

Supplementary information

Table S1. Qualitative LC/MS/MS results for analysis of the degraded RED-106 linker/payload and the surrogate small molecule conjugates.

Small Molecule	Molecular Formula	Theoretical Monoisotopic Mass (m, Da)	Most Abundant Feature Observed			Mass Error (ppm)	Observed Monoisotopic Mass Shift of Modification (Da)	Theoretical Monoisotopic Mass Shift of Modification (Da)	Composition Change of Modification	Observed? (* or #)
			m/z	z	[m+z H] ^{z+} , where H=1.007825 Da					
RED-106	C ₆₂ H ₈₇ C ₁ N ₈ O ₁₆	1234.59 2857	618. 301	2	1236. 6022	5.1	0	0	N/A	Y
RED-106àRED-10 6-H ₂ O	C ₆₂ H ₈₅ C ₁ N ₈ O ₁₅	1216.58 2292	609. 296	2	1218. 5938	3.4	-18.008	-18.015 7	(-H ₂ O)	Y (*)
RED-106àRED-10 6-NCO ₂ H ₃	C ₆₁ H ₈₄ C ₁ N ₇ O ₁₄	1173.57 6478	587. 792	2	1175. 584 and 1175. 587. 793 5	6.9 and 4.4	-61.018 and -61.015	-61.016 4	(-NCO ₂ H ₃)	Y (*)
RED-106àRED-10 6-CH ₂	C ₆₁ H ₈₅ C ₁ N ₈ O ₁₆	1220.57 7207	611. 294	2	1222. 589	3.2	-14.013	-14.015 7	(-CH ₂)	Y (*)
RED-106àRED-10 6-H ₂	C ₆₂ H ₈₅ C ₁ N ₈ O ₁₆	1232.57 7207	617. 293	2	1234. 5878	4.1	-2.014	-2.0157	(-H ₂)	Y (#)
RED-106àRED-10 6+C	C ₆₃ H ₈₇ C ₁ N ₈ O ₁₆	1246.59 2857	624. 301	2	1248. 6022	5.1	12	12	(+C)	Y (#)
IBA	C ₄ H ₈ O	72.0575	N/A	N / A	N/A	N/A	N/A	N/A	N/A	N/A

IBAàRED-106(+IB A) = RED-106(+54.098)*	C ₆₆ H ₉₃ ClN ₈ O 16	1288.63 907 5	645. 325 5	2	1290. 651	2.9	0	0	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆)	Y (*)
IBAàRED-106(+IB A-H ₂ O)	C ₆₆ H ₉₁ ClN ₈ O 15	1270.62 9242 7	636. 320 7	2	1272. 6414	2.7	-18.01	-18.015 7	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆ -H ₂ O)	Y (*)
IBAàRED-106(+IB A-NCO ₂ H ₃)	C ₆₅ H ₉₀ ClN ₇ O 14	1227.62 3429 7	614. 816 7	2	1229. 6334	4.6	-61.018	-61.016 4	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆ -NCO ₂ H ₃)	Y (*)
IBAàRED-106(+IB A-CH ₂)	C ₆₅ H ₉₁ ClN ₈ O 16	1274.62 4157 7	638. 317 7	2	1276. 6354	3.5	-14.016	-14.015 7	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆ -CH ₂)	Y (*)
IBAàRED-106(+IB A-H ₂)	C ₆₆ H ₉₁ ClN ₈ O 16	1286.62 4157	N/A / A	N	N/A	N/ A	N/A	-2.0157	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆ -H ₂)	N (#)
IBAàRED-106(+IB A+C)	C ₆₇ H ₉₃ ClN ₈ O 16	1300.63 9807	N/A / A	N	N/A	N/ A	N/A	12	(+C ₆₆ H ₉₃ ClN ₈ O ₁₆ +C)	N (#)
HMBA	C ₈ H ₈ O ₃	152.047 344	N/A / A	N	N/A	N/ A	N/A	N/A	N/A	N/A
HMBAàRED-106(+HMBA) = RED-106(+134.037) *	C ₇₀ H ₉₃ ClN ₈ O 18	1368.62 936 4	685. 320 4	2	1370. 6408	3.1	0	0	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈)	Y (*)
HMBAàRED-106(+HMBA-H ₂ O)	C ₇₀ H ₉₁ ClN ₈ O 17	1350.61 9072 4	676. 315 4	2	1352. 6308	2.9	-18.01	-18.015 7	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈ -H ₂ O)	Y (*)
HMBAàRED-106(+HMBA-NCO ₂ H ₃)	C ₆₉ H ₉₀ ClN ₇ O 16	1307.61 3258 6	654. 319 6	2	1308. 62	75 5.4 (low w S/ N)	-62.001	-61.016 4	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈ -NCO ₂ H ₃)	Y (*)
HMBAàRED-106(+HMBA-CH ₂)	C ₆₉ H ₉₁ ClN ₈ O 18	1354.61 3986 5	678. 317 5	2	1356. 635	-4	-14.006	-14.015 7	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈ -CH ₂)	Y (*)

HMBAàRED-106(+HMBA-H ₂)	C ₇₀ H ₉₁ ClN ₈ O 18	1366.61 3986	N/A	N / A	N/A	N/ A	N/A	-2.0157	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈ -H ₂)	N (#)
HMBAàRED-106(+HMBA+C)	C ₇₁ H ₉₃ ClN ₈ O 18	1380.62 9636	N/A	N / A	N/A	N/ A	N/A	12	(+C ₇₀ H ₉₃ ClN ₈ O ₁₈ +C)	N (#)

Table S2. Qualitative LC/MS/MS results for peptides from digests of unconjugated antibody and ADC.

Aldehyde tag Peptide from Large Molecule	Molecular Formula	Theoretical Monoisotopic Mass (m, Da)	Most Abundant Feature Observed			Mass Error (ppm)	Observed Monoisotopic Mass Shift of Modification (Da)	Theoretical Monoisotopic Mass Shift of Modification (Da)	Composition Change of Modification	Observed in mAb?	Observed in ADC? (* or #)
			m/z	z	[m+z H] ^{z+} , where H=1. 0078 25 Da						
SLSLSPGSL CTPSR	C ₅₈ H ₁₀₁ N 17O ₂₁ S ₁	1403.7 07864	702 .86 1	2	1405. 7224	0.8	0	0	N/A	Y	Y
CysàfGly (bioconversion)	C ₅₈ H ₉₉ N ₁ 7O ₂₂	1385.7 15058	693 .86 5	2	1387. 7296	0.8	17.993	-17.99 3	(+O-H ₂ S)	Y	Y
CysàfGlyàMe Ox (analytical methoxylamine modification for quantification of bioconversion/ bioorthogonal conjugation)	C ₅₉ H ₁₀₂ N 18O ₂₂	1414.7 41607	708 .37 8	2	1416. 7562	0.7	-11.03 4	11.034	(+HCNO-S)	Y	Y
CysàfGlyàGly	C ₅₇ H ₉₉ N ₁ 7O ₂₁	1357.7 20144	679 .86 7	2	1359. 7346	0.9	45.987 8	-45.98 8	(-H ₂ CS)	Y	Y
CysàfGlyàhydrated fGly	C ₅₈ H ₁₀₁ N 17O ₂₃	1403.7 25623	702 .87	2	1405. 7402	0.8	1405	0.0178	(+H ₂ O ₂ -H ₂ S)	Y	Y
CysàCys (analytical carbamidomethyl modification for	C ₆₀ H ₁₀₄ N 18O ₂₂ S ₁	1460.7 29328	731 .37 2	2	1462. 7438	0.8	-57.02 14	57.022	(+H ₃ C ₂ NO)	Y	Y

quantification of bioconversion/bioorthogonal conjugation)											
Glutathionylation on Cys	$C_{68}H_{116}N_{20}O_{27}S_2$	1708.77602	855.395	2	1710.7906	0.6	-305.0682	305.068	(+H ₁₅ C ₁₀ N ₃ O ₆ S)	Y	Y
CysàfGlyàRE D-106 (bioorthogonal conjugation)	$C_{120}H_{184}N_{25}O_{35}S_1Cl_1$	2602.279592	868.434	3	2605.3014	0.6	-1199.579	1198.57127	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄)	N/A	Y (*)
CysàfGlyàRE D-106-H ₂ O	$C_{120}H_{182}N_{25}O_{34}S_1Cl_1$	2584.269027	862.43	3	2587.2909	0.6	-1181.5685	1180.556	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄ -H ₂ O)	N/A	Y (*)
CysàfGlyàRE D-106-NCO ₂ H ₃	$C_{119}H_{181}N_{24}O_{33}S_1Cl_1$	2541.263214	848.095	3	2544.285	0.7	-1138.5626	1137.5549	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄ -NCO ₂ H ₃)	N/A	Y (*)
CysàfGlyàRE D-106-CH ₂	$C_{119}H_{182}N_{25}O_{35}S_1Cl_1$	2588.263942	863.762	3	2591.2857	0.7	-1185.5633	1184.556	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄ -CH ₂)	N/A	Y (*)
CysàfGlyàRE D-106-H ₂	$C_{120}H_{184}N_{25}O_{36}S_1Cl_1$	2618.274507	N/A	N/A	N/A	N/A	N/A	1196.556	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄ -H ₂)	N/A	N (#)
CysàfGlyàRE D-106+C	$C_{121}H_{186}N_{25}O_{36}S_1Cl_1$	2632.290157	N/A	N/A	N/A	N/A	N/A	1210.5713	(+C ₆₂ H ₈₃ CIN ₈ O ₁₄ +C)	N/A	N (#)

* Conjugatable modifications; # nonconjugatable modifications, Y – yes, N – no, N/A – not applicable.

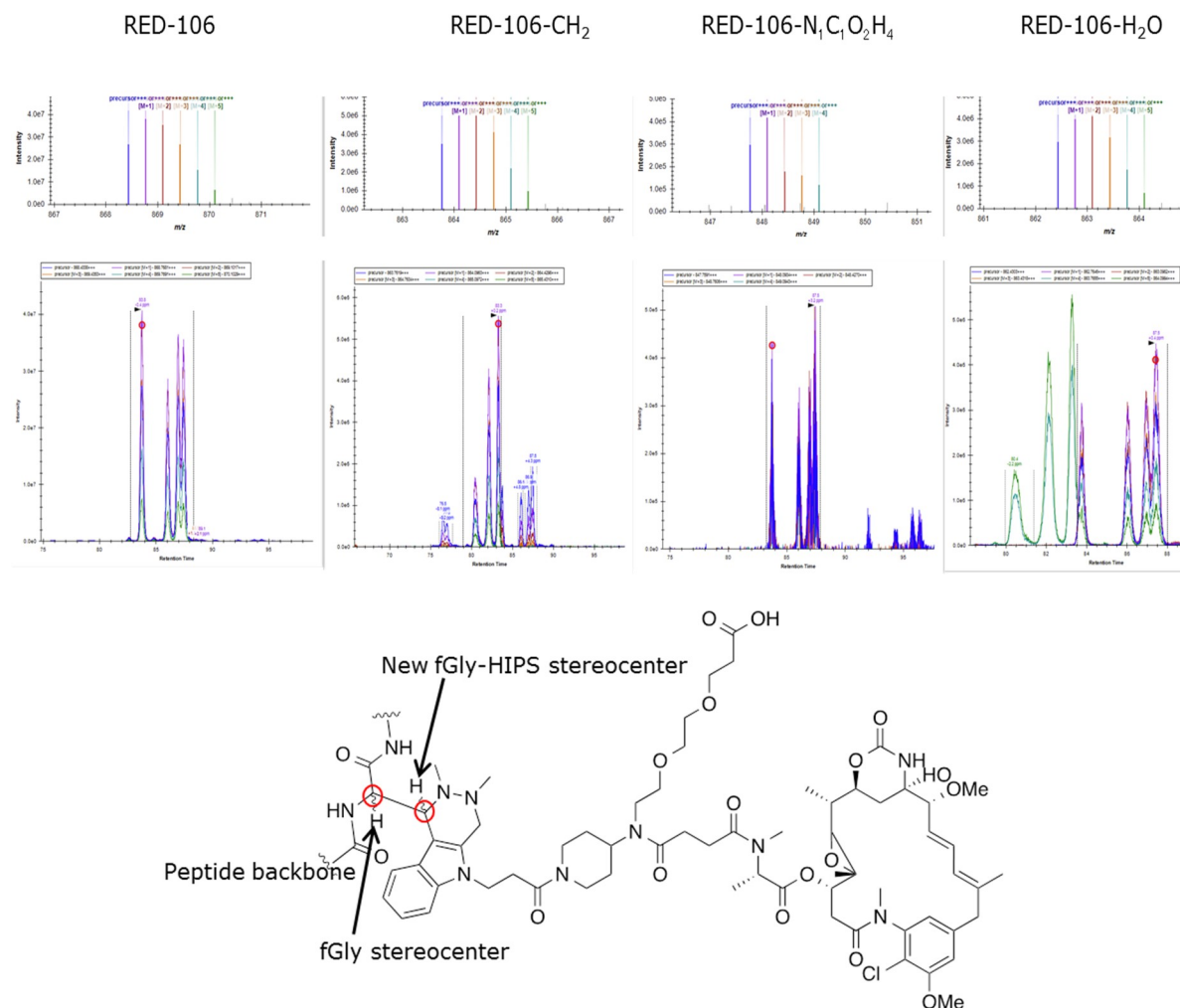


Figure S1. Representative chromatograms and isotopic envelopes for RED-106-, RED-106(-CH₂-), RED-106(-N₁C₁O₂H₃)- and RED-106(-H₂O)-modified SMARTag® peptides.

LC/MS/MS revealed identical conjugatable modifications in the surrogate conjugates and in aldehyde tag containing peptides from digests of the ADC, including full chromatographic resolution for all four expected isobaric (same mass) stereoisomers arising from the 2 fGly and 2 fGly-HIPS stereocenters in (D) for each of the following (from left to right): RED-106-, RED-106(-CH₂-), RED-106(-N₁C₁O₂H₃)- and RED-106(-H₂O)-modified SMARTag® peptides. Strong evidence for the assignment of each chromatographic peak is provided by the consistent isotopic envelopes shown above each extracted ion chromatogram. The structure shown illustrates the position of the fGly and fGly-HIPS stereocenters relative to the peptide backbone in RED-106-modified SMARTag® peptides and conjugation-related modifications of these peptides.