Supporting Information

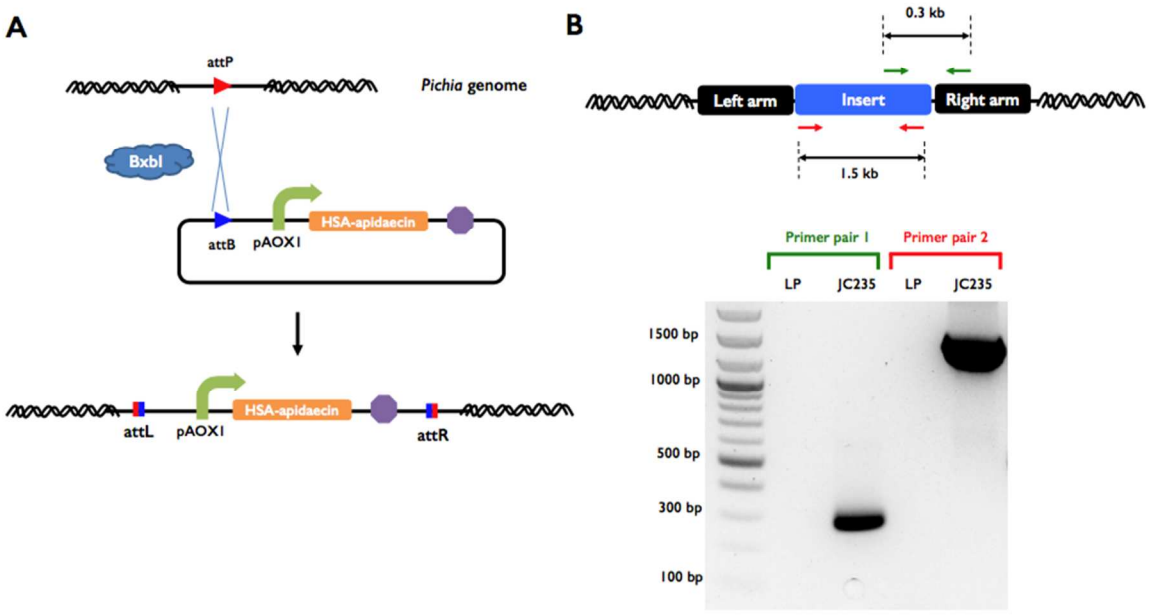
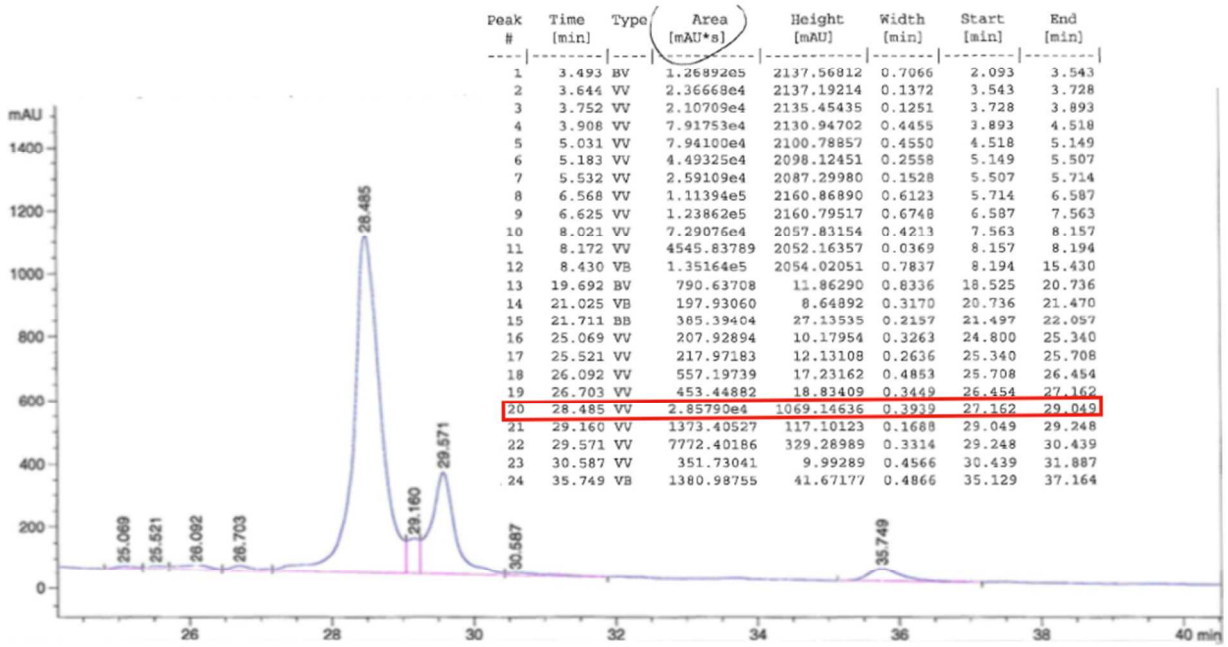


Figure S1. Engineering strategy to generate a HSA-apidaecin fusion protein producing *P. pastoris* strain. (A) Schematic representation of recombinase-based integration of the pAOX1-HSA-apidaecin expression vector into engineered *P. pastoris* cells with the landing pad. The pAOX1-HSA-apidaecin expression vector and a second vector expressing BxbI recombinase were co-transformed into the cells. The BxBI recombinase recognized the attP site within the *P. pastoris* genome and attB site on the expression vector and inserted the whole expression vector into the attP site on *P. pastoris* genome. **(B)** Colony PCR verification of the gene insertion. Primer pair 1 confirmed the correct insertion of the protein expression vector in the desired position on the *Pichia* genome. Primer pair 2 confirmed the insertion of the protein expression vector in the *Pichia* genome. The parental *P. pastoris* strain is labeled as LP, while the HSA-AMP producing strain is labeled as JC235.



Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	3.493	BV	1.2689205	2137.56812	0.7066	2.093	3.543
2	3.644	VV	2.36668e4	2137.19214	0.1372	3.543	3.728
3	3.752	VV	2.10709e4	2135.45435	0.1251	3.728	3.893
4	3.908	VV	7.91753e4	2130.94702	0.4455	3.893	4.518
5	5.031	VV	7.94100e4	2100.78857	0.4550	4.518	5.149
6	5.183	VV	4.49325e4	2098.12451	0.2558	5.149	5.507
7	5.532	VV	2.59109e4	2087.29980	0.1528	5.507	5.714
8	6.568	VV	1.11394e5	2160.86890	0.6123	5.714	6.587
9	6.625	VV	1.23862e5	2160.79517	0.6748	6.587	7.563
10	8.021	VV	7.29076e4	2057.83154	0.4213	7.563	8.157
11	8.172	VV	4545.83789	2052.16357	0.0369	8.157	8.194
12	8.430	VB	1.35164e5	2054.02051	0.7837	8.194	15.430
13	19.692	BV	790.63708	11.86290	0.8336	18.525	20.736
14	21.025	VB	197.93060	8.64892	0.3170	20.736	21.470
15	21.711	BB	385.39404	27.13535	0.2157	21.497	22.057
16	25.069	VV	207.92894	10.17954	0.3263	24.800	25.340
17	25.521	VV	217.97183	12.13108	0.2636	25.340	25.708
18	26.092	VV	557.19739	17.23162	0.4853	25.708	26.454
19	26.703	VV	453.44882	18.83409	0.3449	26.454	27.162
20	28.485	VV	2.85790e4	1069.14636	0.3939	27.162	29.049
21	29.160	VV	1373.40527	117.10123	0.1688	29.049	29.248
22	29.571	VV	7772.40186	329.28989	0.3314	29.248	30.439
23	30.587	VV	351.73041	9.99289	0.4566	30.439	31.887
24	35.749	VB	1380.98755	41.67177	0.4866	35.129	37.164

Figure S2. Chromatogram of the recovered peptide, where the peak at 28.485 corresponds to apidaecin.

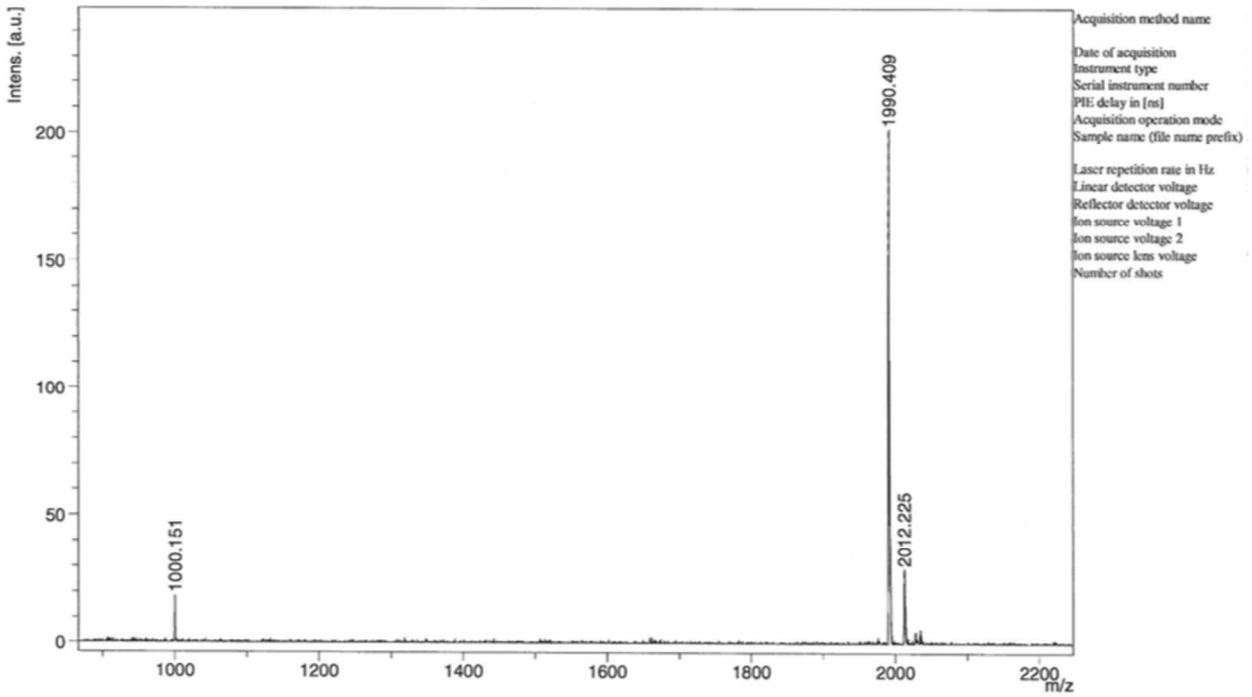


Figure S3. Mass spectrum of the end product (Figure 1 - peak at 28.485 min, GNNRPVYIPQPRPPHPR – ~1.99 kDa).