

Figure S1 Alignment of alpha-toxin amino acid sequences representing toxin types F, I, IVb, IVc, IVd, V, Vd, Ve, Vf, Vg, and VIII. Asterisk indicates identical amino acid. Residues that are different from those of type F are shown in red. The central loop domain which mediates interaction with ganglioside GM1a is marked in blue in the bottom line, and its key residues are indicated with vertical bars. Shadowed portion above the sequence indicates C-domain (membrane-binding region), in which critical amino acid sites for binding of toxin are marked with #.

	Signal peptide	
F	MKRKICKALICATLATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
I	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
VIII	MKRKICKALICATLATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
IVd	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
IVc	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKSEPE	60
IVb	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
Vg	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
Vd	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
Ve	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
V	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
Vf	MKRKICKALICAALATSLWAGASTKYYAWDGKIDGTGTHAMIVTQGVSIENDLSKNEPE	60
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F	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
I	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
VIII	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
IVd	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
IVc	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
IVb	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
Vg	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
Vd	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
Ve	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
V	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120
Vf	SVRKNLEILKENMHLEQLGSTYPDYDKNAYDLYQDHFWDPTDNNFSKDNSWYLAYSIPD	120

F	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
I	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
VIII	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
IVd	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
IVc	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
IVb	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
Vg	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
Vd	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
Ve	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
V	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180
Vf	TGESQIRKFSALARYEWQRGNYKQATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVKFE	180

F	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
I	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
VIII	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
IVd	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
IVc	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
IVb	TFAEERKEQYKINTAGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
Vg	TFAEERKEQYKINTAGCKTNEAFYTDILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
Vd	TFAEERKEQYKINTAGCKTNEAFYTDILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
Ve	TFAEERKEQYKINTAGCKTNEAFYTDILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
V	TFAEERKEQYKINTAGCKTNEAFYTDILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
Vf	TFAEERKEQYKINTAGCKTNEAFYTDILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSH	240
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F	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
I	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
VIII	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
IVd	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
IVc	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
IVb	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
Vg	SWD Y WDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
Vd	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
Ve	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
V	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300
Vf	SWDDWDYAAKVTLAN SQKGTAGYIYRFLHDVSEGN DPSVGKNVKELVAYISTSGEKDAGT	300

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F	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
I	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
VIII	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
IVd	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
IVc	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
IVb	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
Vg	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
Vd	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
Ve	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
V	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360
Vf	DDYMYFGIKTKDGKTQEWMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRYT		360

	#	
F	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
I	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
VIII	AFPDAYKPENIKI V IANGKVVDKDI NEWISGNSTYNIK	398
IVd	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
IVc	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
IVb	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
Vg	A I S D AYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
Vd	AFPD V YKPENIKI V IANGKVVDKDI NEWISGNSTYNIK	398
Ve	AFPD V YKPENIKI V IANGKVVDKDI NEWISGNSTYNIK	398
V	AFPDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398
Vf	AFSDAYKPENIKI IANGKVVDKDI NEWISGNSTYNIK	398

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