SUPPORTING INFORMATION

[^{99m}Tc]Tc-DGA1, a Promising CCK_2R-Antagonist-Based Tracer for Tumor Diagnosis with SPECT

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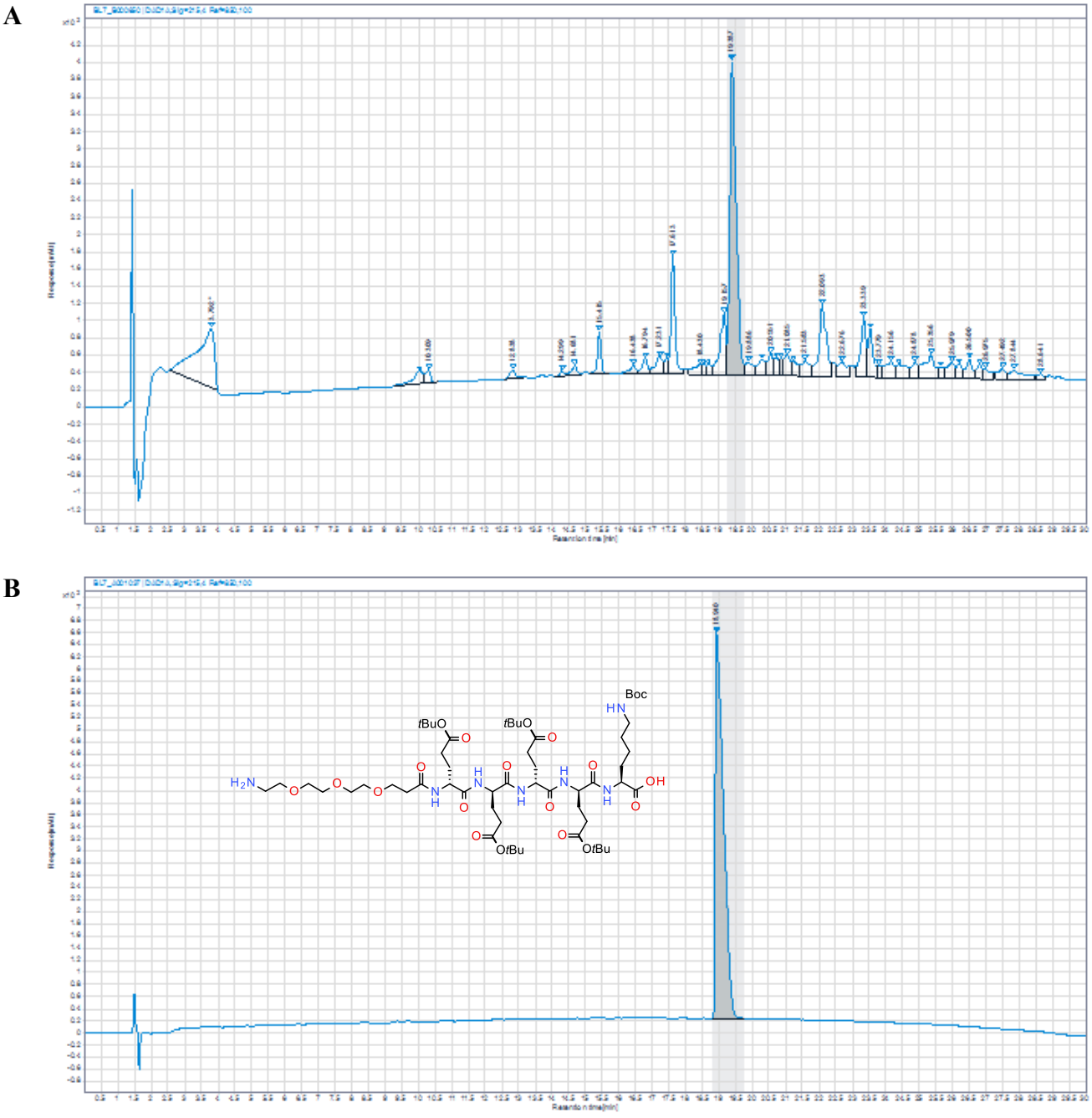


Figure S1. RP-HPLC UV traces (215 nm) of H-PEG$_3$-[DGlu(O^{t}Bu)]$_4$-Lys(Boc)-OH (**A**) before and (**B**) after purification.

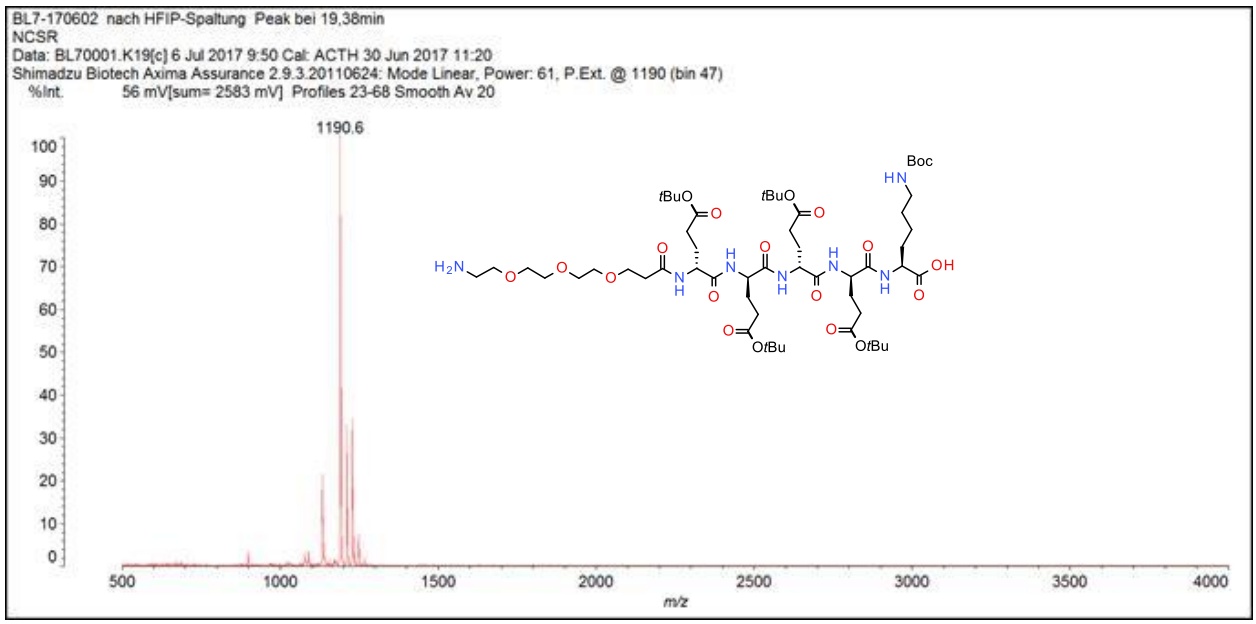


Figure S2. MALDI-TOF-MS spectrum of purified H-PEG$_3$-[DGlu(O^{t}Bu)]$_4$-Lys(Boc)-OH, m/z calculated for $C_{56}H_{99}N_7O_{20}$ $(M+H)^+$: 1190.7, found: 1190.6

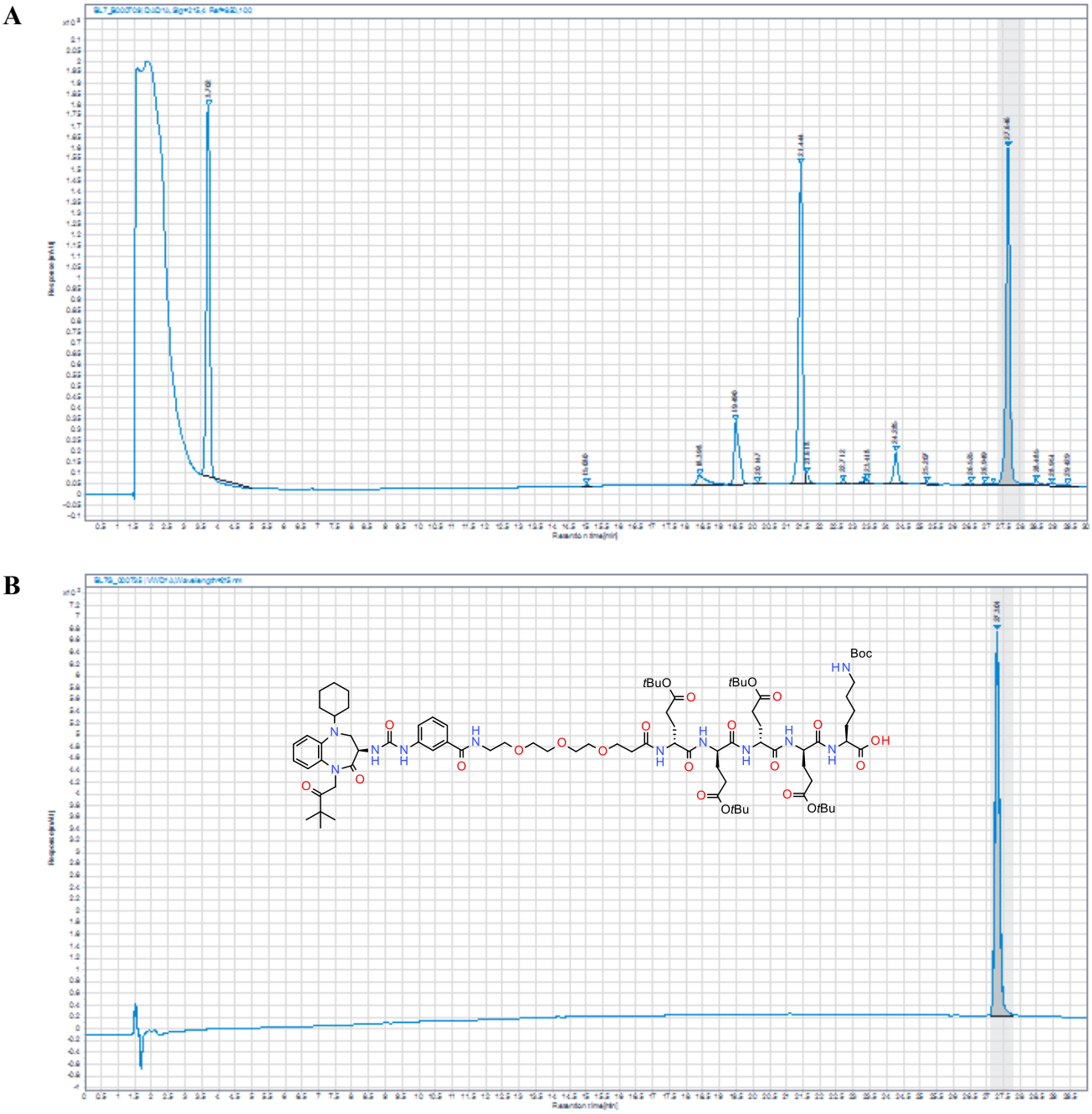


Figure S3. RP-HPLC UV traces (215 nm) of Z-360-PEG$_3$-[DGlu(O^{t}Bu)]$_4$-Lys(Boc)-OH (**A**) before and (**B**) after purification; (Peak at t_R = 21 min corresponds to free Z-360, which was recycled).

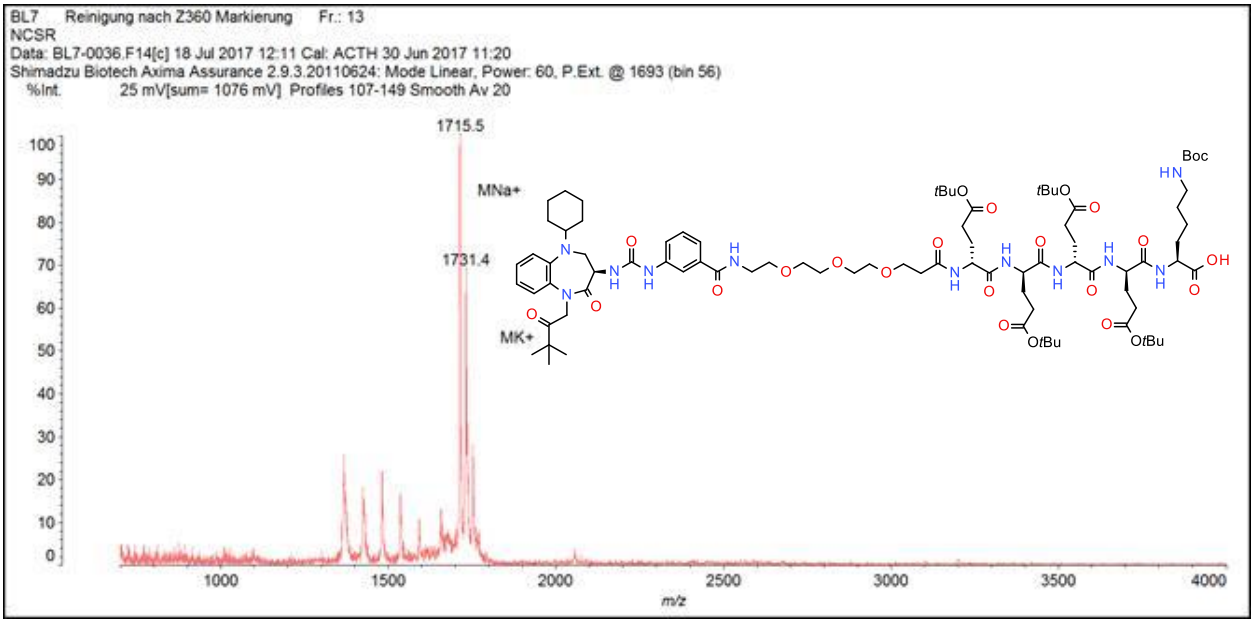


Figure S4. MALDI-TOF-MS spectrum of Z-360-PEG$_3$-[DGlu(O^{t}Bu)]$_4$-Lys(Boc)-OH, m/z calculated for $C_{85}H_{133}N_{11}O_{24}Na$ $(M+Na)^+$: 1715.9, found: 1715.5 and m/z calculated for $(M+K)^+$: 1730.9, found: 1731.4

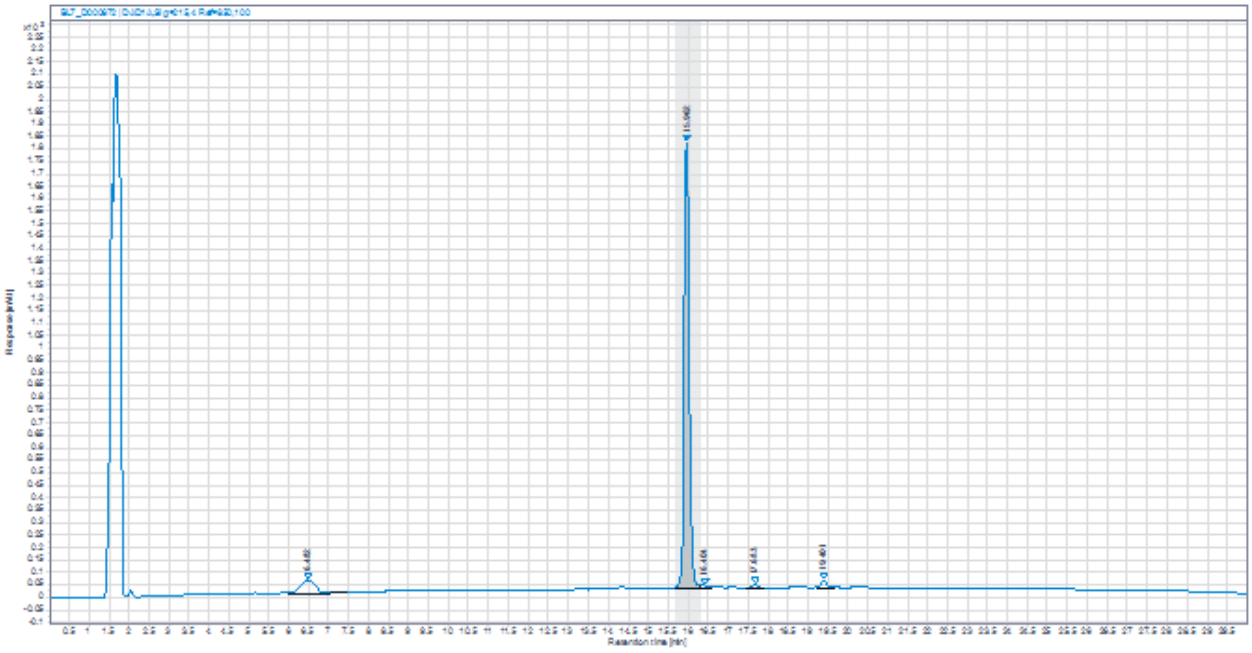


Figure S5. RP-HPLC UV trace (215 nm) of Z-360-PEG$_3$-(DGlu)$_4$-Lys-OH

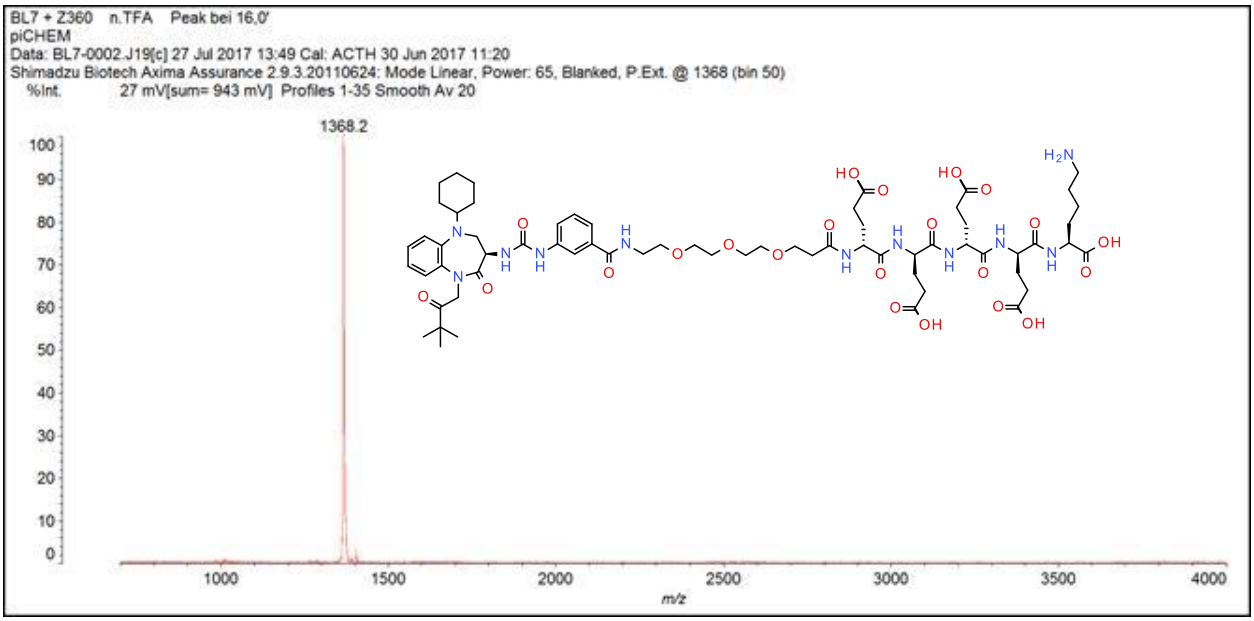


Figure S6. MALDI-TOF-MS spectrum of purified Z-360-PEG$_3$-(DGlu)$_4$-Lys-OH, m/z calculated for $C_{64}H_{93}N_{11}O_{22}$ $(M+H)^+$: 1368.6, found: 1368.2

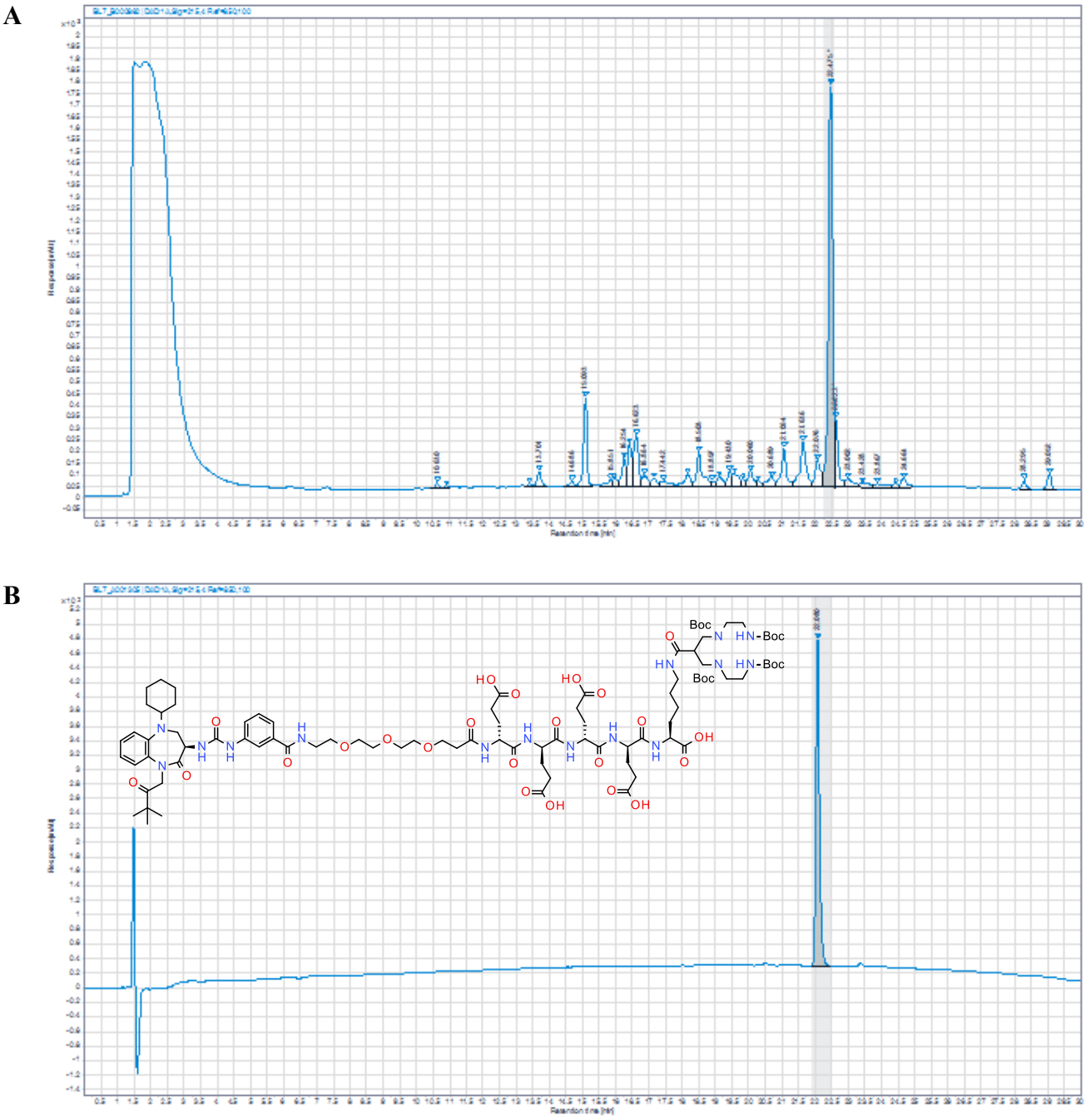
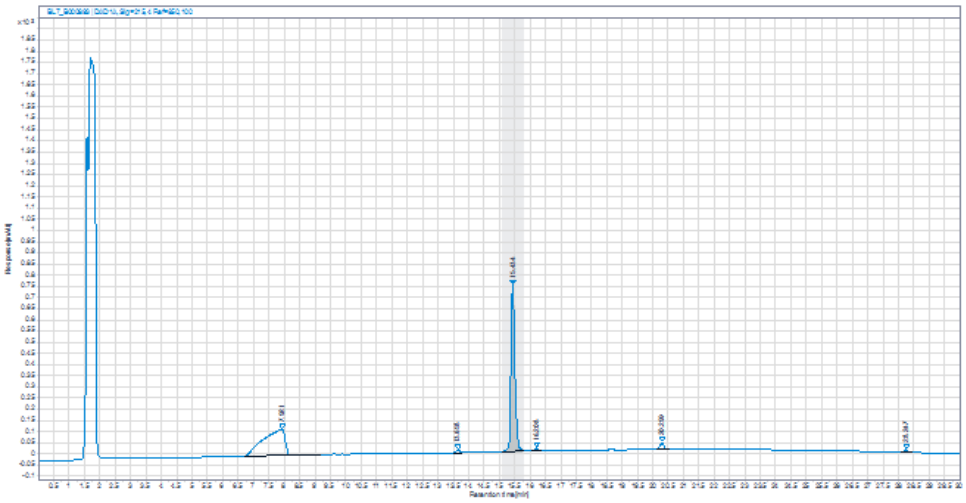
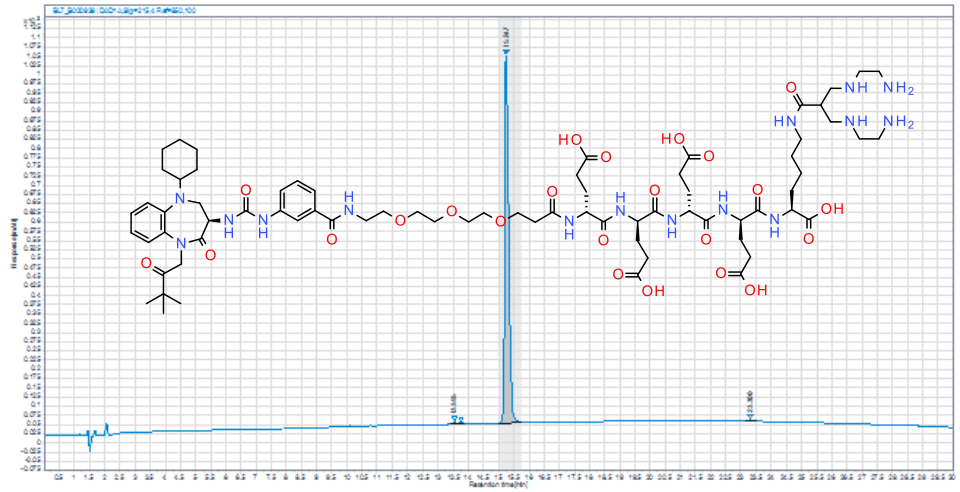


Figure S7. RP-HPLC UV traces (215 nm) of Z-360-PEG$_3$-(DGlu)$_4$-Lys[N$_4$(Boc)$_4$]-OH (**A**) before and (**B**) after purification

A



B



C

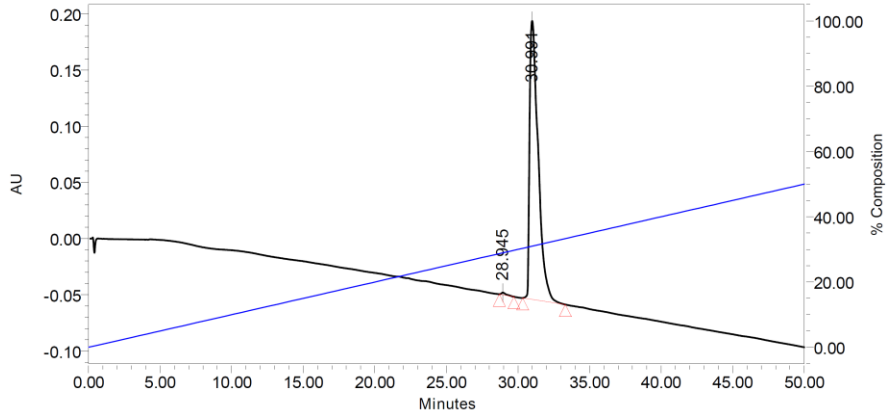


Figure S8. RP-HPLC UV traces (215 nm) of DGA1 (**A**) before and (**B**) after purification applying system 1 or (**C**) system 2, revealing an >96% purity for the lyophilized end-product

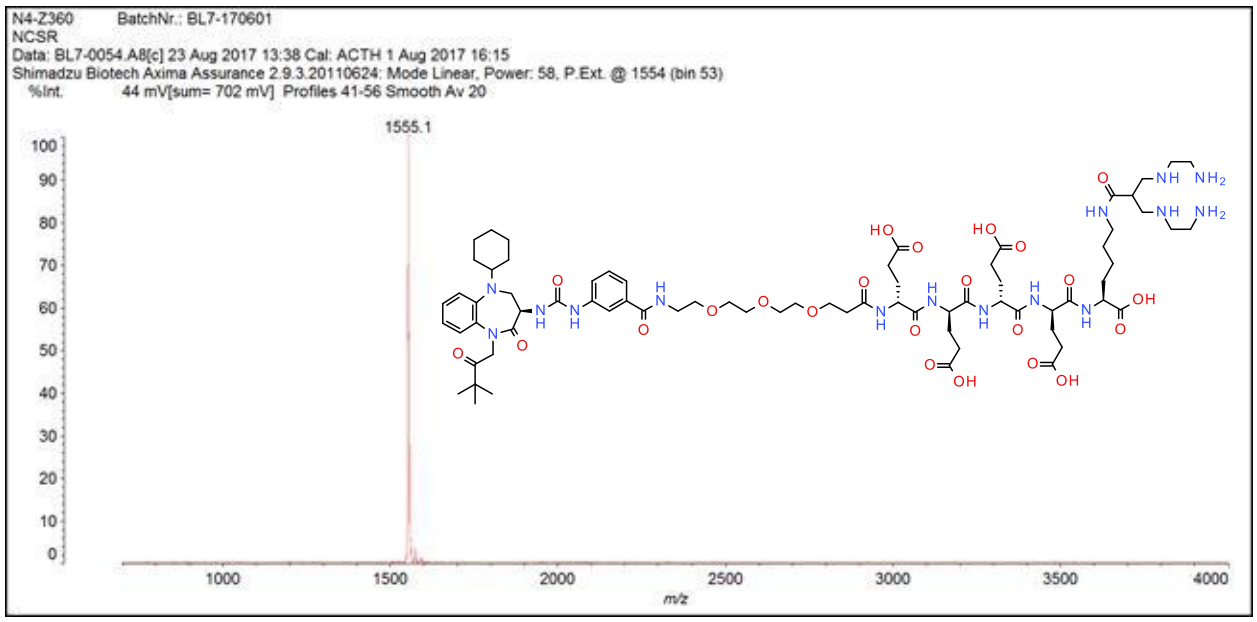


Figure S9. MALDI-TOF-MS spectrum of DGA1, m/z calculated for $C_{72}H_{112}N_{15}O_{23}$ $(M+H)^+$: 1554.8, found: 1555.1

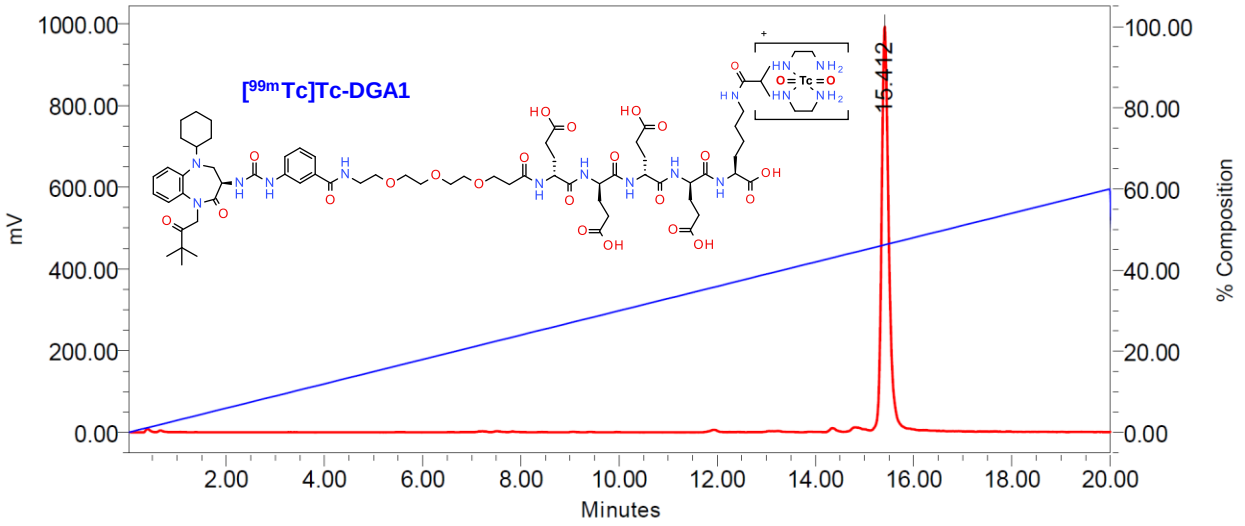


Figure S10. Representative HPLC radiochromatogram of a [^{99m}Tc]Tc-labeling solution of DGA1 applying system 3

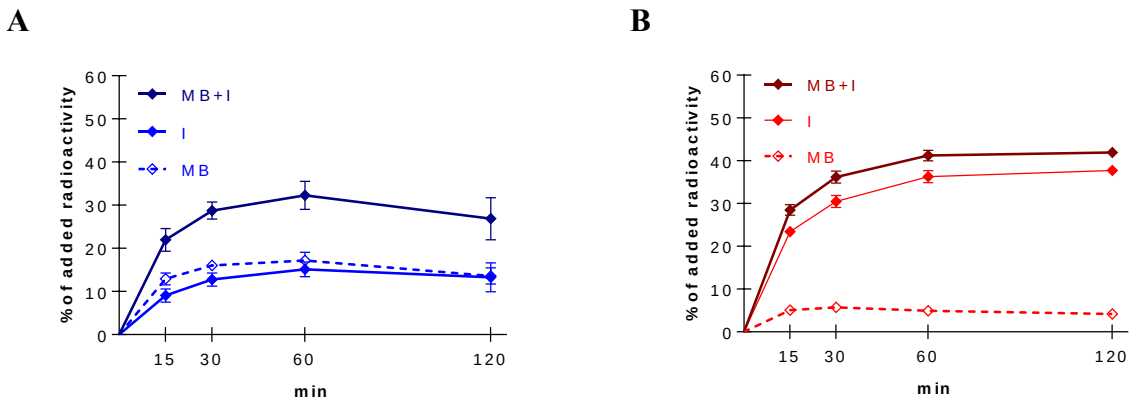


Figure S11. Specific cell-association rates of (**A**) [^{99m}Tc]Tc-DGA1 (blue) and (**B**) [^{99m}Tc]Tc-DG2 (red) in HEK293-CCK$_2$R cells at 37 °C; solid lines represent the internalized (I) and scattered lines the membrane bound fractions (MB), whereas the darker solid lines represent specific total cell uptake (MB+I); results represent mean values±SD, n = 3.

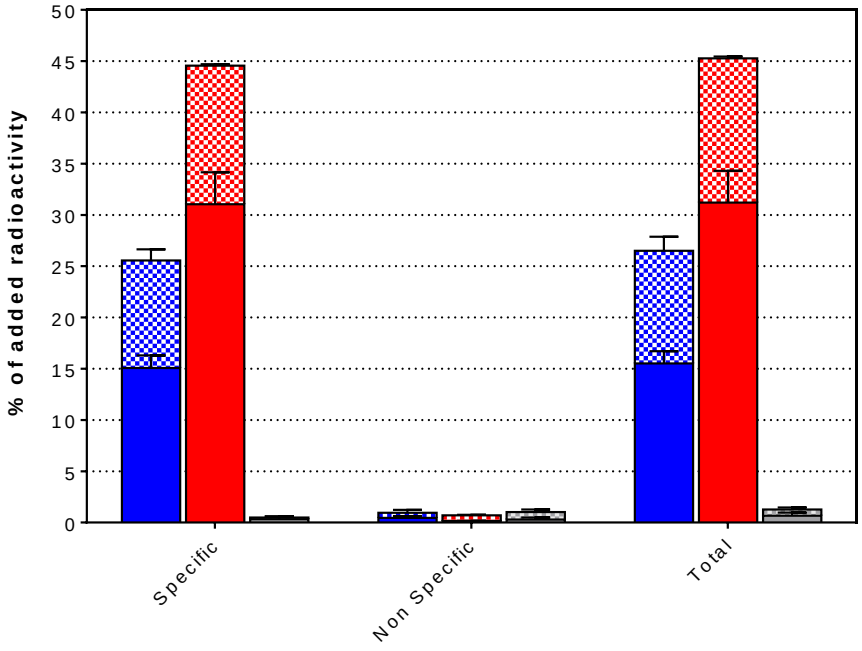


Figure S12. Cell-association (internalized: solid bars and membrane-bound fractions: checkered bars) of [^{99m}Tc]Tc-DGA1 (blue) and [^{99m}Tc]Tc-DG2 (red) in HEK293-CCK$_{2i4sv}$R cells and of [^{99m}Tc]Tc-DGA1 in HEK293T cells at 37 °C at 1 h, including total, non-specific (in the presence of 1 μM DG2) and specific values; results represent mean values±SD, n = 3.

Table S1. Biodistribution of [^{99m}Tc]Tc-DGA1 and [^{99m}Tc]Tc-DG2 in SCID mice bearing twin HEK293-CCK$_2$R positive and HEK293-CCK$_2$R negative tumors at 1, 4 and 24 h pi, expressed as %ID/g and representing mean values±SD, n=4.

Organs	%ID/g ± SD, n=4					
	[^{99m}Tc]Tc-DGA1			[^{99m}Tc]Tc-DG2		
	1 h	4 h	24 h	1 h	4 h	24 h
Blood	10.18±1.11	1.02±0.11	0.09±0.03	0.65±0.02	0.16±0.02	0.34±0.38
Liver	4.62±0.66	1.86±0.19	0.39±0.07	0.55±0.01	0.26±0.03	0.10±0.01
Heart	3.11±0.55	0.64±0.06	0.10±0.02	0.39±0.01	0.13±0.01	0.09±0.01
Kidneys	**133.14±3.01**	**113.3±10.45**	**15.81±1.65**	**82.99±14.51**	**37.28±2.80**	**13.40±3.24**
Stomach	2.49±0.15	0.86±0.15	0.25±0.03	4.77±0.70	2.39±0.56	0.74±0.16
Intestines	1.68±0.21	0.89±0.20	0.41±0.09	0.63±0.19	0.63±0.11	0.34±0.11
Spleen	2.09±0.23	0.82±0.21	0.37±0.06	0.37±0.09	0.19±0.03	0.30±0.00
Muscle	1.01±0.09	0.19±0.01	0.05±0.01	0.16±0.06	0.04±0.01	0.04±0.01
Lungs	4.86±0.44	1.00±0.11	0.19±0.01	0.63±0.18	0.15±0.03	0.07±0.00
Pancreas	2.14±0.12	0.36±0.04	0.07±0.01	1.38±0.06	0.14±0.02	0.08±0.01
HEK293-CCK$_2$R tumor	**39.64±2.84**	**33.58±6.54**	**12.50±2.53**	**11.18±1.93**	**8.71±1.06**	**7.40±2.43**
HEK293T tumor	**2.23±0.25**	**0.55±0.52**	**0.18±0.03**	**0.46±0.09**	**0.27±0.08**	**0.14±0.01**