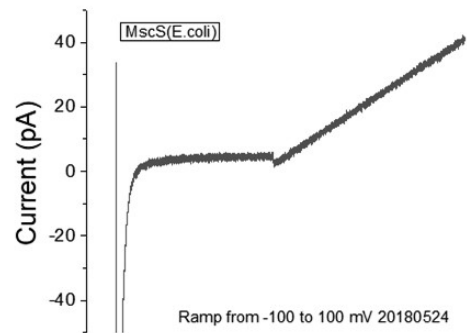


Fig. 26

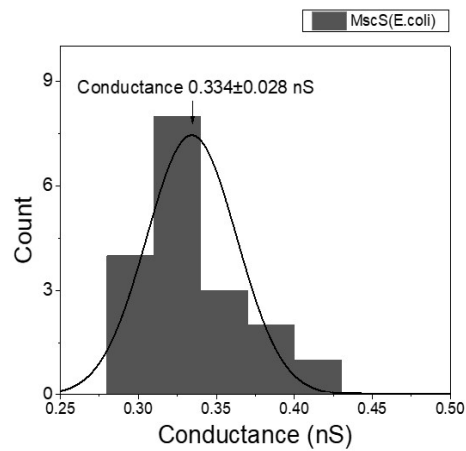
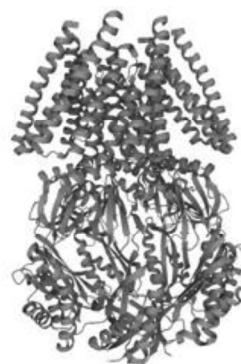


Fig. 27



Schematic diagram of the structure of EcMscS

# Length: 250			
# Identity: 92/250 (36.8%)			
# Similarity: 151/250 (60.4%)			
# Gaps: 1/250 (0.4%)			
# Score: 470			
#			
#			
#=====			
EMBOSS_001	23	LLLSYAVNIVAALATIIIVGLI IARMISNAVNRLMISRKIDATVADFLSAL	72
EMBOSS_001	18	IVLEYSGRVALALLTLAIGWLLINTLTGRVGGLLARRSVDRITLQGFVGSLS	67
EMBOSS_001	73	VRYGIIAFTLIAALGRVGVQIASVIAVLGAAGLAVGLAQGLSLNLAAGV	122
EMBOSS_001	68	VSIVLKILLVSVSMIGIQTTSFVAAGAAGLAIGLALQGLSLANFAGGV	117
EMBOSS_001	123	LLVMFRPFPRAGEYVDLGGVAGTVLSVQIFSTMTADGKIIIVPNGKIIA	172
EMBOSS_001	118	LILLFRPFKVGWIEAQGVAGTVDSILIFHTVLRSGDNKRIIVPNGALSN	167
EMBOSS_001	173	GNIIINFSREPVRKNEFIIGVAYDSIDQVKQILTNI IQSEDRILADREMT	222
EMBOSS_001	168	GTVTNYSAPVRKVIDVGVGIDYDADLKNAQNILL-AMADDPKVLKDPAPV	216
EMBOSS_001	223	VRLNELGASSINFVVRVWSNSGDLQVYWDVLERIKREFDAAGISFPYPQ	272
EMBOSS_001	217	AVVSNLGEAITLSLRVVKADYWDVVMFMFNEKARDALGKEGIGIPFPQ	266

Sequence alignment of PaMscS and EcMscS

Fig. 28a

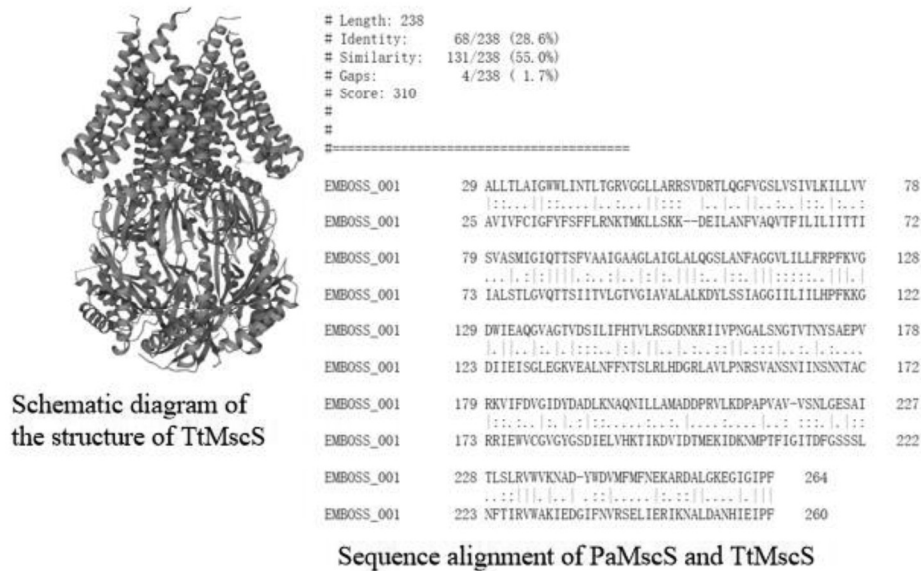


Fig. 28b

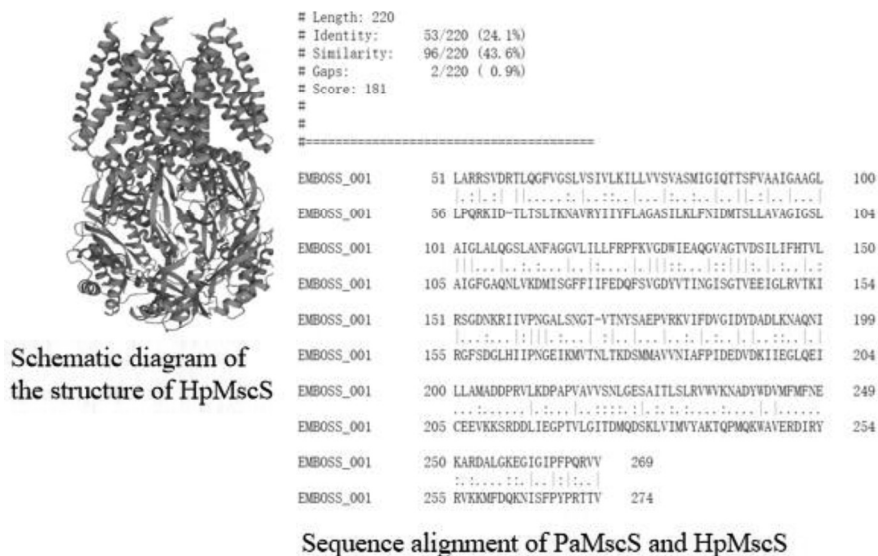


Fig. 28c

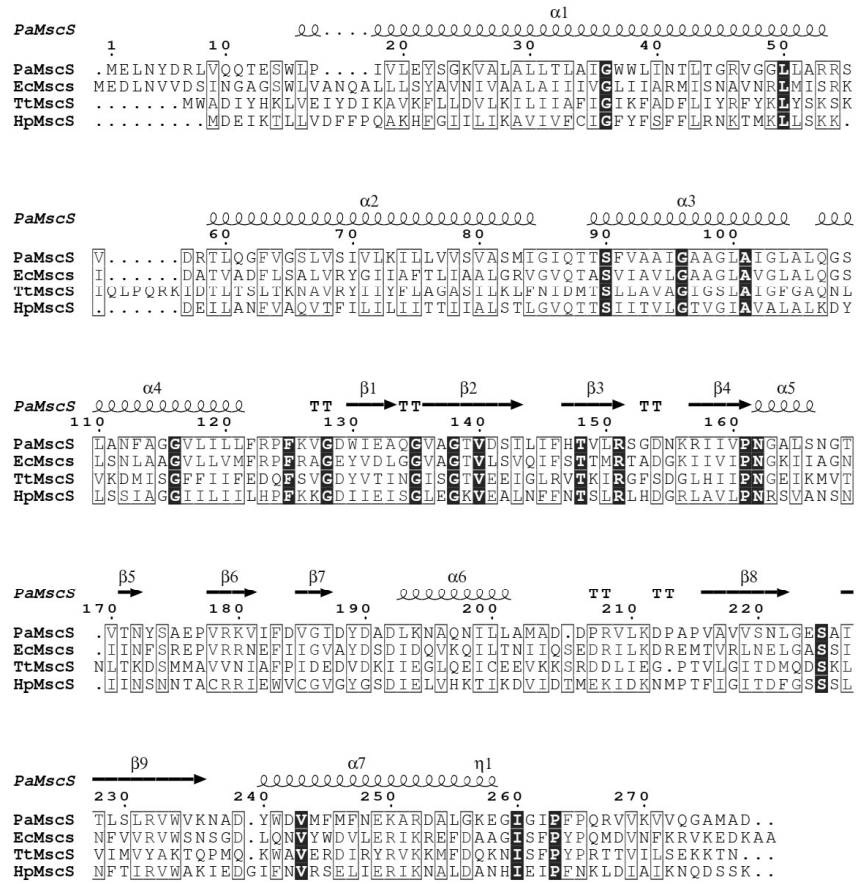


Fig. 28d

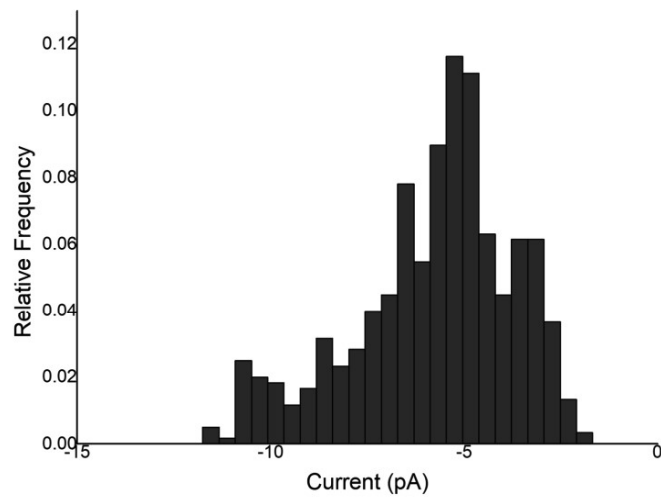


Fig. 29

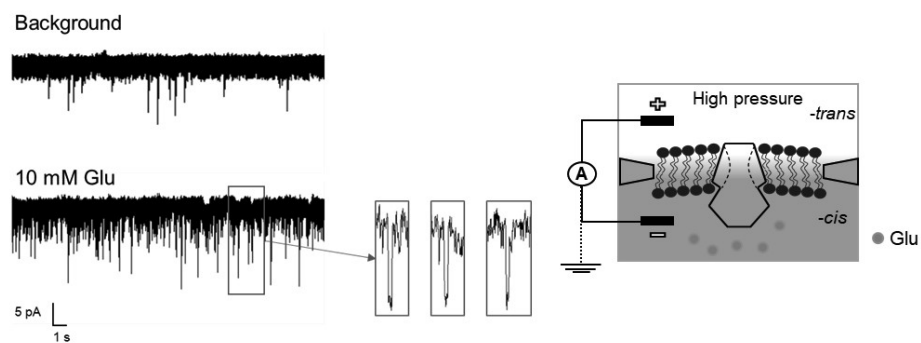


Fig. 30

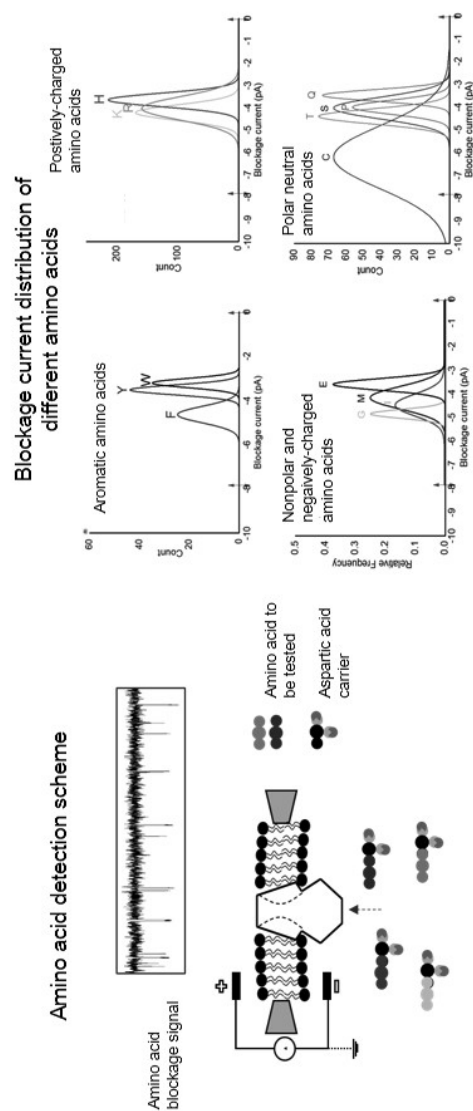


Fig. 31