Supplementary Information

Discovery of Stable and Selective Antibody Mimetics from Combinatorial Libraries of Polyvalent, Loop-Functionalized Peptoid Nanosheets

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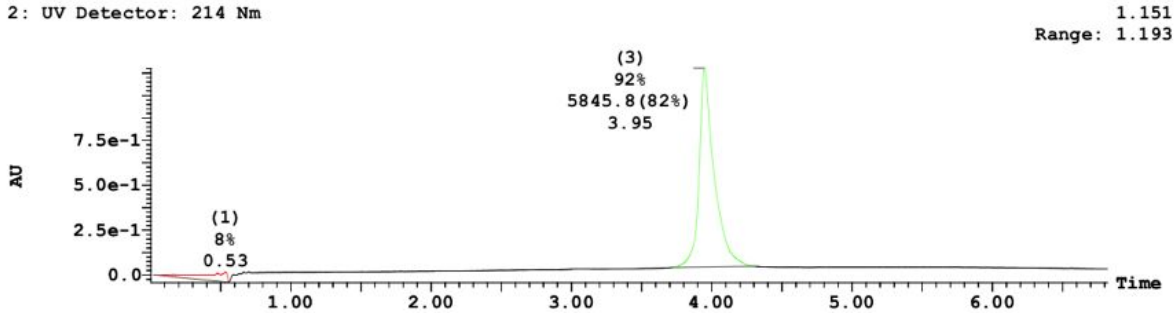
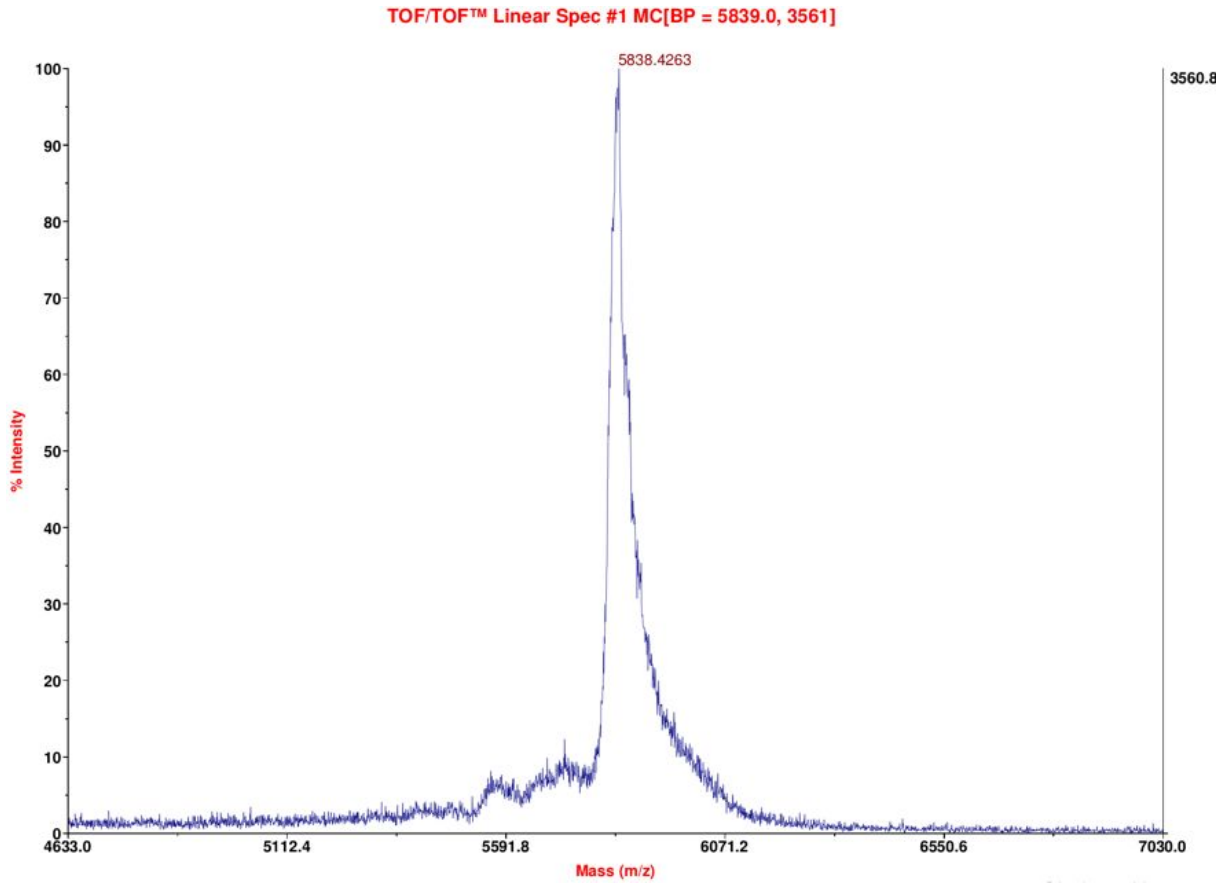
A. LOOPOID LIBRARY

Characterization of free peptoids by analytical HPLC and MALDI-TOF

Several representative peptoid strands are shown in this section.

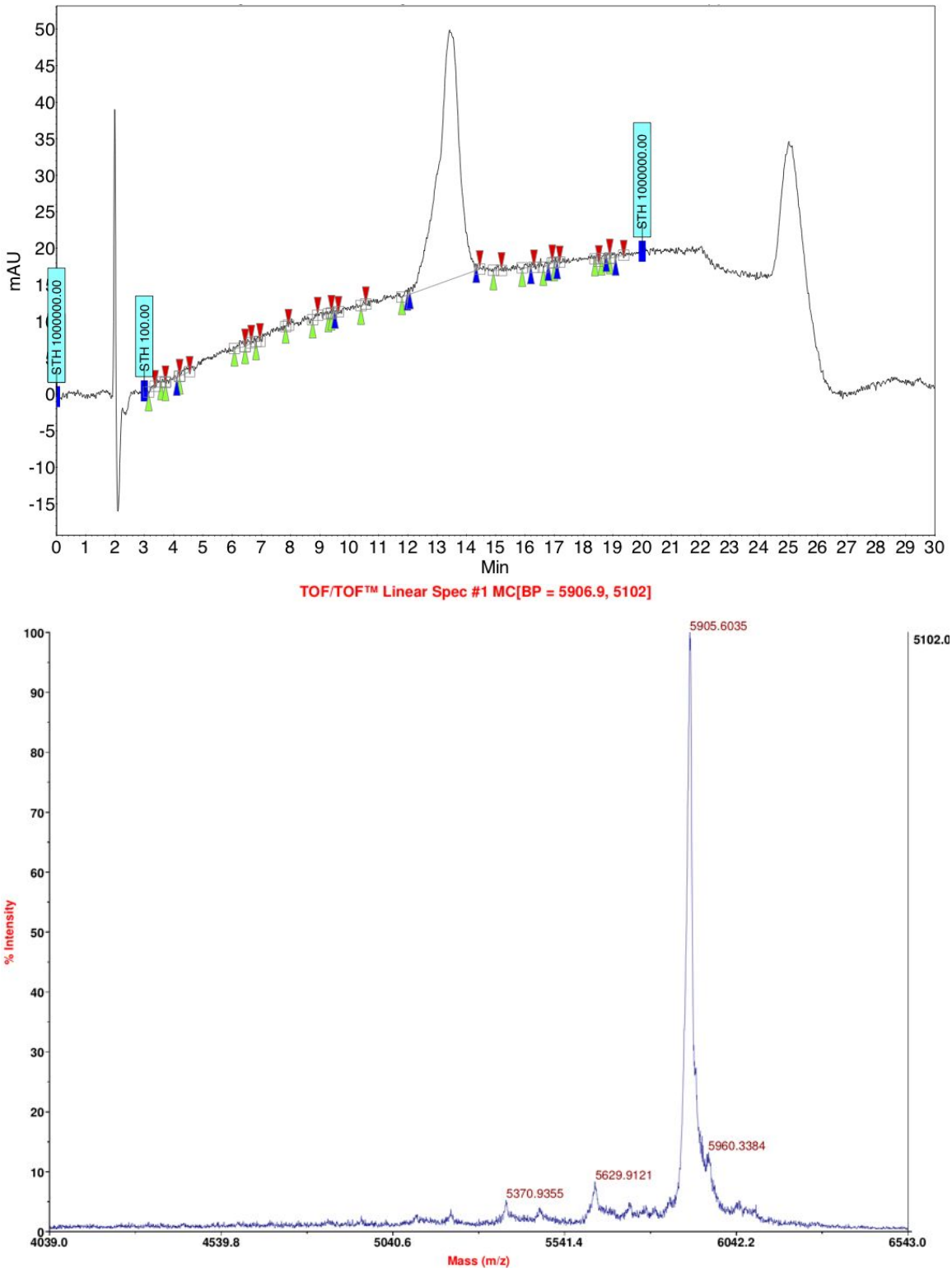
TYWWLD-inserted loopoid strand





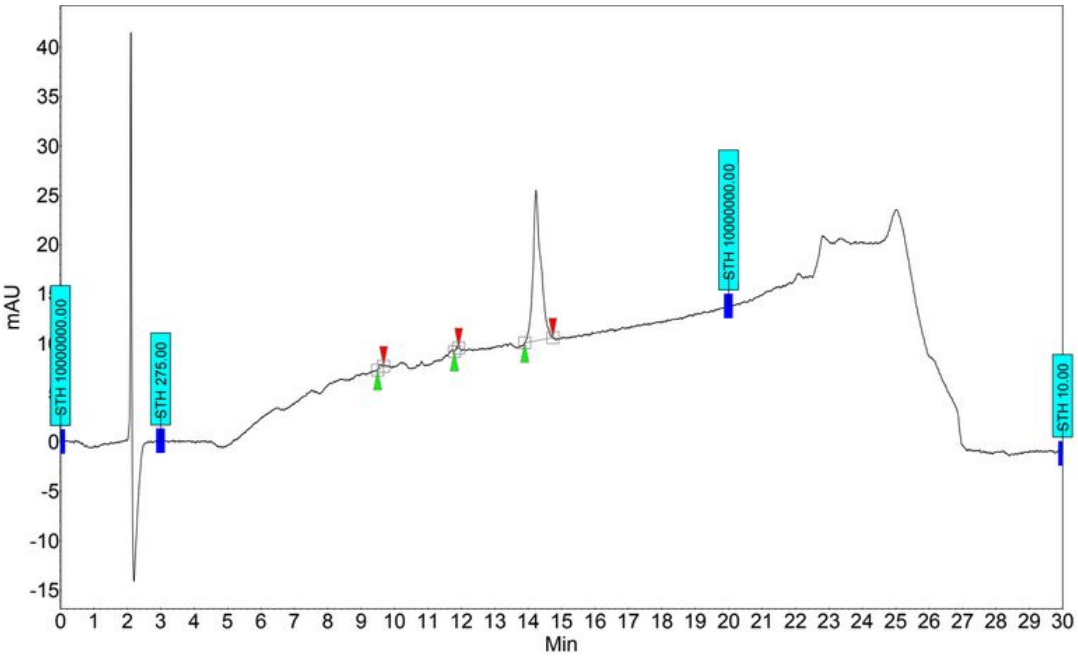
UPLC (5-95% 6.8 min) RT = 3.95 min.
MALDI-TOF calc. $(M+H)^+$ = 5847.78, obs. = 5838.43

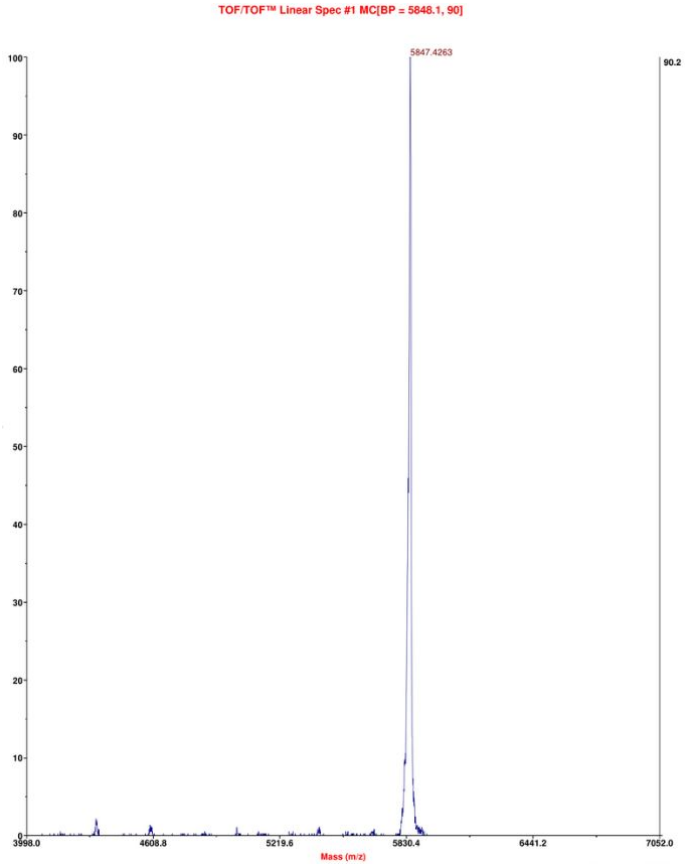
TYWWLD-inspired loopoid strand (Rtoid)



HPLC (5-95% 20 min) RT = 13.44 min
MALDI-TOF calc. $(M+H)^+$ = 5917.92, obs. = 5905.60

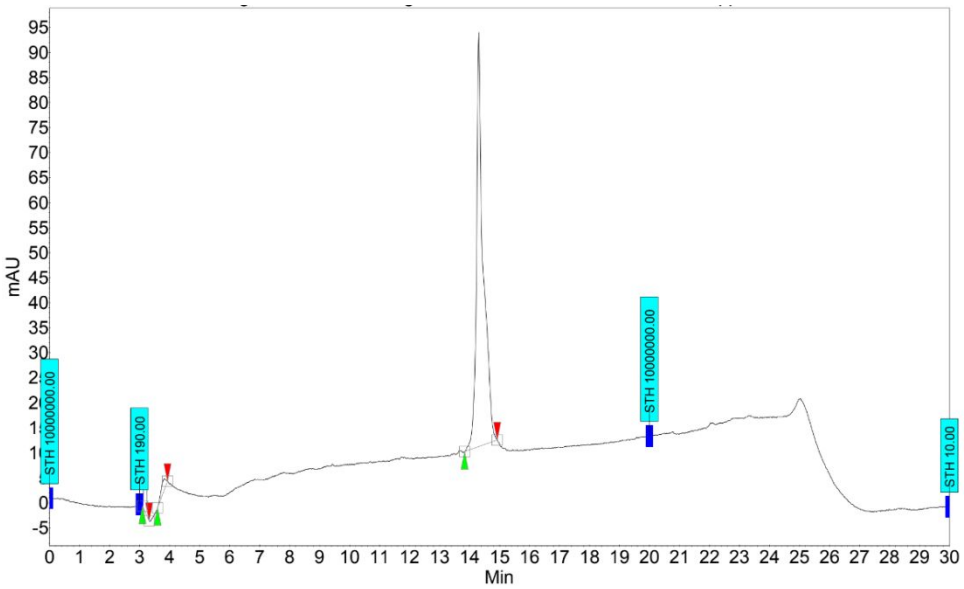
L002 loopoid strand

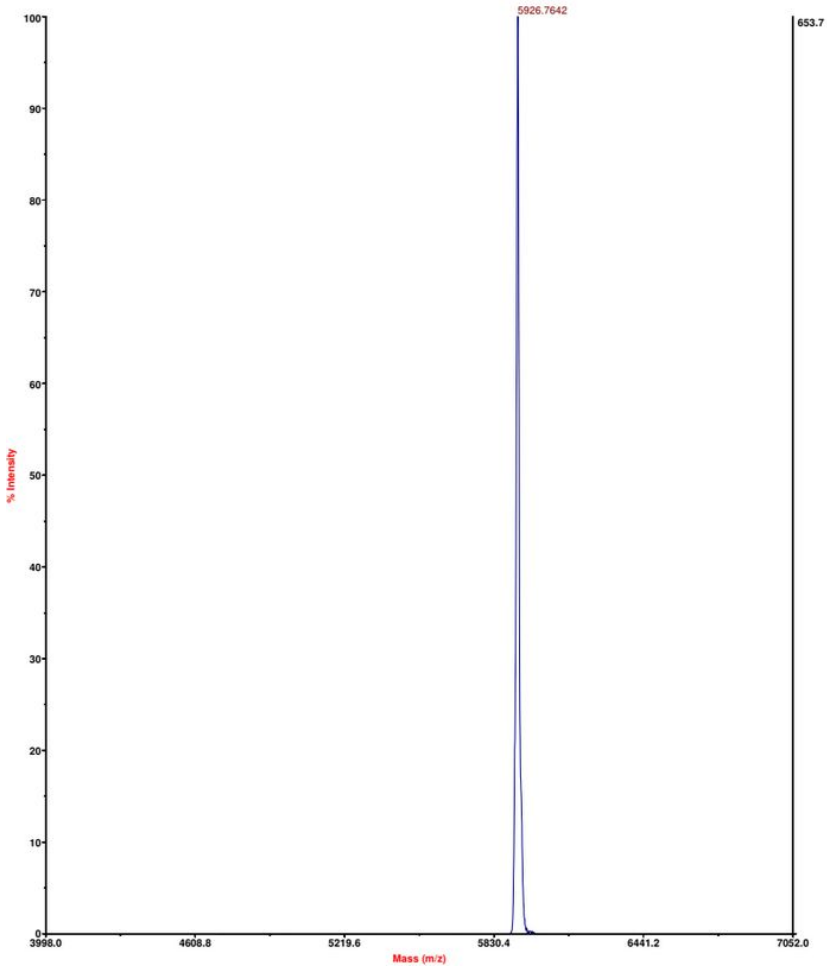




HPLC (5-95% 20 min) RT = 14.23 min
MALDI-TOF calc. $(M+H)^+$ 5855.85, obs. = 5848.1

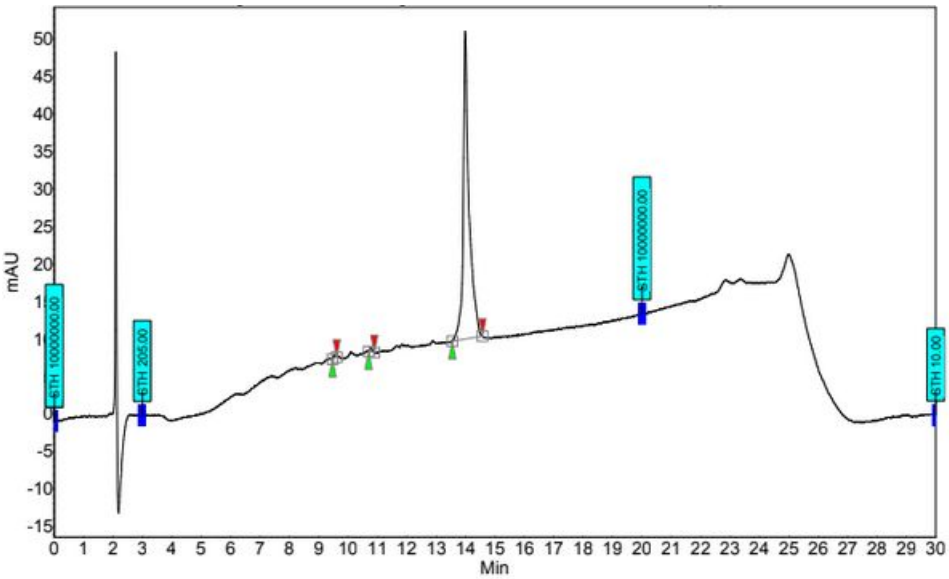
L006 loopoid strand

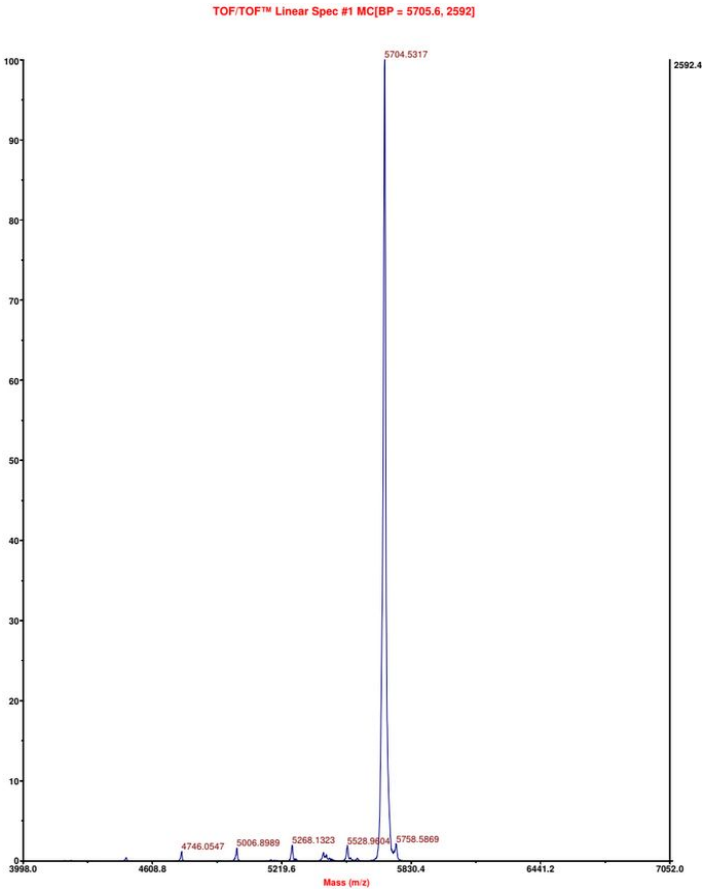




HPLC (5-95% 20 min) RT = 14.31 min
MALDI-TOF calc. $(M+H)^+$ 5932.93, obs. = 5927.8

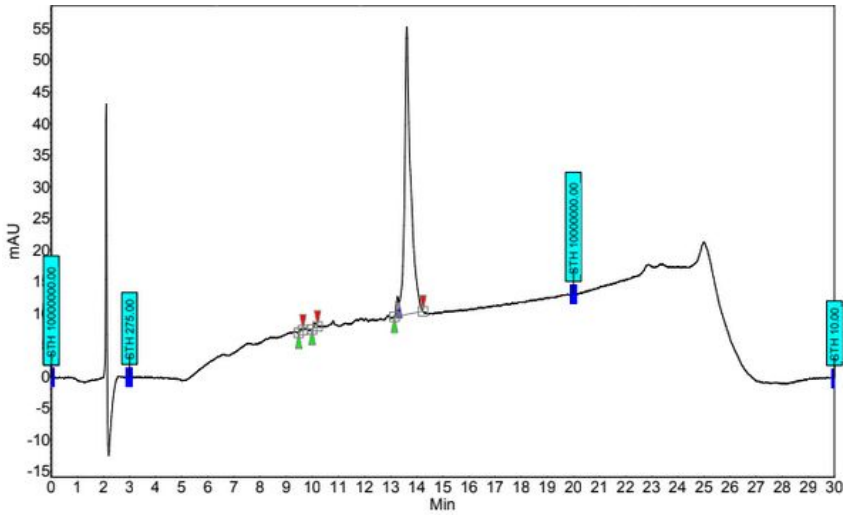
L009 loopoid strand

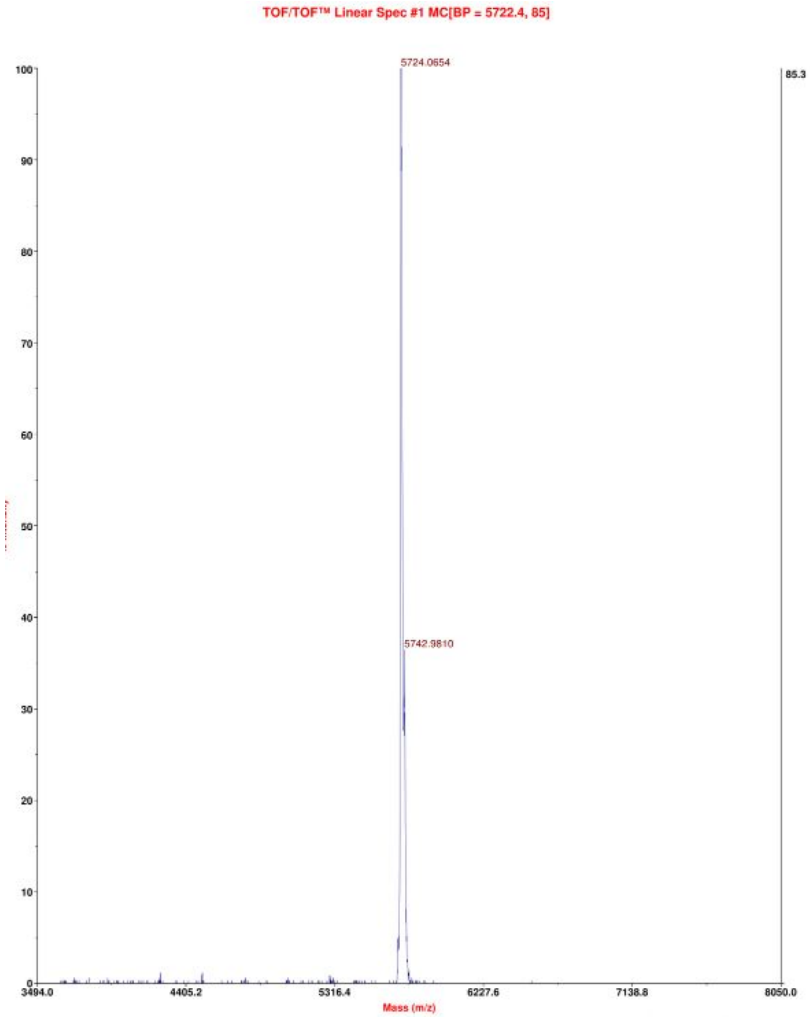




HPLC (5-95% 20 min) RT = 13.99 min
MALDI-TOF calc. $(M+H)^+$ 5710.64, obs. = 5705.6

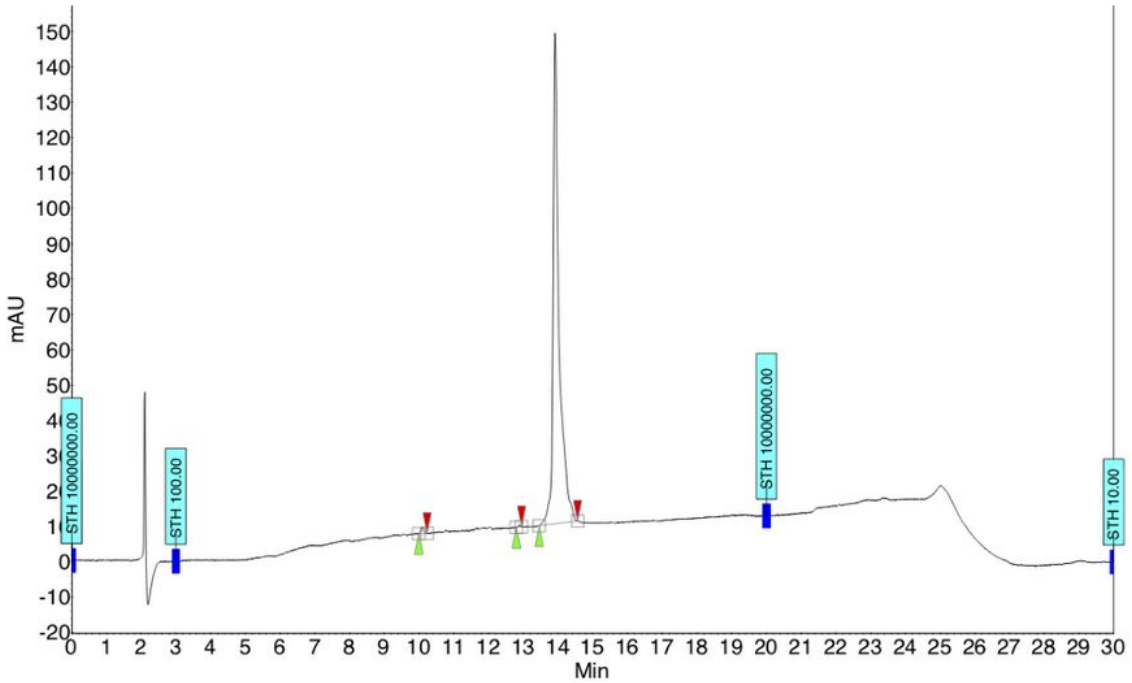
L011 loopoid strand

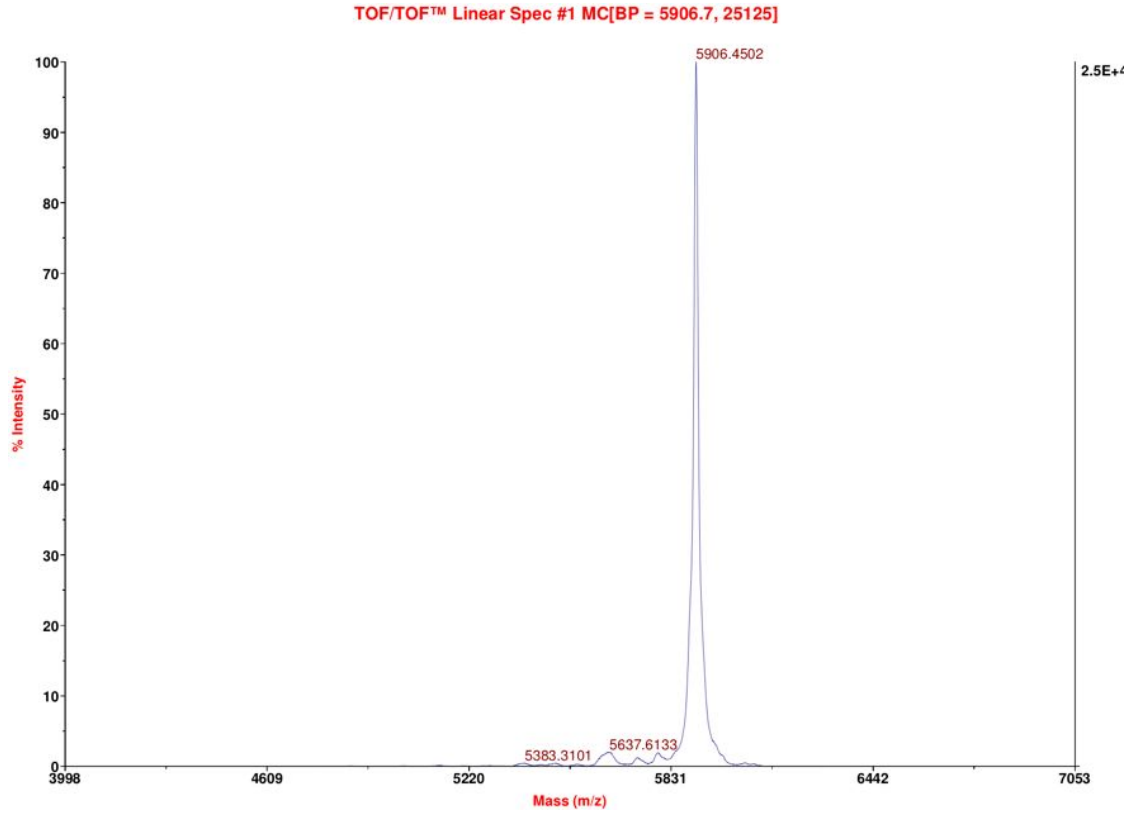




HPLC (5-95% 20 min) RT = 13.61 min
MALDI-TOF calc. $(M+H)^+$ 5939.68, obs. = 5722.4

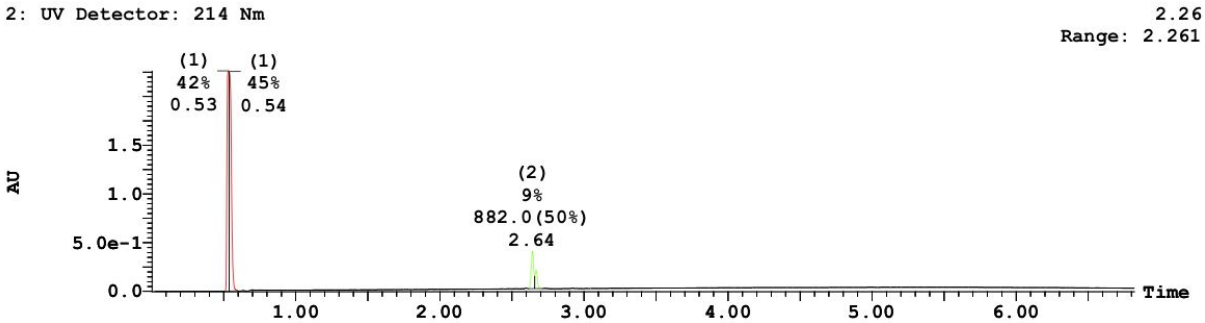
L034 loopoid strand



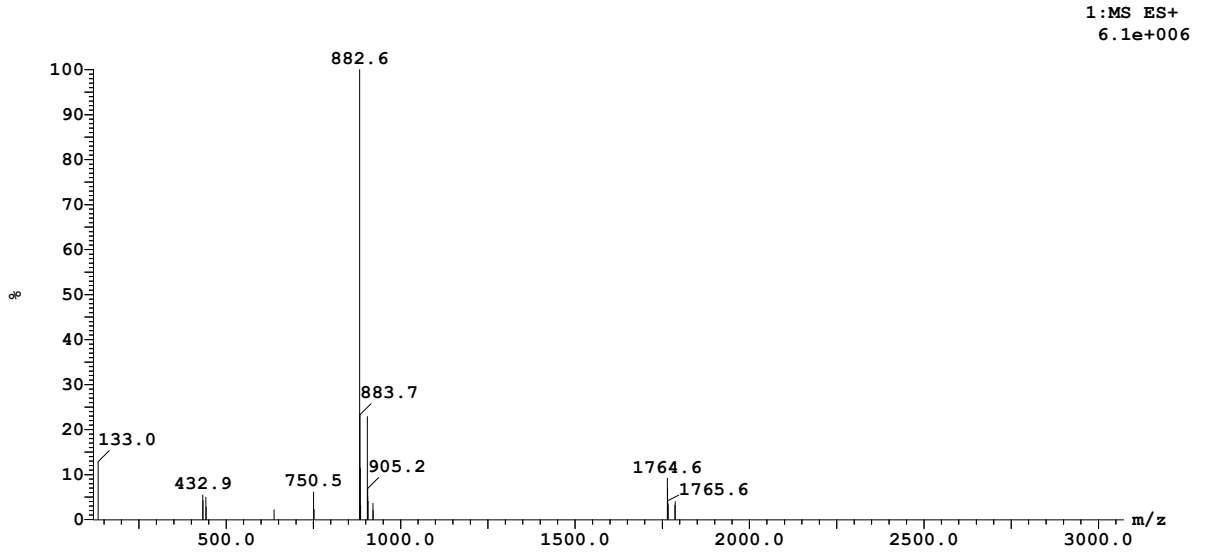


HPLC (5-95% 20 min) RT = 13.91 min
MALDI-TOF calc. $(M+H)^+$ 5919.85, obs. = 5906.45

TYWWLD Peptide



Peak ID	Time	Mass Found
2	2.64	904.75,441.65,882.61



UPLC (5-95% 6.8 min) RT = 2.64 min

ESI-MS calc. $(M+H)^+$ = 882.97, obs. = 882.6

Table S1. HP pattern, sequence, characterization of loopoids

+ and - indicates pass and fail, respectively.

n.a. means that loopoid was not applied to synthesis or test for nanosheet formation.

Abbreviations of monomers are as like below.

Nab: Aminobutyl, Nae: Aminoethyl, Nce: Carboxyethyl, Ncm: Carboxymethyl, Namd: Carboxamide, Nhe: Hydroxyethyl, Npp: Propylpyrrolidinone, Nipr: Isopropyl, Ncpr: Cyclopropylmethy, Nbu: N-butyl, Nia: Isoamyl, Ncpe: Cyclopentyl, Ndpe: Diphenylethyl, Nfu: Furfurylamine, Nph: Phenyl, Npe: Phenylethyl, Nbsa: Benzenesulfonamide, Ntyr: Tyramine, Ntrp: Tryptamine, Npip: Piperonyl

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg	Nanosheet formation
1	HPPHPP	Ndpe-Ncm-Ncm-Ndpe-Ncm-Ncm	5916.783	1480.17 (4H+)	95+%	39	+
2		Ncpe-Nce-Nce-Ncpe-Npp-Npp	5854.845	5847.4263	95+%	18	+
3		Nbn-Ncm-Nab-Nipr-Ncm-Ncm	5701.576	5688.0205	95+%	33	+
4	PHHPPP	Nab-Ntrp-Ntrp-Nab-Nab-Nab	5895.009	5890.1978	95+%	30	+
5		Ncm-Ndpe-Ndpe-Nhe-Nhe-Ncm	5888.817	1472.90(4H+)	95+%	39	+
6		Npp-Nia-Ntrp-Nce-Nce-Npp	5931.931	5926.7642	90+%	25	+
7	PHPPHP	Namd-Ndpe-Namd-Namd-Ndpe-Namd	5912.847	5907.7891	95+%	13	+
8		Nab-Ndpe-Nab-Nab-Ndpe-Namd	5955.06	1489.47(4H+)	90+%	20	+
9		Nce-Nbu-Nae-Nce-Nia-Nce	5709.64	5704.5317	95+%	30	+
10	PPHHPP	Npp-Npp-Ncpr-Ncpr-Npp-Npp	5933.007	5930.852 (M+H)+	95+%	23	-
11		Nhe-Nae-Ntyr-Ntyr-Nhe-Nae	5738.685	5724.0654	95+%	22	+
12		Npp-Npp-Ntrp-Ncpe-Nab-Nab	5928.035	5922.5142	95+%	26	+
13	HHPHPP	Nipr-Nipr-Nab-Nipr-Nab-Nab	5663.751	5659.6748	95+%	28	-
14		Nipr-Nipr-Nce-Nipr-Nae-Nce	5637.577	95+%	95+%	80	+
15		Nia-Nfu-Ncm-Nfu-Npp-Ncm	5795.689	5792.328 (M+H)+	85+%	18	+
16	HHPPHP	Nbu-Nbu-Npp-Npp-Nbu-Npp	5867.976	5865.745 (M+H)+	95+%	21	-
17		Nbsa-Nbsa-Npp-Npp-Nbsa-Namd	6181.208	6176.3267	95+%	28	+
18		Nbsa-Ncpr-Namd-Nhe-Ncpr-Nhe	5760.706	5754.2998	95+%	18	+
19	HHPPPH	Ncpr-Ncpr-Npp-Npp-Npp-Ncpr	5861.928	1466.59(4H+)	95+%	43	+
20		Ncpr-Ncpr-Nab-Npp-Nab-Ncpr	5753.832	5748.436	95+%	24	+
21		Ncpe-Nfu-Nab-Nab-Namd-Nfu	5751.728	5739.7236	95+%	28	+
22	HPHHPP	Ntrp-Namd-Ntrp-Ntrp-Namd-Namd	5924.862	5920.917	95+%	11	+
23		Nipr-Nab-Nipr-Nipr-Npp-Nab	5717.799	5705.4771	93%	15	+
24		Nipr-Nce-Nbu-Nbu-Nae-Nae	5636.637	5634.1123	95+%	16	+
25	PHHHPP	Nae-Ncpe-Ncpe-Ncpe-Nae-Nae	5657.703	943.77(6H+)	95+%	82	+
26		Npp-Npip-Npip-Npip-Npp-Npp	6102.054	1528.08(4H+)	95+%	52	+
27		Namd-Nipr-Nipr-Npip-Npp-Npp	5849.829	1463.22(4H+)	90+%	51	+
28	PHHPHP	Nae-Ncpr-Ncpr-Nae-Ncpr-Nae	5615.622	1404.86(4H+)	90+%	14	+
29		Nhe-Nipr-Nipr-Nce-Nipr-Nce	5638.561	1410.48(4H+)	85+%	18	+
30		Nhe-Nbu-Nia-Nhe-Nia-Npp	5733.794	1433.9 (M+4H)4+	90+%	22	+
31	PPPHHH	Nce-Nce-Nce-Npip-Npip-Npip	5942.73	1189.34(5H+)	95+%	62	+
32		Nhe-Nhe-Npp-Nia-Nia-Nia	5747.821	5745.711 (M+H)+	90+%	17	-
33		Npp-Nhe-Nhe-Ndpe-Ndpe-Npe	6002.068	1501.33(4H+)	95+%	28	+
34	PHHHHP	Namd-Ntyr-Ntyr-Ntyr-Ntyr-Namd	5918.847	5904.1196	95+%	36	+
35		Npp-Nbu-Nbu-Nbu-Nbu-Namd	5730.794	1432.9 (M+4H)4+	90+%	3	+
36		Ncm-Ncpr-Npip-Ncpr-Npip-Npp	5883.798	5879.6567	90+%	13.9	+

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg	Nanosheet formation
37	HPHPPP	Ndpe-Ncm-Ncm-Ndpe-Ncm-Ncm	5908.985	1477.85 [M+4H]	95%	25	+
38		Ncpe-Nce-Nce-Ncpe-Npp-Npp	6149.205	6135.4141 [M+H]+	95%	10	+
39		Nbn-Ncm-Nab-Nipr-Ncm-Ncm	6005.076	1201.9 (M+5H)5+	90+%	12	-
40	HPPPPH	Nab-Ntrp-Ntrp-Nab-Nab-Nab	5640.621	1411.0 (M+4H)4+	95+%	18	n.a.
41		Ncm-Ndpe-Ndpe-Nhe-Nhe-Ncm	5678.626	5669.4976 [M+H]+	95%	23	+
42		Npp-Nia-Ntrp-Nce-Nce-Npp	5759.568	5751.0220 [M+H]+	95+%	16	+
43	PHPHPP	Namd-Ndpe-Namd-Namd-Ndpe-Namd	5664.467	1416.71 [M+4H]	95%	22	+
44		Nab-Ndpe-Nab-Nab-Ndpe-Namd	5780.902	1446.0 (M+4H)4+	95+%	10	-
45		Nce-Nbu-Nae-Nce-Nia-Nce	5642.604	5630.5684 [M+H]+	90+%	17	-
46	PHPPPH	Npp-Npp-Ncpr-Ncpr-Npp-Npp	5604.599	1121.76 [M+5H]	85%	50	-
47		Nhe-Nae-Ntyr-Ntyr-Nhe-Nae	5756.699	1439.9 (M+4H)4+	95%	17	+
48		Npp-Npp-Ntrp-Ncpe-Nab-Nab	5815.727	1454.73 [M+4H]	70%	9	+
49	PPPHHP	Nipr-Nipr-Nab-Nipr-Nab-Nab	5902.985	1476.9 (M+4H)4+	n.a.	n.a.	-
50		Nipr-Nipr-Nce-Nipr-Nae-Nce	5698.58	1425.34 [M+4H]	50%	10	+
51		Nia-Nfu-Ncm-Nfu-Npp-Ncm	5954.965	1489.32 [M+4H]	95+%	44	+
52	HHHPPP	Nbu-Nbu-Npp-Npp-Nbu-Npp	5847.949	5841.3472 [M+H]+	95%	6	+
53		Nbsa-Nbsa-Npp-Npp-Nbsa-Namd	5887.922	---	n.a.	n.a.	n.a.
54		Nbsa-Ncpr-Namd-Nhe-Ncpr-Nhe	5778.658	5769.9619 [M+H]+	95+%	13	+
55	HPPHHP	Ncpr-Ncpr-Npp-Npp-Npp-Ncpr	5666.571	1417.1 (M+4H)4+	90+%	25	-
56		Ncpr-Ncpr-Nab-Npp-Nab-Ncpr	5665.682	1417.08 [M+4H]	95+%	54	-
57		Ncpe-Nfu-Nab-Nab-Namd-Nfu	5769.61	5764.9434 [M+H]+	95%	8	+
58	HPPHPH	Ntrp-Namd-Ntrp-Ntrp-Namd-Namd	5967.075	5987.4419 [M+Na]+	90+%	14	-
59		Nipr-Nab-Nipr-Nipr-Npp-Nab	5711.795	1428.9 (M+4H)4+	95+%%	20	+
60		Nipr-Nce-Nbu-Nbu-Nae-Nae	5810.766	5802.439 [M+H]+	95+%	19	+
61	PHHPPH	Nae-Ncpe-Ncpe-Ncpe-Nae-Nae	5904.009	1476.57 [M+4H]	95+%	57	+
62		Npp-Npip-Npip-Npip-Npp-Npp	5833.789	1459.0 (M+4H)4+	n.a.	n.a.	n.a.
63		Namd-Nipr-Nipr-Npip-Npp-Npp	5744.6	5735.6455 [M+H]+	95+%	9	+
64	PPHHHP	Nae-Ncpr-Ncpr-Nae-Ncpr-Nae	5702.604	1426.46 [M+4H]	95+%	67	+
65		Nhe-Nipr-Nipr-Nce-Nipr-Nce	5680.6	1424.8 (M+4H)4+	90%	16	n.a.
66		Nhe-Nbu-Nia-Nhe-Nia-Npp	5680.598	5672.7271 [M+H]+	95+%	29	-
67	PPHHPH	Nce-Nce-Nce-Npip-Npip-Npip	5882.913	5890.3662 [M+Na]+	95+%	20	-
68		Nhe-Nhe-Npp-Nia-Nia-Nia	5900.828	1475.52 [M+4H]	95+%	66	+
69		Npp-Nhe-Nhe-Ndpe-Ndpe-Npe	5955.909	1489.9 (M+4H)4+	90%	20	-
70	PPHPHH	Namd-Ntyr-Ntyr-Ntyr-Ntyr-Namd	5768.754	1443.0 (M+4H)4+	n.a.	n.a.	n.a.
71		Npp-Nbu-Nbu-Nbu-Nbu-Namd	5782.646	1446.34 [M+4H]	---	41	+
72		Ncm-Ncpr-Npip-Ncpr-Npip-Npp	5920.951	1480.77 [M+4H]	---	60	-

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg	Nanosheet formation
73	HHPPPP	Ndpe-Ncm-Ncm-Ndpe-Ncm-Ncm	5634.621	1409.96 [M+4H]	95+%	80	-
74		Ncpe-Nce-Nce-Ncpe-Npp-Npp	5756.656	1440.41 [M+4H]	95+%	57	+
75		Nbn-Ncm-Nab-Nipr-Ncm-Ncm	5913.87	1479.0 [M+4H]4+	90%	30	n.a.
76	HPPPHP	Nab-Ntrp-Ntrp-Nab-Nab-Nab	5694.673	1424.89 [M+4H]	95%	35	+
77		Ncm-Ndpe-Ndpe-Nhe-Nhe-Ncm	5628.663	1408[M+4H]4+	95%	30	n.a.
78		Npp-Nia-Ntrp-Nce-Nce-Npp	5672.5532	n.a.	n.a.	n.a.	n.a.
79	PPHPHP	Namd-Ndpe-Namd-Namd-Ndpe-Namd	5750.871	1438.09 [M+4H]	90%	27	n.a.
80		Nab-Ndpe-Nab-Nab-Ndpe-Namd	5747.6228	n.a.	n.a.	n.a.	n.a.
81		Nce-Nbu-Nae-Nce-Nia-Nce	5907.91	1478.49 (M+4H)4+	85%	5	+
82	PPHPPH	Npp-Npp-Ncpr-Ncpr-Npp-Npp	6028.9764	n.a.	n.a.	n.a.	n.a.
83		Nhe-Nae-Ntyr-Ntyr-Nhe-Nae	5974.955	5962.3091 [M+H]+	90%	12	+
84		Npp-Npp-Ntrp-Ncpe-Nab-Nab	5945.1118	1487.45 (M+4H)4+	90%	25	+
85	PPPHPH	Nipr-Nipr-Nab-Nipr-Nab-Nab	6057.2445	1515.97 (M+4H)4+	90%	10	n.a.
86		Nipr-Nipr-Nce-Nipr-Nae-Nce	5701.576	1426.16 [M+4H]	95+%	26	n.a.
87		Nia-Nfu-Ncm-Nfu-Npp-Ncm	5758.6862				n.a.
88	PPPPHH	Nbu-Nbu-Npp-Npp-Nbu-Npp	5809.672	1453.0 (M+4H)4+	<85%	5	n.a.
89		Nbsa-Nbsa-Npp-Npp-Nbsa-Namd	5854.7284	n.a.	n.a.	n.a.	n.a.
90		Nbsa-Ncpr-Namd-Nhe-Ncpr-Nhe	5678.582	1420.16 [M+4H]	90%	29	n.a.
91	HPHPPH	Ncpr-Ncpr-Npp-Npp-Npp-Ncpr	5758.76	1440.26 [M+4H]	95%	46	n.a.
92		Ncpr-Ncpr-Nab-Npp-Nab-Ncpr	5769.746	n.a.	n.a.	n.a.	n.a.
93		Ncpe-Nfu-Nab-Nab-Namd-Nfu	5711.6762	n.a.	n.a.	n.a.	n.a.
94	HPPPHH	Ntrp-Namd-Ntrp-Ntrp-Namd-Namd	6017.004	n.a.	n.a.	n.a.	n.a.
95		Nipr-Nab-Nipr-Nipr-Npp-Nab	5944.827	5931.6548 [M+H]+	90%	14	+
96		Nipr-Nce-Nbu-Nbu-Nae-Nae	5693.648	5684.2407 [M+H]+	92%	14	+
97	PHPHHP	Nae-Ncpe-Ncpe-Ncpe-Nae-Nae	5679.746	1420.76 [M+4H]	95%	43	n.a.
98		Npp-Npip-Npip-Npip-Npp-Npp	5699.738	1425.9 [M+4H]+	95%	12	n.a.
99		Namd-Nipr-Nipr-Npip-Npp-Npp	5792.681	n.a.	n.a.	n.a.	n.a.
100	PHPPHH	Nae-Ncpr-Ncpr-Nae-Ncpr-Nae	5629.605	1408.16 [M+4H]	80%	9	n.a.
101		Nhe-Nipr-Nipr-Nce-Nipr-Nce	5907.911	1477.9 [M+4H]4+	87-89%	10	n.a.
102		Nhe-Nbu-Nia-Nhe-Nia-Npp	5717.707	1430.29 [M+4H]	80%	7	n.a.
103	HPHPHP	Nce-Nce-Nce-Npip-Npip-Npip	5645.5708	5634.0264 [M+H]+	85%	9	n.a.
104		Nhe-Nhe-Npp-Nia-Nia-Nia	5853.86	5845.3564 [M+H]+	94%	14	+
105		Npp-Nhe-Nhe-Ndpe-Ndpe-Npe	5775.884	n.a.	n.a.	n.a.	+
106	HHPPHH	Namd-Ntyr-Ntyr-Ntyr-Ntyr-Namd	5682.753	1421.44 [M+4H]	95%	45	-
107		Npp-Nbu-Nbu-Nbu-Nbu-Namd	5993.149	1499.15 [M+4H]	95%	49	-
108		Ncm-Ncpr-Npip-Ncpr-Npip-Npp	5724.839	1431.9 [M+4H]4+	90%	24	-

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg
109	HPPHPP	Nipr-Nhe-Nhe-Ncpe-Nhe-Nhe	5610.551	1403.88 [M+4H]	95%	2
110		Nph-Namd-Namd-Ncpr-Ncm-Ncm	5684.51	n.a.	n.a.	n.a.
111		Nipr-Nmp-Nmp-Ntrp-Nab-Nce	5866.819	5855.0308 [M+H]+	93%	15
112	PHHPPP	Npp-Ncpe-Ntyr-Npp-Npp-Npp	6013.093	7155.413 [M+H]+	95+%	24
113		Npp-Nbsa-Nia-Nae-Nae-Npp	5913.98	1183.9 [M+4H]4+	95%	17
114		Nab-Nph-Nfu-Nmp-Npp-Nab	5854.852	5843.3057 [M+H]+	92%	28
115	PHPPHP	Ncm-Nia-Ncm-Ncm-Nipr-Ncm	5668.499	1418.06 [M+4H]	90%	26
116		Namd-Ncpr-Namd-Nae-Ncpe-Nae	5646.5616	n.a.	n.a.	n.a.
117		Nae-Npe-Nae-Ncm-Nia-Nme	5700.68	1426.24 [M+4H]	90%	42
118	PPHHPP	Nhe-Nhe-Ndpe-Ncpr-Nhe-Nhe	5734.693	1434.49 [M+4H]	95%	5
119		Nce-Nce-Nipr-Nph-Namd-Namd	5700.55	n.a.	n.a.	n.a.
120		Npp-Nab-Ncpr-Ntyr-Nce-Npp	5891.91	5877.7261 [M+H]+	95%	24
121	HHPHPP	Ntyr-Nipr-Nme-Nipr-Nme-Nme	5702.692	5695.7388 [M+H]+	95%	28
122		Nia-Ntyr-Nae-Ntyr-Nce-Nce	5821.771	5819.2891 [M+H]+	95%	36
123		Ndpe-Ndpe-Nce-Ncpr-Namd-Nae	5910.92	n.a.	n.a.	n.a.
124	HHPPHP	Ntrp-Ncpr-Nme-Nme-Ncpr-Nme	5749.752	n.a.	n.a.	n.a.
125		Nbu-Nbu-Namd-Ncm-Ndpe-Ncm	5789.729	1448.44 [M+4H]	90%	9
126		Nspe-Nspe-Npp-Nce-Nbu-Nab	5842.93	n.a.	n.a.	n.a.
127	HHPPPH	Npip-Nbu-Nce-Nce-Nce-Npip	5864.704	1467.12 [M+4H]	90%	42
128		Ndpe-Ncpr-Nab-Ncm-Ncm-Ndpe	5925.926	1482.35 [M+4]	90%	18
129		Nipr-Nspe-Nme-Nab-Nmp-Nipr	5747.78	5739.9175 [M+H]+	95%	35
130	HPHHPP	Ntrp-Nme-Ntrp-Nfu-Nme-Nme	5864.8309	n.a.	n.a.	n.a.
131		Ndpe-Nae-Nipr-Nipr-Nae-Npp	5799.86	1450.77 [M+4H]	95%	26
132		Nfu-Ncm-Nfu-Nspe-Nhe-Nhe	5762.66	n.a.	n.a.	n.a.
133	PHHHPP	Ncm-Nbn-Ncpe-Nbn-Ncm-Ncm	5746.616	1437.64 [M+4H]	90%	16
134		Namd-Ncpr-Ncpr-Nph-Nab-Nab	5707.72	n.a.	n.a.	n.a.
135		Nab-Ncpr-Ncpr-Nbn-Ncm-Nhe	5695.66	1424.66 [M+4H]	90%	13
136	PHHPHP	Npp-Nspe-Nbu-Npp-Nspe-Npp	5964.06	n.a.	90%	32
137		Npp-Nipr-Nipr-Nae-Ndpe-Nae	5799.86	1450.92 [M+4H]	90%	20
138		Nmp-Nia-Nia-Namd-Ndpe-Nab	5879.914	5868.7896 [M+H]+	75%	9
139	PPPHHH	Nce-Nce-Nce-Ncpr-Nbsa-Nbsa	5960.87	n.a.	n.a.	n.a.
140		Nae-Nfu-Nae-Nipr-Ncpe-Nipr	5642.6134	5632.5654 [M+H]+	86%	17
141		Nae-Nme-Nce-Nipr-Nipr-Nia	5651.648	1413.93 [M+4H]	90%	48
142	PHHHHP	Nab-Ncpr-Nph-Ncpr-Ncpr-Nab	5704.76	5904.1196	95+%	45
143		Nmp-Npip-Nipr-Npip-Nipr-Namd	5840.7046	1432.9 (M+4H)4+	90+%	49
144		Nae-Ncpe-Ncpr-Ncpr-Nce-Namd	5672.63	5879.6567	90+%	24

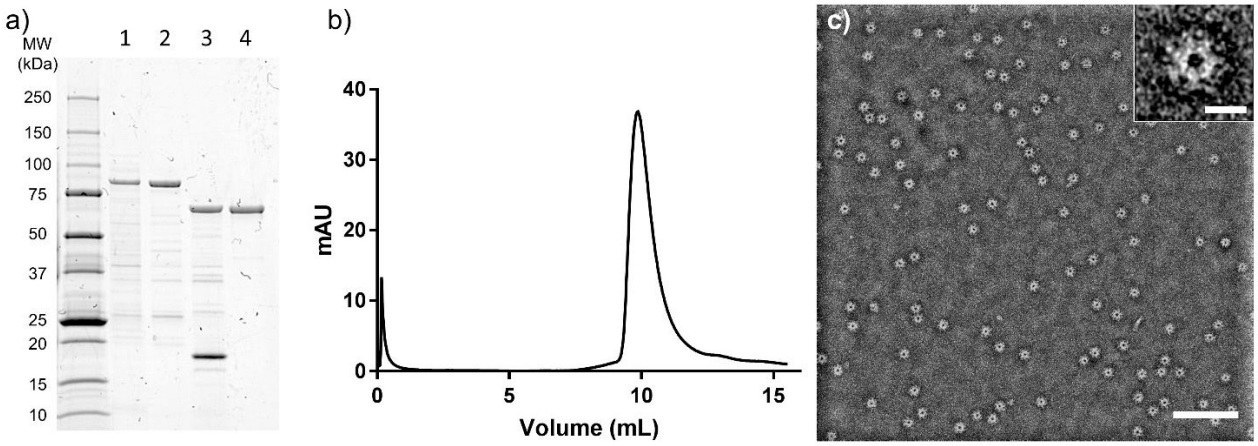
ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg
145	HPHPPP	Ncpr-Nce-Ncpr-Nce-Npp-Nce	5773.683	1444.09 [M+4H]	95%	83
146		Nipr-Namd-Nfu-Nab-Nab-Namd	5702.66	n.a.	n.a.	n.a.
147		Nbn-Namd-Nbu-Nae-Nae-Ncm	5671.6	n.a.	n.a.	n.a.
148	HPPPPH	Nph-Namd-Namd-Nfu-Namd-Nph	5727.5486	n.a.	n.a.	n.a.
149		Nfu-Nhe-Nme-Nhe-Nme-Ntyr	5728.6317	5721.6099 [M+H]+	75%	6
150		Npip-Nmp-Nab-Ncm-Ncm-Nia	5822.6868	n.a.	n.a.	n.a.
151	PHPHPP	Npp-Nipr-Nme-Nipr-Npp-Npp	5841.894	1461.64 [M+4H]	95%	56
152		Nmp-Nph-Nae-Nbu-Nae-Nmp	5756.6941	5747.9019 [M+H]+	95%	8
153		Namd-Ncpr-Nce-Nia-Nab-Nab	5719.6962	n.a.	n.a.	n.a.
154	PHPPPH	Ncm-Ndpe-Nhe-Nhe-Ncm-Ndpe	5888.82	n.a.	n.a.	n.a.
155		Npp-Ndpe-Nab-Nab-Npp-Nph	5973.075	n.a.	n.a.	n.a.
156		Nme-Ndpe-Npp-Npp-Nae-Ncpr	5909.972	1478.60 [M+4H]	90%	97
157	PPPHHP	Nme-Nae-Nme-Ndpe-Ndpe-Nae	5886.937	1472.45 [M+4H]	95%	64
158		Nce-Nab-Nce-Nia-Ncpr-Nce	5735.678	1434.71 [M+4H]	95%	55
159		Npp-Npp-Nmp-Ntrp-Nipr-Namd	5923.8836	n.a.	n.a.	n.a.
160	HHHPPP	Nipr-Nipr-Nipr-Ncm-Nhe-Ncm	5610.507	1403.58 [M+4H]	95%	33
161		Nfu-Nipr-Nipr-Nab-Nab-Nce	5702.696	1426.69 [M+4H]	95%	96
162		Ncpr-Npip-Ncpr-Namd-Npp-Nhe	5792.7038	n.a.	n.a.	n.a.
163	HPPHHP	Nbu-Ncm-Nhe-Nbu-Nbu-Ncm	5652.588	1413.93 [M+4H]	90%	60
164		Nipr-Nae-Namd-Nbu-Nipr-Nae	5607.5682	n.a.	n.a.	n.a.
165		Nfu-Nme-Nab-Nspe-Nfu-Nhe	5761.72	n.a.	n.a.	n.a.
166	HPPHPH	Nbsa-Namd-Ncm-Nbsa-Namd-Nbsa	6045.9618	6036.9316 [M+H]+	95%	15
167		Npip-Ncm-Nab-Ncpr-Nab-Ncpr	5766.739	1442.66 [M+4H]	95%	63
168		Nbu-Nae-Npp-Ndpe-Ncm-Nbu	5842.881	1462.02 [M+4H]	95%	51
169	PHHPPH	Npp-Nia-Nia-Nmp-Nmp-Nia	5873.9256	5865.2129 [M+H]+	90%	22
170		Nae-Ncpr-Nspe-Npp-Npp-Nspe	5879.95	1470.9 [M+4H]4+	95%	34
171		Nae-Nspe-Nspe-Ncm-Nhe-Nipr	5719.68	n.a.	n.a.	n.a.
172	PPHHHP	Nhe-Nce-Ncpe-Ncpe-Ncpe-Nce	5716.675	1430.29 [M+4H]	90%	35
173		Nhe-Nme-Nph-Npe-Npe-Nme	5768.75	n.a.	n.a.	n.a.
174		Nme-Namd-Nia-Nbsa-Ncpe-Nce	5832.81	n.a.	n.a.	n.a.
175	PPHHPH	Nmp-Nce-Ncpr-Ncpr-Nce-Ncpr	5737.6246	n.a.	n.a.	n.a.
176		Nme-Ncm-Ntrp-Ncpr-Nme-Ntrp	5838.793	n.a.	n.a.	n.a.
177		Nmp-Nab-Ntyr-Nipr-Nce-Nipr	5778.738	5765.2773 [M+H]+	95%	27
178	PPHPHH	Nab-Ncm-Ncpr-Nab-Ncpr-Ncpr	5686.697	1422.71 [M+4H]	95%	38
179		Nce-Nab-Ntyr-Nab-Nipr-Nipr	5742.7484	5730.5815 [M+H]+	95%	32
180		Nae-Ncm-Nbsa-Namd-Nbsa-Ndpe	6029	n.a.	n.a.	n.a.

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg
181	HHPPPP	Ncpe-Ncpe-Nae-Nhe-Nae-Nhe	5634.621	1409.81 [M+4H]	90%	45
182		Nbsa-Nbu-Npp-Npp-Nce-Nce	6218.8909	n.a.	90%	35
183		Ndpe-Nia-Nme-Nhe-Nhe-Nhe	5764.763	1442.51 [M+4H]	95%	22
184	HPPPHP	Nipr-Nce-Nce-Nae-Nipr-Nce	5667.559	1417.76 [M+4H]	95%	67
185		Ndpe-Ncm-Ncm-Ncm-Ncpr-Nab	5803.712	1451.89 [M+4H]	90%	60
186		Nph-Ncm-Ncm-Npp-Ncpr-Ncm	5753.5982	n.a.	n.a.	n.a.
187	PPHPHP	Namd-Nce-Ndpe-Nce-Ndpe-Nce	5957.8694	n.a.	n.a.	n.a.
188		Nae-Ncm-Nbsa-Ncm-Nipr-Nae	5751.6501	n.a.	n.a.	n.a.
189		Nab-Nhe-Nia-Nab-Ncpr-Nhe	5678.718	1420.76 [M+4H]	90%	55
190	PPHPPH	Ncm-Ncm-Nia-Ncm-Nme-Nia	5696.597	1425.11 [M+4H]	90%	28
191		Npp-Nae-Nbu-Nae-Npp-Nipr	5758.808	1440.49 [M+4H]	90%	43
192		Nhe-Nhe-Ndpe-Nab-Nhe-Nfu	5787.757	1447.87 [M+4H]	90%	17
193	PPPHPH	Namd-Nae-Namd-Ntrp-Nae-Ntrp	5810.7276	n.a.	n.a.	n.a.
194		Namd-Namd-Nae-Ntyr-Nae-Ndpe	5824.782	5814.7749 [M+H]+	85%	26
195		Nme-Nme-Nme-Nph-Nae-Ncpe	5685.67	n.a.	n.a.	n.a.
196	PPPPHH	Npp-Npp-Nme-Nme-Nfu-Nfu	5850.813	1463.74 [M+4H]	95%	39
197		Nae-Nce-Nce-Nce-Nbu-Ntyr	5759.6458	5751.9385 [M+H]+	95%	34
198		Nme-Nae-Nae-Nme-Ncpr-Ntrp	5723.705	n.a.	n.a.	n.a.
199	HPHPPH	Nipr-Nhe-Nipr-Nhe-Nab-Nipr	5609.611	1403.58 [M+4H]	95%	58
200		Npip-Npp-Npip-Npp-Nab-Nspe	6018.0118	n.a.	n.a.	n.a.
201		Nfu-Nhe-Nbn-Nce-Nce-Nspe	5786.681	n.a.	n.a.	n.a.
202	HPPPHH	Ncpr-Namd-Namd-Nme-Ncpr-Ncpr	5658.5871	n.a.	n.a.	n.a.
203		Ndpe-Nme-Ncm-Nme-Nia-Nia	5818.855	1455.72 [M+4H]	95%	78
204		Ncpe-Namd-Nce-Nce-Npe-Nipr	5739.658	n.a.	n.a.	n.a.
205	PHPHHP	Npp-Ncpr-Npp-Ncpr-Ncpr-Nmp	5843.856	5829.4287 [M+H]+	92%	23
206		Npp-Nph-Npp-Ncpr-Ncpr-Nme	5816.84	n.a.	n.a.	n.a.
207		Nab-Ntyr-Nme-Ncpe-Nipr-Nme	5741.7606	5731.7388 [M+H]+	92%	38
208	PHPPHH	Nce-Ncpr-Namd-Namd-Ncpr-Ncpr	5672.58	n.a.	n.a.	n.a.
209		Nae-Nipr-Namd-Namd-Npip-Nipr	5699.5788	n.a.	n.a.	n.a.
210		Nae-Nbn-Nmp-Nmp-Nspe-Nbu	5831.804	5824.9771 [M+H]+	90%	28
211	HPHPHP	Ncpe-Nab-Ncpe-Nmp-Ncpe-Nab	5777.8218	n.a.	n.a.	n.a.
212		Nspe-Nab-Ntrp-Nce-Nspe-Nab	5889.9274	n.a.	n.a.	n.a.
213		Nipr-Nab-Ntrp-Nab-Nph-Npp	5852.9097	5845.0396 [M+H]+	70%	16
214	HHPPHH	Nipr-Nipr-Namd-Namd-Nipr-Nipr	5606.5372	n.a.	n.a.	n.a.
215		Nfu-Nspe-Ncm-Nab-Npe-Npe	5845.84	n.a.	n.a.	n.a.
216		Ncpr-Npip-Nae-Ncm-Ncpr-Ndpe	5847.812	1463.29 [M+4H]	95%	68

ID	HP pattern	Sequence	M. W.	MALDI (MH+)	Purity	Purified wt. /mg
217	HPPPPH	Ndpe-Namd-Namd-Nme-Nme-Ndpe	5910.94	n.a.	n.a.	n.a.
218		Ncpr-Nce-Npp-Npp-Nce-Ntrp	5917.904	5905.8164 [M+H]+	60%	13
219		Nia-Npp-Nce-Nce-Nce-Ndpe	5915.884	1479.87 [M+4H]	95%	106
220	PHPPHP	Nab-Ndpe-Npp-Nab-Ndpe-Npp	6077.227	1519.78 [M+4H]	90%	118
221		Npp-Nia-Npp-Nae-Nipr-Nae	5772.835	1444.09 [M+4H]	95%	88
222		Nhe-Ndpe-Nab-Nhe-Nbu-Nab	5790.849	1448.52 [M+4H]	95%	110
223	PPHPPH	Ncm-Nme-Nfu-Nme-Ncm-Nfu	5716.543	1430.21 [M+4H]	90%	21
224		Nfu-Nhe-Ncpr-Nhe-Nhe-Npip	5724.5826	n.a.	n.a.	n.a.
225		Nce-Nme-Nph-Nme-Nce-Nspe	5764.68	n.a.	n.a.	n.a.
226	HHHPPP	Nipr-Nipr-Nipr-Nmp-Nme-Nme	5673.6244	n.a.	n.a.	n.a.
227		Ncpr-Ncpr-Ntrp-Nhe-Nae-Nae	5705.6898	n.a.	n.a.	n.a.
228		Nspe-Nia-Npe-Namd-Ncm-Namd	5774.72	n.a.	n.a.	n.a.
229	HHPPHP	Nia-Nia-Ncm-Nab-Nia-Ncm	5721.739	1431.64 [M+4H]	95%	16
230		Nipr-Ntrp-Nae-Nhe-Nipr-Nae	5681.6678	n.a.	n.a.	n.a.
231		Nspe-Ncpe-Nhe-Npp-Nipr-Npp	5832.89	n.a.	n.a.	n.a.
232	HPHHPP	Nipr-Namd-Nipr-Nipr-Nme-Namd	5622.57	n.a.	n.a.	n.a.
233		Npip-Ncm-Ncpr-Ncpr-Nab-Ncm	5753.652	1439.59 [M+4H]	95%	70
234		Nph-Nhe-Ncpr-Nbu-Ncm-Ncm	5638.52	n.a.	n.a.	n.a.
235	HPHPPH	Ntyr-Nce-Ntyr-Nhe-Nce-Ntyr	5872.7613	5863.5210 [M+H]+	95%	29
236		Nipr-Nce-Nipr-Npp-Npp-Nbsa	5913.93	n.a.	n.a.	n.a.
237		Nfu-Nmp-Ndpe-Nmp-Nab-Npip	6003.944	n.a.	n.a.	n.a.
238	HPPHPH	Nbsa-Nce-Nab-Nbsa-Nab-Nbsa	6088.12	1218.8 [M+5H]5+	95%	36
239		Nbu-Namd-Nab-Ndpe-Nab-Ndpe	5940.0122	n.a.	n.a.	n.a.
240		Nph-Namd-Nme-Nph-Nme-Nipr	5691.599	5683.2041 [M+H]+	73%	17
241	PHHPHP	Nab-Nipr-Nipr-Ncm-Nipr-Nab	5650.664	1413.71 [M+4H]	90%	51
242		Ncm-Nbn-Nfu-Ncm-Nbn-Namd	5757.5718	n.a.	n.a.	n.a.
243		Nae-Npip-Ndpe-Nae-Nipr-Ncm	5824.778	1457.29 [M+4H]	95%	92
244	PHPHHP	Nae-Ncpr-Namd-Ncpr-Ncpr-Nae	5629.605	1408.46[M+4H]	90%	27
245		Ncm-Nbu-Nab-Nbu-Ncpr-Ncm	5677.642	1420.31 [M+4H]	90%	64
246		Nab-Nspe-Nab-Ndpe-Nbu-Npp	5932.08	n.a.	n.a.	n.a.
247	PPHHPH	Nme-Nme-Ntyr-Ntyr-Namd-Ntyr	5857.804	n.a.	n.a.	n.a.
248		Nce-Nmp-Ncpe-Nipr-Nmp-Ncpe	5788.7332	5775.3403 [M+H]+	95%	23
249		Nae-Namd-Ncpr-Nph-Namd-Nia	5681.64	n.a.	n.a.	n.a.
250	HHPPHH	Ncpe-Ncpe-Namd-Namd-Ncpe-Ncpe	5710.6884	n.a.	n.a.	n.a.
251		Nipr-Ntyr-Nae-Nce-Ntyr-Nipr	5763.7234	5756.9761 [M+H]+	95+%	40
252		Ncpe-Ncpe-Npp-Nce-Nipr-Nbsa	5882.92	n.a.	n.a.	n.a.
253	PHHHHP	Nhe-Ncpr-Ncpr-Ncpr-Ncpr-Npp	5709.731	1428.41 [M+4H]	90%	15
254		Nmp-Ncpr-Ncpr-Nspe-Ncpr-Nae	5740.7172	n.a.	n.a.	n.a.
255		Namd-Nia-Ntyr-Nia-Nph-Nae	5760.7661	5749.7959 [M+H]+	93%	33
256		Npp-Nspe-Nipr-Nfu-Nfu-Ncm	5813.75	n.a.	n.a.	n.a.

B. SUPPLEMENTARY DATA

Anthrax protective antigen (PA63)7 preparation.



(PA63)7 expression, purification, and characterization. a) SDS-PAGE gel of $(PA63)_7$ at different stages of purification. 1) Soluble whole cell lysate containing PA83, 2) PA83 contained in fraction eluted from anion exchange column, 3) PA63 and PA20 after trypsin cleavage of PA83, 4) $(PA63)_7$ contained in fraction eluted from second round of anion exchange chromatography. b) UV absorbance spectrum (mAU) versus elution volume (mL) from size exclusion chromatography of Alexa Fluor-647 conjugated $(PA63)_7$. c) Survey view of $(PA63)_7$ by transmission electron microscopy with negative staining. Scale bar = 100 nm. Inset in upper right corner shows higher magnification of a representative particle of $(PA63)_7$. Scale bar in inset = 10 nm.

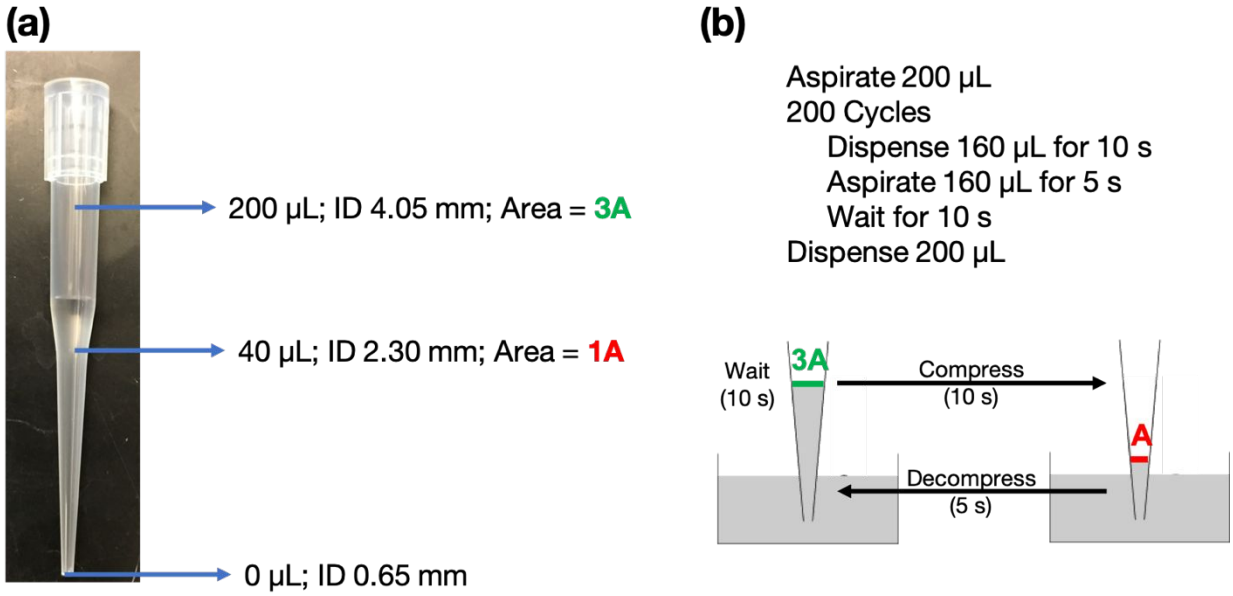


Figure S1. Pipet tip geometry for interfacial compression.

Nanosheets are formed by repeated interfacial compression of a peptoid solution. (a) The inner diameter of a P250 pipet tip defines the air/water interfacial area at different volumes of aspirated liquid. Area compression ratio of 3 can be achieved by changing the volume between the 200 µL and 40 µL positions. (b) The robotic pipettor is programmed to perform 200 compression cycles. By controlling the aspirate and dispense flow rates (32 µL/s and 16 µL/s, respectively) and the post-aspiration wait time (10 s), the peptoid molecules have enough time to re-populate the newly formed air/water interface during each cycle.

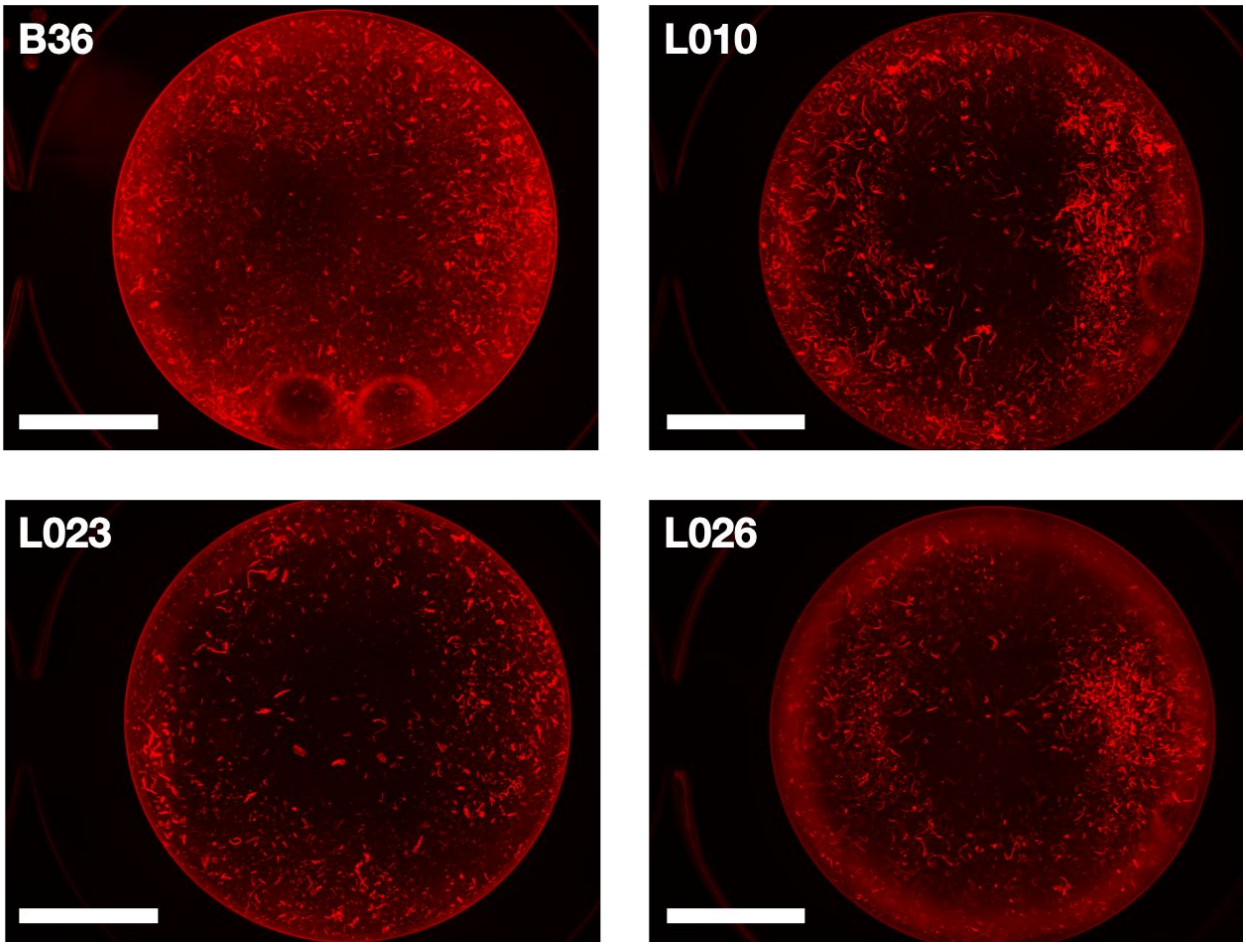


Figure S2. Fluorescence microscopic images of pipet-generated nanosheets.

Representative fluorescence images of nanosheets (loopoid ID's: B36, L010, L023, L026) produced in a 96-well plate produced by the robotic pipetting method. The scale bar is 2 mm.

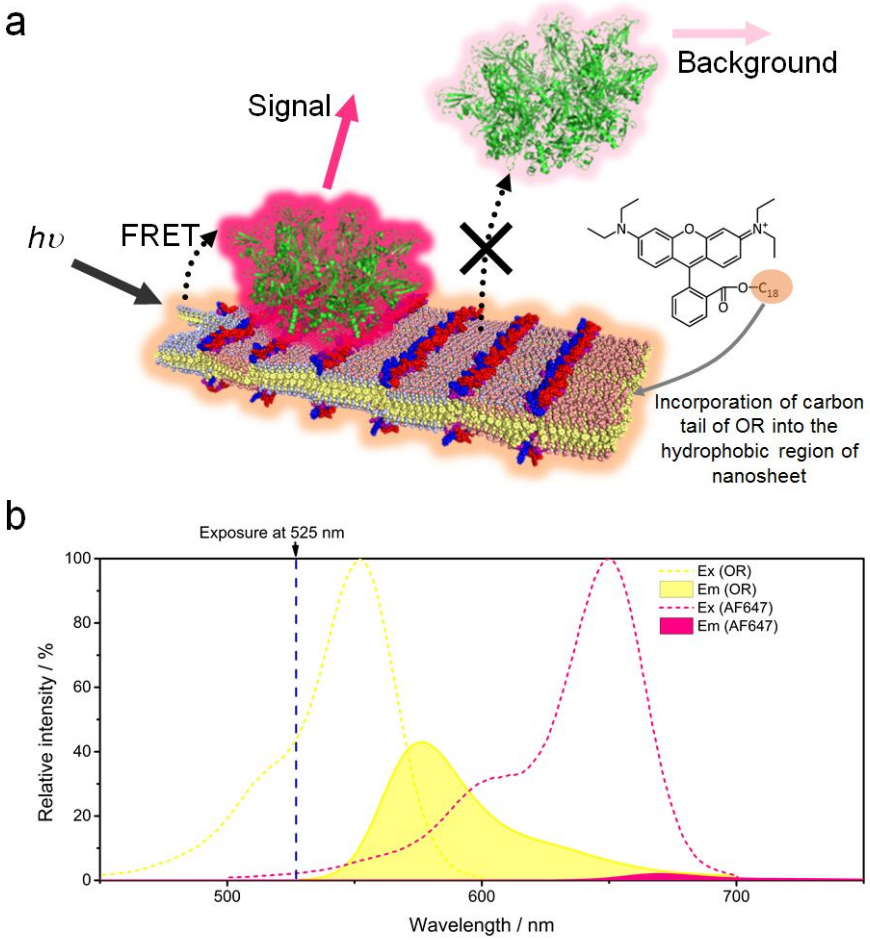


Figure S3. Homogeneous FRET assay for the identification of binding affinity of loopoid nanosheet.

(a) Schematic illustration of FRET assay using the incorporation of octadecyl rhodamine (OR) into nanosheet and Alexa Fluor 647 (AF647)-conjugated protein substrate. Long hydrocarbon chain of OR facilitates insertion into the hydrophobic core of peptoid bilayer. When AF647-conjugated protein is bound on the nanosheet surface, the fluorescence of OR (FRET donor) is transferred into Alexa Fluor 647 (FRET acceptor) via FRET phenomenon. (b) Absorbance (dotted line) and fluorescence (filled area) of OR (yellow) and AF647 (red). The fluorescence emission spectra are normalized to show the relative fluorescence intensities by direct excitation at 525 nm.

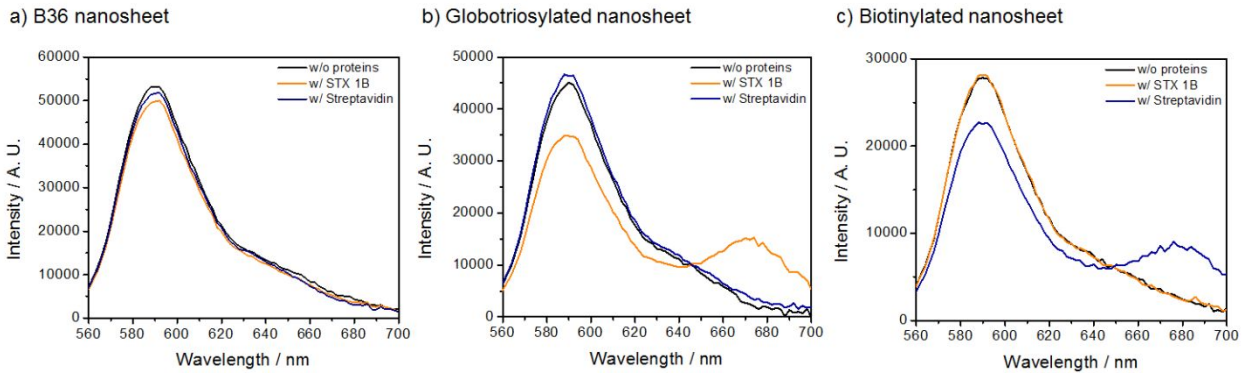


Figure S4. FRET assay to identify protein binding to peptoid nanosheet.

Fluorescence spectra of a) B36, b) globotriosylated, and c) biotinylated nanosheet in the absence (black line) and presence of STX 1B (orange line) and streptavidin (blue line). All spectra were obtained under the excitation wavelength at 525 nm. Globotriose and biotin are binding elements for STX 1B and streptavidin, respectively.

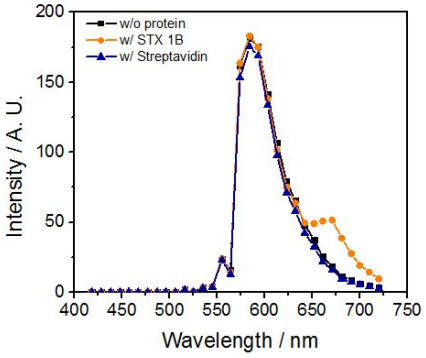


Figure S5. Identification of the origin of FRET signal by confocal microscopy.

Spectra were obtained by spectral scanning of globotriosylated nanosheet in the absence and presence of STX 1B and streptavidin.

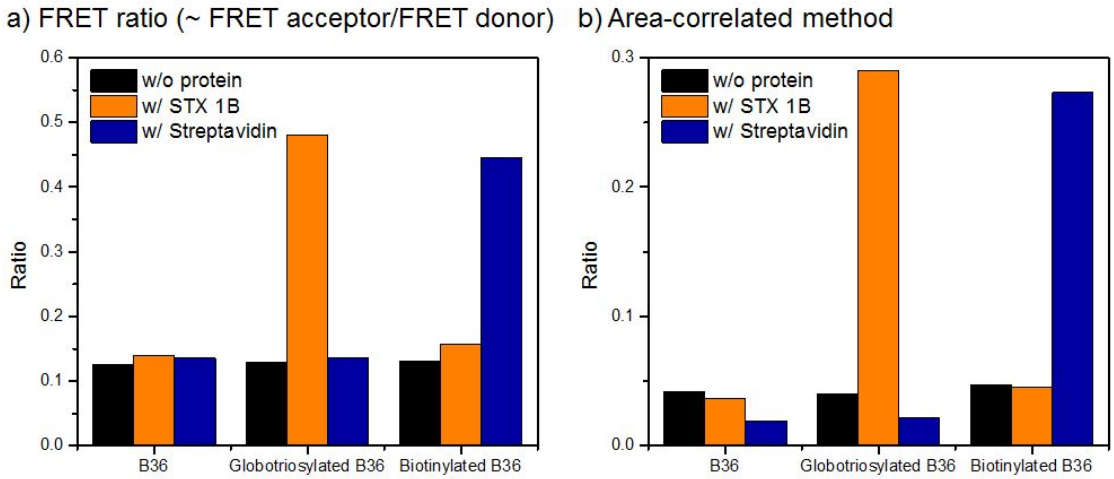


Figure S6. Curve fitting method provides more accurate measure of FRET efficiency.

FRET ratio obtained by a) calculating a simple ratio of donor and acceptor fluorescence intensities ($I_{Alexa647}$ / I_{OR}) and b) curve fitting fluorescence spectra with a linear combination of donor and acceptor emission spectra and calculating the ratio of the regression coefficients.

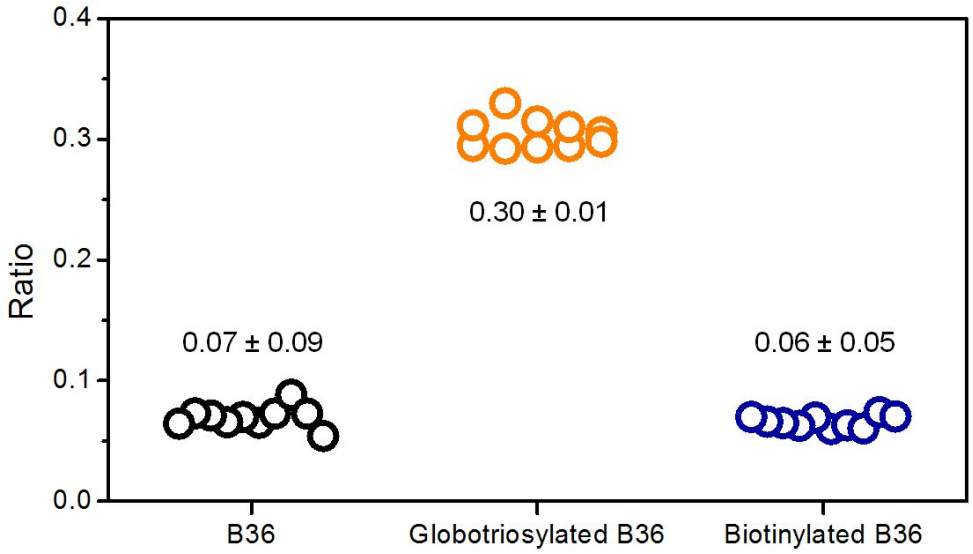


Figure S7. Z-factor calculation validates the reliability of developed FRET assay.

FRET ratio obtained from 10 samples of B36, globotriosylated, and biotinylated nanosheet in the presence of STX 1B. Based on the value of average and standard deviation, Z-factor of our screening assay is approximately 0.73.

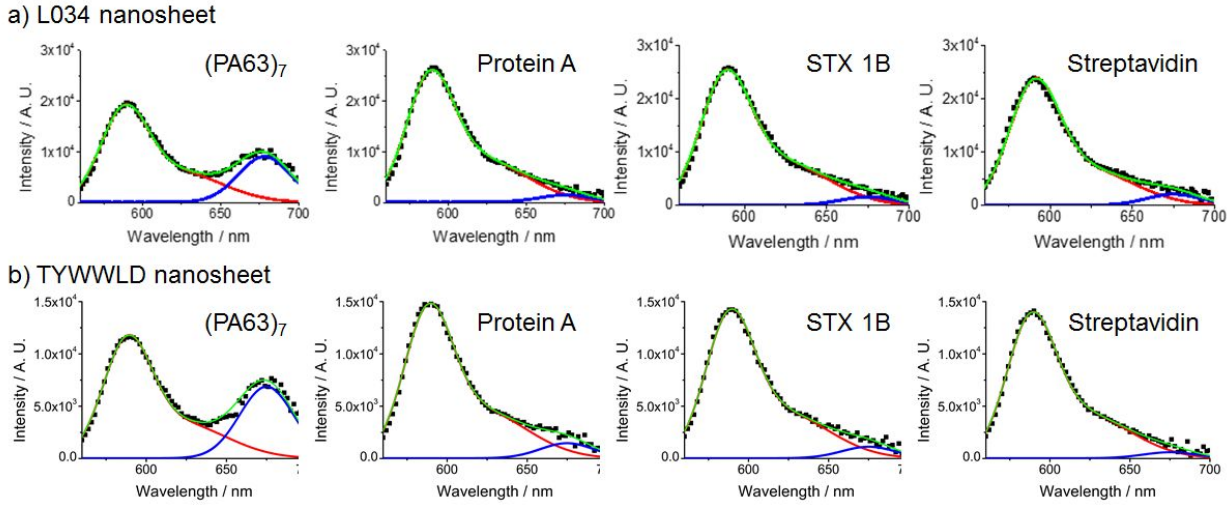


Figure S8. Validation of binding specificity of L034 and TYWWLD nanosheet by FRET assay.

All spectra were obtained under the excitation wavelength at 525 nm with 2 nm interval for data acquisition. By curve fitting using Gaussian function-derived donor and acceptor spectra, the emission spectra can be decomposed into OR (red line) and AF647 (blue line) components. Green line represents the sum of OR and AF647 spectra. All nanosheets were prepared by vial-rocking method. Positive FRET signal is clearly observed only in the presence of $(PA63)_7$.

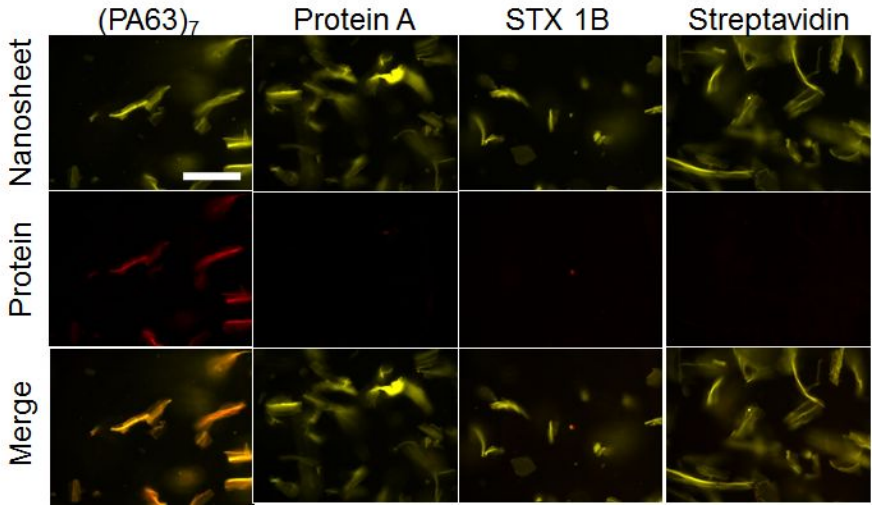


Figure S9. Validation of binding specificity of TYWWLD nanosheet by fluorescent microscopy.

OR-stained nanosheets are visualized with TR filter (yellow color). AF647-conjugated proteins are detected in Cy5 filter (red color). The colocalization of fluorescence signals in the merged image shows the binding specificity of TYWWLD nanosheets. Scale bar represents 100 μm. All images were acquired with the same magnification.

Table S2. Comparison of HP pattern and chemical property of monomers between L034 and TYWWLD loop sequences.

ID	HP pattern		1st	2nd	3rd	4th	5th	6th
L034	**PHHHHP**	Monomer	Namd	Ntyr	Ntyr	Ntyr	Ntyr	Namd
		Chemical property	Hd	**Ar**	**Ar**	**Ar**	Ar	Hd
TYWWLD	**PHHHHP**	Monomer	Thr	Tyr	Trp	Trp	Leu	Asp
		Chemical property	Hd	**Ar**	**Ar**	**Ar**	Sa	An

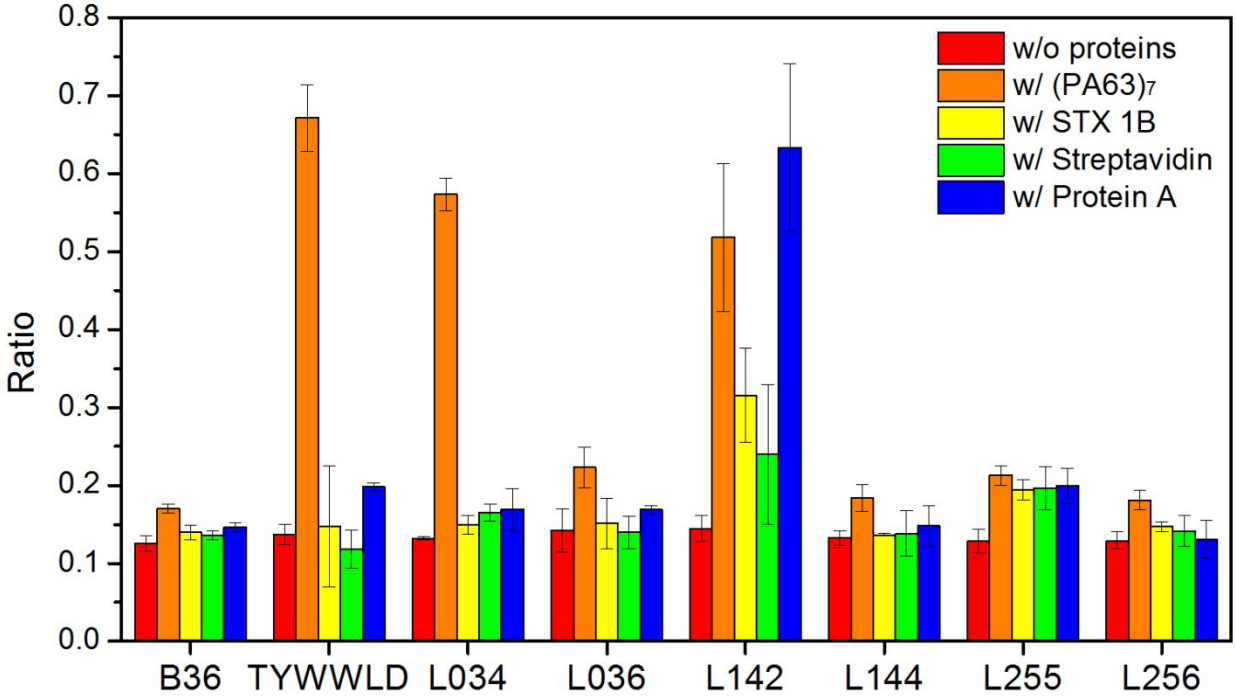


Figure S10. FRET-based validation of protein binding to nanosheets classified as PHHHHP pattern.

Among various nanosheets, only TYWWLD and L034 nanosheets showed high $(PA63)_7$ binding specificity. L142 represents non-specific binding to multiple target proteins.

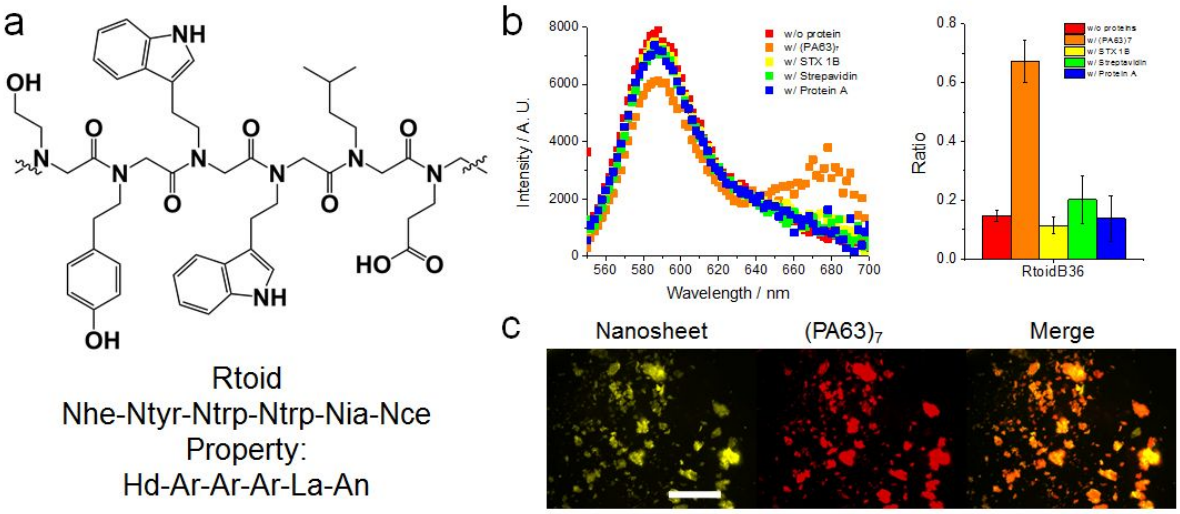


Figure S11. Chemical structure and $(PA63)_7$ binding specificity of Rtoid.

(a) Sequence and chemical property of Rtoid loop. (b) FRET-based validation of selective $(PA63)_7$ binding to Rtoid nanosheet. (c) Fluorescent images of Rtoid nanosheet in the presence of $(PA63)_7$.

Table S3. Binding parameters of B36, TYWWLD, and L034 nanosheet measured by bio-layer interferometry.

	Kd (nM)	k_{on} (M^{-1} s^{-1})	k_{dis} (s^{-1})
B36 nanosheet	-	-	-
TYWWLD nanosheet	1.59	8.71×10^{4}	1.38×10^{-4}
L034 nanosheet	1.95	4.74×10^{4}	9.24×10^{-5}

To obtain all binding parameters, all binding curves (Figure 5a) were fitted with 2:1 binding model. No binding observed in B36 nanosheet.