Appendix

Table of content

Appendix Figures and Figure legends

Appendix Figure S1: The syntaxin-1 R151A, I155A mutations do not influence the release kinetics. Appendix Figure S2: Competitive effect of the cytoplasmic domain of syntaxin-1 (residues 2–253) in the binding between the fluorescent dye-labeled syntaxin-1 linker peptide (residues 148–162) and the MUN-BC fragment.

Appendix Figure S3: The syntaxin-1 R210E mutant does not influence the transit of syntaxin-1 from the Munc18-1/syntaxin-1 complex to the ternary SNARE complex mediated by the MUN domain.

Appendix Tables

Appendix Table S1: Data summary table for the results shown in Figure 4 for the specified mutants of uncomplexed syntaxin-1-CC and syntaxin-1-CC (RIAA: R151A/I155A, LEAA: L165A/E166A, LEAA+RIAA: R151A/I155A/L165A/E166A).

Appendix Table S2: Data summary table for results shown in Figure 4 for syntaxin-1-CC. Appendix Table S3: Data summary table for results shown in Figure 4 for syntaxin-1-MN.

Appendix Supplementary Figures and Figure legends



Appendix Figure S1

Appendix Figure S1

The syntaxin-1 R151A, I155A mutations do not influence the release kinetics.

A. Summary graphs of rise times (left), decay times τ_{fast} (center), and decay times τ_{slow} (right) of the evoked-IPSC experiments shown in Fig 2B.

B. Three additional example recordings illustrate the variability of the evoked-IPSC experiments shown in Fig 2B.

C. Three additional example recordings illustrate the variability of RRPs experiments shown in Fig 2C. Data are presented as means \pm SEM.

Appendix Figure S2



Appendix Figure S2

Competitive effect of the cytoplasmic domain of syntaxin-1 (residues 2–253) in the binding between the fluorescent dye-labeled syntaxin-1 linker peptide (residues 148–162) and the MUN-BC fragment. The concentrations of the MUN-BC fragment and the rhodamine B-labeled syntaxin peptide are 60 μ M and 50 nM, respectively. Measurements are shown as means \pm SEM (n = 10). A single exponential decay curve was fit to the data (solid line).

Appendix Figure S3



Appendix Figure S3

The syntaxin-1 R210E mutant does not influence the transit of syntaxin-1 from the Munc18-1/syntaxin-1 complex to the ternary SNARE complex mediated by the MUN domain.

A, B. Measurements of the transition from the Munc18-1/syntaxin-1 complex to the SNARE complex by native gel experiments. Representative Coomassie brilliant blue-stained native electrophoresis gels from one of three independent experiments are shown. The data were processed by Image J (NIH).

C, D. Measurements of the transit of syntaxin-1 from the Munc18-1/syntaxin-1

complex to the ternary SNARE complex using an ensemble FRET assay. Measurements are shown as means \pm SD and the significance was assessed by the Student's t-test using n = 3 technical replicates.

Appendix Tables

Appendix Table S1

Data summary table for the results shown in Figure 4 for the specified mutants of uncomplexed syntaxin-1-CC and syntaxin-1-CC (RIAA: R151A/I155A, LEAA: L165A/E166A, LEAA+RIAA: R151A/I155A/L165A/E166A)*

	FRET efficiency	FRET efficiency	% population of	
	(state 1)	(state 2)	state 1	
WT	0.311 ± 0.025	0.584 ± 0.006	33.07 ± 6.83	
RIAA	0.278 ± 0.003	0.592 ± 0.015	29.11 ± 13.5	
LEAA	0.347 ± 0.002	0.646 ± 0.013	90.15 ± 0.49	
LEAA+RIAA	0.338 ± 0.027	0.649 ± 0.013	87.60 ± 4.38	

* Shown are means \pm SD.

	Conditions	FRET efficiency	Number of analyzed	Student's t-test
			traces	(p value)
WT	uncomplexed	0.584 ± 0.006	90	0.007
	<u>M18</u>	0.747 ± 0.018	66	
	S25+SB	0.156 ± 0.027	77	0.002
	M18+S25+SB	0.742 ± 0.028	70	0.706
	M18+MUN	0.714 ± 0.008	57	0.131
	M18+S25+SB+MUN	0.217 ± 0.005	105	0.001
	M18+MUN NFAA	0.728 ± 0.011	65	0.319
	M18+S25+SB+MUN NFAA	0.729 ± 0.002	80	0.270
	uncomplexed	0.592 ± 0.015	99	0.015
RIAA	M18	0.764 ± 0.026	105	
	S25+SB	0.135 ± 0.029	93	0.002
	M18+S25+SB	0.729 ± 0.015	97	0.243
	M18+MUN	0.713 ± 0.024	136	0.179
	M18+S25+SB+MUN	0.718 ± 0.016	129	0.172
LEAA	uncomplexed	0.347 ± 0.002	104	0.002
	M18	0.701 ± 0.007	131	
	M18+MUN	0.693 ± 0.004	133	0.304
	M18+S25+SB	0.205 ± 0.007	90	0.0002
	M18+S25+SB+MUN	0.196 ± 0.012	102	0.0004
LEAA+RI AA	uncomplexed	0.338 ± 0.027	99	0.004
	M18	0.716 ± 0.023	116	
	M18+MUN	0.713 ± 0.010	98	0.879
	M18+S25+SB	0.203 ± 0.003	107	0.001
	M18+S25+SB+MUN	0.199 ± 0.017	104	0.002

Appendix Table S2 Data summary table for results shown in Figure 4 for syntaxin-1-CC*

* Shown are means \pm SD.

	Conditions	FRET efficiency	Number of	Student's
			analyzed	t-test
			traces	(p value)
WT	uncomplexed	0.521 ± 0.001	79	0.003
	M18	0.603 ± 0.006	94	
	S25+SB	0.403 ± 0.010	92	0.002
	M18+S25+SB	0.617 ± 0.010	46	0.264
	M18+MUN	0.513 ± 0.010	80	0.008
	M18+S25+SB+MUN	0.412 ± 0.003	90	0.001
	M18+MUN NFAA	0.594 ± 0.004	82	0.221
	M18+S25+SB+MUN	0.596 ± 0.005	58	0.344
	NFAA		38	0.344
RIAA	uncomplexed	0.518 ± 0.009	93	0.007
	M18	0.599 ± 0.003	128	
	S25+SB	0.406 ± 0.001	153	0.0001
	M18+S25+SB	0.610 ± 0.004	70	0.078
	M18+MUN	0.613 ± 0.018	112	0.399
	M18+S25+SB+MUN	0.611 ± 0.016	105	0.396
LEAA	uncomplexed	0.441 ± 0.015	141	0.402
	M18	0.456 ± 0.013	58	
	M18+MUN	0.450 ± 0.020	91	0.746
	M18+S25+SB	0.437 ± 0.019	114	0.366
	M18+S25+SB+MUN	0.425 ± 0.016	103	0.161
LEAA+RI AA	uncomplexed	0.435 ± 0.013	76	0.670
	M18	0.444 ± 0.022	90	
	M18+MUN	0.450 ± 0.028	51	0.857
	M18+S25+SB	0.425 ± 0.014	117	0.400
	M18+S25+SB+MUN	0.435 ± 0.008	113	0.625

Appendix Table S3 Data summary table for results shown in Figure 4 for syntaxin-1-MN*

* Shown are means \pm SD.