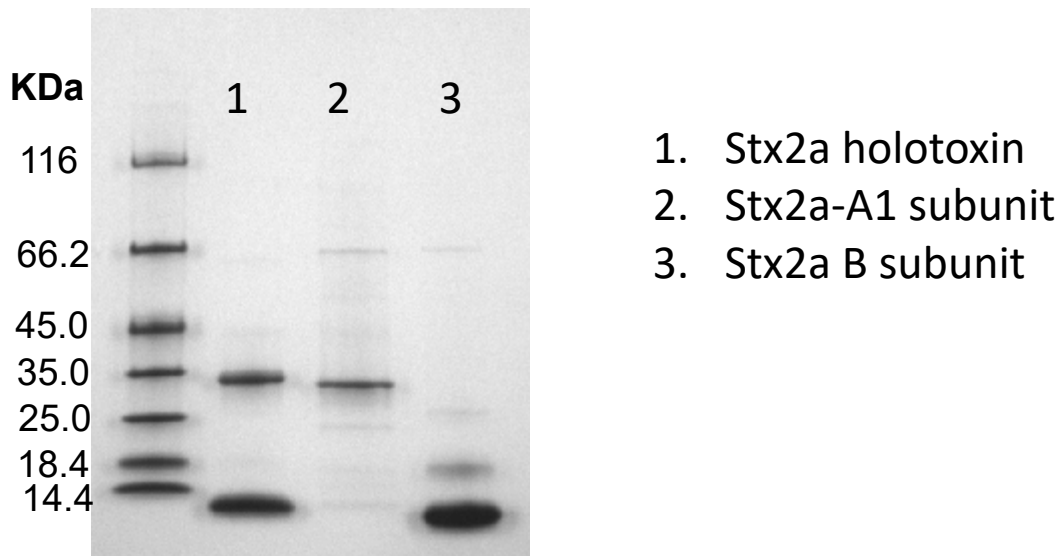


Supplementary Information



Amino acid sequences:

Stx2a holotoxin:

MKCILFKWVLCLLLGFSVSYSREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSVSVINHTPPGSYFAVDIRGLDVYQARFDHLR
LIIEQNPLYVAGFVNTATNTFYRFSDFTHSVPGVTTVSMTTDSSYTTLQRVAALERSGMQISRHSLSVSSYLALMEFSGNTMTRDA
SRVLRFTVTAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTNLWGRISNVLPEYRGEDGVRVGRISFNNISAILGTVAVILNC
HHQGARSVRVNEESQPECQITGDRPVIKINNTLWESNTAAFLNRKSQFLYTTGK

taaaggagttaagc

MKKMFMAVLFALASVNAMAADCAKGKIEFSKYNEDDTFTVKVDGKEYWTSRWNLQPLLQSAQLTGMTVTIKSSTCESGSGFAE
VQFNNDLEHHHHHH

DNA sequence sandwiched between the A and B subunit

Signal peptide

Stx2a-A1:

MKCILFKWVLCLLLGFSVSYSREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSVSVINHTPPGSYFAVDIRGLDVYQARFDHLR
LIIEQNPLYVAGFVNTATNTFYRFSDFTHSVPGVTTVSMTTDSSYTTLQRVAALERSGMQISRHSLSVSSYLALMEFSGNTMTRDA
SRVLRFTVTAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTNLWGRISNVLPEYRGEDGVRVGRISFNNISAILGTVAVILNC
HHQGARSVRVNEESQPEGGSLEHHHHHH

Stx2a-B:

MKKMFMAVLFALASVNAMAADCAKGKIEFSKYNEDDTFTVKVDGKEYWTSRWNLQPLLQSAQLTGMTVTIKSSTCESGSGFAE
VQFNNDHHHHHH

Figure S1. An SDS-PAGE (4-15%) image of the purified proteins under reducing conditions and their protein sequences.

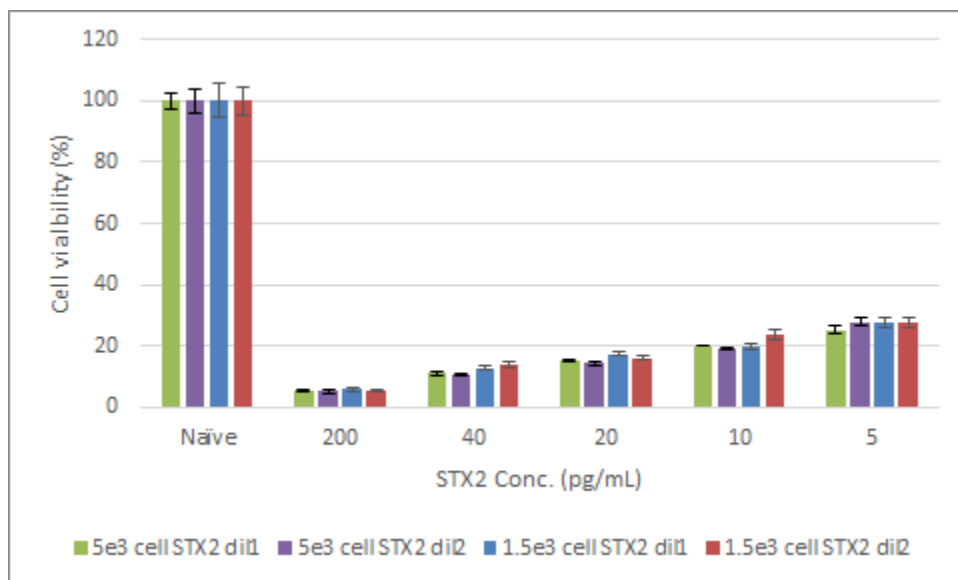
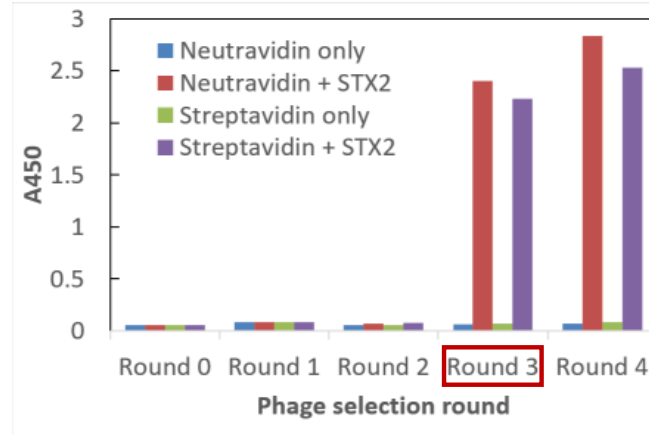


Figure S2. Toxicity of holotoxin Stx2a. Vero E6 cells (1.5×10^3 cells/well) were mixed with the appropriately diluted Stx2a and the mixture was added to 96-well plate. The cell viability was quantified 3 days later using the CellTiterGlo assay.



Cloned into pET28a and transformed BL21(DE3) cells

752 clones were picked and DARPin expressions were induced by IPTG (0.5 mM)

48 clones were chosen, DARPins were expressed in AI medium, and ELISA and neutralization assay were performed

Figure S3. Enrichment of STX2-binding DARPins after phage panning. Successive rounds of a DARPin-phage library were panned against STX2 using streptavidin-coated magnetic beads coated with 100 nM biotinylated-STX2 and MaxiSorp 96-well plates coated with neutravidin (66 nM) and 100 nM biotin-STX2 in alternative rounds. The binding of phage recovered from successive rounds of panning to STX2 was quantified using ELISA. Significant binding was observed after three rounds of panning.

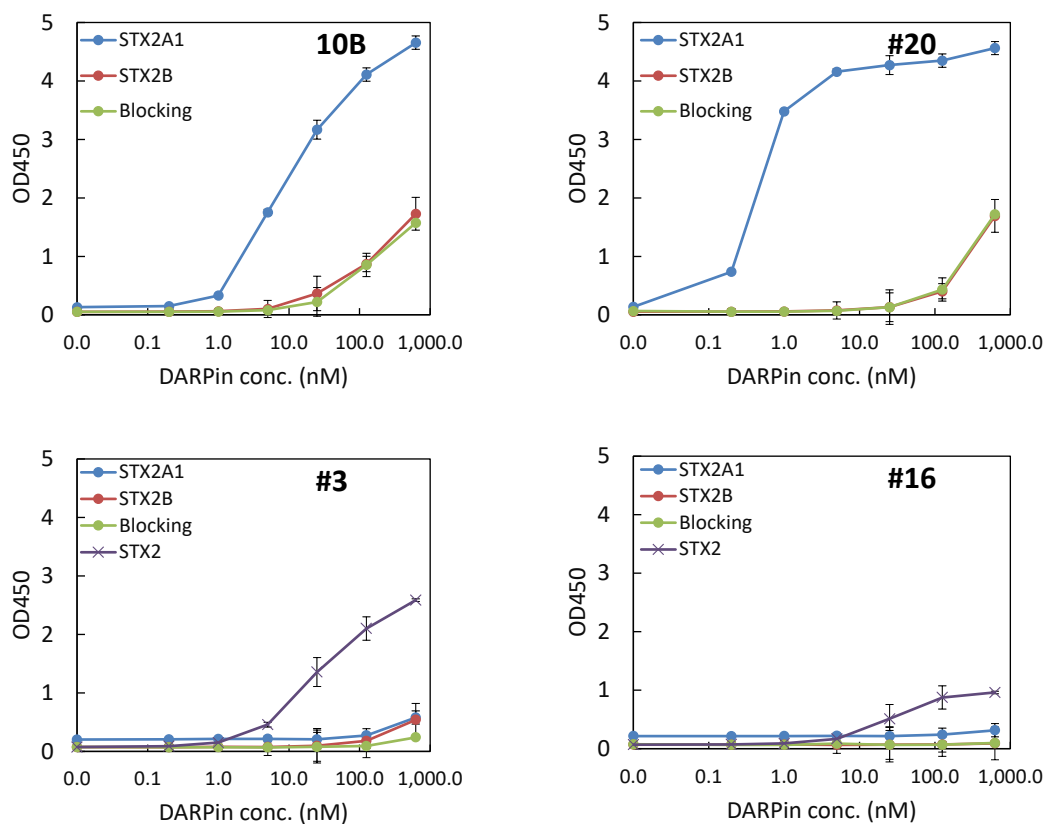
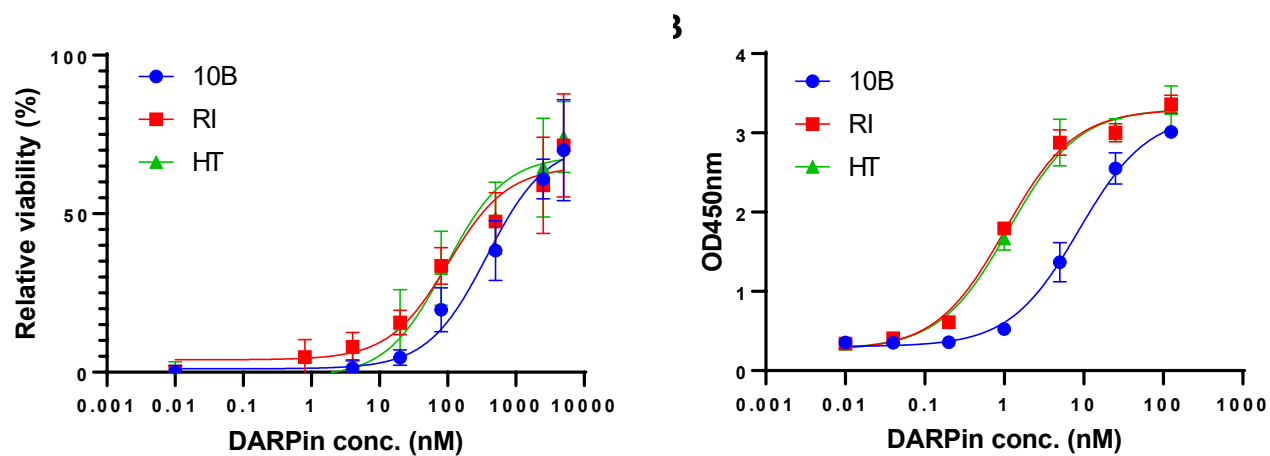


Figure S4. ELISA-based assay to evaluate the ability of monomeric DARPins to bind the A- and B-subunits of Stx2a. The error bars represent the mean deviation of duplicate samples from one representative experiment.



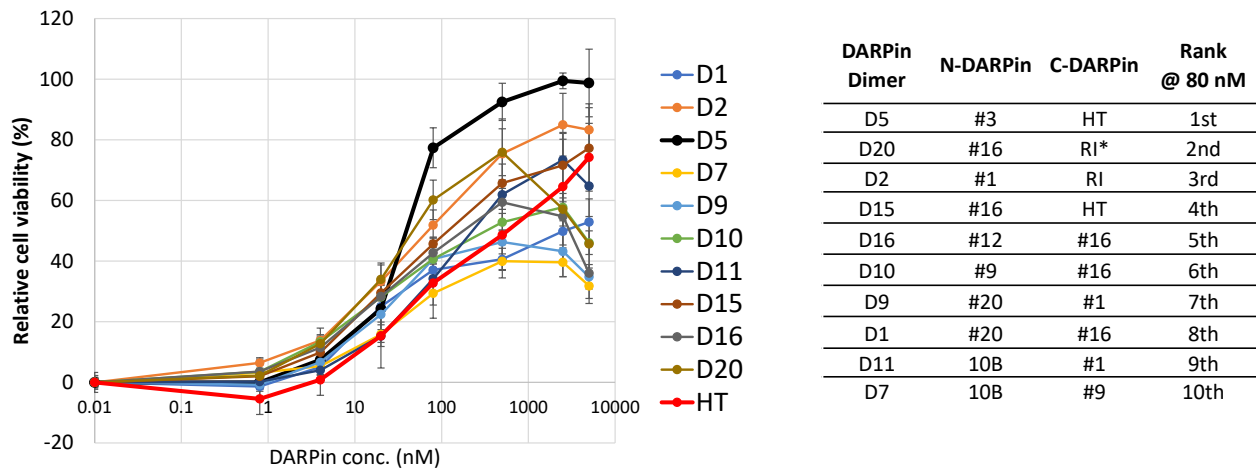
HT:

GKKLLEAARAGQDDEVRLMANGADVNA/GDPFGFTPLHLAAMFGHLEIVEVLLKNGADVNA/HDEYGF TPLHLAA VVGHL EIVEVLLKNGADVNA/CDNQGGTPLHLAAHTGHLEIVEVLLKHGADVNA/QDKFGKTAFDISIDNGNEDLA EILQ

RI:

GKKLLEAARAGQDDEVRLMANGADVNA/GDPFGFTPLHLAAMFGHLEIVEVLLKNGADVNA/HDEYGF TPLHLAA VVGHL EIVEVLLKNGADVNA/CDNQGGTPLHLAARI GHLEIVEVLLKHGADVNA/QDKFGKTAFDISIDNGNEDLA EILQ

Figure S5. Relative viability **(A)** and binding ability **(B)** of DARPin HT, RI and 10B. **(C)** Amino acid sequences of DARPin HT and RI. The ELISA plates were coated with the full-length Stx2a.



* Variant contains additional point mutations

Figure S6. Activity comparison of DARPin dimers.

Figure S7. Sequence alignment of off-rate mutants.

ID	Motif	NCAP	AR1	AR2	AR3	CCAP
		1-----10-----20-----30-----40-----50-----60-----70-----80-----90-----100-----110-----120-----130-----140-----150				
		GKKLLEAARAGQDDEVRI LMANGADVNA/	XDXXGXTPLHLAAXXGHLEIVEVLLKXGADVNA/	XDXXGXTPLHLAAXXGHLEIVEVLLKXGADVNA/	XDXXGXTPLHLAAXXGHLEIVEVLLKXGADVNA/	QDKFGKTAFDISIDNGNEDLAEILQ
	RI	GKKLLEAARAGQDDEVRI LMANGADVNA/	GDPFGFTPLHLAAMFGHLEIVEVLLKNGADVNA/	HDEYGFTPLHLAAVVGHLEIVEVLLKNGADVNA/	CDNQGGTPLHLAARTGHLEIVEVLLKHGADVNA/	QDKFGKTAFDISIDNGNEDLAEILQ
	HT	GKKLLEAARAGQDDEVRI LMANGADVNA/	GDPFGFTPLHLAAMFGHLEIVEVLLKNGADVNA/	HDEYGFTPLHLAAVVGHLEIVEVLLKNGADVNA/	CDNQGGTPLHLAARTGHLEIVEVLLKHGADVNA/	QDKFGKTAFDISIDNGNEDLAEILQ
#1	#1-A4	-----/-----/-----E-----N-----/-----HT-----/-----I-----				
#2	#1-A10	----V-----/-----/-----E-----/-----HT-----/-----				
#3	#2-A9	-----/-----/-----E-----S-M-----/-----HT-----/-----				
#4	#2-G5	-----/-----/-----E-----/-----RM-----M-----/-----				
#5	#2-H7	-----/-----/-----E-----/-----RI-----/-----				
#6	#2-H8	-----V-----/-----/-----E-----R-----/-----HT-----/-----				
#7	#3-A6	-----V-----/-----/-----E-----R-----/-----HT-----/-----				
#8	#3-A7	-----/-----/-----/-----E-----/-----HT-----/-----				
#9	#3-A8	-----/-----/-----/-----E-----/-----HT-----/-----				
#10	#3-A10	-----/-----/-----/-----E-----L-----/-----HT-----/-----GY-----				
#11	#3-B2	-----V-----/-----/-----E-----/-----HT-----/-----				
#12	#3-C4	-----/-----/-----LY-----/-----E-----/-----HT-----/-----				
#13	#3-D10	-----/-----/-----Y-----/-----E-----/-----HT-----/-----Y-----				
#14	#3-D12	-----V-----/-----A-----S-----/-----E-----G-----/-----RI-----/-----				
#15	#3-E9	-----/-----/-----/-----E-----/-----HT-----/-----				
#16	#3-E10	----D---T-----/-----L-----/-----E-----/-----RI-----Q-----/-----				
#17	#3-E11	-----/-----/-----M-----/-----E-----G-----/S-----RI-----/-----				
#18	#3-F8	-----/-----/-----G-----/-----E-----/-----RI-----/-----I-----				
#19	#3-F12	-----/-----/-----F-----/-----E-----/-----HT-----/-----I-----				
#20	#4-A2	-----T-----/-----Y-----/-----E-----/-----HT-----/-----				
#21	#4-A10	-----/-----/-----/-----E-----/-----HT-----/-----				
#22	#4-B5	-----/-----G-----/-----E-----L-----/R-----S-----HT-----R-----/-----				
#23	#4-E1	-----/C-----/-----E-----/-----HT-----/-----				
#24	#4-F2	-----/-----/-----/-----E-----N-----/-----HT-----/-----				
#25	#4-F9	-----/-----M-----A-----/-----E-----/-----HT-----/-----				
#26	#4-G7	-----/-----/-----/-----E-----/-----SHT-----/-----T-----				
#27	#4-H5	-----F-----/-----E-----/-----E-----/-----HT-----/-----				
#28	#4-H7	-----/-----Y-----/-----E-----/-----RI-----/-----				
Syn	SHT	-----V-----/-----LY-----/-----E-----S-M-----N-----/R-----S-----SHT-----Q-----/-----Y-----I-----				

A		
Stx2a-A	MKCILFKWVLCLLLGFSVSVYSREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSV	60
Stx2c-A	MKCILFKWVLCLLLGFSVSVYSREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSV	60

Stx2a-A	SVINHTPPGSYFAVDIRGLDVYQARFDHLRLIEQNNLYVAGFVNTATNTFYRFSDFTHI	120
Stx2c-A	SVINHTPPGSYFAVDIRGLDVYQARFDHLRLIEQNNLYVAGFVNTATNTFYRFSDFTHI	120

Stx2a-A	SVPGVTTVSMTTDSSYTTLQRVAALERSGMQISRHSVLSSYLALMEFSGNTMTRDASRAV	180
Stx2c-A	SVPGVTTVSMTTDSSYTTLQRVAALERSGMQISRHSVLSSYLALMEFSGNTMTRDASRAV	180

Stx2a-A	LRFVTVTAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTLNWGRISNVLPFYRGEDGV	240
Stx2c-A	LRFVTVTAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTLNWGRISNVLPFYRGEDGV	240

Stx2a-A	RVGRISFNNISAILGTVAVILNCHHQGARSVRVNEESQPECQITGDRPVIKINNTLWES	300
Stx2c-A	RVGRISFNNISAILGTVAVILNCHHQGARSVRVNEESQPECQITGDRPVIKINNTLWES	300

Stx2a-A	NTAAAFNLRKSQFLYTTGK	319
Stx2c-A	NTAAAFNLRKSQFLYTTGK	319

Stx2a-B	MKKMFMAVLFALASVNAMAADCAKKGKIEFSKYNEDDTFTVKVDGKEYWTSRWNLQPLLQS	60
Stx2c-B	MKKMFMAVLFALVSVNAMAADCAKKGKIEFSKYNEDDTFTVKVAGKEYWTSRWNLQPLLQS	60

Stx2a-B	AQLTGMTVTIKSSTCESGSGFAEVQFNND	89
Stx2c-B	AQLTGMTVTIKSSTCESGSGFAEVQFNND	89

B

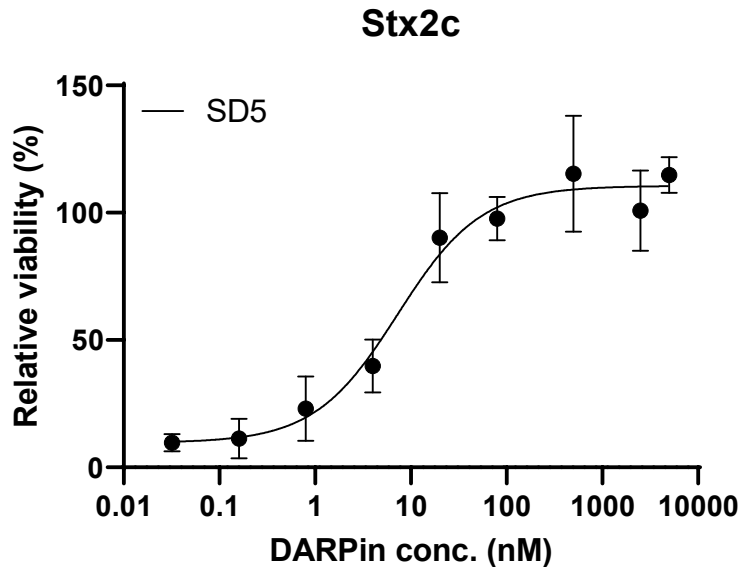


Figure S8. (A) Sequence alignment of Stx2a and Stx2c. (B) Protection of Vero cells by SD5. Vero E6 cells (1.5×10^3 cells/well) were incubated with 60 pg/mL Stx2c and the appropriately diluted DARPin for 3 days. Error bars represent the standard deviation of two independent experiments performed in duplicate.

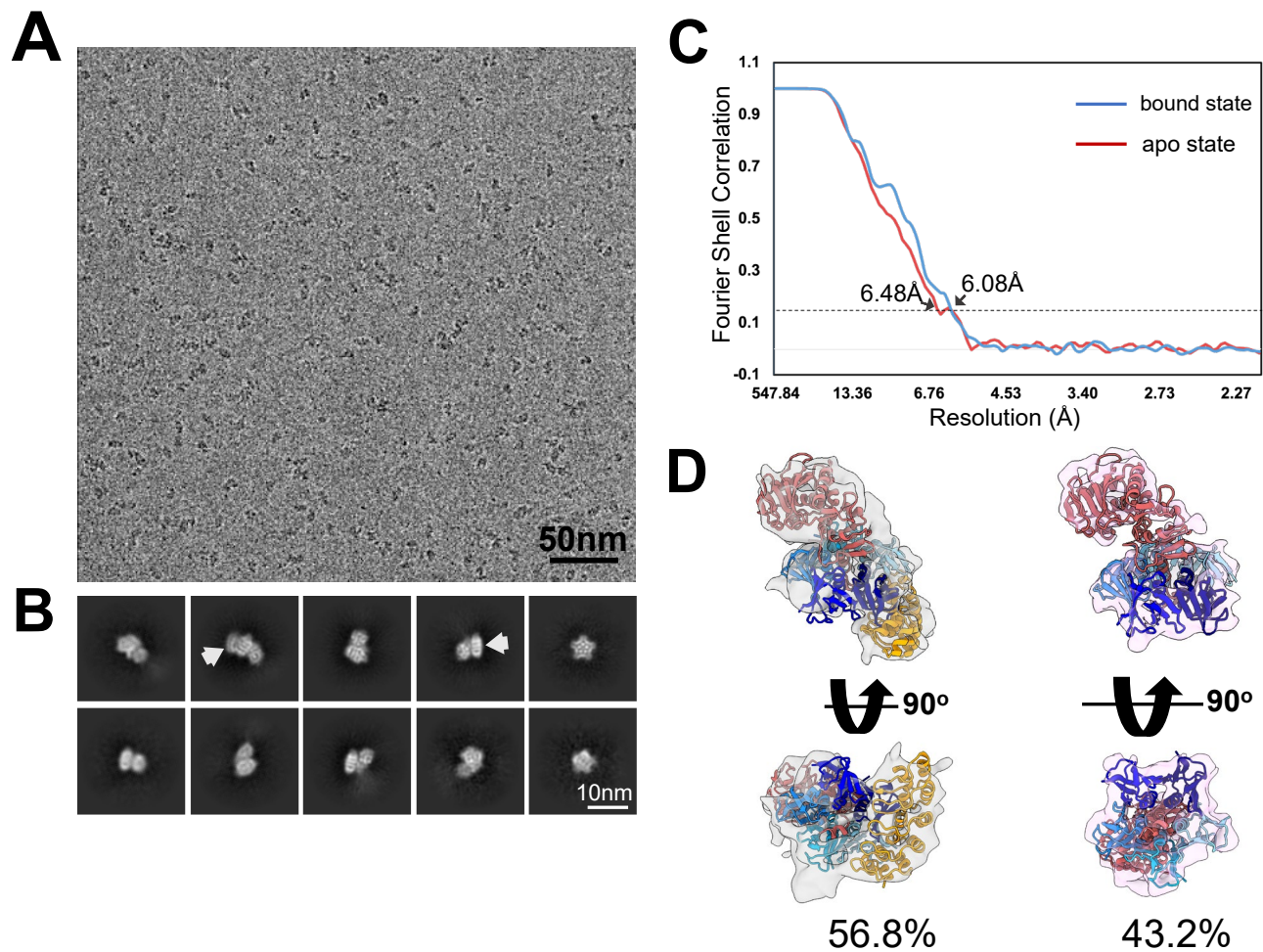


Figure S9. Cryo-EM analysis on Stx2a and DARPin #3 complex. **(A)** Representative micrograph of the cryo-EM data. **(B)** Representative 2D classification of the complex. The white arrows highlight the extra density of DARPin. **(C)** FSC of the bound-state map and apo-state map. **(D)** The density maps of the bound state (left) and the apo state (right) with the refined models docked in. The A subunit is colored red. The B subunit is colored blue. The DARPin is colored orange.

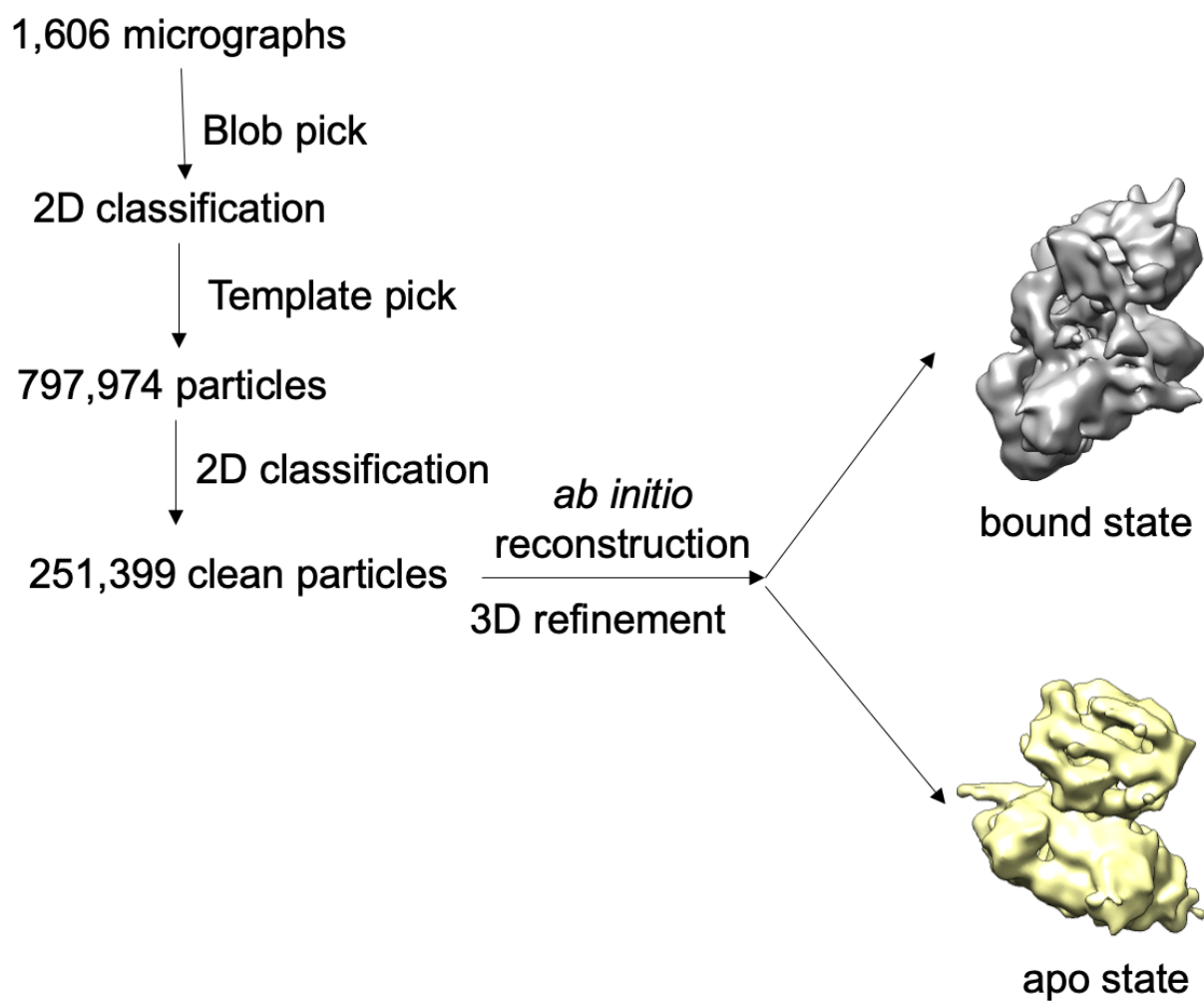


Figure S10. Data processing for the complex between Stx2a and DARPin #3.