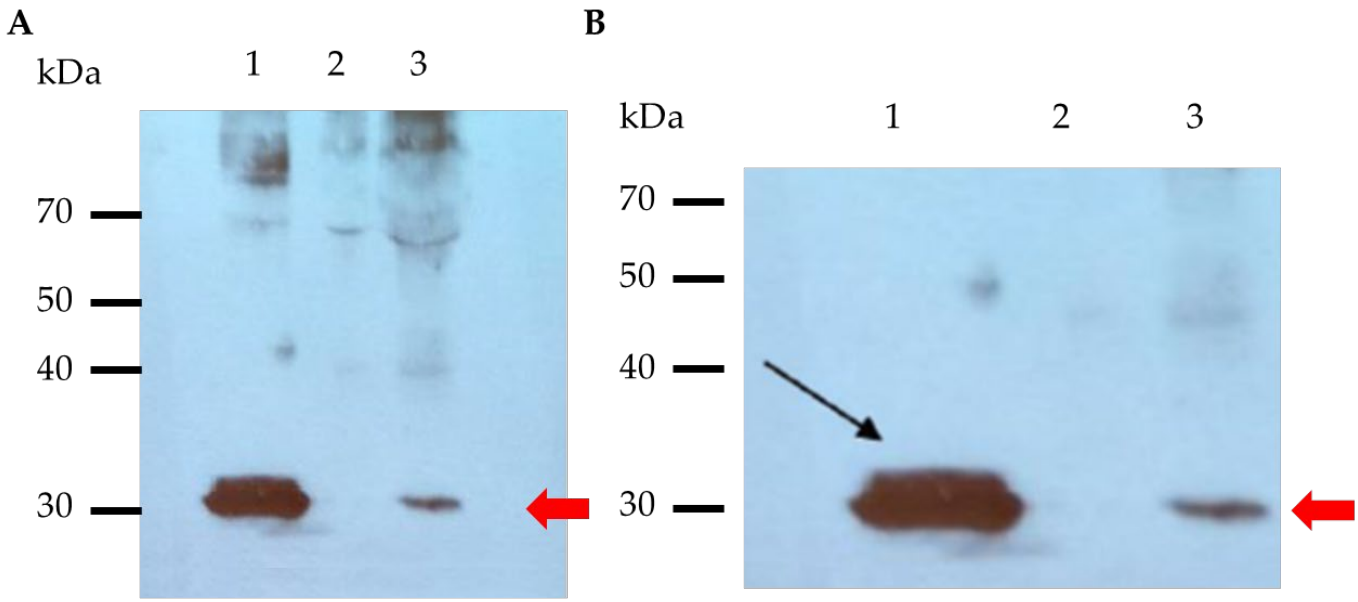


Figure S1. Western blot evaluation with anti-loxoscelic antivenom. *Samples obtained during purification of wtSphD (panel A) and dSphD (panel B) from S. frugiperda larvae homogenates were analyzed by the Western blot, using anti-loxoscelic antivenom as primary antibody. The identity of the lanes is as follows: Lanes: 1, IMAC eluate; 2 pass.through; 3, total larvae homogante.*

Table S1: Identity of 32 kDa SDS-PAGE gel band by PMF

MW gel band	Uniprot ID	Theor. mass	Score	Expect.	Matches
32 kDa	Q1KY80.1 RecName: Full=Phospholipase D LlSicToxalphaIII1ii	32085	267	2.8e-19	26

Table S2: Peptide list used during PMF identification.

m/z	S/N	Intensity	m/z	S/N	Intensity	m/z	S/N	Intensity
650.051	10.1	1262.25	1152.415	6.1	855.41	1776.777	6.8	795.76
662.257	35.9	4473.05	1153.395	8.7	1204.09	1790.753	20	2323.86
683.806	9.7	1200.9	1171.403	11.5	1597.46	1794.809	6.6	759.9
685.308	11.7	1457.18	1188.421	16.9	2366.1	1797.724	20.4	2364.76
806.359	8.1	1028.28	1202.438	6.2	862.17	1804.774	10.6	1222.37
832.244	53.5	6847.76	1209.445	13.9	1951.64	1809.919	16	1830.21
833.162	22.2	2851.07	1265.578	12.1	1725.05	**1842.874**	**54.8**	**5962.47**
869.427	6.8	878.77	1266.345	34.5	4923.11	1870.761	6.3	647.59
883.394	48.4	6322.27	1267.396	73.7	10528.26	1914.743	19.3	1857.16
954.364	7.5	973.35	1337.567	12	1698.32	1928.76	8.3	775.56
971.384	17.9	2347.76	1339.511	6.4	900.95	**1977.892**	**103.5**	**8606.54**
1001.369	7.4	981.21	**1432.609**	**508.9**	**72116.28**	1978.886	59.8	5242.06
1002.329	16.4	2177.88	1446.621	53.8	7606.54	1991.922	40.4	3354.15
1006.459	18.6	2458.2	1454.645	10	1422.48	2035.993	7.3	542.84
1007.418	9.5	1269.15	1489.611	10.4	1467.32	2210.983	15.7	838.3
1014.468	9	1205.16	**1599.602**	**77.5**	**10455.27**	2481.178	21.6	605.87
1020.412	**83.8**	**11181.79**	1613.627	12.9	1718.88	2489.841	19.1	463.71
1030.432	25.2	3381.01	1621.635	9.1	1162.26	**2529.169**	**78.5**	**2007.8**
1034.424	55.3	7431.98	1722.652	21.7	2619.92	2545.142	10.3	238.66
1046.351	41.5	5578.85	1731.748	11.3	1370.01	2555.068	7.3	152.78
1060.366	12.1	1640.84	1732.492	23.4	2857.8	2570.098	18.9	444.25
1073.424	23.9	3266.6	1733.702	47.7	5761.68	2641.198	9.5	198.83

1087.458	7.1	977.47	1740.665	126	15138.06	2769.33	12.3	192.6
1113.391	40.5	5564.76	1750.638	165	17852.17			
1131.406	**42.6**	**5857.64**	1756.729	8.5	1006.06			

Peptides selected for fragmentation and MS/MS analysis are indicated in bold