

Supplementary information

Scrutiny of *Mycobacterium tuberculosis* 19 kDa antigen proteoforms provides new insights in the lipoglycoprotein biogenesis paradigm

Julien Parra^{1,+}, Julien Marcoux^{1,+}, Isabelle Poncin², Stéphane Canaan², Jean Louis Herrmann³, Jérôme Nigou¹, Odile Burlet-Schiltz^{1,*}, Michel Rivière^{1,*}

¹Institut de Pharmacologie et de Biologie Structurale, Université de Toulouse, CNRS, UPS, France

²CNRS – Aix-Marseille Université, Enzymologie Interfaciale et Physiologie de la Lipolyse UMR7282, Marseille, France

³UMR1173, INSERM, Université de Versailles St Quentin, 78180, Montigny le Bretonneux, France

*Correspondence should be addressed to M.R. (Michel.riviere@ipbs.fr) or O.B-S. (email: Odile.schiltz@ipbs.fr)

+these authors contributed equally to this work

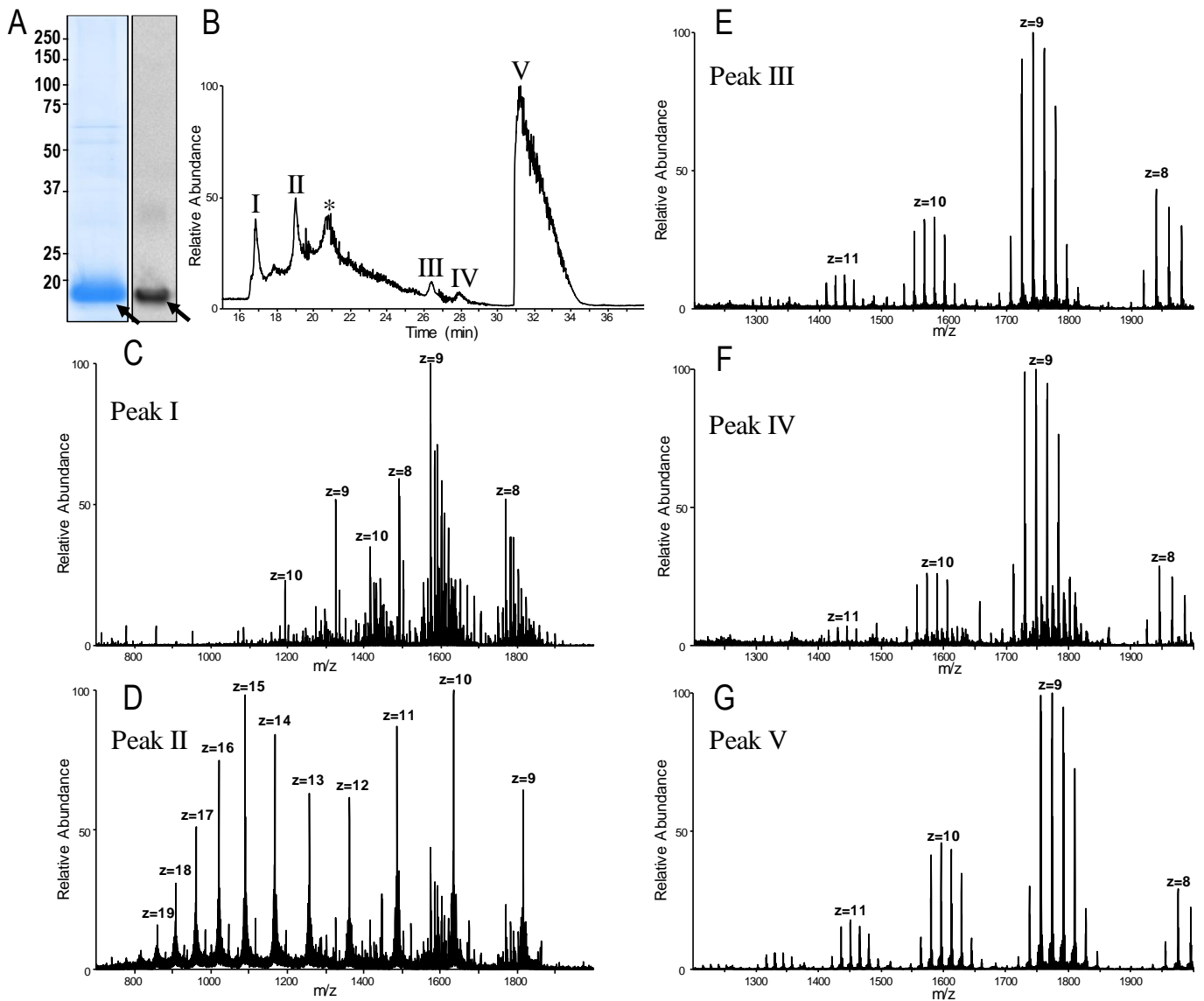


Figure S1. A single band showing different chromatographic peaks upon LC-MS analysis. (A) SDS-PAGE and anti His-tag Western Blotting of the recombinant LpqH^{His} (arrows). **(B to F).** Averaged full MS scans of the chromatographic peaks I, II, III, IV and V attributed to the different classes of LpqH proteoforms observed by the LC-MS analysis. These spectra show charge state distributions ranging from 8+ to 19+.

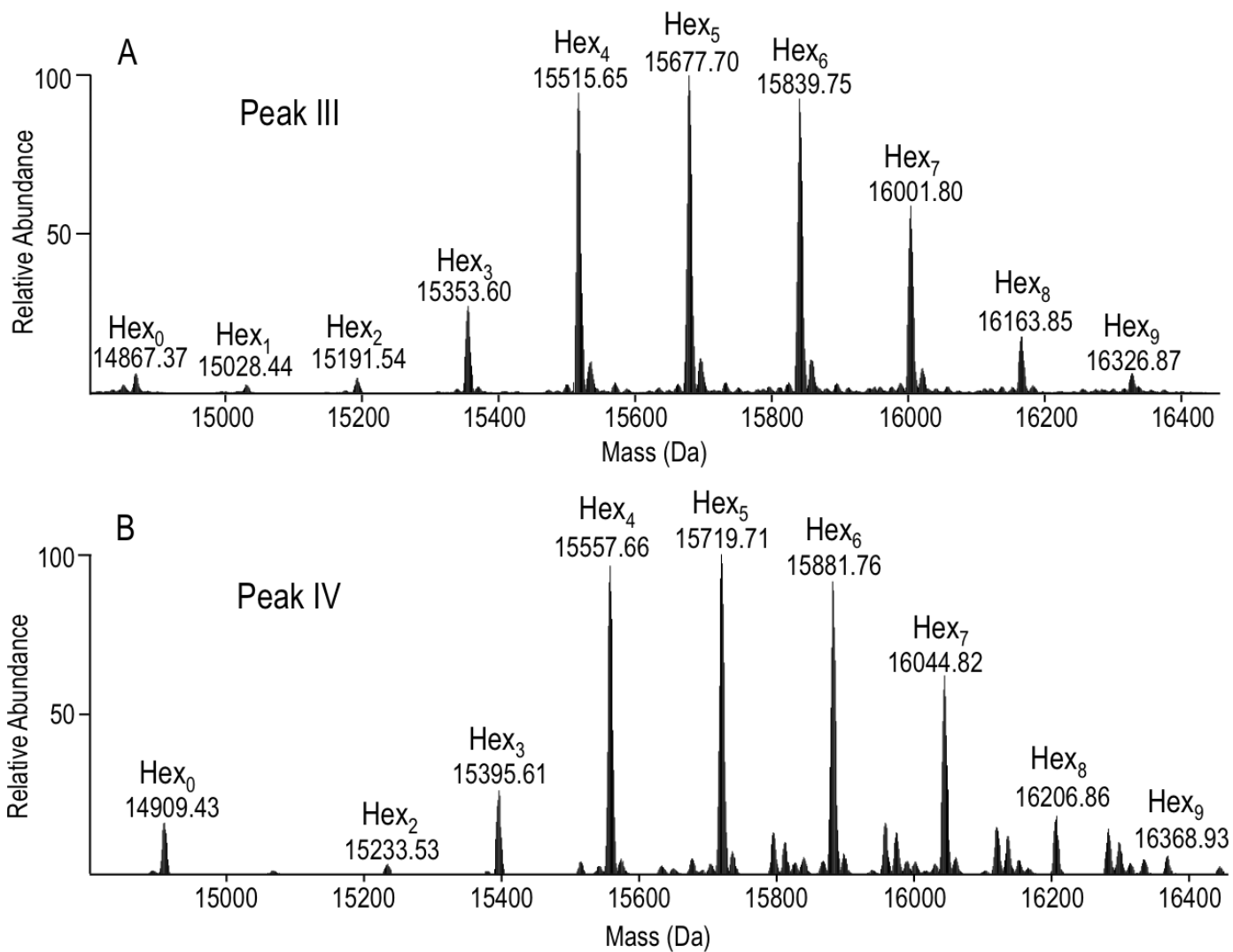


Figure S2. Deconvoluted MS spectra of the diacylated species of rLpqH^{His}. Different glycoforms of rLpqH^{His} [C₂₂-H₁₆₈] acylated with (A) a di-palmitoyl-glycerol (GroC₁₆C₁₆), or (B) a tuberculostearoyl-palmitoyl-glycerol (GroC₁₆C₁₉).

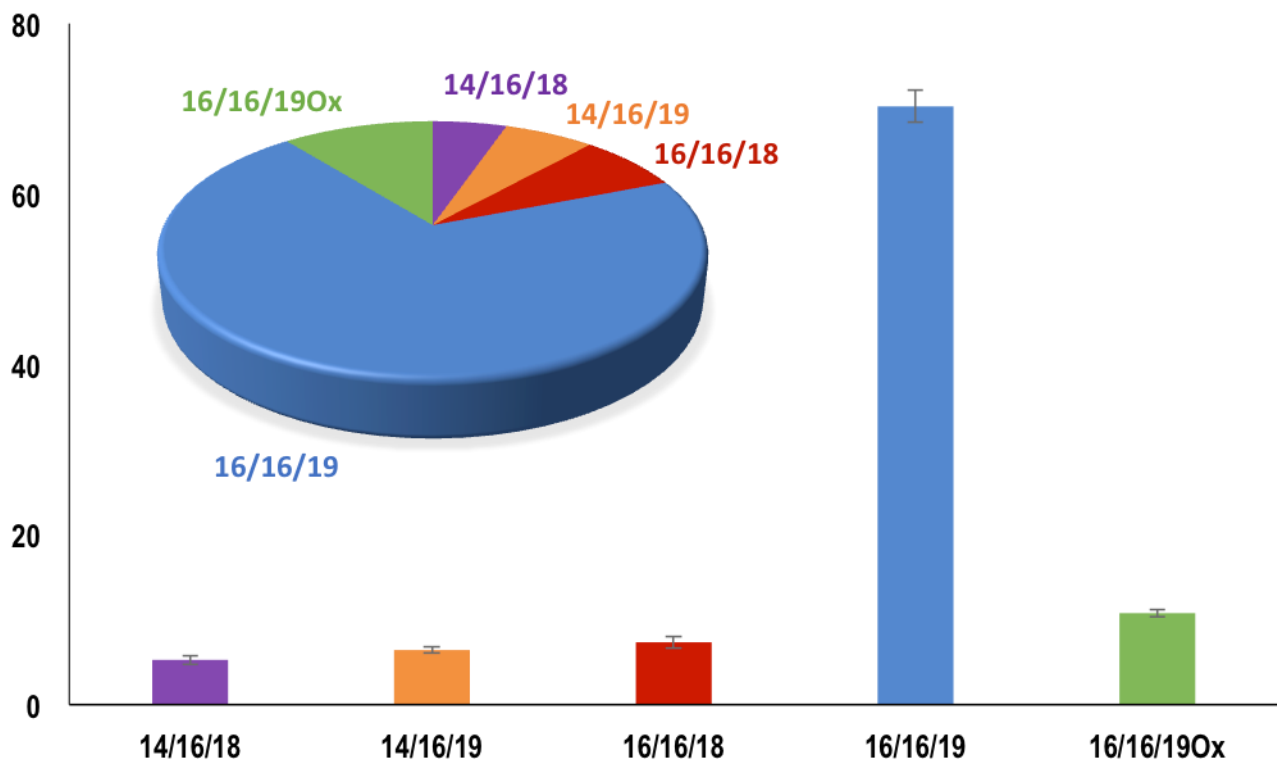


Figure S3. Relative abundance of each lipidic composition harbored by the tri-acylated proteoforms of rLpqH^{His}. The error bars represent the standard deviation from the mean of 5 deconvoluted glycoforms.

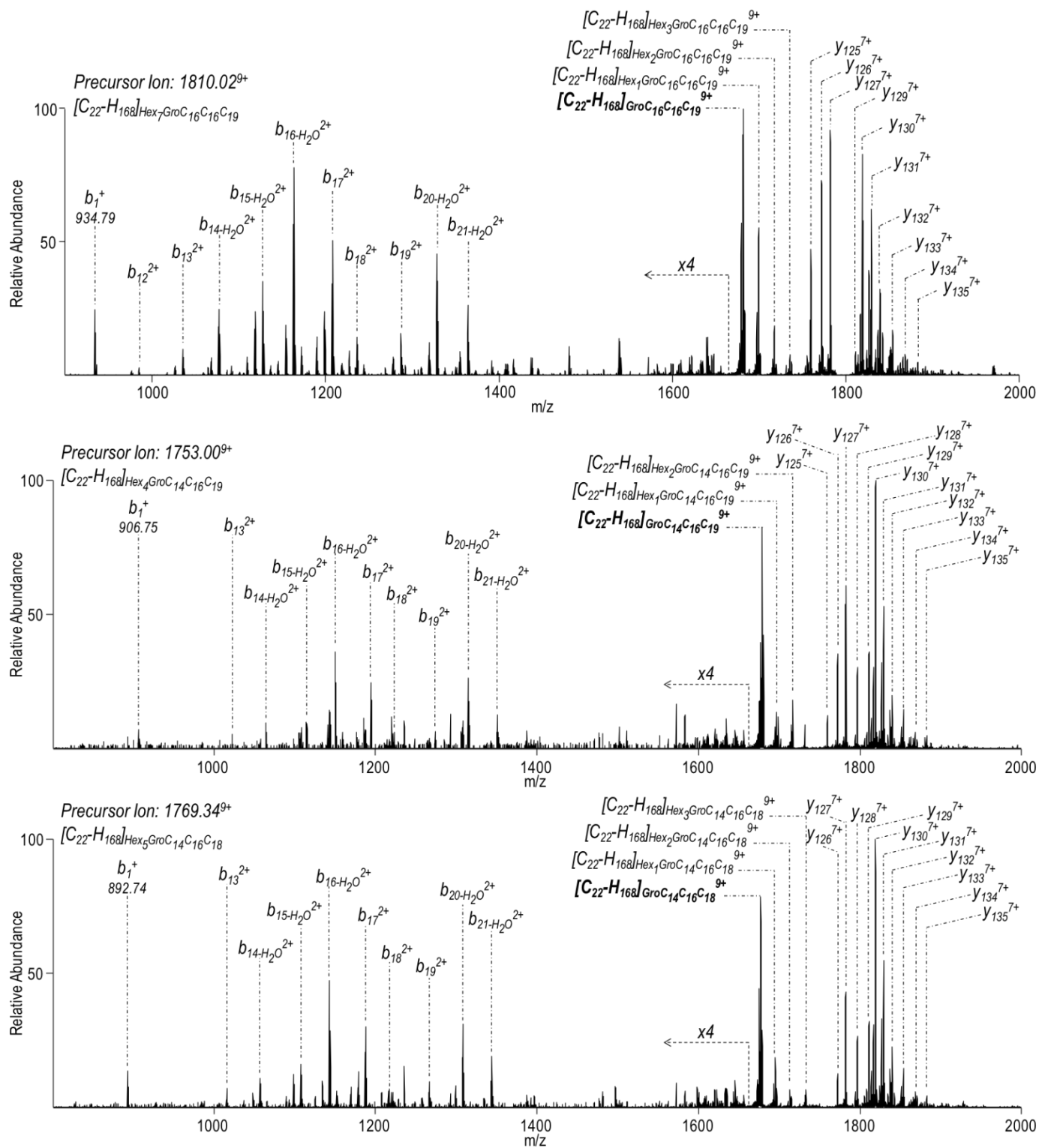


Figure S4. Top-down CID fragmentation of triacylated rLpQH^{His}. (A) [C₂₂-H₁₆₈]Hex₇GroC₁₆C₁₆C₁₉ (Precursor ion: 1810.029⁺), (B) [C₂₂-H₁₆₈]Hex₄GroC₁₄C₁₆C₁₉ (Precursor ion: 1753.009⁺) and (C) [C₂₂-H₁₆₈]Hex₅GroC₁₄C₁₆C₁₈ (Precursor ion: 1769.349⁺).

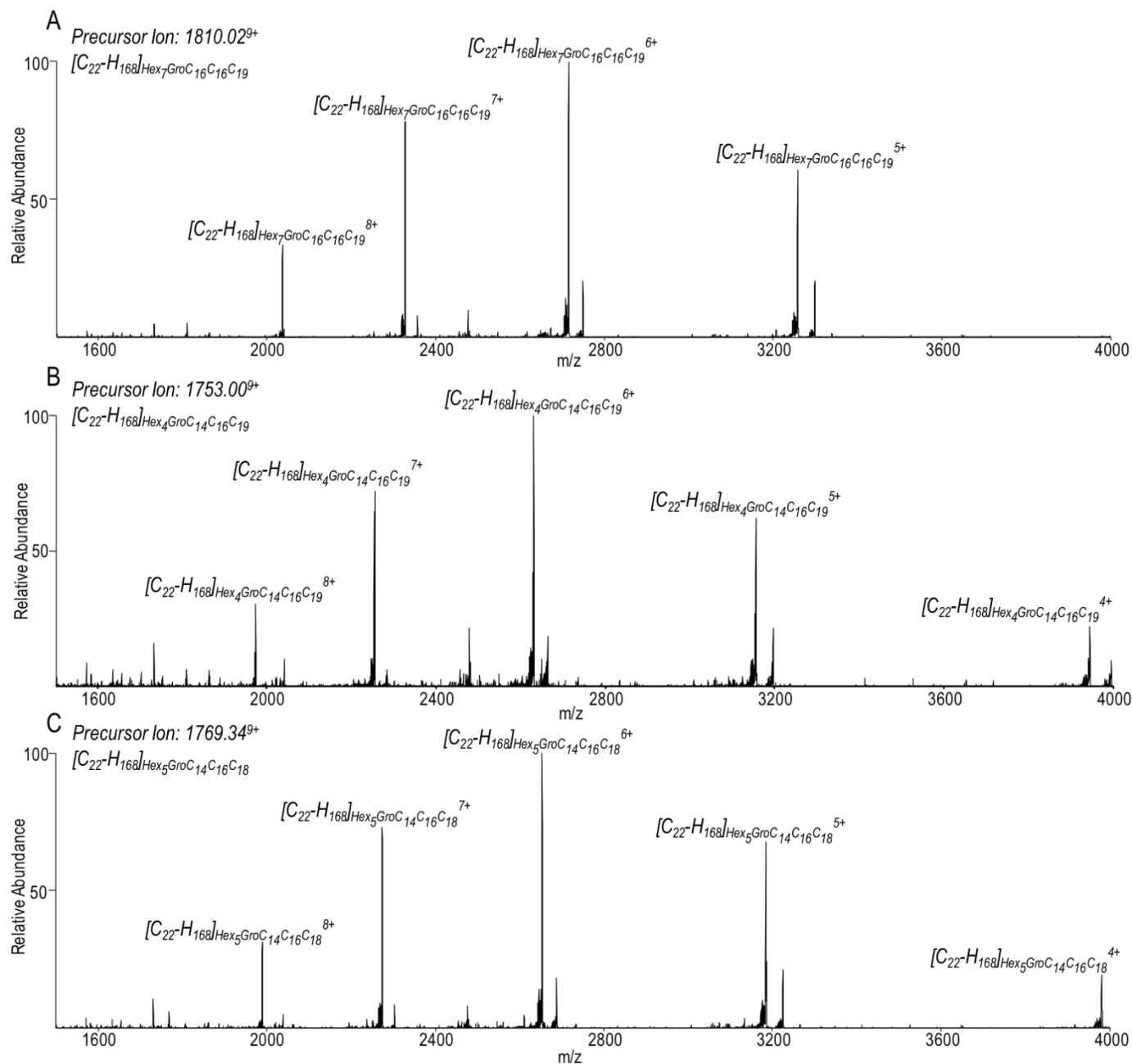


Figure S5. Top-down ETnOD spectra of the triacylated rLpQH^{His}. (A) $[C_{22}-H_{168}]Hex_7GroC_{16}C_{16}C_{19}$ (Precursor ion: 1810.02⁹⁺), (B) $[C_{22}-H_{168}]Hex_4GroC_{14}C_{16}C_{19}$ (Precursor ion: 1753.00⁹⁺) and (C) $[C_{22}-H_{168}]Hex_5GroC_{14}C_{16}C_{18}$ (Precursor ion: 1769.34⁹⁺).

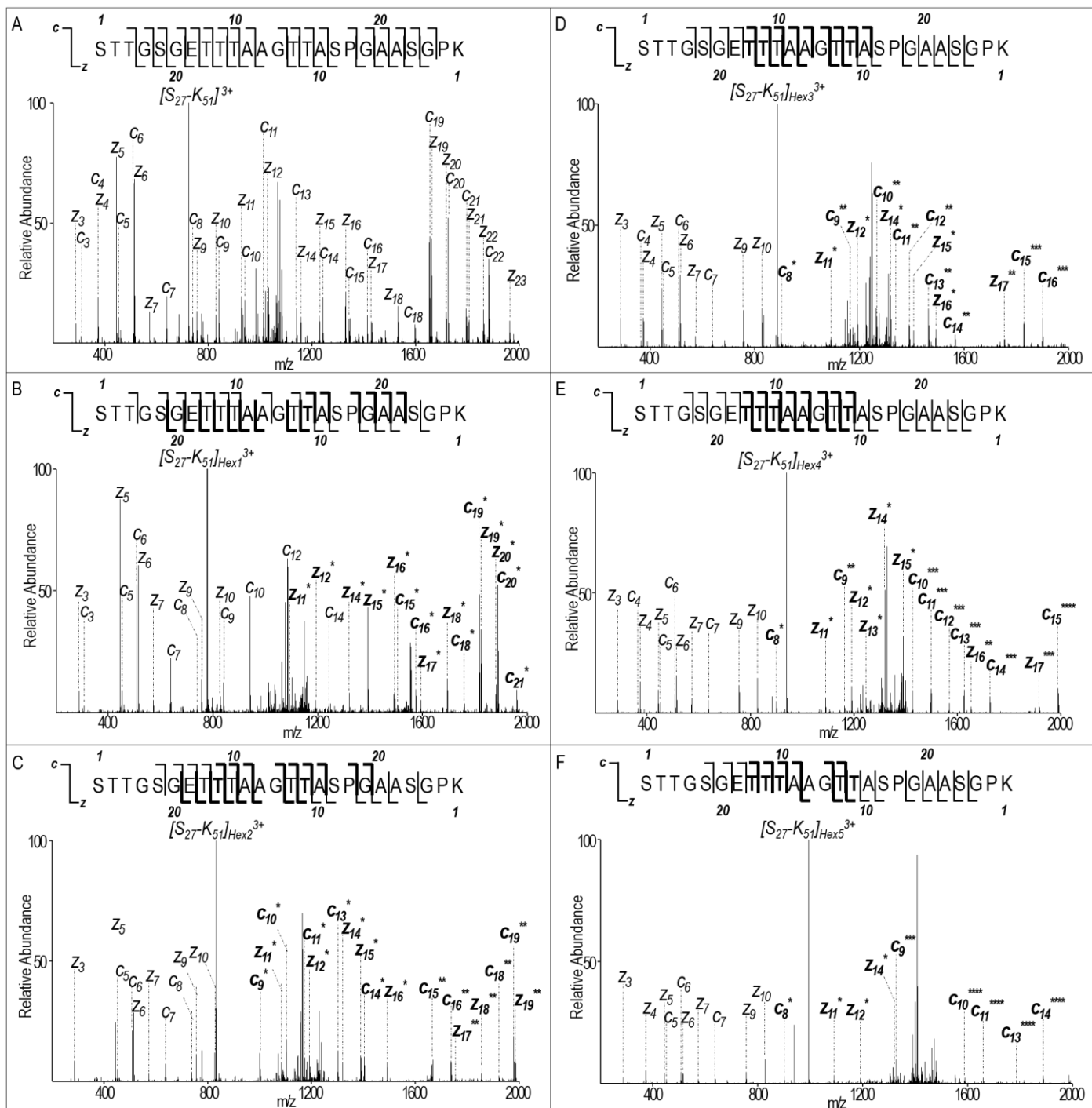


Figure S6. Bottom-up ETD fragmentation of tryptic peptide $S_{27}-K_{51}$. (A) non glycosylated (Precursor ion: 723.013+), (B) mono-glycosylated (Precursor ion: 777.033+), (C) di-glycosylated (Precursor ion: 831.043+), (D) tri-glycosylated (Precursor ion: 885.063+), (E) tetra-glycosylated (Precursor ion: 939.083+) and (F) penta-glycosylated (Precursor ion: 993.103+). Glycosylation sites and fragments are marked in bold, and number of glycosylation units are indicated by stars on spectra.

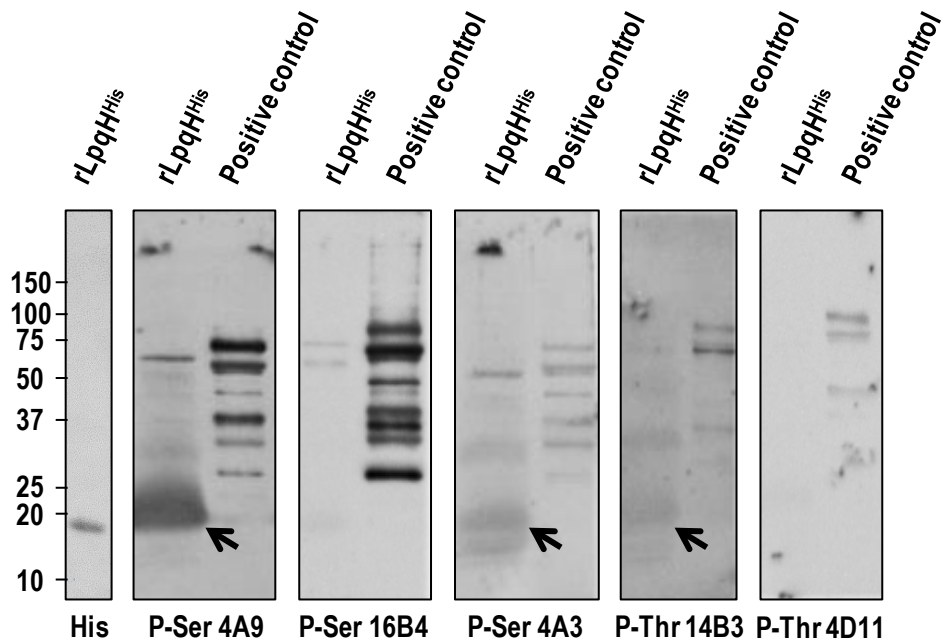


Figure S7. Western blotting of rLpqH^{His} with Anti-Phospho-Serine and Anti-Phospho-Threonine antibodies. Positive controls are phosphoproteins mixture provided by antibodies manufacturers.

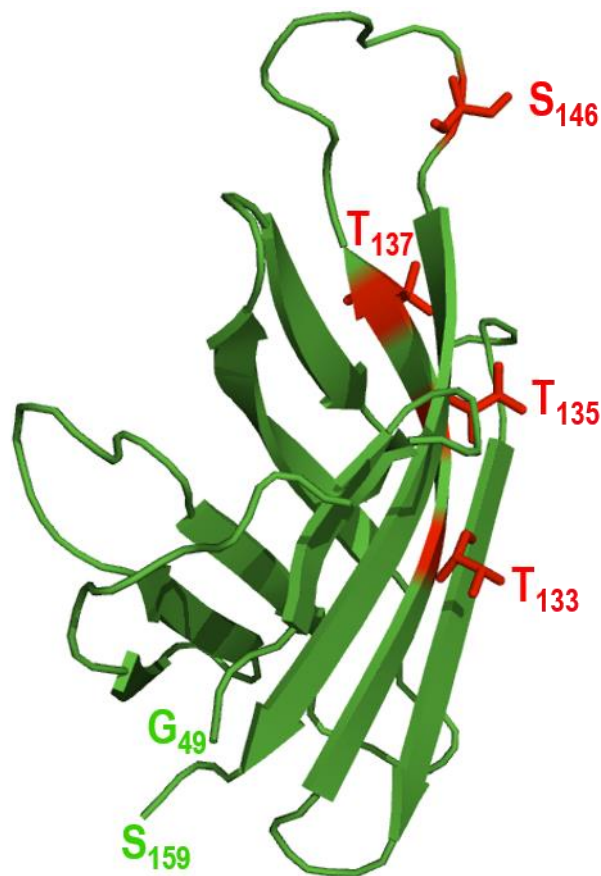


Figure S8. Structural model of LpqH (PDB 4ZJM), and localization of the four potential phosphorylation sites (indicated in red). Only the fragment [G₄₉-S₁₅₉] has been resolved in this model, excluding the N-terminal part of the protein encompassing all of the glycosylation and acylation sites.

Table S1. List of proteoforms of rLpqH^{His} identified. ΔM tolerance was set to 2.5 Da.

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
I	11 221.44	11 222.19	0.75	[G ₅₆ -H ₁₆₈]	
I	11 648.69	11 648.70	0.01	[V ₅₂ -H ₁₆₈]	
I	11 930.87	11 931.03	0.16	[G ₄₉ -H ₁₆₈]	
I	12 017.90	12 018.11	0.21	[S ₄₈ -H ₁₆₈]	
I	12 088.94	12 089.19	0.25	[A ₄₇ -H ₁₆₈]	
I	12 158.97	12 160.27	1.30	[A ₄₆ -H ₁₆₈]	
I	12 401.09	12 401.51	0.42	[S ₄₃ -H ₁₆₈]	
I	12 472.12	12 472.59	0.47	[A ₄₂ -H ₁₆₈]	
I	12 735.23	12 735.74	0.51	[T ₄₁ -H ₁₆₈]	Hex ₁
I	13 933.69	13 932.79	0.90	[T ₂₉ -H ₁₆₈]	Hex ₂
I	13 993.75	13 993.74	0.01	[G ₃₀ -H ₁₆₈]	Hex ₃
I	14 095.78	14 094.84	0.94	[T ₂₉ -H ₁₆₈]	Hex ₃
I	14 155.79	14 155.79	0.00	[G ₃₀ -H ₁₆₈]	Hex ₄
I	14 195.82	14 195.94	0.12	[T ₂₈ -H ₁₆₈]	Hex ₃
I	14 256.84	14 256.89	0.05	[T ₂₉ -H ₁₆₈]	Hex ₄
I	14 283.81	14 283.04	0.77	[S ₂₇ -H ₁₆₈]	Hex ₃

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
I	14 317.84	14 317.84	0.00	[G ₃₀ -H ₁₆₈]	Hex ₅
I	14 357.88	14 357.99	0.11	[T ₂₈ -H ₁₆₈]	Hex ₄
I	14 418.89	14 418.94	0.05	[T ₂₉ -H ₁₆₈]	Hex ₅
I	14 444.89	14 445.09	0.20	[S ₂₇ -H ₁₆₈]	Hex ₄
I	14 479.90	14 479.89	0.01	[G ₃₀ -H ₁₆₈]	Hex ₆
I	14 519.94	14 520.04	0.10	[T ₂₈ -H ₁₆₈]	Hex ₅
I	14 580.94	14 580.99	0.05	[T ₂₉ -H ₁₆₈]	Hex ₆
I	14 607.00	14 607.14	0.14	[S ₂₇ -H ₁₆₈]	Hex ₅
I	14 641.96	14 641.94	0.02	[G ₃₀ -H ₁₆₈]	Hex ₇
I	14 682.00	14 682.09	0.09	[T ₂₈ -H ₁₆₈]	Hex ₆
I	14 699.13	14 699.50	0.37	[S ₂₃ -H ₁₆₈]	Hex ₃
I	14 743.00	14 743.04	0.04	[T ₂₉ -H ₁₆₈]	Hex ₇
I	14 769.04	14 769.19	0.15	[S ₂₇ -H ₁₆₈]	Hex ₆
I	14 804.02	14 803.99	0.03	[G ₃₀ -H ₁₆₈]	Hex ₈
I	14 844.04	14 844.14	0.10	[T ₂₈ -H ₁₆₈]	Hex ₇
I	14 861.09	14 861.55	0.46	[S ₂₃ -H ₁₆₈]	Hex ₄
I	14 905.05	14 905.09	0.04	[T ₂₉ -H ₁₆₈]	Hex ₈

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
I	14 932.11	14 931.24	0.87	[S ₂₃ -H ₁₆₈]	Hex ₇
I	15 024.18	15 023.60	0.58	[S ₂₃ -H ₁₆₈]	Hex ₅
I	15 186.23	15 185.65	0.58	[S ₂₃ -H ₁₆₈]	Hex ₆
I	15 348.35	15 347.70	0.65	[S ₂₃ -H ₁₆₈]	Hex ₇
I	15 510.34	15 509.75	0.59	[S ₂₃ -H ₁₆₈]	Hex ₈
II	16 335.01	16 334.74	0.27	[M ₁ -H ₁₆₈]	HPO ₃
III	14 867.37	14 867.35	0.02	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₆
III	15 028.44	15 029.40	0.96	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₆ C ₁₆
III	15 191.54	15 191.45	0.09	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₆
III	15 353.60	15 353.50	0.10	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₆
III	15 515.65	15 515.55	0.10	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₆
III	15 677.70	15 677.60	0.10	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₆
III	15 839.75	15 839.65	0.10	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₆
III	16 001.80	16 001.70	0.10	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₆
III	16 163.85	16 163.75	0.10	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₆
III	16 326.87	16 325.80	1.07	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₆
IV	14 909.43	14 909.43	0.00	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₉

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
IV	15 233.53	15 233.53	0.00	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₉
IV	15 395.61	15 395.58	0.03	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₉
IV	15 557.66	15 557.63	0.03	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₉
IV	15 719.71	15 719.68	0.03	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₉
IV	15 881.76	15 881.73	0.03	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₉
IV	16 044.82	16 043.78	1.04	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₉
IV	16 206.86	16 205.83	1.03	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₉
IV	16 368.93	16 367.88	1.05	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₉
V	15 106.64	15 105.76	0.88	[C ₂₂ -H ₁₆₈]	GroC ₁₄ C ₁₆ C ₁₈
V	15 117.64	15 119.79	2.15	[C ₂₂ -H ₁₆₈]	GroC ₁₄ C ₁₆ C ₁₉
V	15 131.64	15 133.81	2.17	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₆ C ₁₈
V	15 146.68	15 147.84	1.16	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₆ C ₁₉
V	15 163.67	15 163.83	0.16	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₆ C ₁₉ OX ₁
V	15 177.64	15 179.83	2.19	[C ₂₂ -H ₁₆₈]	GroC ₁₆ C ₁₆ C ₁₉ OX ₂
V	15 251.67	15 253.79	2.12	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₄ C ₁₄ C ₁₉
V	15 267.74	15 267.81	0.07	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₄ C ₁₆ C ₁₈
V	15 280.70	15 281.84	1.14	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₄ C ₁₆ C ₁₉

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
V	15 294.74	15 295.86	1.12	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₆ C ₁₆ C ₁₈
V	15 307.73	15 309.89	2.16	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₆ C ₁₆ C ₁₉
V	15 323.72	15 325.88	2.16	[C ₂₂ -H ₁₆₈]	Hex ₁ GroC ₁₆ C ₁₆ C ₁₉ OX ₁
V	15 427.79	15 429.86	2.07	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₄ C ₁₆ C ₁₈
V	15 442.80	15 443.89	1.09	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₄ C ₁₆ C ₁₉
V	15 455.80	15 457.91	2.11	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₆ C ₁₈
V	15 470.83	15 471.94	1.11	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₆ C ₁₉
V	15 488.83	15 487.93	0.90	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₆ C ₁₉ OX ₁
V	15 503.80	15 503.93	0.13	[C ₂₂ -H ₁₆₈]	Hex ₂ GroC ₁₆ C ₁₆ C ₁₉ OX ₂
V	15 576.85	15 577.89	1.04	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₄ C ₁₄ C ₁₉
V	15 591.87	15 591.91	0.04	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₄ C ₁₆ C ₁₈
V	15 605.88	15 605.94	0.06	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₄ C ₁₆ C ₁₉
V	15 618.88	15 619.96	1.08	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₆ C ₁₈
V	15 632.91	15 633.99	1.08	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₆ C ₁₉
V	15 649.90	15 649.98	0.08	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₆ C ₁₉ OX ₁
V	15 665.90	15 665.98	0.08	[C ₂₂ -H ₁₆₈]	Hex ₃ GroC ₁₆ C ₁₆ C ₁₉ OX ₂
V	15 725.89	15 725.91	0.02	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₄ C ₁₄ C ₁₈

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
V	15 739.91	15 739.94	0.03	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₄ C ₁₄ C ₁₉
V	15 753.92	15 753.96	0.04	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₄ C ₁₆ C ₁₈
V	15 767.93	15 767.99	0.06	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₄ C ₁₆ C ₁₉
V	15 781.94	15 782.01	0.07	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₆ C ₁₈
V	15 795.96	15 796.04	0.08	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₆ C ₁₉
V	15 812.96	15 812.03	0.93	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	15 827.95	15 828.03	0.08	[C ₂₂ -H ₁₆₈]	Hex ₄ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂
V	15 887.94	15 887.96	0.02	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₄ C ₁₄ C ₁₈
V	15 900.95	15 901.99	1.04	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₄ C ₁₄ C ₁₉
V	15 915.97	15 916.01	0.04	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₄ C ₁₆ C ₁₈
V	15 929.98	15 930.04	0.06	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₄ C ₁₆ C ₁₉
V	15 943.99	15 944.06	0.07	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₆ C ₁₈
V	15 958.00	15 958.09	0.09	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₆ C ₁₉
V	15 975.00	15 974.08	0.92	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	15 989.99	15 990.08	0.09	[C ₂₂ -H ₁₆₈]	Hex ₅ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂
V	16 049.98	16 050.01	0.03	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₄ C ₁₄ C ₁₈
V	16 062.01	16 064.04	2.03	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₄ C ₁₄ C ₁₉

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
V	16 078.01	16 078.06	0.05	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₄ C ₁₆ C ₁₈
V	16 092.02	16 092.09	0.07	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₄ C ₁₆ C ₁₉
V	16 106.03	16 106.11	0.08	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₆ C ₁₈
V	16 120.05	16 120.14	0.09	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₆ C ₁₉
V	16 137.05	16 136.13	0.92	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	16 153.04	16 152.13	0.91	[C ₂₂ -H ₁₆₈]	Hex ₆ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂
V	16 211.05	16 212.06	1.01	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₄ C ₁₄ C ₁₈
V	16 226.06	16 226.09	0.03	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₄ C ₁₄ C ₁₉
V	16 240.06	16 240.11	0.05	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₄ C ₁₆ C ₁₈
V	16 254.07	16 254.14	0.07	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₄ C ₁₆ C ₁₉
V	16 268.08	16 268.16	0.08	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₆ C ₁₈
V	16 282.09	16 282.19	0.10	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₆ C ₁₉
V	16 298.10	16 298.18	0.08	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	16 315.09	16 314.18	0.91	[C ₂₂ -H ₁₆₈]	Hex ₇ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂
V	16 375.09	16 374.11	0.98	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₄ C ₁₄ C ₁₈
V	16 402.12	16 402.16	0.04	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₄ C ₁₆ C ₁₈
V	16 417.13	16 416.19	0.94	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₄ C ₁₆ C ₁₉

Chromatographic peak	Experimental Mass (Da)	Theoretical Mass (Da)	ΔM (Da)	Sequence	PTMs
V	16 430.16	16 430.21	0.05	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₆ C ₁₈
V	16 444.14	16 444.24	0.10	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₆ C ₁₉
V	16 461.15	16 460.23	0.92	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	16 477.15	16 476.23	0.92	[C ₂₂ -H ₁₆₈]	Hex ₈ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂
V	16 550.16	16 550.19	0.03	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₄ C ₁₄ C ₁₉
V	16 564.13	16 564.21	0.08	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₄ C ₁₆ C ₁₈
V	16 578.18	16 578.24	0.06	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₄ C ₁₆ C ₁₉
V	16 592.21	16 592.26	0.05	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₆ C ₁₈
V	16 606.21	16 606.29	0.08	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₆ C ₁₉
V	16 623.23	16 622.28	0.95	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₆ C ₁₉ Ox ₁
V	16 636.20	16 638.28	2.08	[C ₂₂ -H ₁₆₈]	Hex ₉ GroC ₁₆ C ₁₆ C ₁₉ Ox ₂