Electronic Supplementary Information for

Enzyme-Containing Spin Membranes for Rapid Digestion and Characterization of Single Proteins

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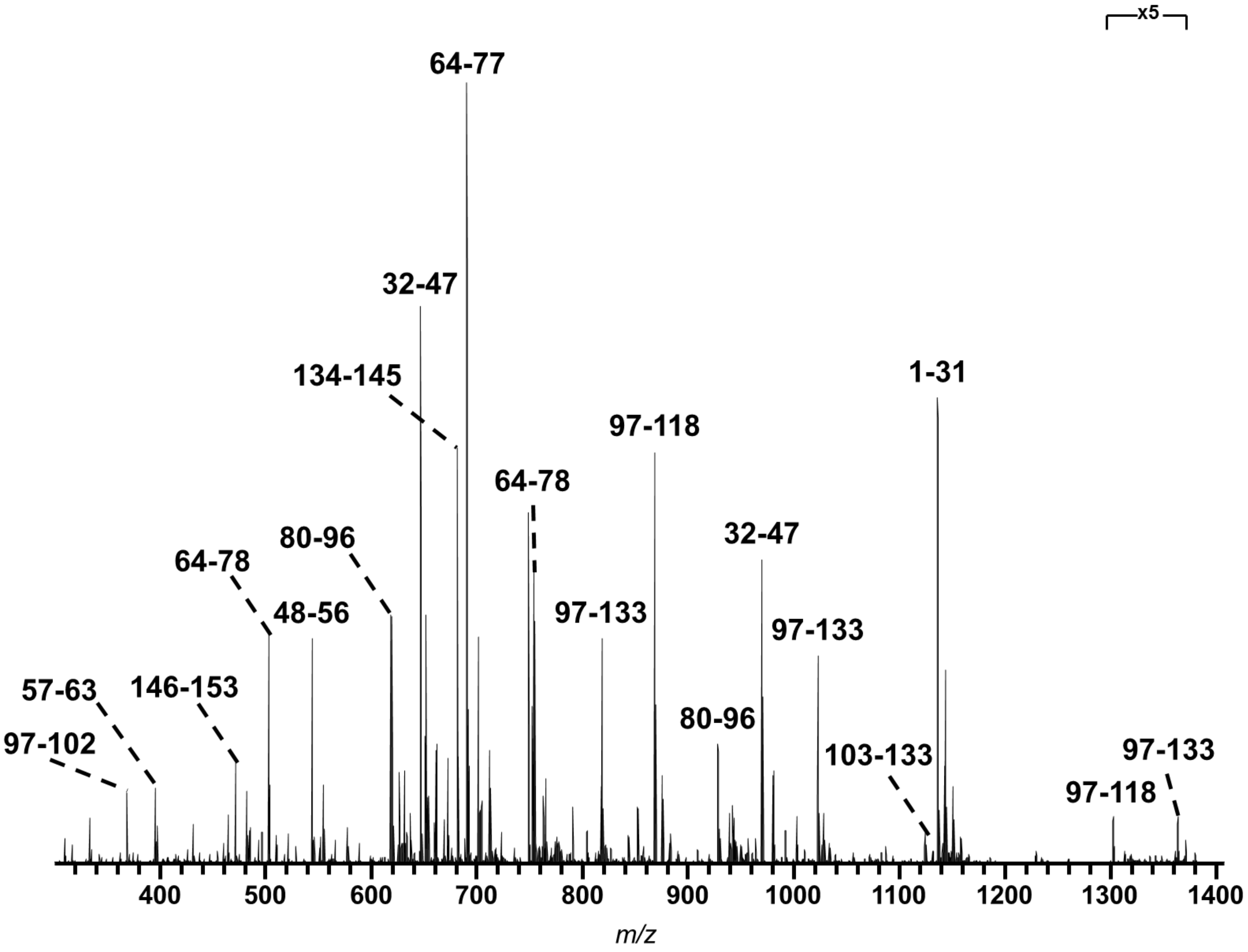


Figure S-1. Part of the mass spectrum of a tryptic spin digest (spun at 500 *g*) of apomyoglobin. Labels show the amino acids in the sequence (not all of the peptide signals are labelled)

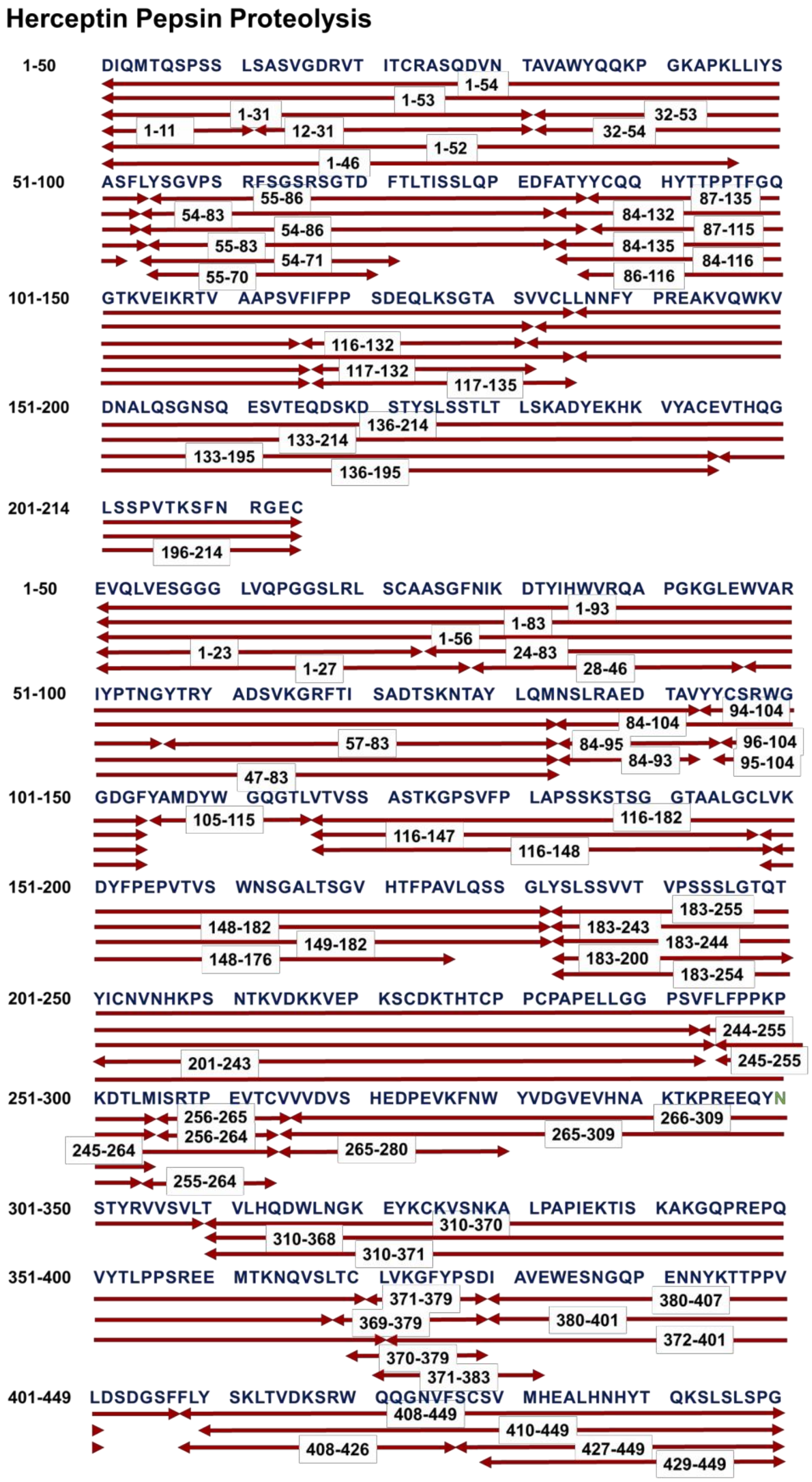

Herceptin Pepsin Proteolysis

Figure S-2. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane peptic digest of Herceptin. The light green “N” represents the glycosylation site.

Figure S-3. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane peptic digest of Avastin. The light green “N” represents the glycosylation site, and the red “K” denotes the C-terminal lysine clipping.

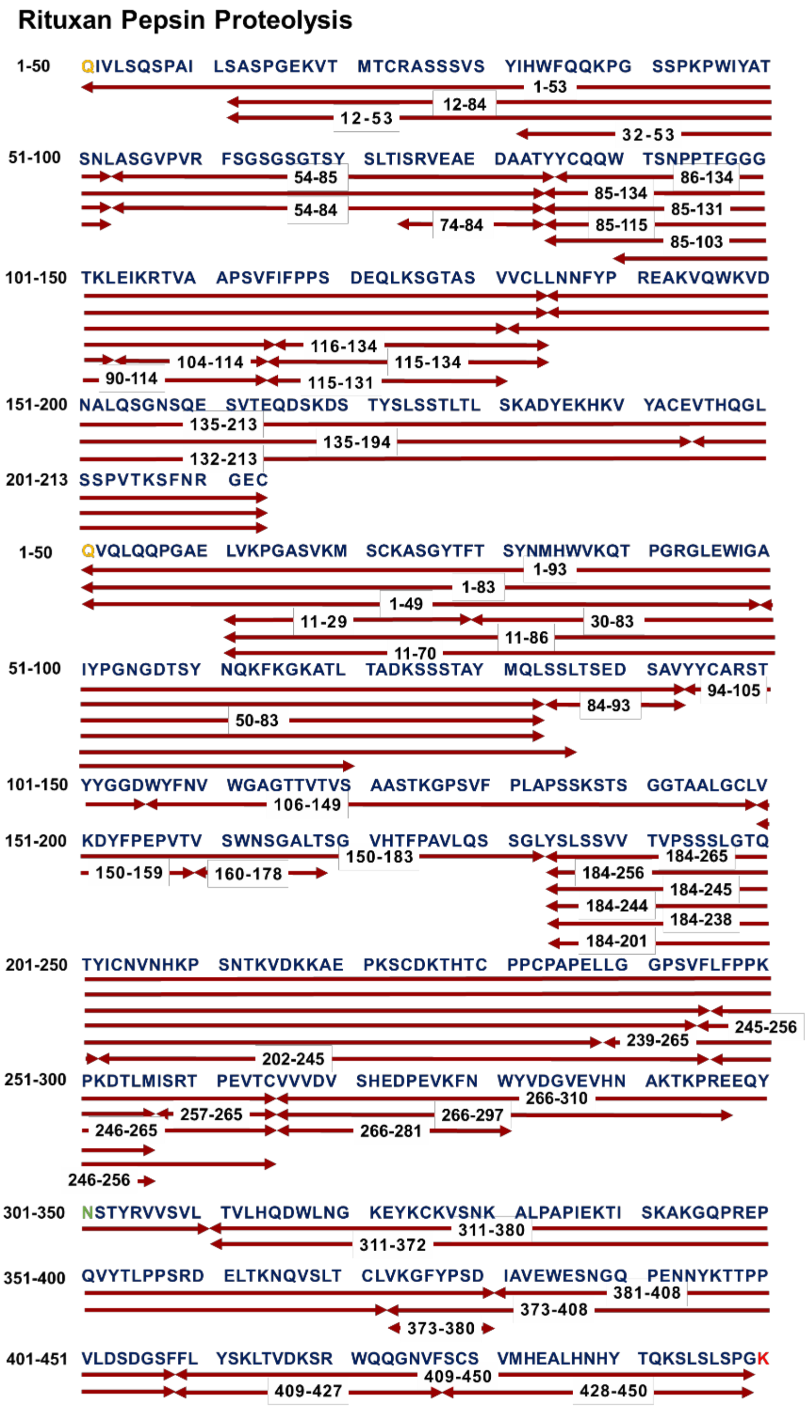
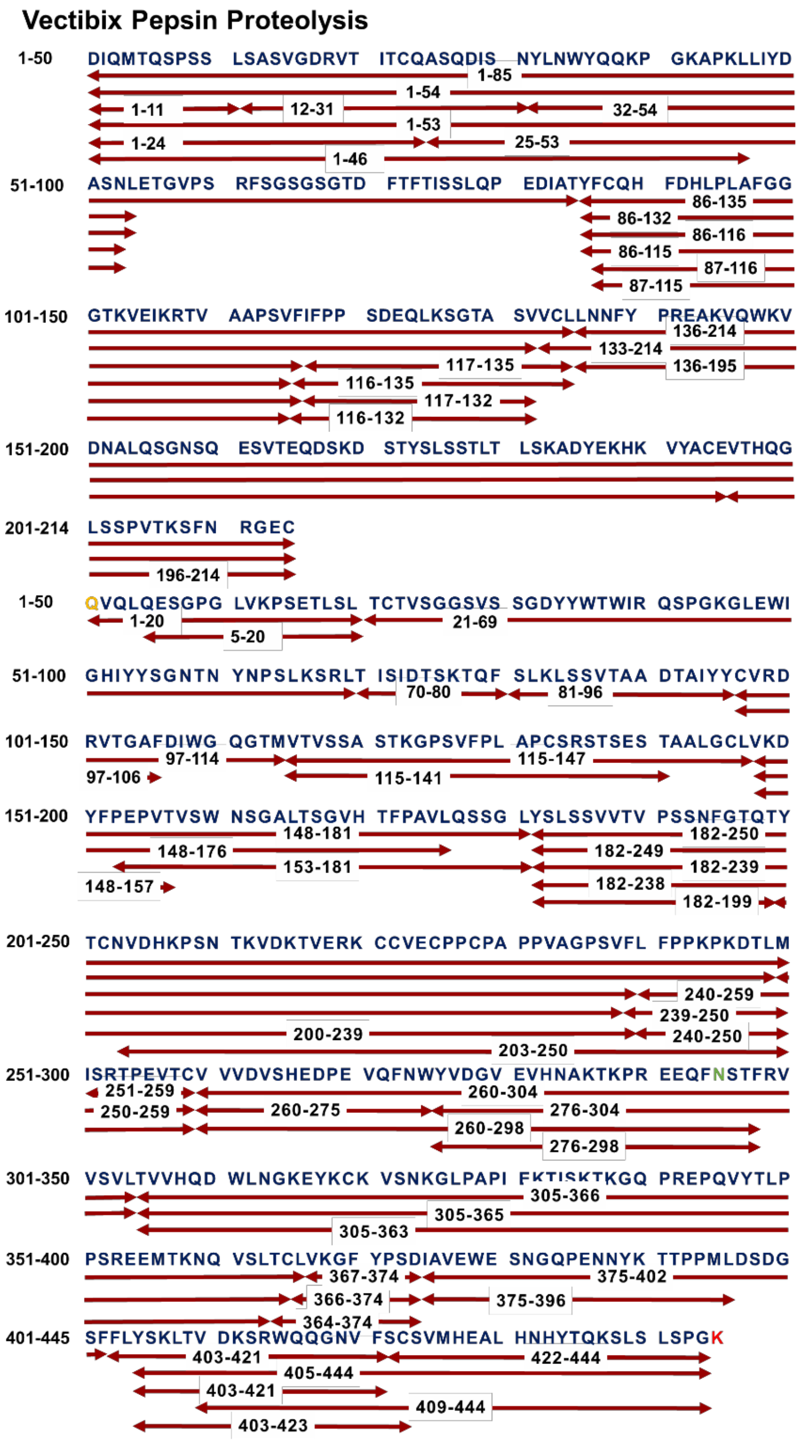

Rituxan Pepsin Proteolysis

Figure S-4. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane peptic digest of Rituxan. The orange "Q" indicates N-terminal pyroglutamate formation, the light green "N" denotes the glycosylation site, and the red "K" represents the C-terminal lysine clipping.



Vectibix Pepsin Proteolysis

Figure S-5. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane peptic digest of Vectibix. The orange “Q” indicates N-terminal pyroglutamate formation, the light green “N” denotes the glycosylation site, and the red “K” represents the C-terminal lysine clipping.

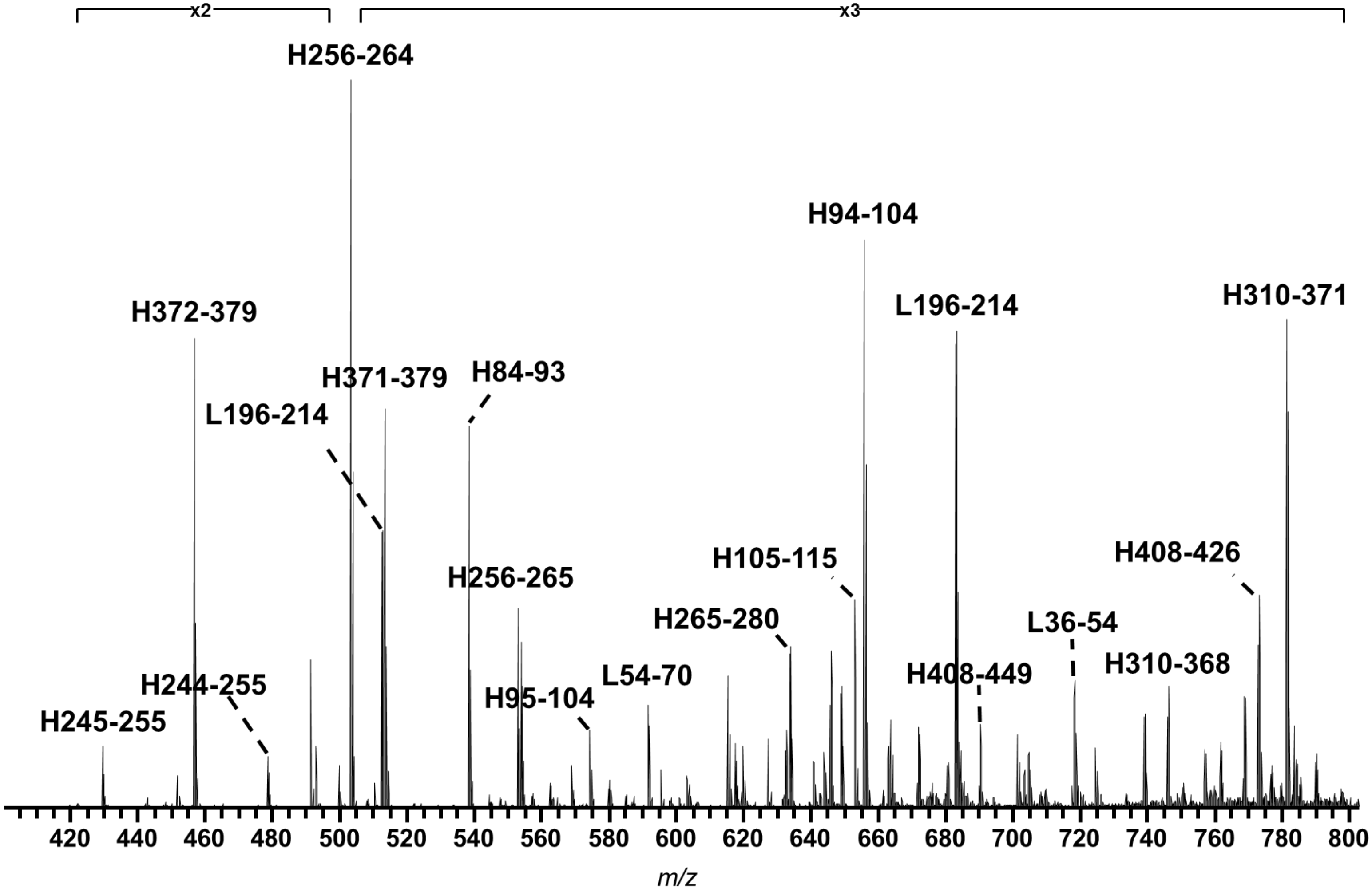


Figure S-6. Part of the mass spectrum of a peptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

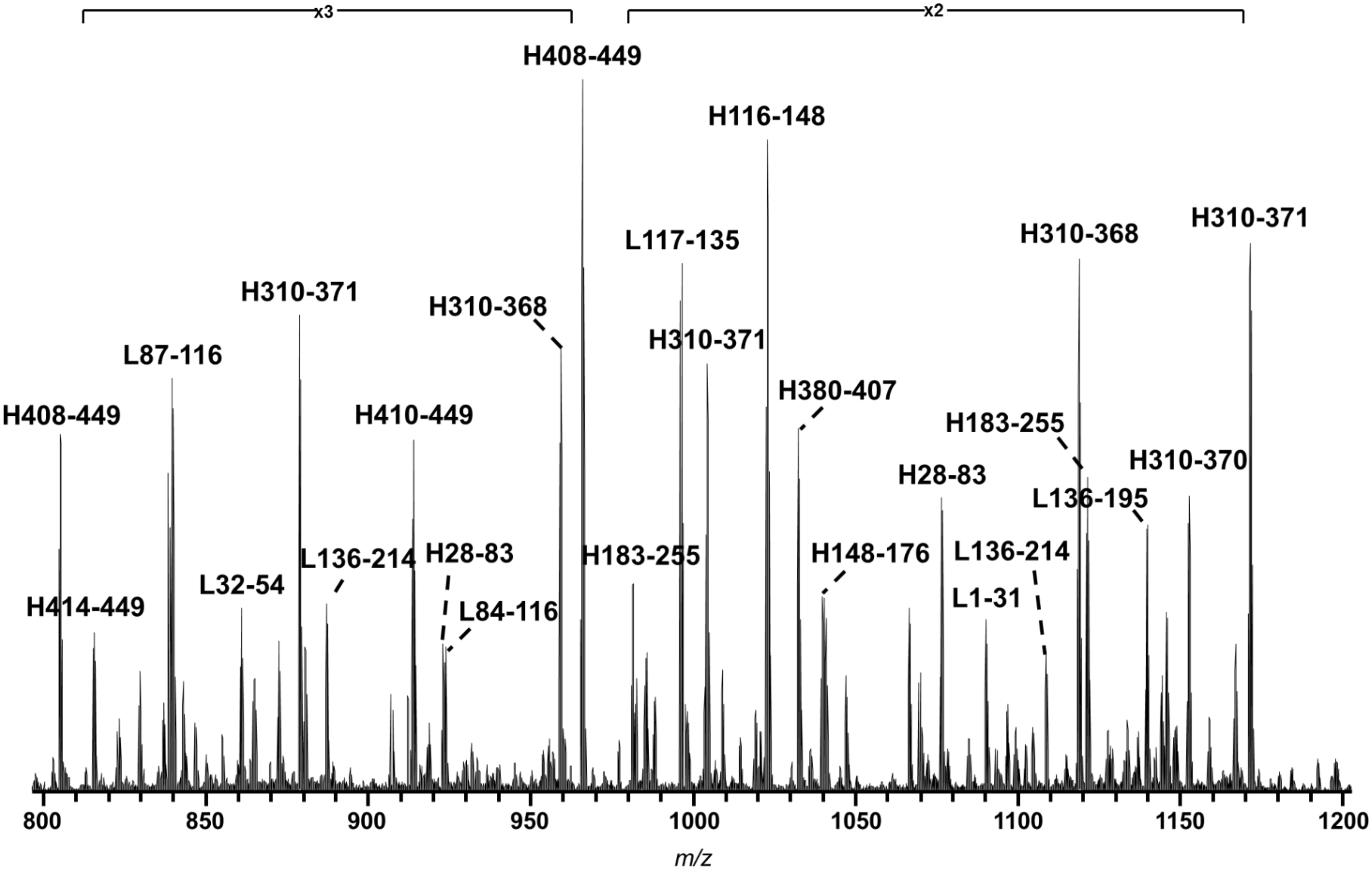


Figure S-6 (continued). Part of the mass spectrum of a peptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

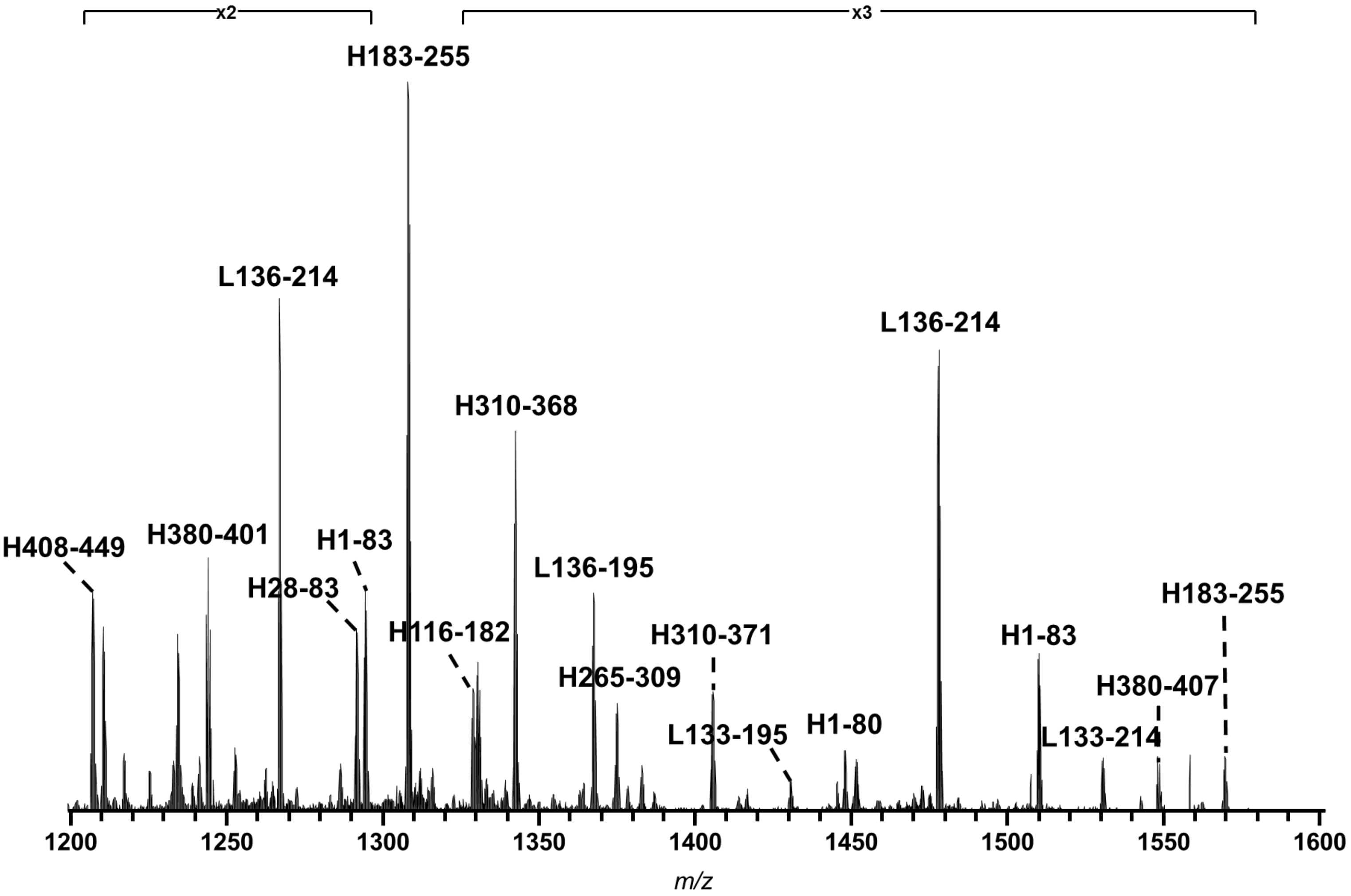


Figure S-6 (continued). Part of the mass spectrum of a peptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

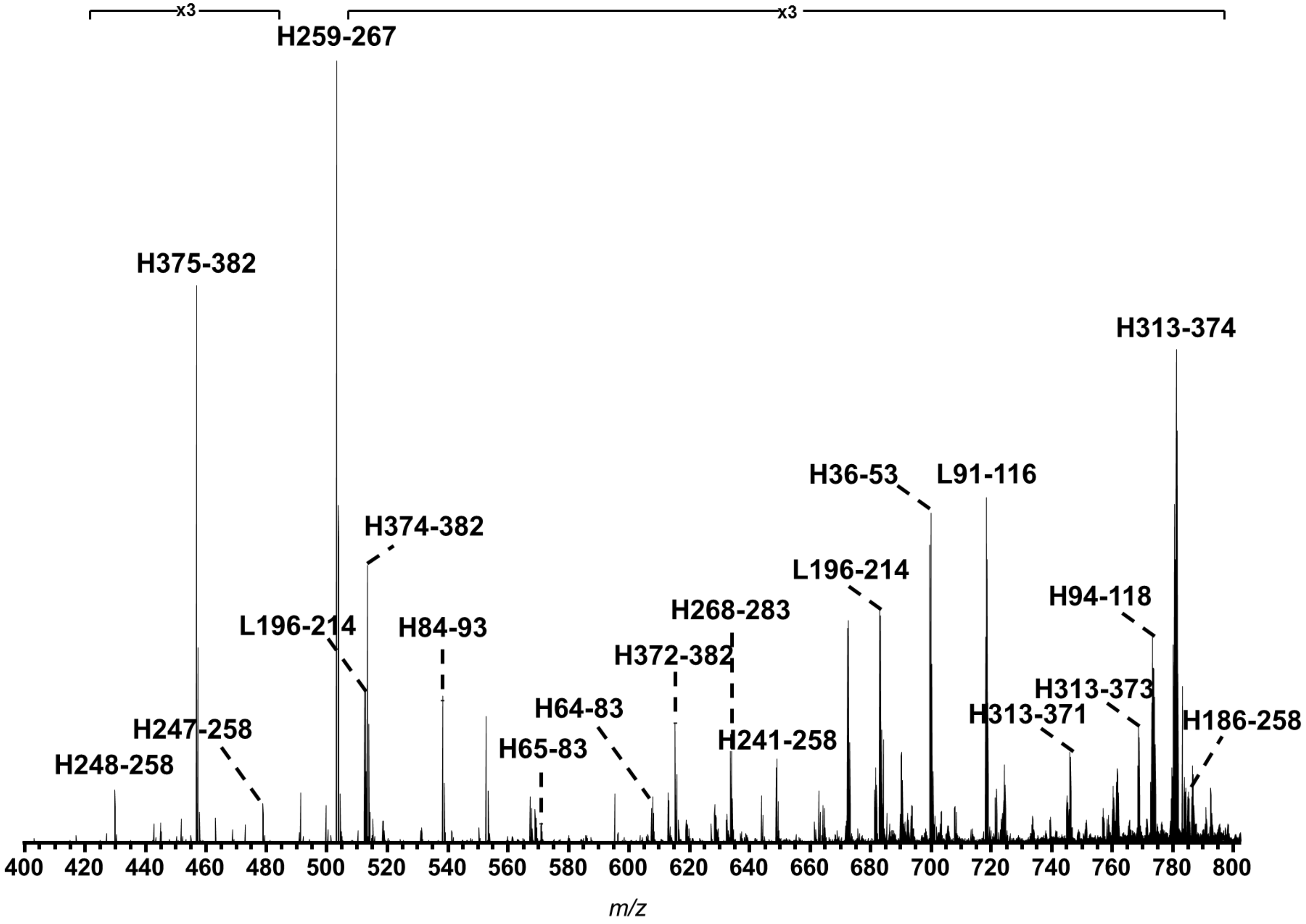


Figure S-7. Part of the mass spectrum of a peptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

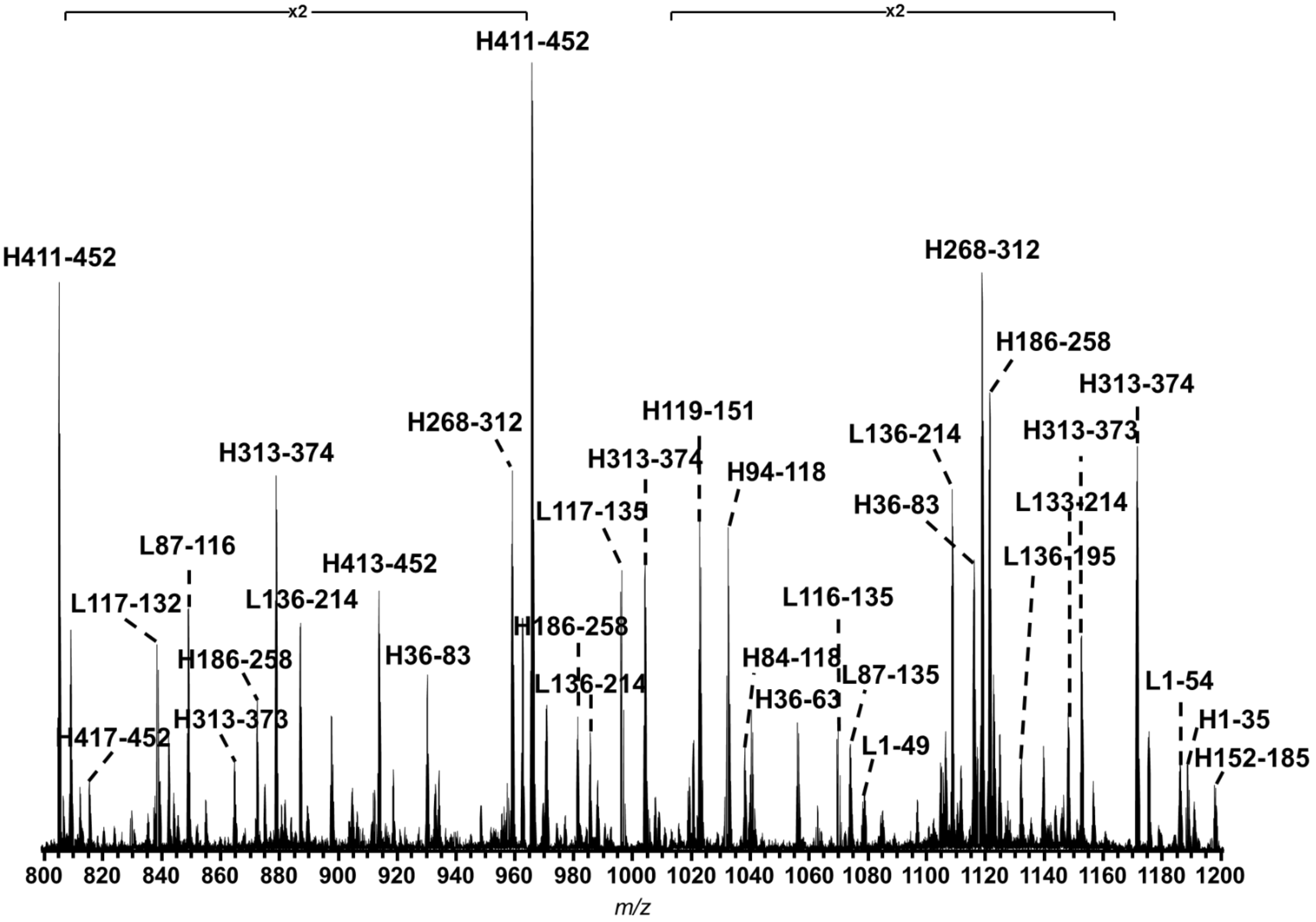


Figure S-7 (continued). Part of the mass spectrum of a peptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

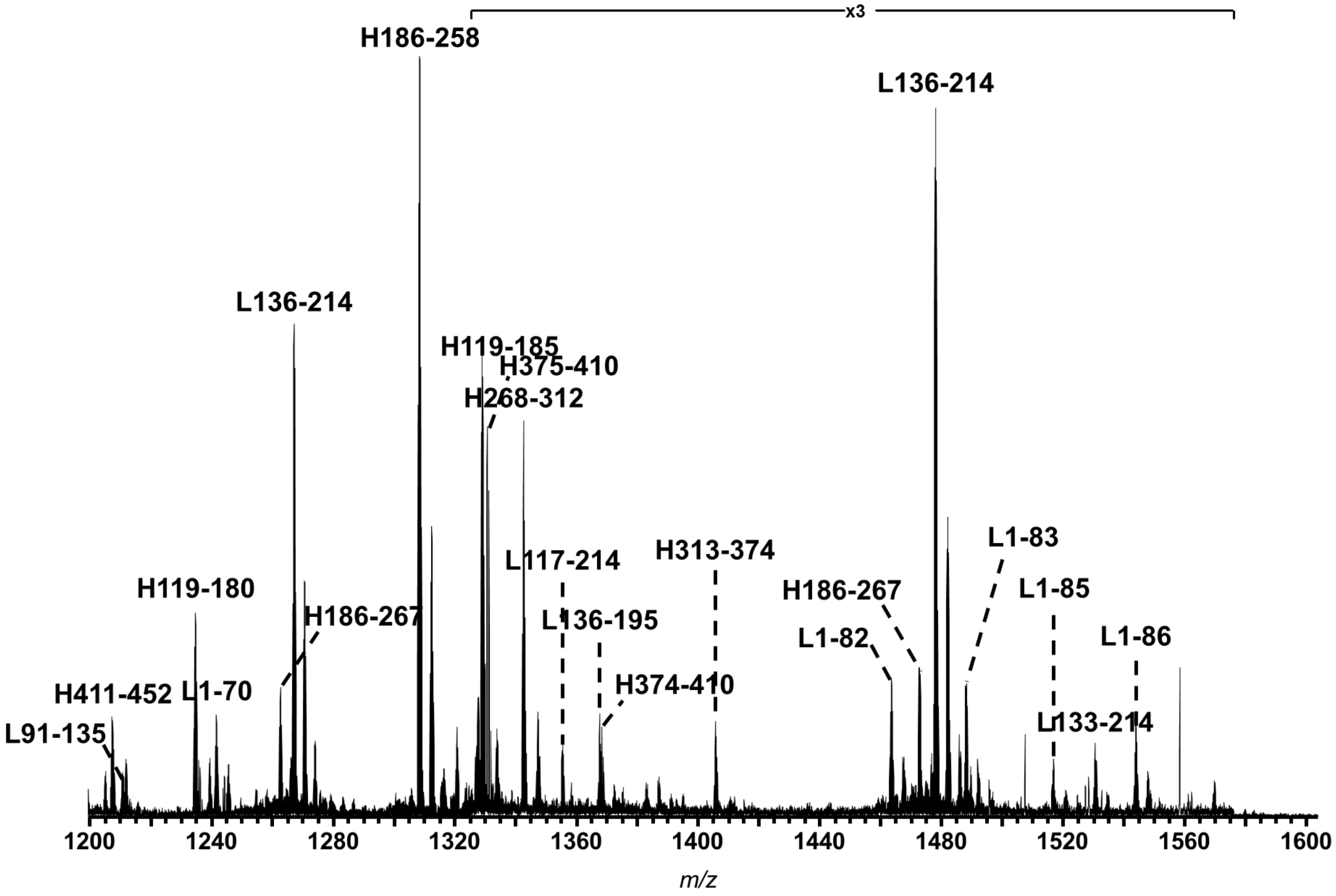


Figure S-7 (continued). Part of the mass spectrum of a peptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

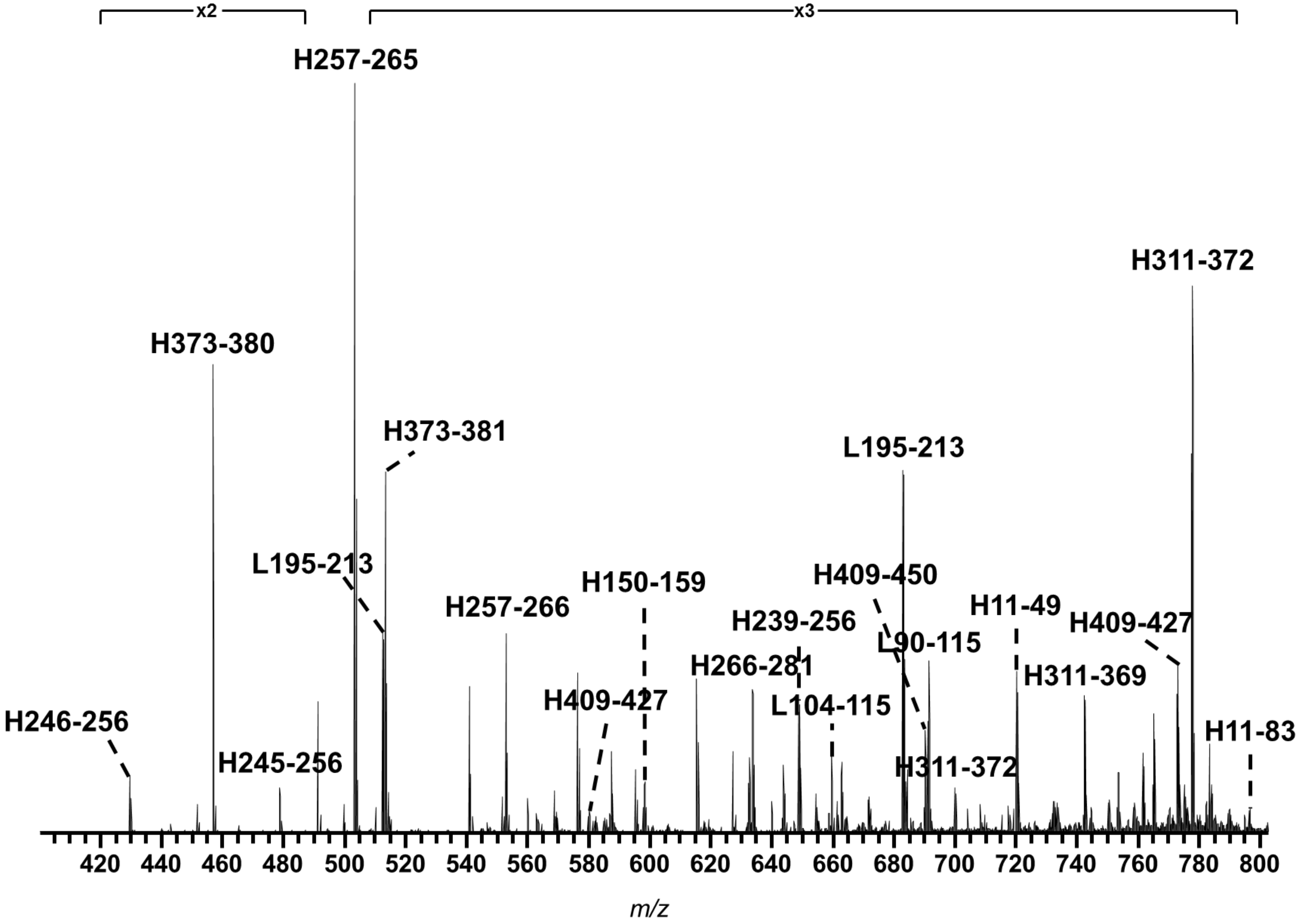


Figure S-8. Part of the mass spectrum of a peptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

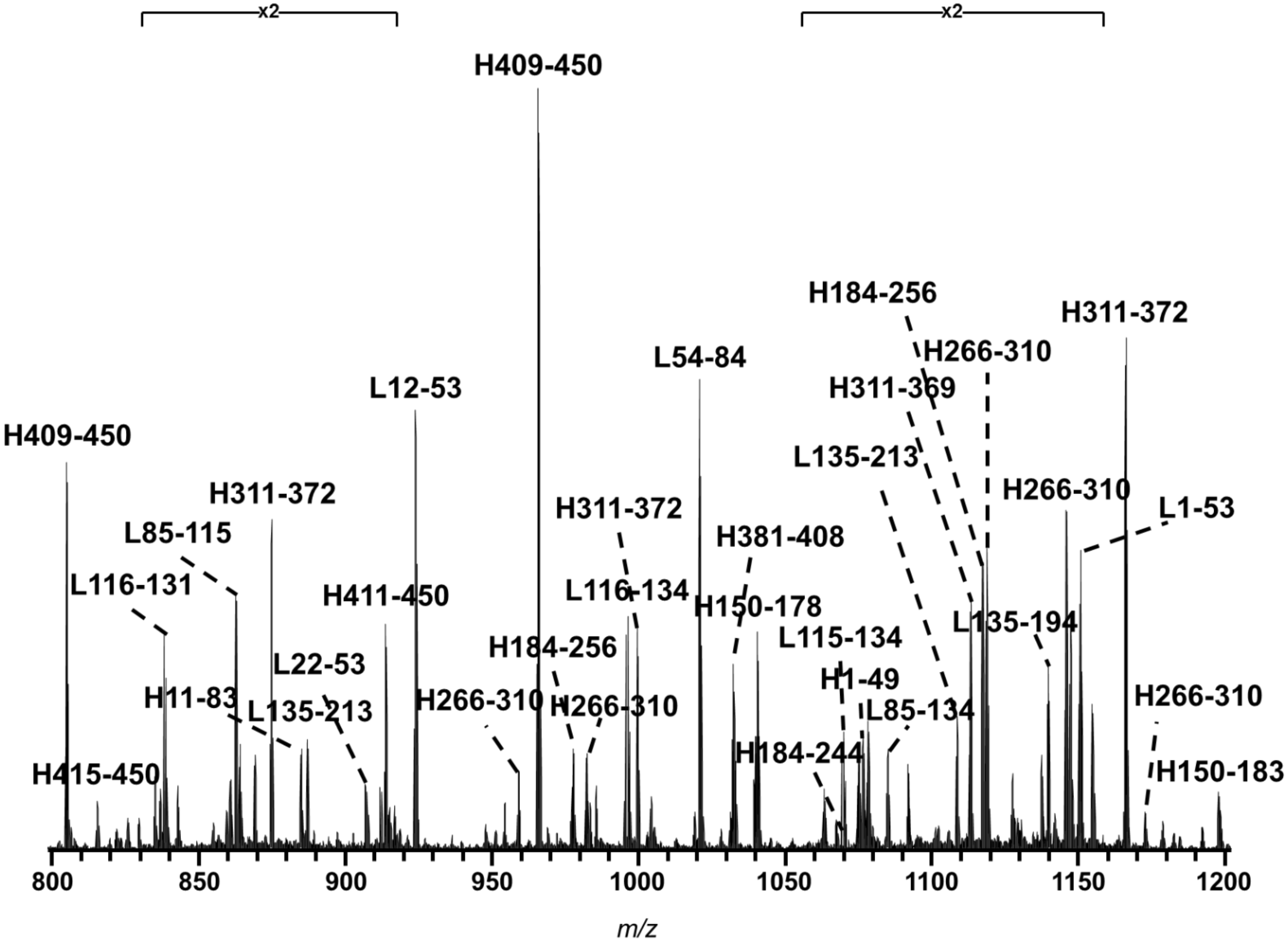


Figure S-8 (continued). Part of the mass spectrum of a peptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

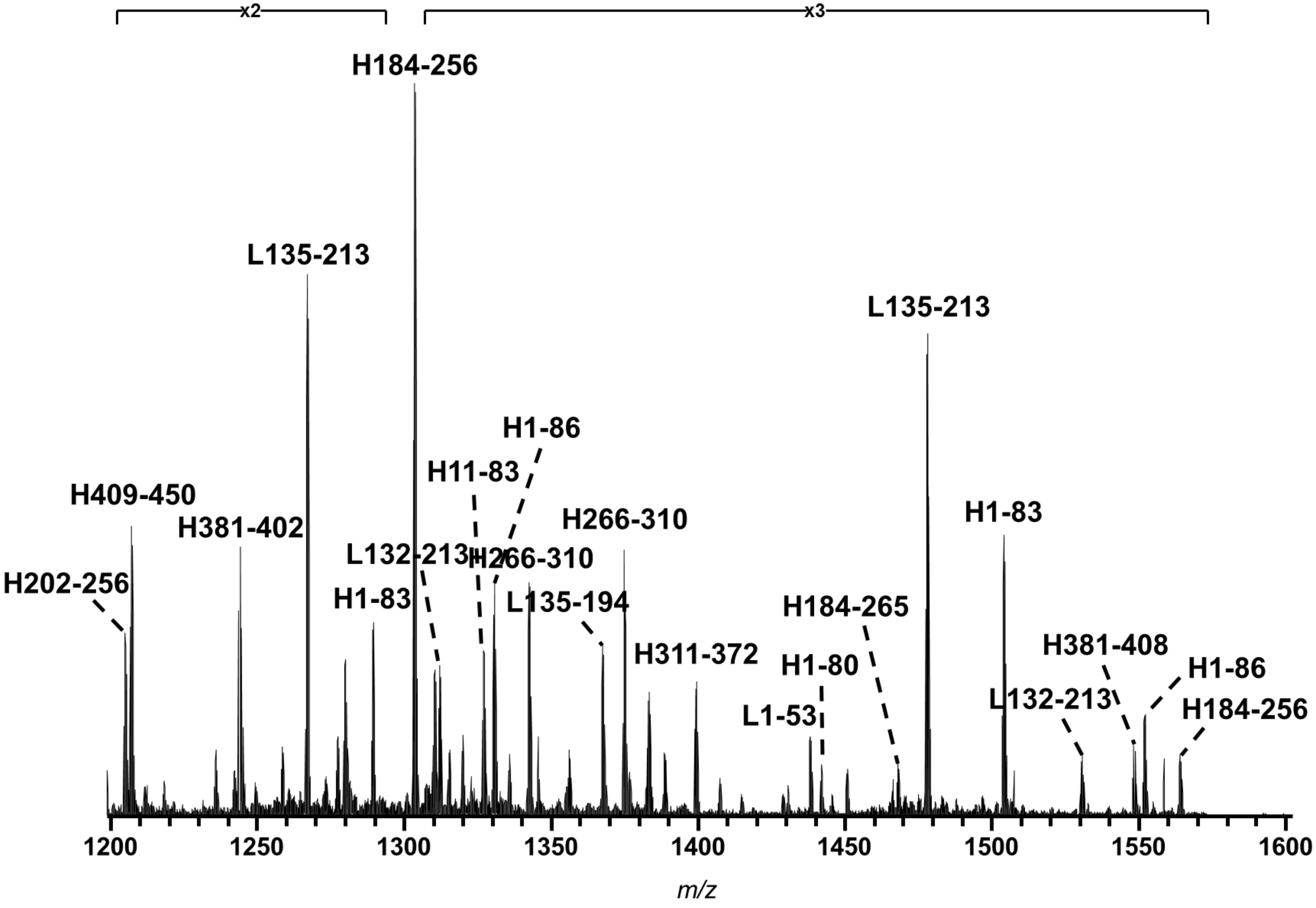


Figure S-8 (continued). Part of the mass spectrum of a peptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

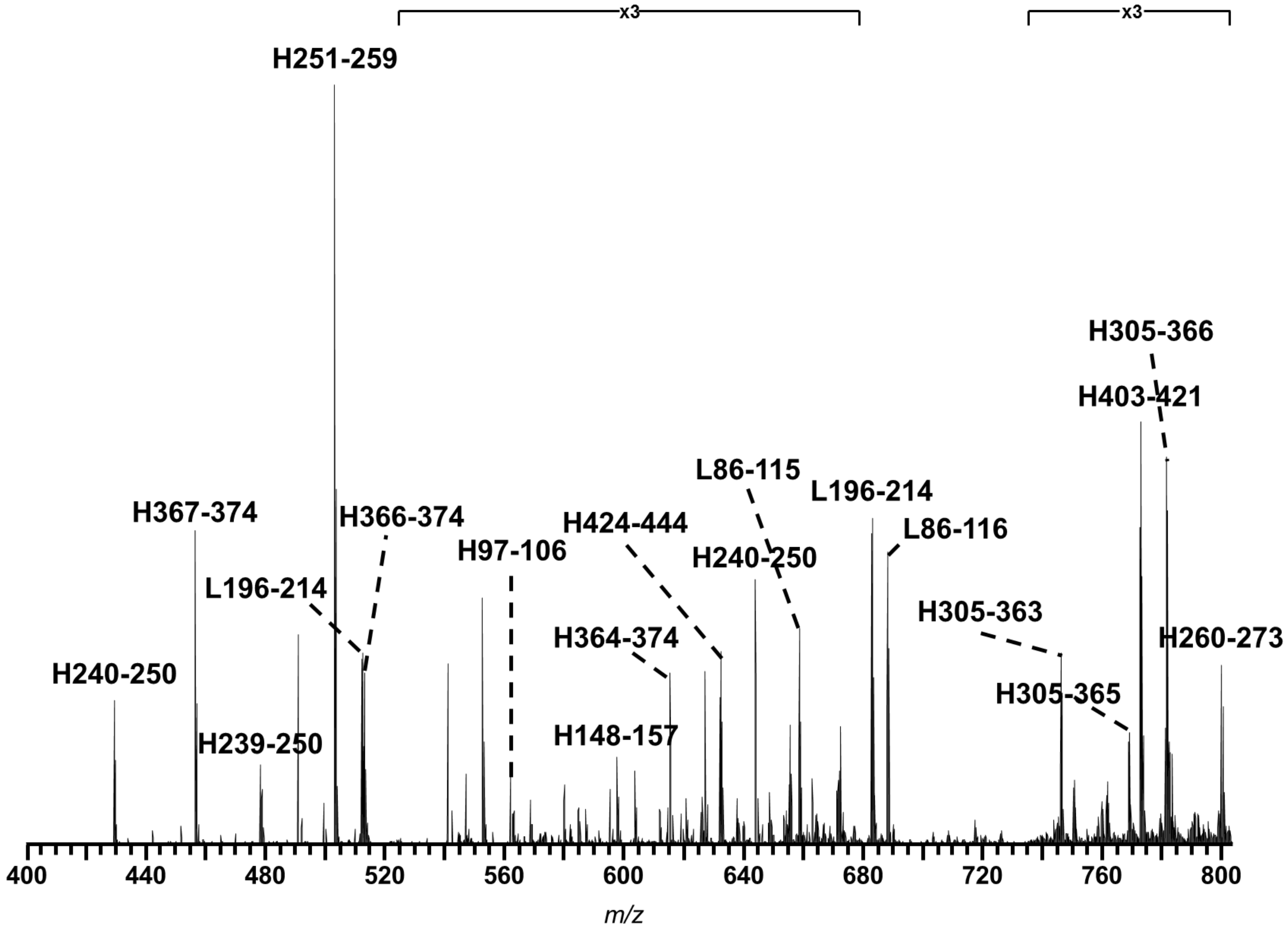


Figure S-9. Part of the mass spectrum of a peptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

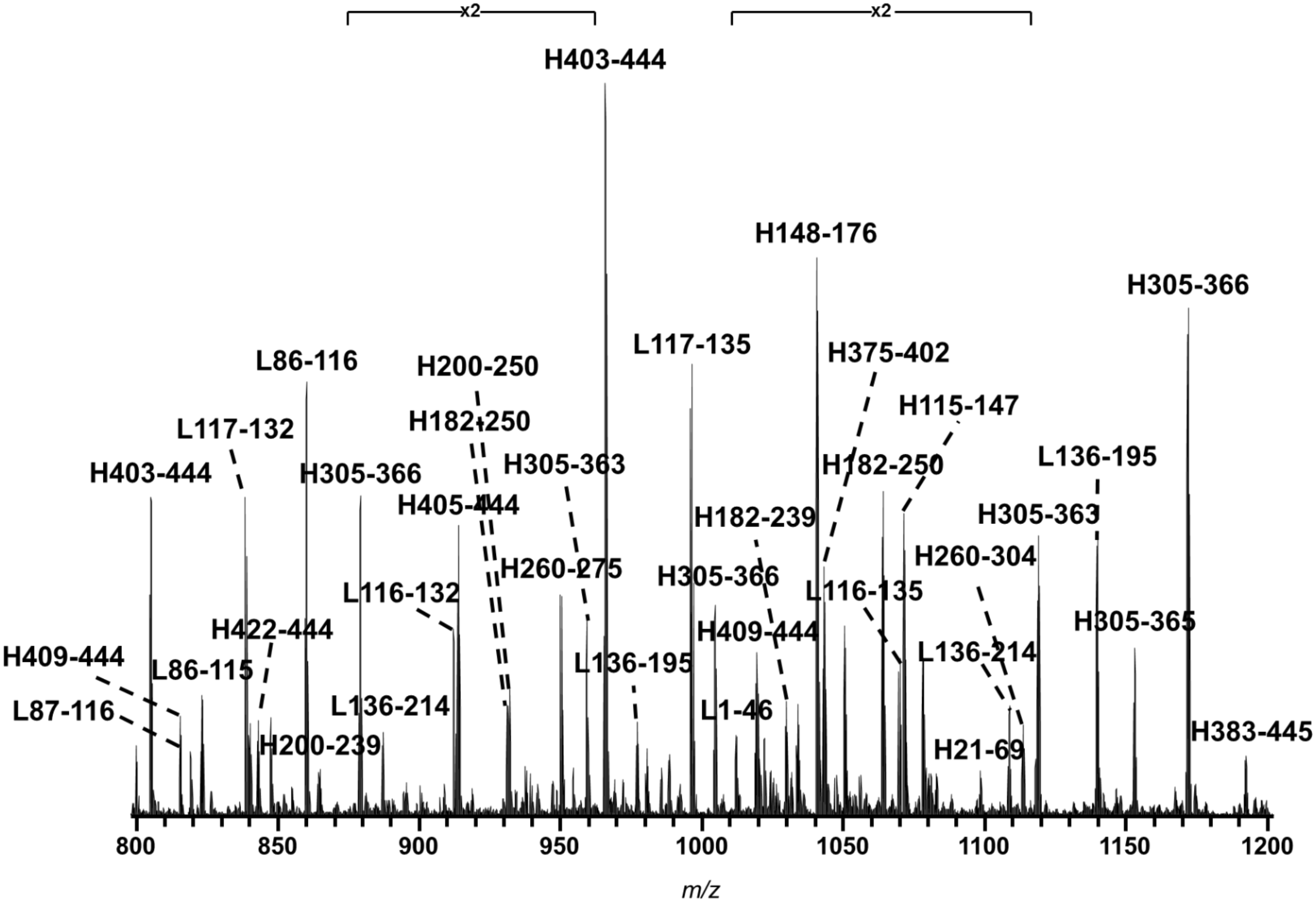


Figure S-9 (continued). Part of the mass spectrum of a peptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

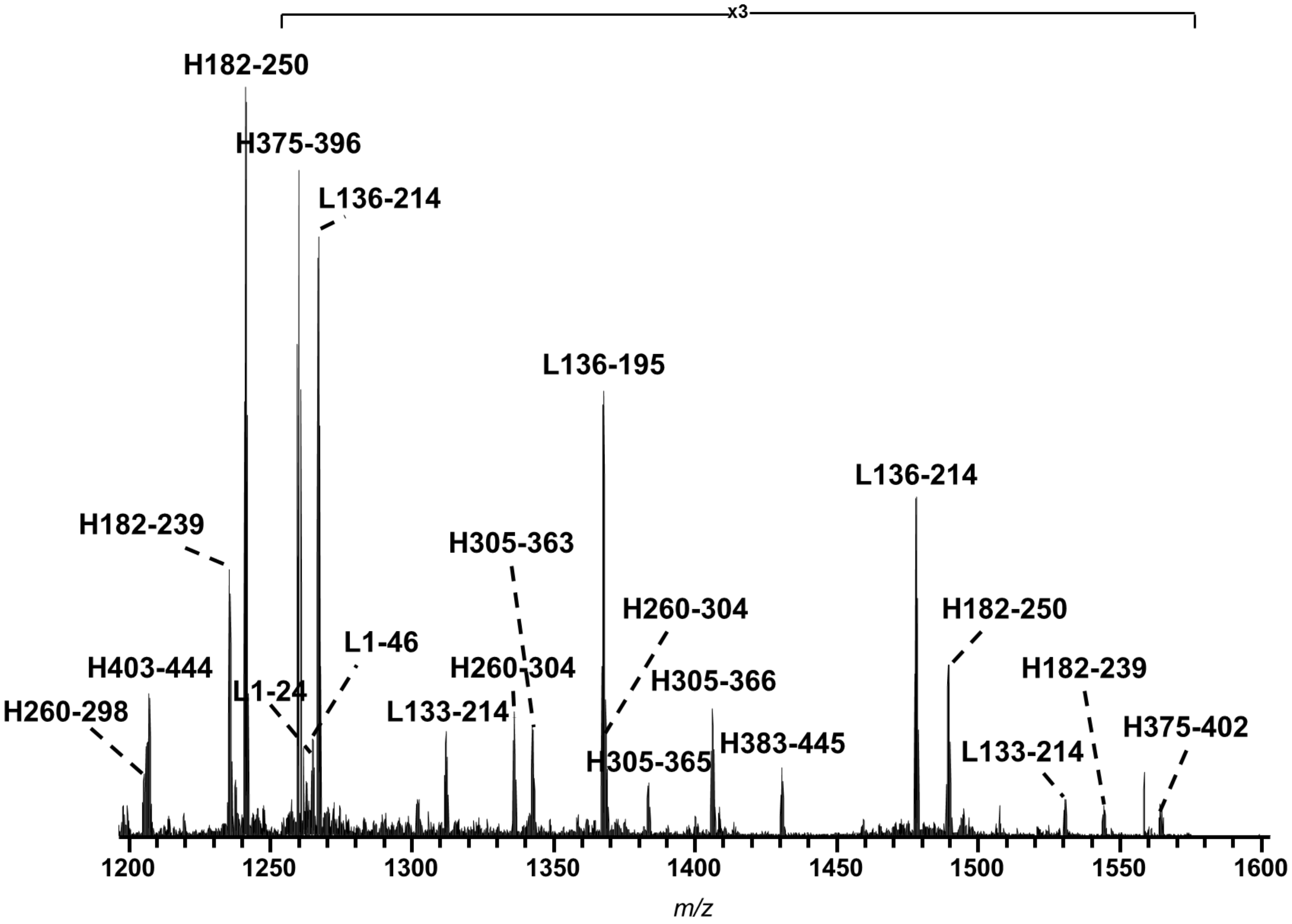


Figure S-9 (continued). Part of the mass spectrum of a peptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

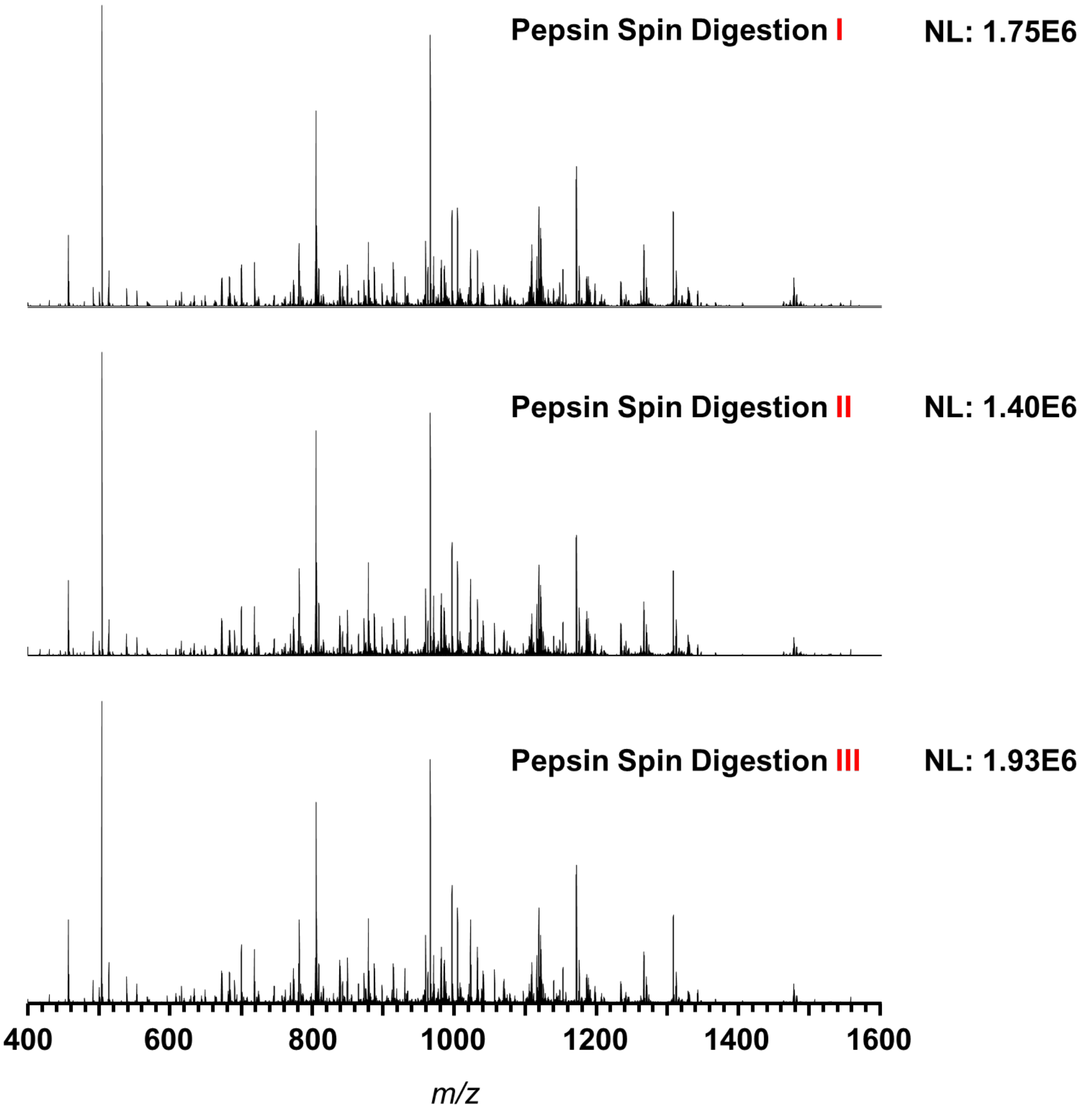


Figure S-10. Mass spectra of 3 different spin-membrane digests of Avastin. Each digestion employed a different peptic spin membrane. For the twenty highest signals in the mass spectra, standard deviations of the signals (relative to the base peak) from triplicate digestion are <6%.

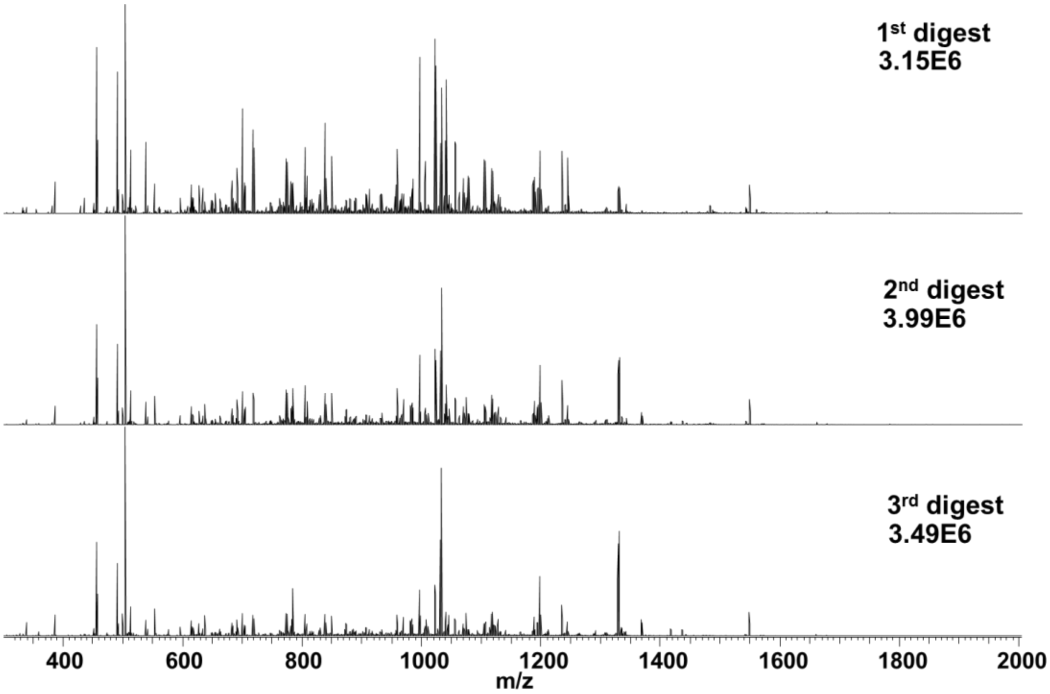


Figure S-11. Infusion-MS spectra from three consecutive Av peptic spin digests obtained using the same spin membrane.

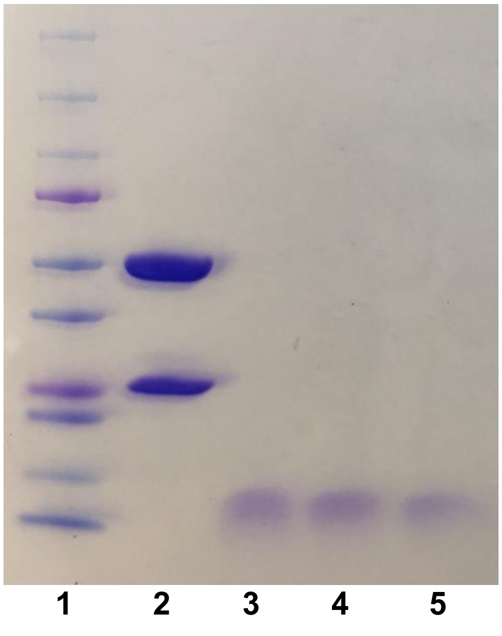


Figure S-12. Gel electrophoresis (SDS-PAGE) analysis of the reusability of a pepsin spin membrane. Lane 1: protein standards; Lane 2: 5 µg of Avastin; Lanes 3, 4 and 5: 5 µg of Avastin peptic spin digests (spun at 500 *g*) obtained sequentially using the same membrane.

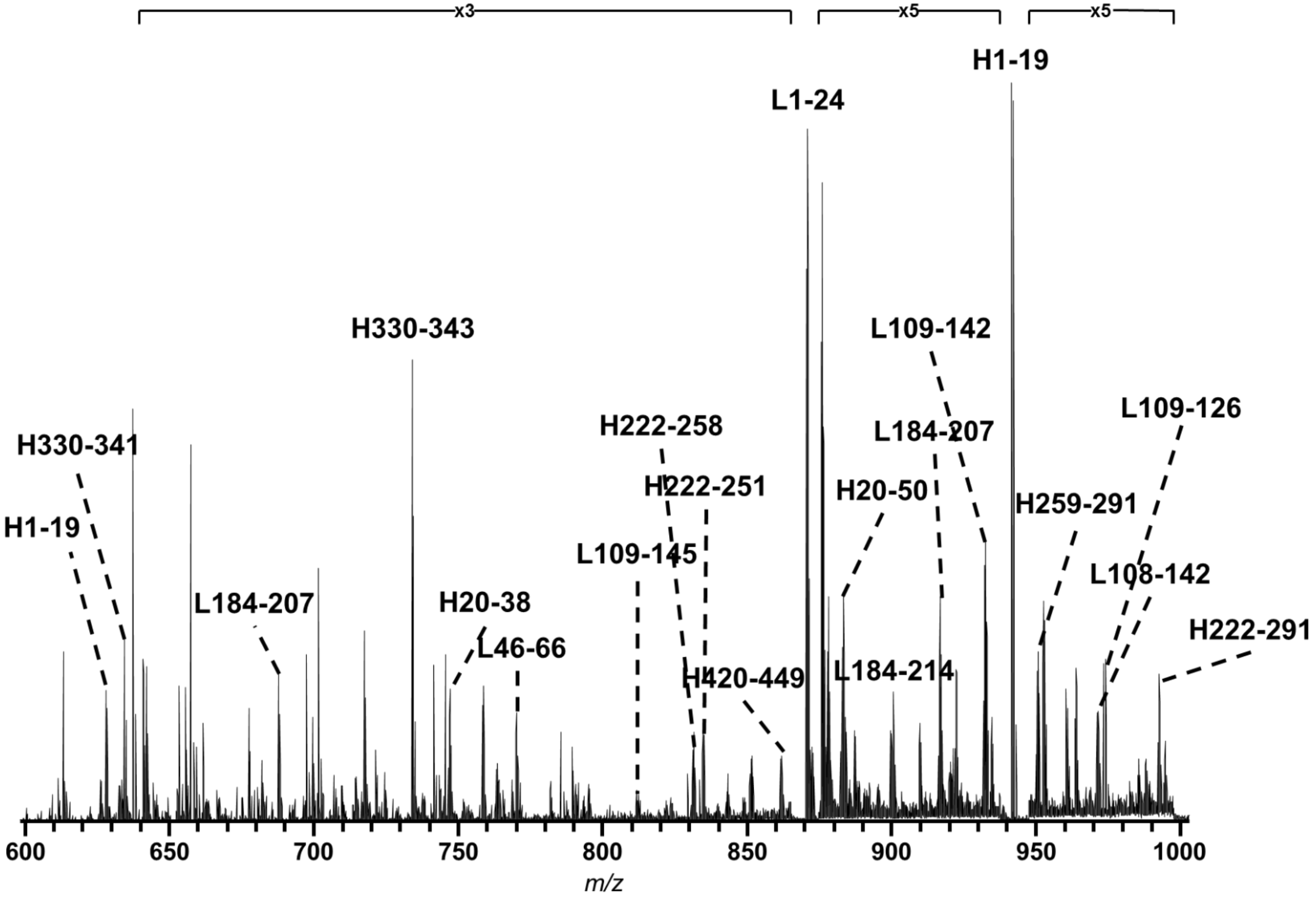


Figure S-13. Part of the mass spectrum of a tryptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

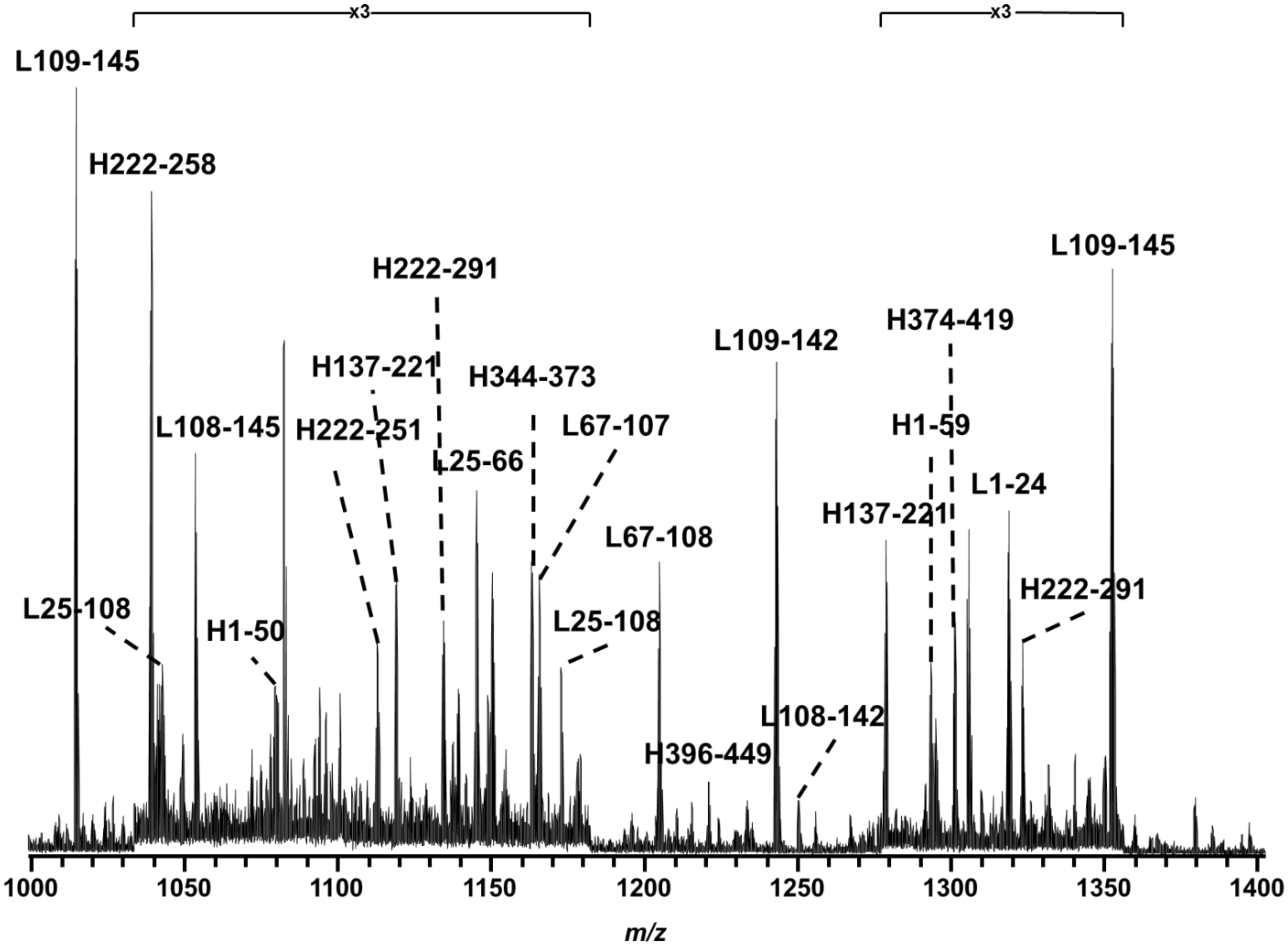


Figure S-13 (continued). Part of the mass spectrum of a tryptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

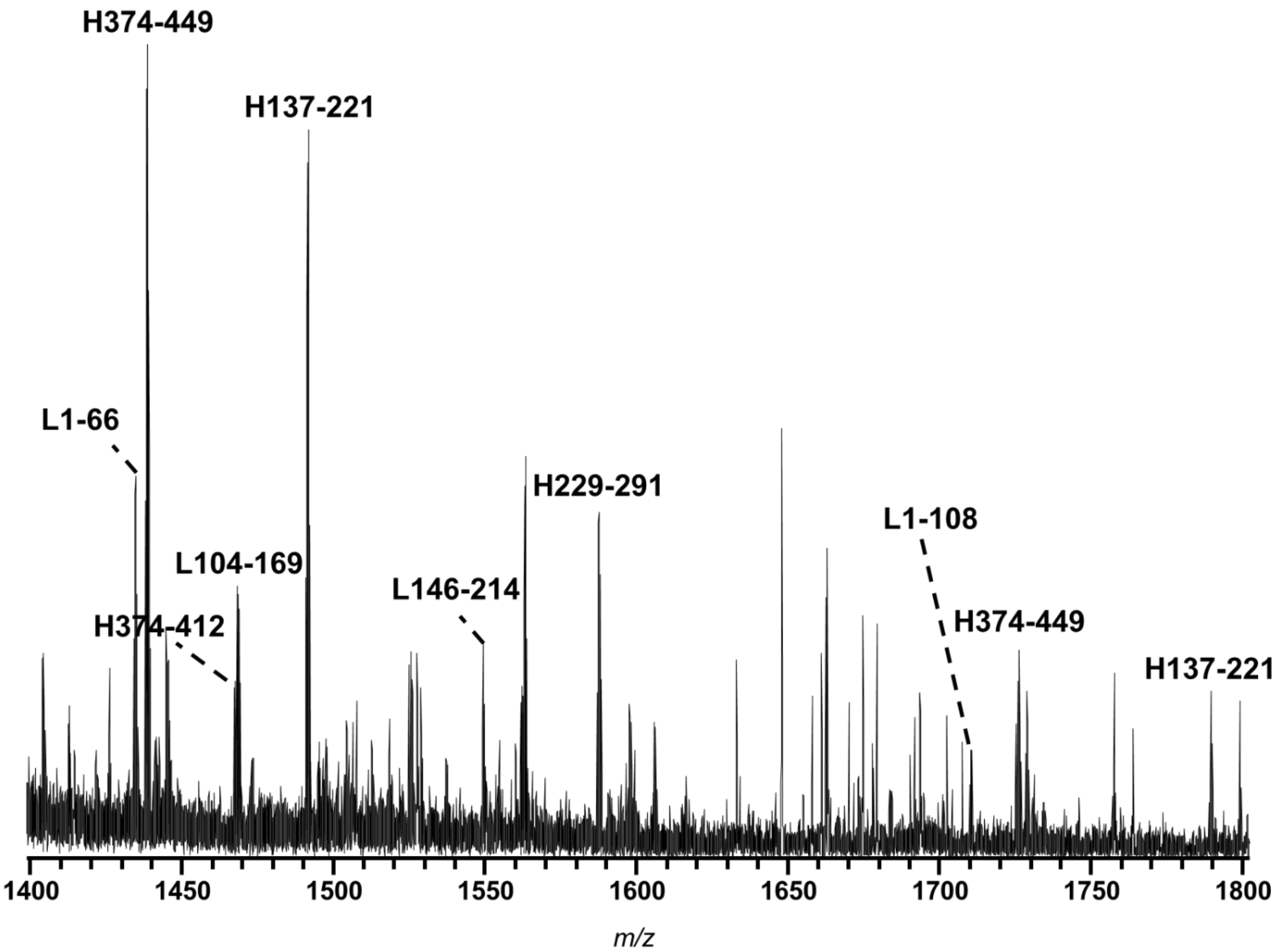


Figure S-13 (continued). Part of the mass spectrum of a tryptic spin digest of Herceptin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

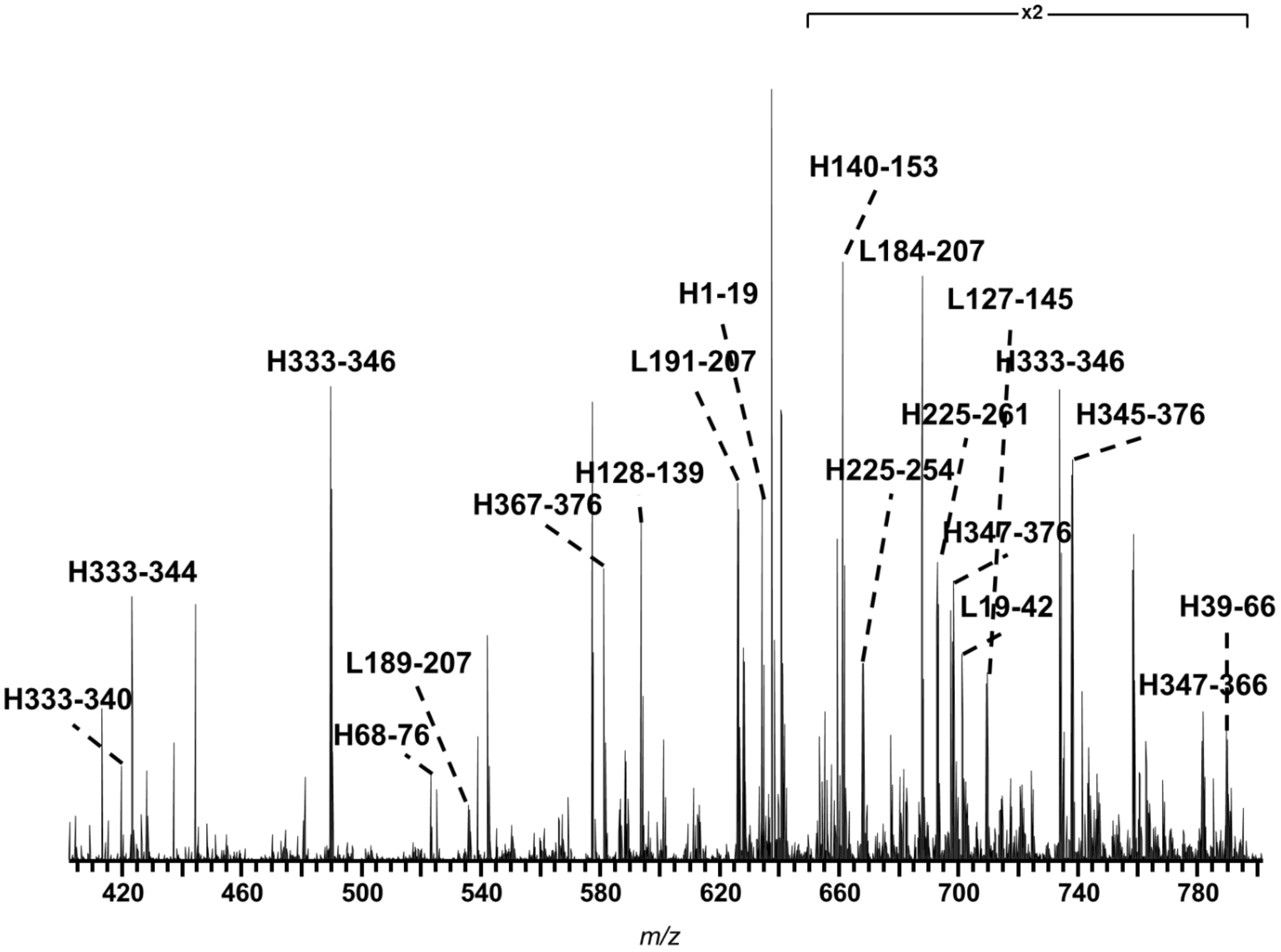


Figure S-14. Part of the mass spectrum of a tryptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

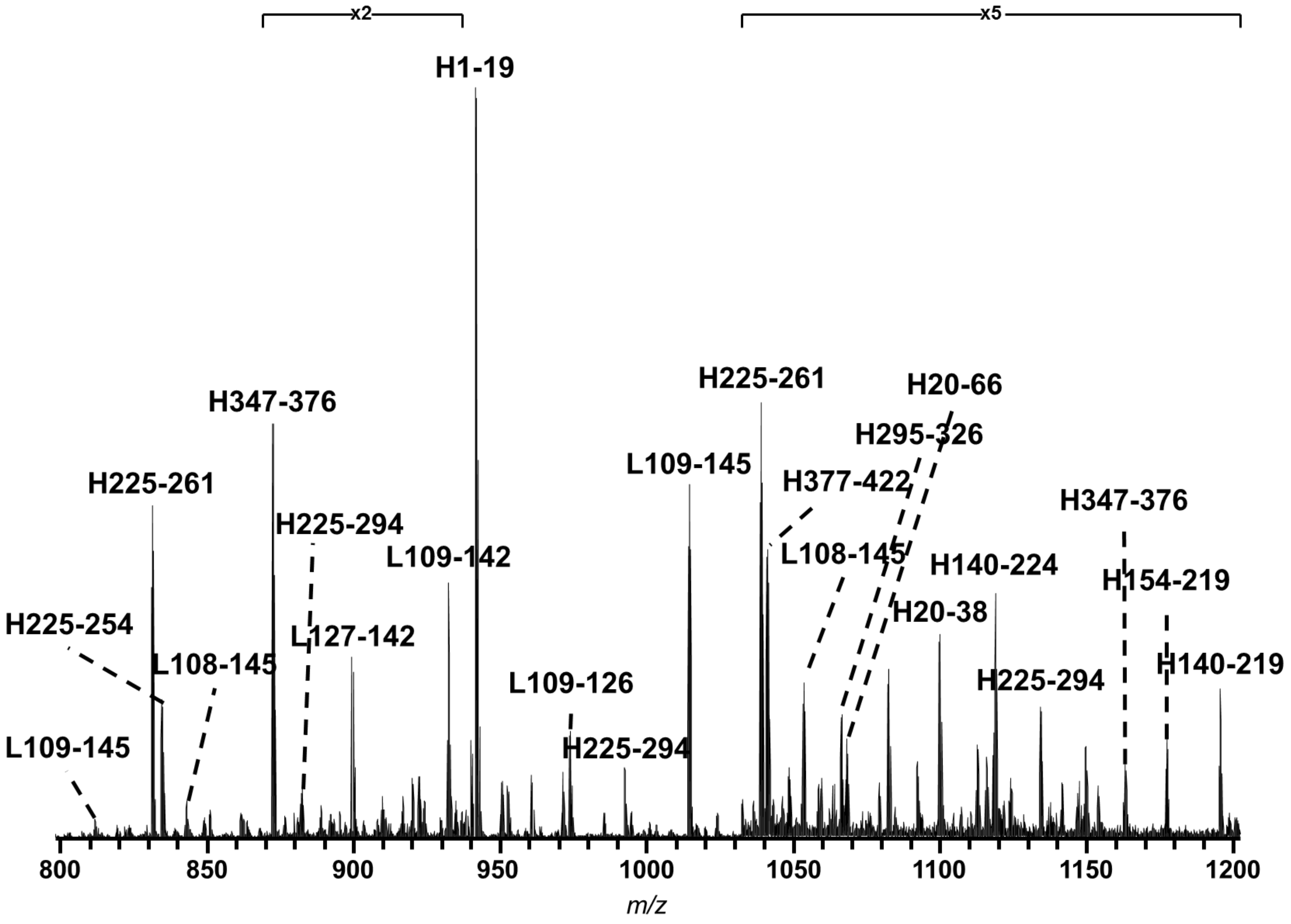


Figure S-14 (continued). Part of the mass spectrum of a tryptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

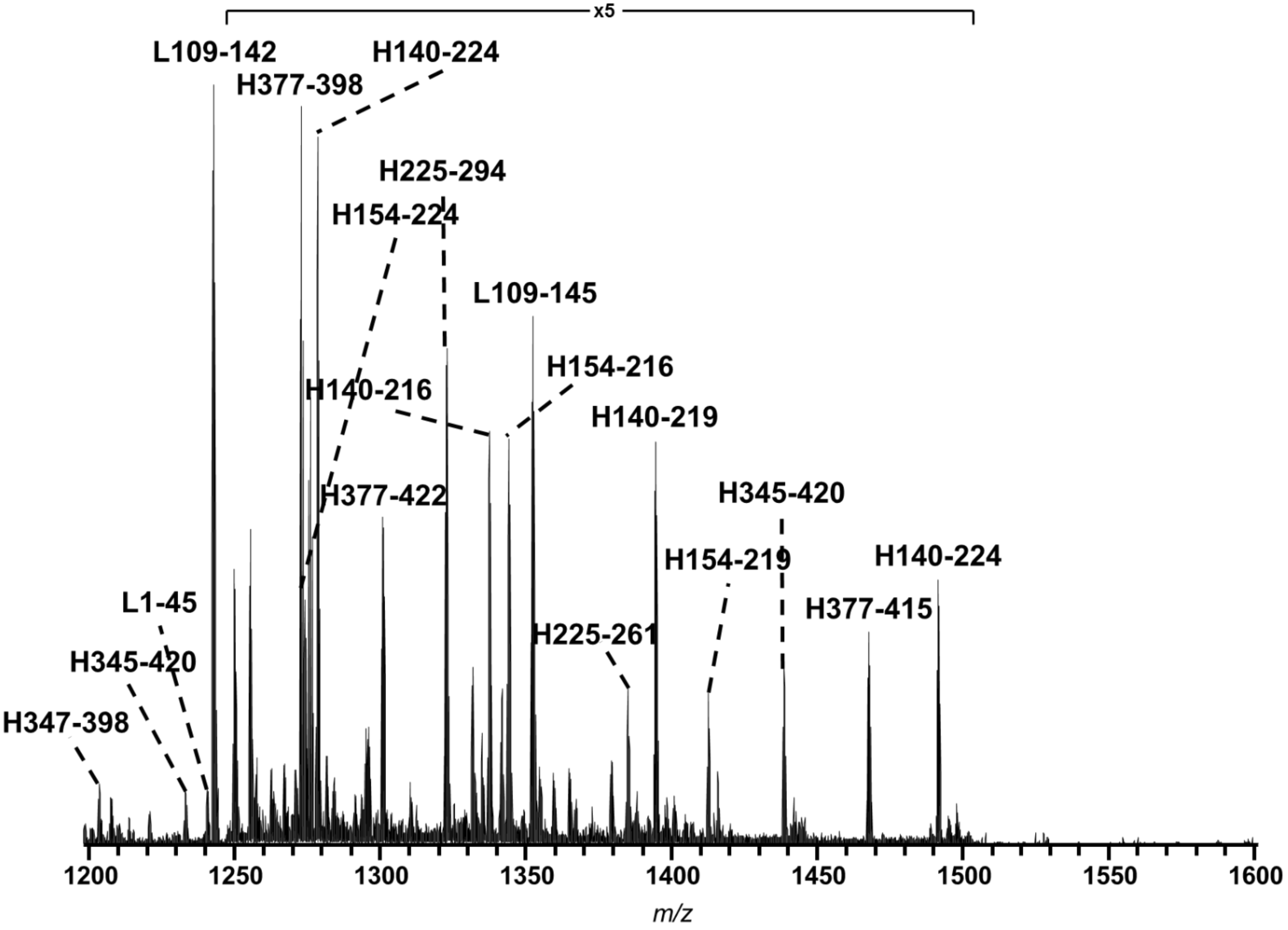


Figure S-14 (continued). Part of the mass spectrum of a tryptic spin digest of Avastin. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

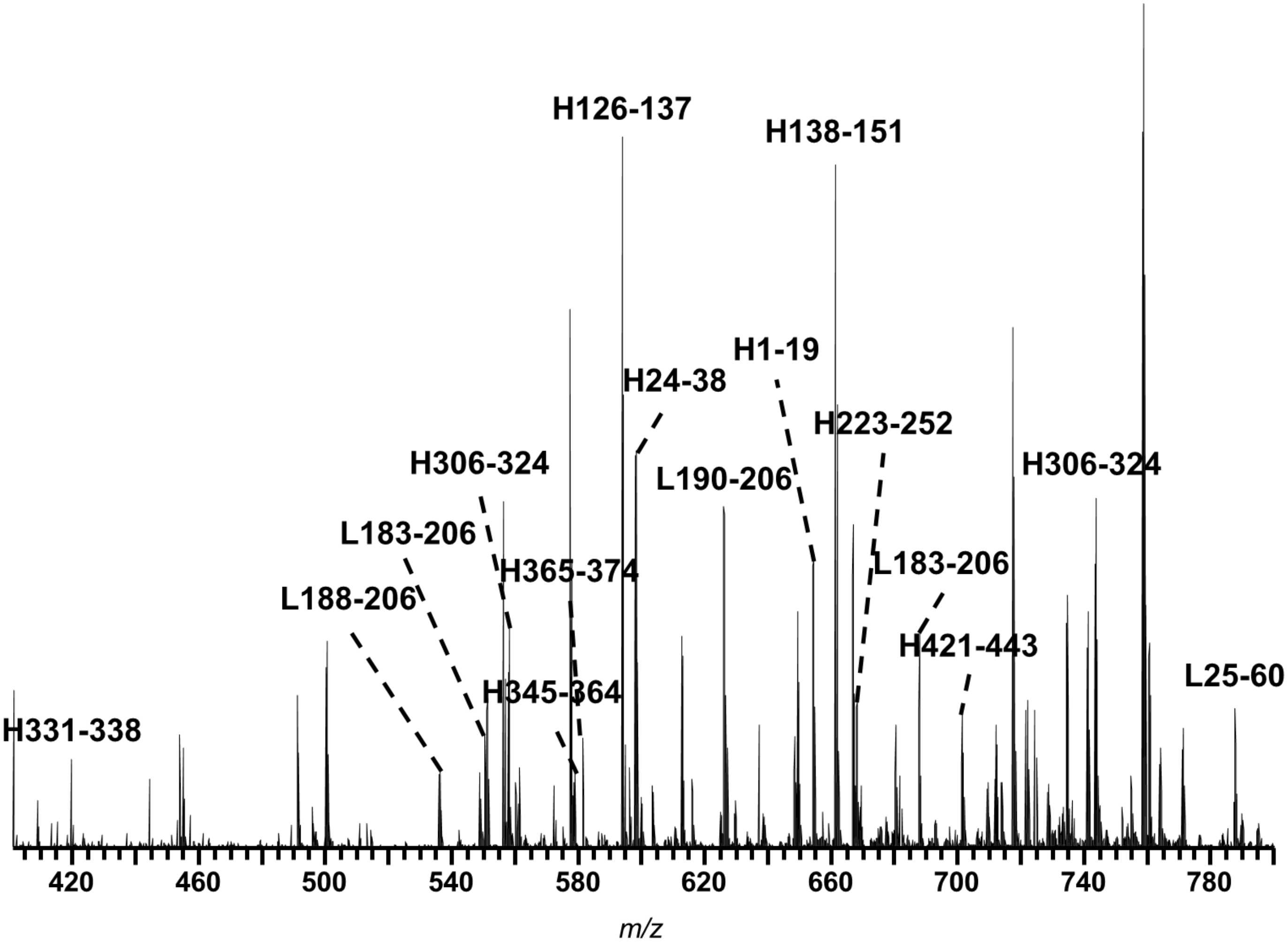


Figure S-15. Part of the mass spectrum of a tryptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

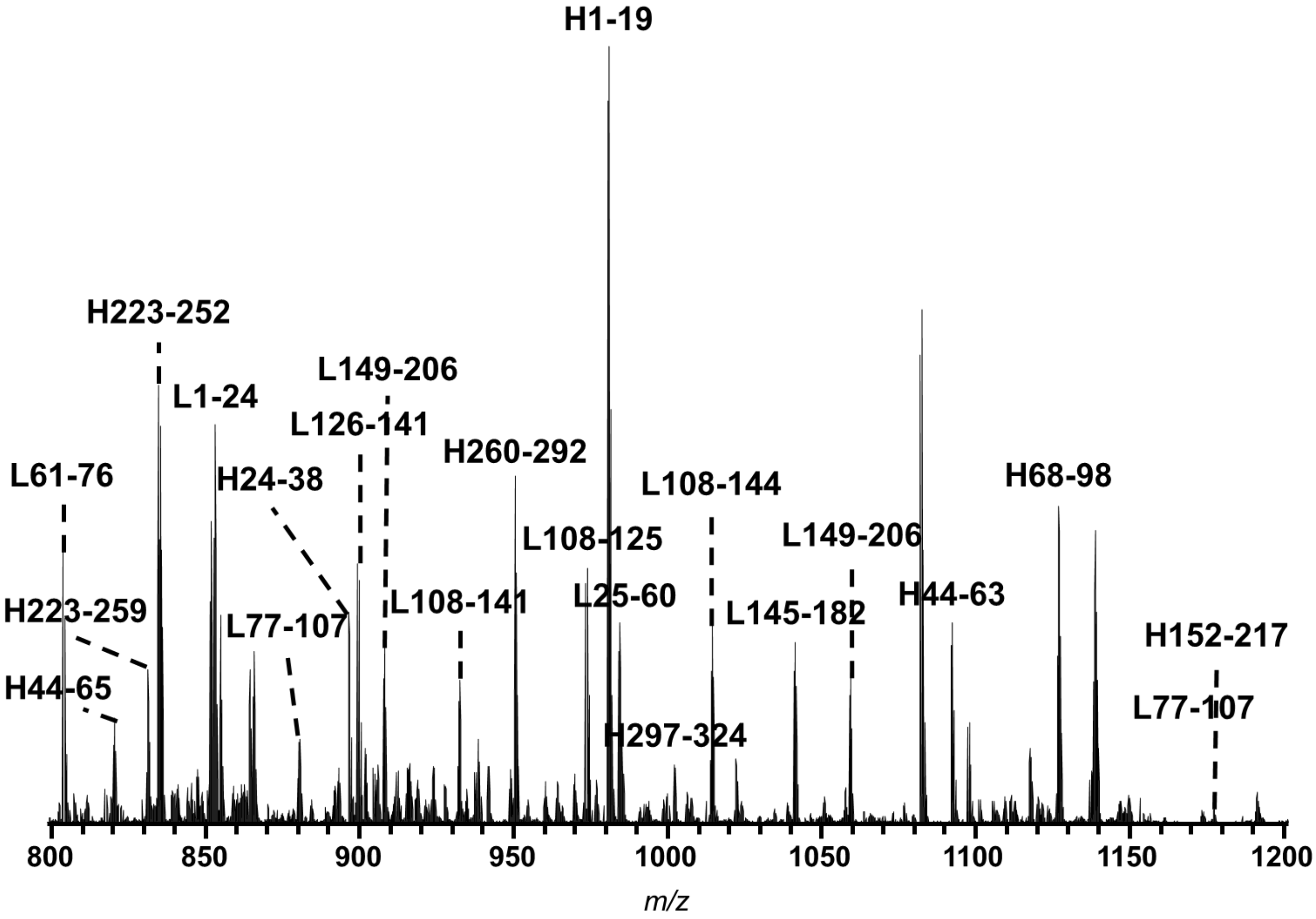


Figure S-15 (continued). Part of the mass spectrum of a tryptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

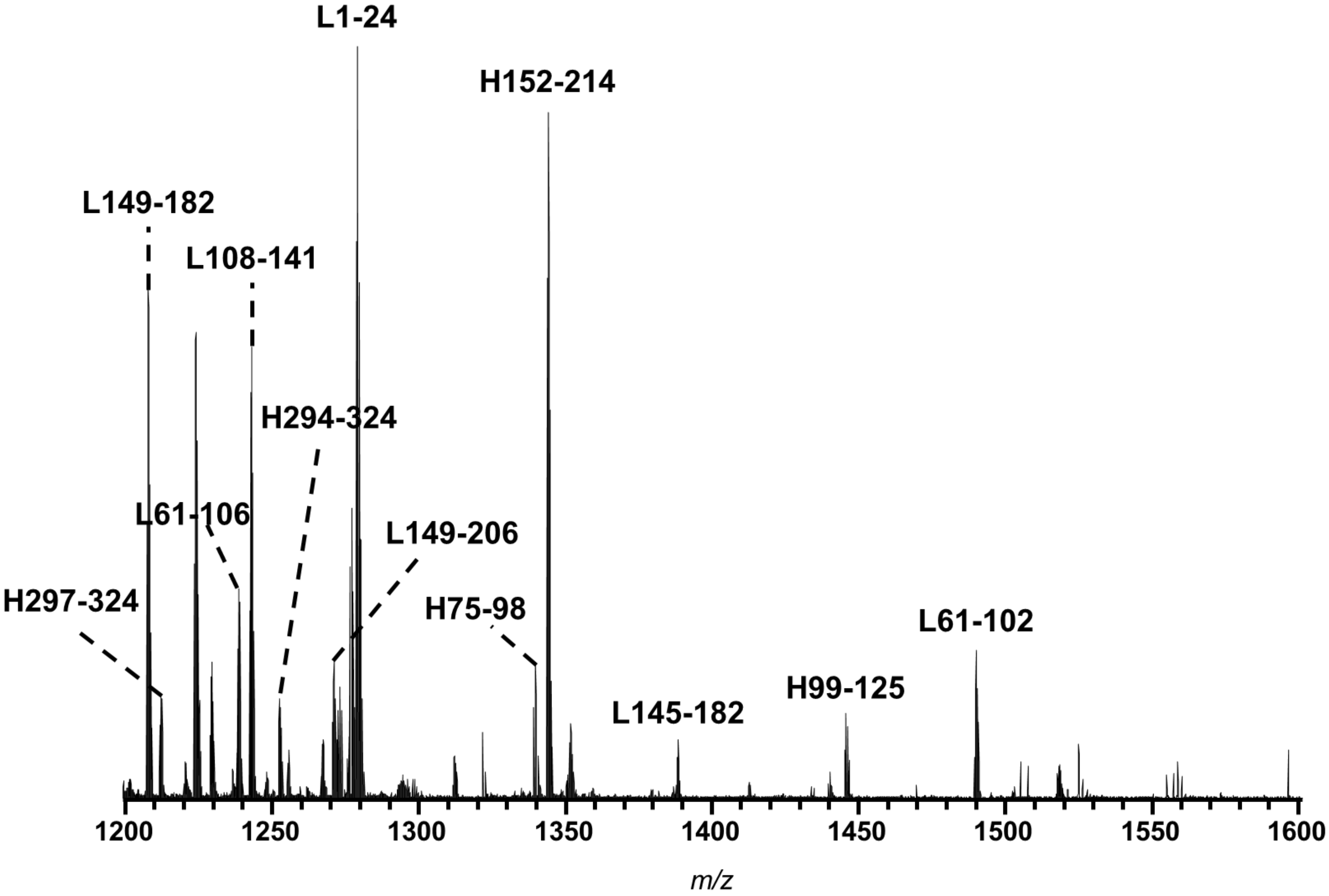


Figure S-15 (continued). Part of the mass spectrum of a tryptic spin digest of Rituxan. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

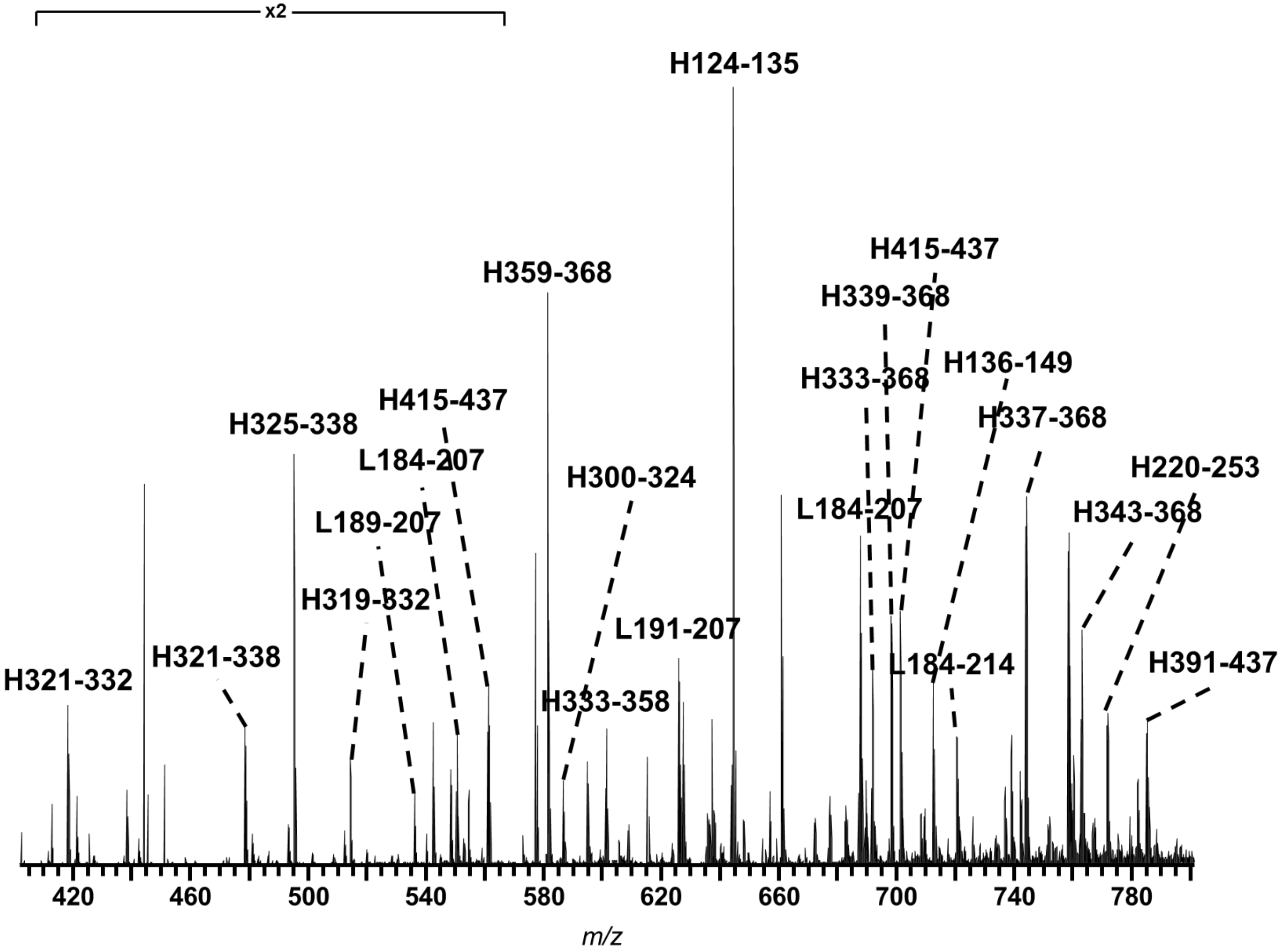


Figure S-16. Part of the mass spectrum of a tryptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

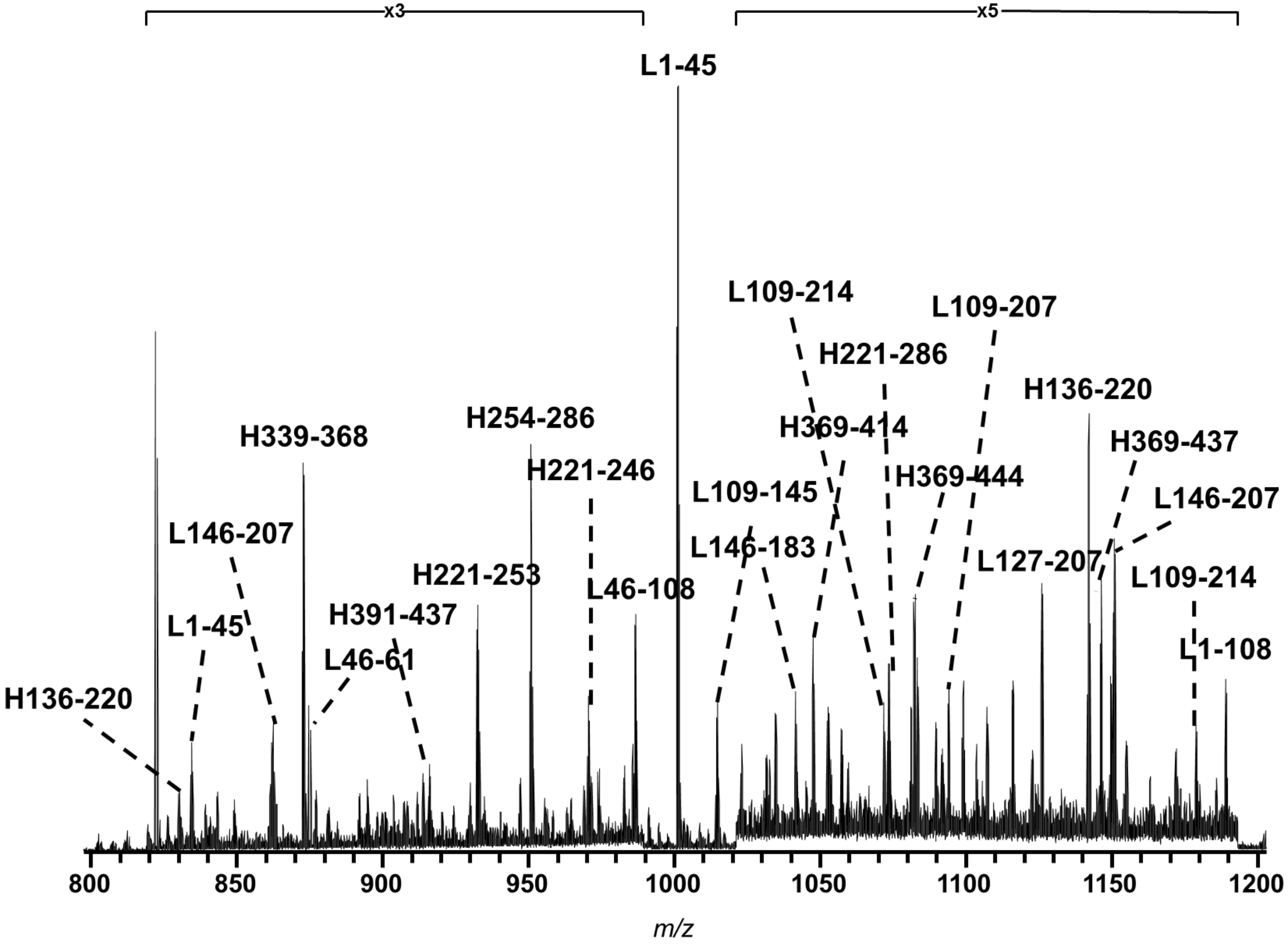


Figure S-16 (continued)**.** Part of the mass spectrum of a tryptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

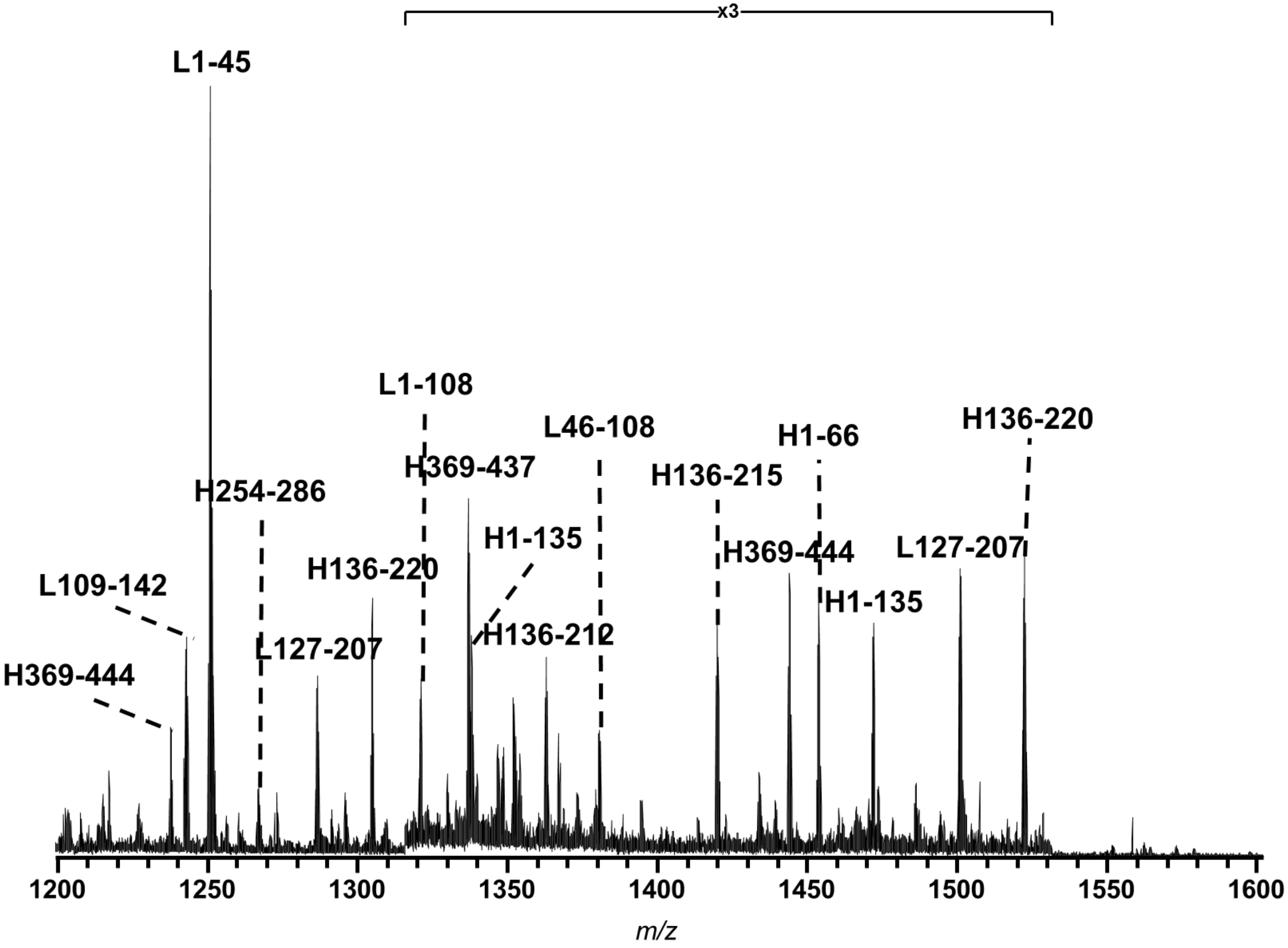


Figure S-16 (continued)**.** Part of the mass spectrum of a tryptic spin digest of Vectibix. Labels show the amino acids on the Hc and Lc (not all of the peptide signals are labelled).

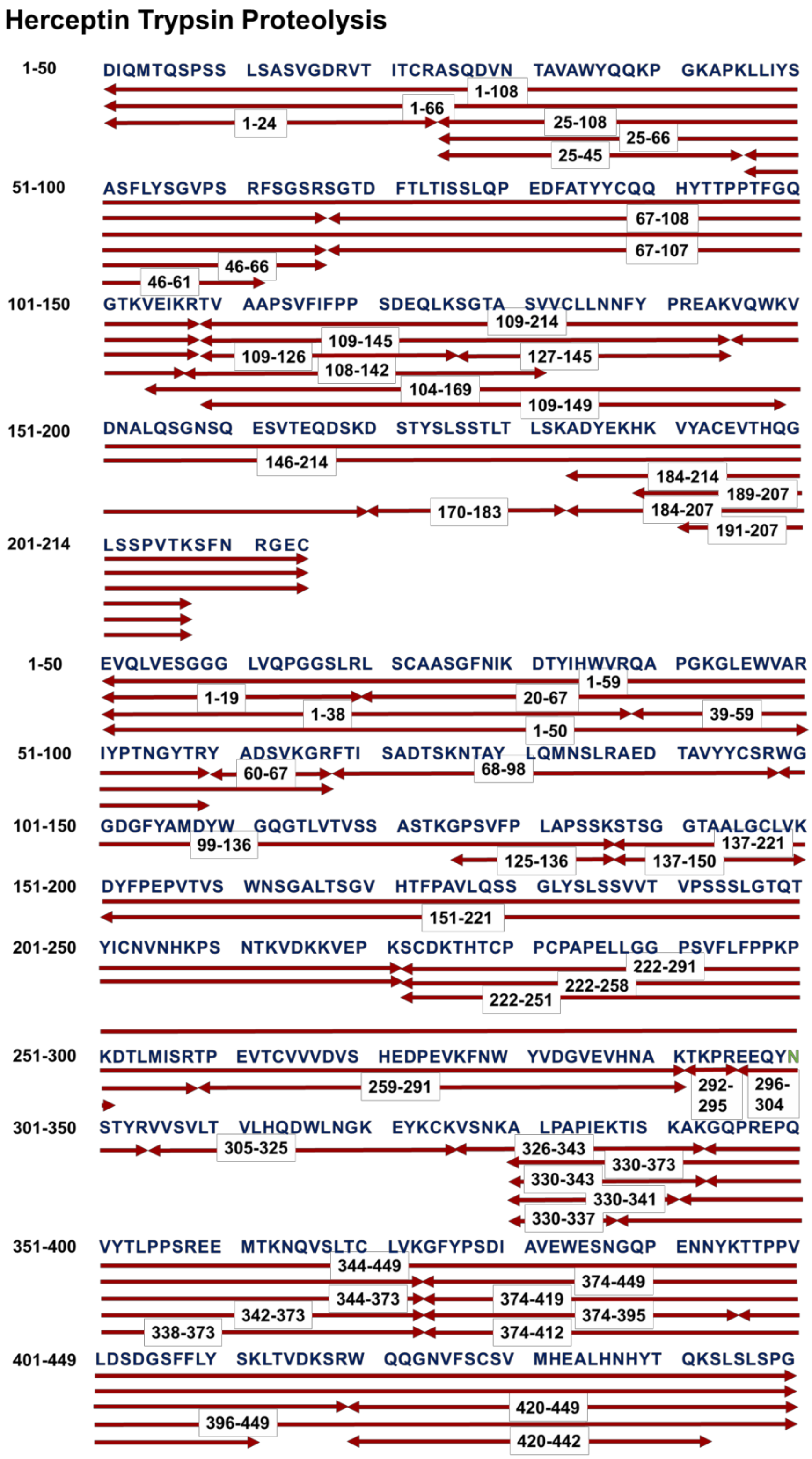


Figure S-17. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane tryptic digest of Herceptin. The light green “N” represents the glycosylation site.

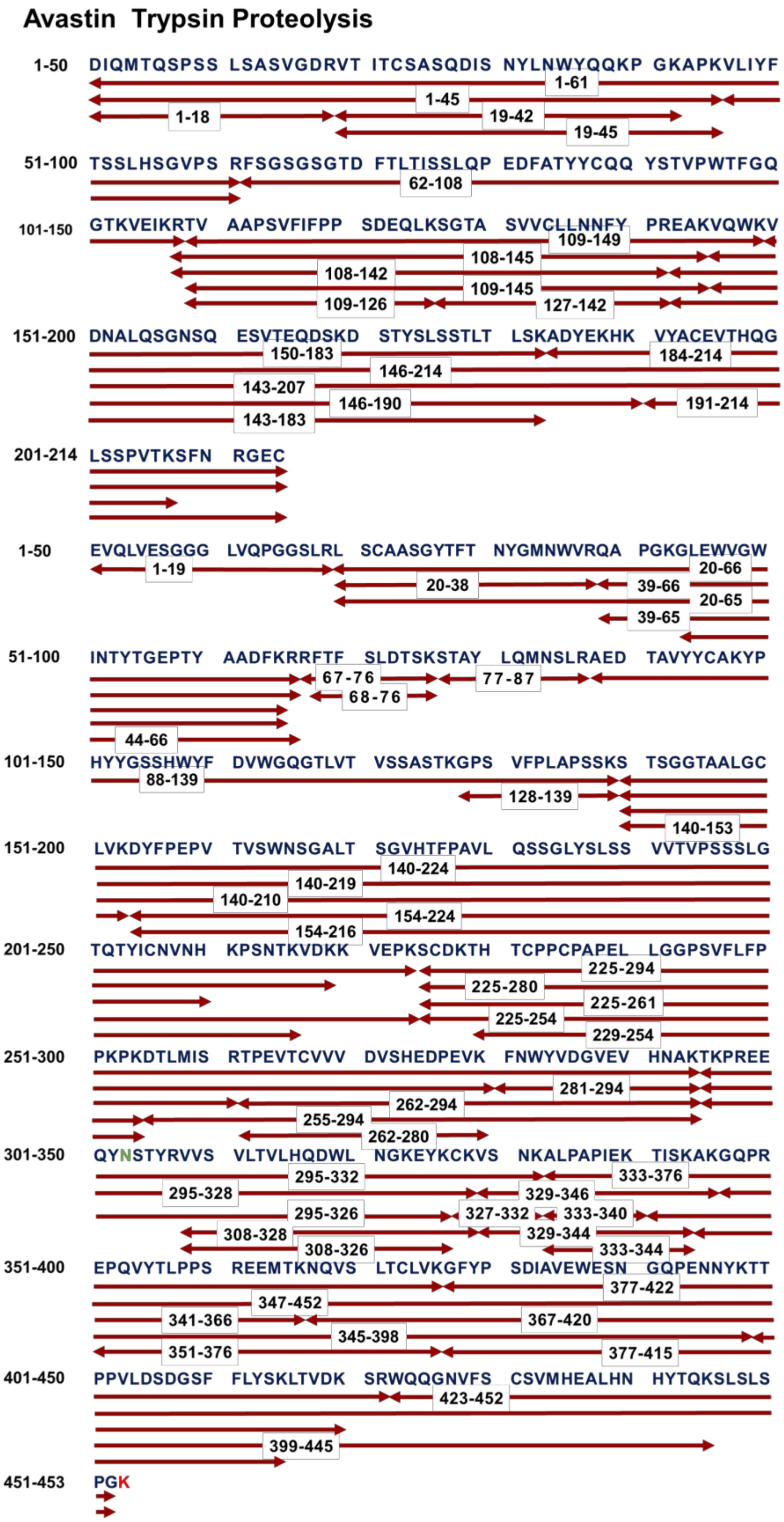


Figure S-18. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane tryptic spin digest of Avastin. The light green "N" represents the glycosylation site, and the red "K" indicates C-terminal lysine clipping.

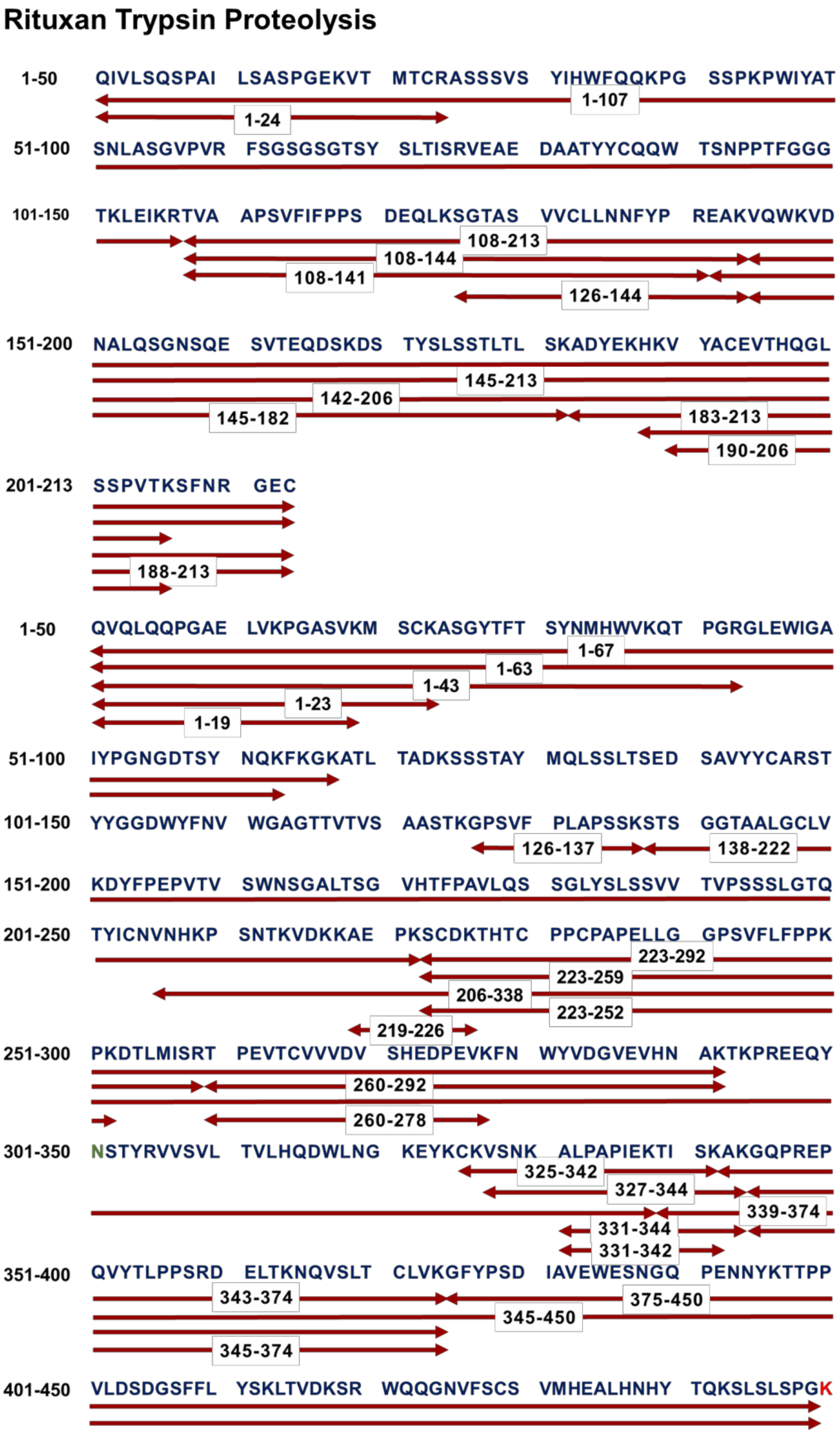


Figure S-19. Sequence map of the peptides identified from infusion ESI-Orbitrap analysis of an in-membrane tryptic digest of Rituxan. The light green "N" represents the glycosylation site, and the red "K" denotes C-terminal lysine clipping.

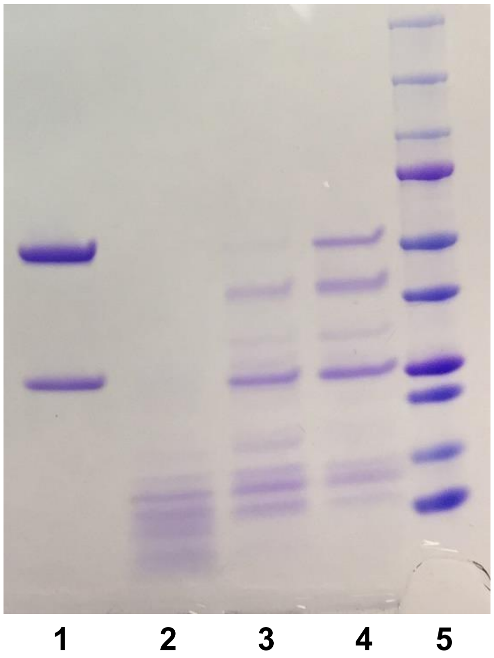


Figure S-20 Gel electrophoresis (SDS-PAGE) analysis of the reusability of a trypsin spin membrane. Lane 1: 3 µg of Avastin; Lanes 2, 3 and 4: 3 µg of Avastin tryptic spin digests (spun at 500 *g*) obtained consecutively from the same membrane; Lane 5: protein standards.

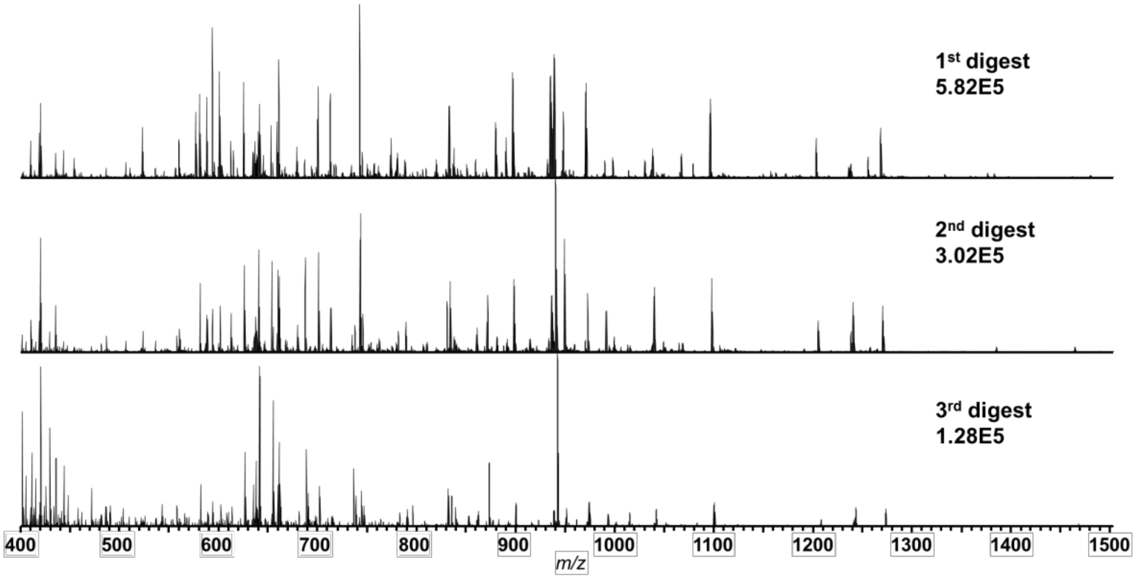


Figure S-21 Infusion-MS spectra from three consecutive Av tryptic spin digests obtained using the same spin membrane. Digestion occurred at 500 *g*.

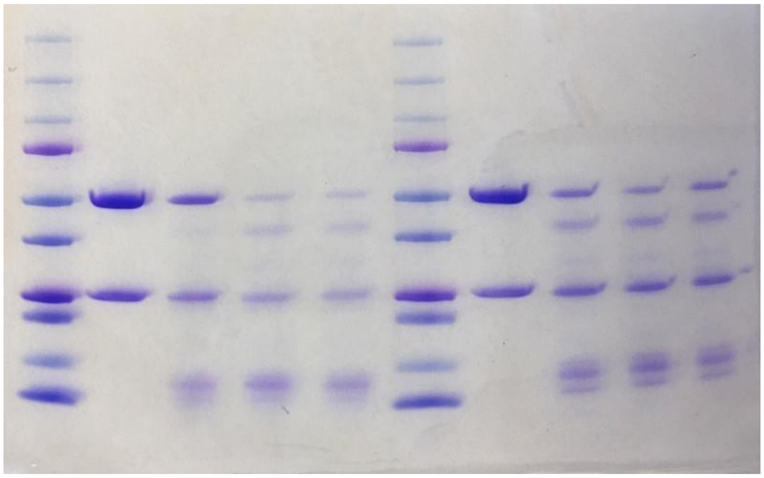


Figure S-22. Gel electrophoresis (SDS-PAGE) analysis of tryptic (TPCK-treated) in-solution digestion of He and Av with different incubation times. Lanes 1 and 6: protein standards; Lane 2: 3 µg of He; Lanes 3, 4 and 5: 3 µg of in-solution He digests obtained with incubation times of 5, 30, and 60 min respectively; Lane 7: 3 µg of Av; Lanes 8, 9 and 10: 3 µg of in-solution Av digests with incubation times of 5, 30, and 60 min, respectively.

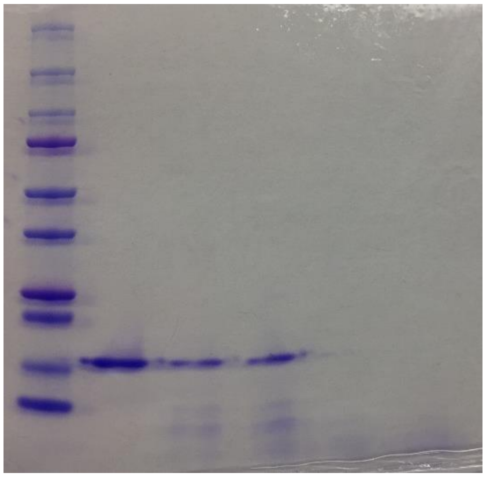


Figure S-23 Gel electrophoresis (SDS-PAGE) analysis of tryptic (sequencing grade) in-solution digestion of apomyoglobin with different incubation times. Lane 1: protein standards; Lane 2: 3 µg of apomyoglobin; Lanes 3, 4, 5 and 6: 3 µg of apomyoglobin tryptic in-solution digests obtained with incubation times of 5, 15, 30, and 60 min respectively.

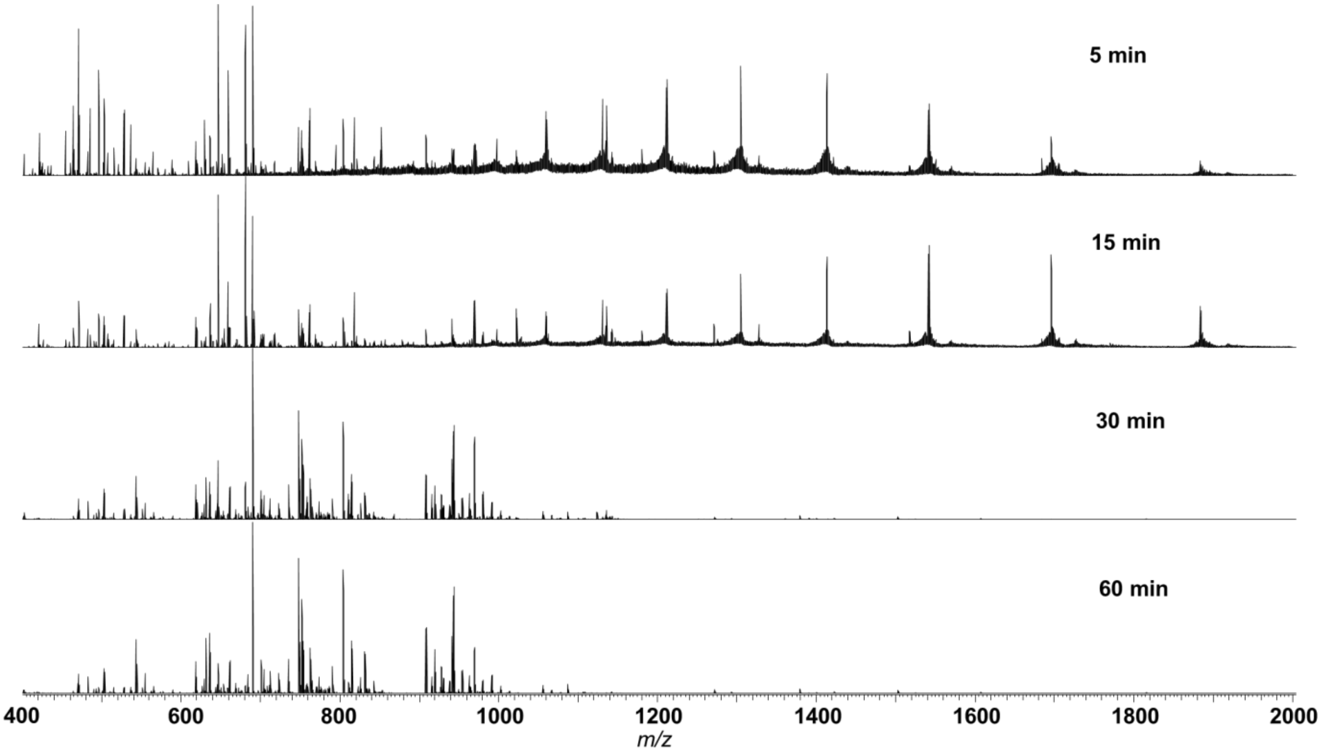


Figure S-24 Mass spectra of tryptic in-solution digests of apomyoglobin obtained with incubation times of 5, 15, 30, and 60 min (from top to bottom). This digestion employed sequencing-grade trypsin.

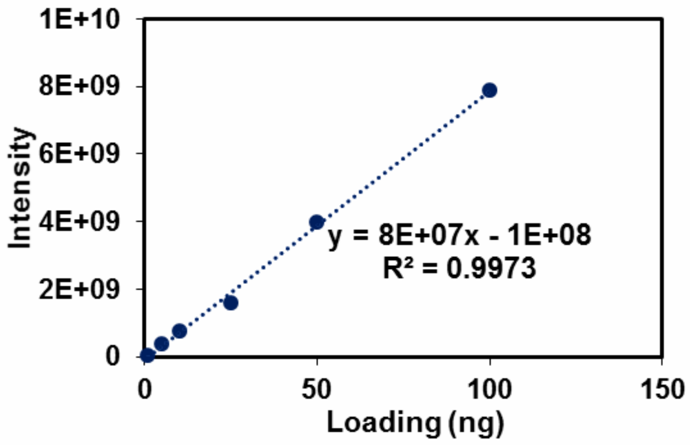


Figure S-25. Intensities of peptide ions (nanoLC-MS/MS) from tryptic spin digests of 1, 5, 10, 25, 50, and 100 ng of He in 0.1 mL. The intensities are the sum of the signals for all peptides that were detected at every concentration.

Table S-1. Apomyoglobin peptides identified from a spin-membrane (spun at 500 *g*) peptic digest.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids
3134.5542	(-)GLSDGEWQQVLNVWGKVEADIAGHGQEVL(I)	1-29
4651.5069	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVL(T)	30-69
8764.8436	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEF(I)	30-106
4132.3546	(L)TALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEF(I)	70-106
3242.6627	(F)ISDAIIHVLHSKHPGDFGADAQGAMTKALEL(F)	107-137
2927.5196	(D)AIIHVLHSKHPGDFGADAQGAMTKALEL(F)	110-137
1856.9654	(L)FRNDIAAKYKELGFQG(-)	138-153

Table S-2. Apomyoglobin peptides identified from a spin-membrane (spun at 10,000 *g*) peptic digest.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids
3134.5542	(-)GLSDGEWQQVLNVWGKVEADIAGHGQEVL(I)	1-29
4651.5069	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVL(T)	30-69
8764.8436	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEF(I)	30-106
9079.9867	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISD(A)	30-109
11988.4885	(L)IRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSKHPGDFGADAQGAMTKALEL(F)	30-137
4132.3546	(L)TALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEF(I)	70-106
3242.6627	(F)ISDAIIHVLHSKHPGDFGADAQGAMTKALEL(F)	107-137
5080.6102	(F)ISDAIIHVLHSKHPGDFGADAQGAMTKALELFRNDIAAKYKELGFQG(-)	107-153
2927.5196	(D)AIIHVLHSKHPGDFGADAQGAMTKALEL(F)	110-137
1856.9654	(L)FRNDIAAKYKELGFQG(-)	138-153

Table S-3. Apomyoglobin peptides identified from a spin-membrane (spun at 500 *g*) tryptic digest.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids	Missed Cleavages
1815.9024	(-)GLSDGEWQQVLNVWGK(V)	1-16	0
3403.7393	(-)GLSDGEWQQVLNVWGKVEADIAGHGQEVLIR(L)	1-31	1
1606.8547	(K)VEADIAGHGQEVLIR(L)	17-31	0
1271.663	(R)LFTGHPETLEK(F)	32-42	0
1937.0167	(R)LFTGHPETLEKFDKFK(H)	32-47	2
3004.5601	(R)LFTGHPETLEKFDKFKHLKTEAEMK(A)	32-56	4
1086.5612	(K)HLKTEAEMK(A)	48-56	1
1857.9739	(K)HLKTEAEMKASEDLKK(H)	48-63	3
790.4305	(K)ASEDLKK(H)	57-63	1
1378.8417	(K)HGTVVLTALGGILK(K)	64-77	0
1506.9366	(K)HGTVVLTALGGILKK(K)	64-78	1
1635.0316	(K)HGTVVLTALGGILKKK(G)	64-79	2
2110.1516	(K)KKGHHEAELKPLAQSHATK(H)	78-96	2
1982.0566	(K)KGHHEAELKPLAQSHATK(H)	79-96	1
1853.9617	(K)GHHEAELKPLAQSHATK(H)	80-96	0
735.4876	(K)HKIPIK(Y)	97-102	1
2601.4915	(K)HKIPIKYLEFISDAIIHVLHSK(H)	97-118	2
4085.143	(K)HKIPIKYLEFISDAIIHVLHSKHPGDFGADAQGAMTK(A)	97-133	3
3819.9891	(K)IPIKYLEFISDAIIHVLHSKHPGDFGADAQGAMTK(A)	99-133	2
1885.0218	(K)YLEFISDAIIHVLHSK(H)	103-118	0
3368.6732	(K)YLEFISDAIIHVLHSKHPGDFGADAQGAMTK(A)	103-133	1
1502.6693	(K)HPGDFGADAQGAMTK(A)	119-133	0
1360.7583	(K)ALELFRNDIAAK(Y)	134-145	1
2283.2132	(K)ALELFRNDIAAKYKELGFQG(-)	134-153	3
922.4993	(R)NDIAAKYK(E)	140-147	1
941.4727	(K)YKELGFQG(-)	146-153	1

Table S-4. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) peptic digest of **Herceptin**.

m/z of [M+H]+	Peptide Sequence	Amino Acids
1206.5671	(-)DIQMTQSPSSL(S)	L1-11
3267.558	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNT(A)	L1-31
3694.7799	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAW(Y)	L1-35
4933.4935	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKL(L)	L1-46
5567.8261	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSAS(F)	L1-52
5714.8945	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASF(L)	L1-53
5827.9786	(-)DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFL(Y)	L1-54
2080.0088	(L)SASVGDRVTITCRASQDVNT(A)	L12-31
3745.9443	(L)SASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKL(L)	L12-46
1684.9533	(T)AVAWYQQKPGKAPKL(L)	L32-46
2466.3544	(T)AVAWYQQKPGKAPKLLIYSASF(L)	L32-53
2579.4384	(T)AVAWYQQKPGKAPKLLIYSASFL(Y)	L32-54
2039.1324	(W)YQQKPGKAPKLLIYSASF(L)	L36-53
2152.2165	(W)YQQKPGKAPKLLIYSASFL(Y)	L36-54
1772.8562	(F)LYSGVPSRFSGSRSGTD(F)	L54-70
1919.9246	(F)LYSGVPSRFSGSRSGTDF(T)	L54-71
3104.5171	(F)LYSGVPSRFSGSRSGTDFTLTISSLQPED(F)	L54-82
3251.5855	(F)LYSGVPSRFSGSRSGTDFTLTISSLQPEDF(A)	L54-83
3586.7336	(F)LYSGVPSRFSGSRSGTDFTLTISSLQPEDFATY(Y)	L54-86
1659.7721	(L)YSGVPSRFSGSRSGTD(F)	L55-70
1806.8406	(L)YSGVPSRFSGSRSGTDF(T)	L55-71
2991.433	(L)YSGVPSRFSGSRSGTDFTLTISSLQPED(F)	L55-82
3138.5014	(L)YSGVPSRFSGSRSGTDFTLTISSLQPEDF(A)	L55-83
3473.6496	(L)YSGVPSRFSGSRSGTDFTLTISSLQPEDFATY(Y)	L55-86
3689.8421	(F)ATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L84-116
5346.678	(F)ATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L84-132
5661.8396	(F)ATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L84-135
3517.7573	(T)YYCQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L86-116
5174.5932	(T)YYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L86-132

5489.7549	(T)YYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L86-135
3207.6255	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSV(F)	L87-115
3354.694	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L87-116
5011.5299	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L87-132
5326.6915	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L87-135
3191.6306	(Y)CQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L88-116
1822.9222	(V)FIFPPSDEQLKSGTASV(V)	L116-132
2138.0838	(V)FIFPPSDEQLKSGTASVVCL(L)	L116-135
1675.8537	(F)IFPPSDEQLKSGTASV(V)	L117-132
1991.0154	(F)IFPPSDEQLKSGTASVVCL(L)	L117-135
7145.4419	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L133-195
9173.4266	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L133-214
6830.2803	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L136-195
8858.265	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L136-214
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
2256.1653	(-)EVQLVESGGGLVQPGGSLRLSCA(A)	H1-23
2618.3243	(-)EVQLVESGGGLVQPGGSLRLSCAASGF(N)	H1-27
5982.0872	(-)EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNG(Y)	H1-56
8678.4066	(-)EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY(L)	H1-80
9050.5897	(-)EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQM(N)	H1-83
10107.1097	(-)EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAV(Y)	H1-93
4775.3576	(L)SCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYAD(S)	H21-62
7074.5207	(L)SCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQM(N)	H21-83
6813.4423	(A)ASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQM(N)	H24-83
2225.1826	(F)NIKDTYIHWVRQAPGKGLE(W)	H28-46
2411.2619	(F)NIKDTYIHWVRQAPGKGLEW(V)	H28-47

3382.7807	(F)NIKDTYIHWVRQAPGKGLEWVARIYPTNG(Y)	H28-56
6079.1002	(F)NIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY(L)	H28-80
6451.2833	(F)NIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQM(N)	H28-83
7507.8033	(F)NIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAV(Y)	H28-93
4245.1186	(E)WVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQM(N)	H47-83
3087.5204	(G)YTRYADSVKGRFTISADTSKNTAYLQM(N)	H57-83
1447.721	(Y)LQMNSLRAEDTAV(Y)	H81-93
2367.0459	(M)NSLRAEDTAVYYCSRWGGDGF(Y)	H84-104
1075.5378	(M)NSLRAEDTAV(Y)	H84-93
1401.6645	(M)NSLRAEDTAVYY(C)	H84-95
1310.5259	(V)YYCSRWGGDGF(Y)	H94-104
1147.4626	(Y)YCSRWGGDGF(Y)	H95-104
984.3992	(Y)CSRWGGDGF(Y)	H96-104
1304.5616	(F)YAMDYWGQGTL(V)	H105-115
2952.4983	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGC(L)	H116-147
3065.5823	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL(V)	H116-148
6637.3811	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H116-182
3118.5884	(C)LVKDYFPEPVTVSWNSGALTSGVHTFPAV(L)	H148-176
3703.9006	(C)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H148-182
3590.8166	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H149-182
1812.9226	(L)YSLSSVVTVPSSSLGTQT(Y)	H183-200
5914.9122	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL(L)	H183-237
6425.1924	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV(F)	H183-243
6572.2608	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF(L)	H183-244
7708.9202	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL(M)	H183-254
7839.9607	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM(I)	H183-255
4631.2877	(T)YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV(F)	H201-243
1944.0663	(L)LGGPSVFLFPPKPKDTLM(I)	H238-255
1433.7861	(V)FLFPPKPKDTLM(I)	H244-255

1286.7177	(F)LFPPKPKDTLM(I)	H245-255
2273.2032	(F)LFPPKPKDTLMISRTPEVTC(V)	H245-264
1136.5438	(L)MISRTPEVTC(V)	H255-264
1005.5034	(M)ISRTPEVTC(V)	H256-264
1104.5718	(M)ISRTPEVTCV(V)	H256-265
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H265-280
6705.1696	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)*	H265-309
6867.2114	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)**	H265-309
1799.8599	(V)VVDVSHEDPEVKFNW(Y)	H266-280
6606.0918	(V)VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)***	H266-309
6703.5491	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL(T)	H310-368
6907.606	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(L)	H310-370
7020.69	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL(V)	H310-371
1229.5871	(L)TCLVKGFYPSD(I)	H369-379
1128.5394	(T)CLVKGFYPSD(I)	H370-379
1025.5302	(C)LVKGFYPSD(I)	H371-379
1437.7624	(C)LVKGFYPSDIAVE(W)	H371-383
912.4462	(L)VKGFYPSD(I)	H372-379
1324.6783	(L)VKGFYPSDIAVE(W)	H372-383
3379.6481	(L)VKGFYPSDIAVEWESNGQPENNYKTTPPVL(D)	H372-401
2486.2198	(D)IAVEWESNGQPENNYKTTPPVL(D)	H380-401
3094.4276	(D)IAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H380-407
2316.2135	(F)FLYSKLTVDKSRWQQGNVF(S)	H408-426
4823.3821	(F)FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(-)	H408-449
4563.2296	(L)YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(-)	H410-449
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(-)	H427-449
2336.1452	(C)SVMHEALHNHYTQKSLSLSPG(-)	H429-449

*6705.1696 is the monoisotopic mass for H265-309 with G0F glycosylation.

**6867.2114 is the monoisotopic mass for H265-309 with G1F glycosylation.

***6606.0918 is the monoisotopic mass for H266-309 with G0F glycosylation.

Table S-5. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) peptic digest of **Avastin**.

m/z of [M+H]+	Peptide Sequence	Amino Acids
5388.6879	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIY(F)	L1-49
5923.9521	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSL(H)	L1-54
7439.6223	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTD(F)	L1-70
8771.2832	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPED(F)	L1-82
8918.3517	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPEDF(A)	L1-83
9090.4364	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFAT(Y)	L1-85
9253.4998	(-)DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATY(Y)	L1-86
2069.9523	(Y)FTSSLHSGVPSRFSGSGSGTD(F)	L50-70
3013.4174	(L)HSGVPSRFSGSGSGTDFTLTISSLQPEDF(A)	L55-83
3185.5022	(L)HSGVPSRFSGSGSGTDFTLTISSLQPEDFAT(Y)	L55-85
3726.8625	(F)ATYYCQQYSTVPWTFGQGTKVEIKRTVAAPSVF(I)	L84-116
3244.6459	(Y)YCQQYSTVPWTFGQGTKVEIKRTVAAPSV(F)	L87-115
3391.7144	(Y)YCQQYSTVPWTFGQGTKVEIKRTVAAPSVF(I)	L87-116
5048.5503	(Y)YCQQYSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L87-132
5363.7119	(Y)YCQQYSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L87-135
2722.4563	(Q)YSTVPWTFGQGTKVEIKRTVAAPSV(F)	L91-115
2869.5247	(Q)YSTVPWTFGQGTKVEIKRTVAAPSVF(I)	L91-116
4526.3606	(Q)YSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L91-132
4841.5223	(Q)YSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L91-135
1822.9222	(V)FIFPPSDEQLKSGTASV(V)	L116-132
2138.0838	(V)FIFPPSDEQLKSGTASVVCL(L)	L116-135
1675.8537	(F)IFPPSDEQLKSGTASV(V)	L117-132
1991.0154	(F)IFPPSDEQLKSGTASVVCL(L)	L117-135

10830.2625	(F)IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L117-214
7145.4419	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L133-195
9173.4266	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L133-214
6830.2803	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L136-195
8858.265	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L136-214
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
3562.6941	(-)EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMN(W)	H1-35
2097.1029	(N)WVRQAPGKGLEWVGWINT(Y)	H36-53
3165.5429	(N)WVRQAPGKGLEWVGWINTYTGEPTYAAD(F)	H36-63
3312.6113	(N)WVRQAPGKGLEWVGWINTYTGEPTYAADF(K)	H36-64
5573.7739	(N)WVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTAYLQM(N)	H36-83
6630.2939	(N)WVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTAYLQMNSLRAEDTAV(Y)	H36-93
3495.6889	(T)YTGEPTYAADFKRRFTFSLDTSKSTAYLQM(N)	H54-83
2427.2489	(D)FKRRFTFSLDTSKSTAYLQM(N)	H64-83
2280.1805	(F)KRRFTFSLDTSKSTAYLQM(N)	H65-83
4147.8708	(M)NSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL(V)	H54-118
1075.5378	(M)NSLRAEDTAV(Y)	H84-93
3091.3508	(V)YYCAKYPHYYGSSHWYFDVWGQGTL(V)	H94-118
3065.5823	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL(V)	H119-151
6165.1529	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL(Q)	H119-180
6637.3811	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H119-185
3118.5884	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVL(Q)	H152-180
3590.8166	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H152-185
6425.1924	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV(F)	H186-246
6572.2608	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF(L)	H186-247

7839.9607	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM(I)	H186-258
8826.4462	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC(V)	H186-267
6046.056	(T)YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM(I)	H204-258
1944.0663	(L)LGGPSVFLFPPKPKDTLM(I)	H241-258
1433.7861	(V)FLFPPKPKDTLM(I)	H247-258
1286.7177	(F)LFPPKPKDTLM(I)	H248-258
2273.2032	(F)LFPPKPKDTLMISRTPEVTC(V)	H248-267
1005.5034	(M)ISRTPEVTC(V)	H259-267
998.4789	(C)VVVDVSHED(P)	H268-276
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H268-283
6705.1942	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)*	H268-312
6867.244	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)**	H268-312
5725.726	(D)PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)***	H277-312
6703.5491	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL(T)	H313-371
6907.606	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(L)	H313-373
7020.69	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL(V)	H313-374
7914.1183	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD(I)	H313-382
1229.5871	(L)TCLVKGFYPSD(I)	H372-382
1025.5302	(C)LVKGFYPSD(I)	H374-382
4100.94	(C)LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H374-410
912.4462	(L)VKGFYPSD(I)	H375-382
3987.8559	(L)VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H375-410
2486.2198	(D)IAVEWESNGQPENNYKTTPPVL(D)	H383-404
3094.4276	(D)IAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H383-410
2316.2135	(F)FLYSKLTVDKSRWQQGNVF(S)	H411-429
4823.3821	(F)FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H411-452
4563.2296	(L)YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H413-452

4071.9552	(L)TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H417-452
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H430-452

*6705.1942 is the monoisotopic mass for H268-312 with G0F glycosylation.

**6867.244 is the monoisotopic mass for H268-312 with G1F glycosylation.

***5725.726 is the monoisotopic mass for H277-312 with G0F glycosylation.

Table S-6. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) peptic digest of **Rituxan**.

m/z of [M+H]+	Peptide Sequence	Amino Acids
5763.9302	(-)QIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNL(A)	L1-53
4614.2544	(L)SASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNL(A)	L12-53
7654.7282	(L)SASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAAT(Y)	L12-84
3626.7849	(M)TCRASSSVSYIHWFQQKPGSSPKPWIYATSNL(A)	L22-53
2585.33	(Y)IHWFQQKPGSSPKPWIYATSNL(A)	L32-53
3059.4916	(L)ASGVPVRFSGSGSGTSYSLTISRVEAEDAAT(Y)	L54-84
3222.5549	(L)ASGVPVRFSGSGSGTSYSLTISRVEAEDAATY(Y)	L54-85
1161.5746	(T)ISRVEAEDAAT(Y)	L74-84
2147.9855	(T)YYCQQWTSNPPTFGGGTKL(E)	L85-103
3446.7202	(T)YYCQQWTSNPPTFGGGTKLEIKRTVAAPSVF(I)	L85-115
5103.5561	(T)YYCQQWTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L85-131
5418.7177	(T)YYCQQWTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L85-134
3283.6568	(Y)YCQQWTSNPPTFGGGTKLEIKRTVAAPSVF(I)	L86-115
5255.6544	(Y)YCQQWTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L86-134
2614.3988	(Q)WTSNPPTFGGGTKLEIKRTVAAPSV(F)	L90-114
2761.4672	(Q)WTSNPPTFGGGTKLEIKRTVAAPSVF(I)	L90-115
4733.4647	(Q)WTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L90-134
1170.6841	(L)EIKRTVAAPSV(F)	L104-114

1317.7525	(L)EIKRTVAAPSVF(I)	L104-115
2974.5884	(L)EIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L104-131
3289.7501	(L)EIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L104-134
1822.9222	(V)FIFPPSDEQLKSGTASV(V)	L115-131
2138.0838	(V)FIFPPSDEQLKSGTASVVCL(L)	L115-134
1675.8537	(F)IFPPSDEQLKSGTASV(V)	L116-131
1991.0154	(F)IFPPSDEQLKSGTASVVCL(L)	L116-134
9173.4266	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L132-213
6830.2803	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L135-194
8858.265	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L135-213
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L195-213
5393.702	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIG(A)	H1-49
7647.8403	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATL(T)	H1-70
8659.2912	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAY(M)	H1-80
9031.4743	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL(S)	H1-83
9318.6224	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSL(T)	H1-86
10007.9092	(-)QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAV(Y)	H1-93
1974.0187	(E)LVKPGASVKMSCKASGYTF(T)	H11-29
4315.1613	(E)LVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIG(A)	H11-49
6569.2996	(E)LVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATL(T)	H11-70
7952.9336	(E)LVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL(S)	H11-83
8240.0817	(E)LVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSL(T)	H11-86
5997.9327	(F)TSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL(S)	H30-83

3656.7901	(G)AIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL(S)	H50-83
995.4528	(L)SSLTSEDSAV(Y)	H84-93
1418.5681	(V)YYCARSTYYGGD(W)	H94-105
4332.1645	(D)WYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCL(V)	H106-149
1194.6041	(L)VKDYFPEPVT(V)	H150-159
3118.5884	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVL(Q)	H150-178
3590.8166	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H150-183
1943.0021	(T)VSWNSGALTSGVHTFPAVL(Q)	H160-178
1812.9226	(L)YSLSSVVTVPSSSLGTQT(Y)	H184-201
5886.8809	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPEL(L)	H184-238
6397.1611	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSV(F)	H184-244
6544.2295	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVF(L)	H184-245
7811.9294	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM(I)	H184-256
8798.4149	(L)YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC(V)	H184-265
4092.9762	(T)YICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPEL(L)	H202-238
4750.3248	(T)YICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVF(L)	H202-245
6018.0247	(T)YICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM(I)	H202-256
1944.0663	(L)LGGPSVFLFPPKPKDTLM(I)	H239-256
2930.5518	(L)LGGPSVFLFPPKPKDTLMISRTPEVTC(V)	H239-265
1433.7861	(V)FLFPPKPKDTLM(I)	H245-256
1286.7177	(F)LFPPKPKDTLM(I)	H246-256
2273.2032	(F)LFPPKPKDTLMISRTPEVTC(V)	H246-265
1005.5034	(M)ISRTPEVTC(V)	H257-265
1104.5718	(M)ISRTPEVTCV(V)	H257-266
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H266-281
3721.8609	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE(E)	H266-297
6705.1660	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)*	H266-310
6867.2164	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)**	H266-310

7029.2668	(C)VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL(T)***	H266-310
6671.577	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL(T)	H311-369
6988.718	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL(V)	H311-372
7882.1463	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD(I)	H311-380
912.4462	(L)VKGFYPSD(I)	H373-380
1025.5302	(L)VKGFYPSDI(A)	H373-381
3987.8559	(L)VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H373-408
2486.2198	(D)IAVEWESNGQPENNYKTTPPVL(D)	H381-402
3094.4276	(D)IAVEWESNGQPENNYKTTPPVLDSDGSF(F)	H381-408
2316.2135	(F)FLYSKLTVDKSRWQQGNVF(S)	H409-427
4823.3821	(F)FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H409-450
4563.2296	(L)YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H411-450
4071.9552	(L)TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H415-450
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H428-450

*6705.1660 is the monoisotopic mass for H266-310 with G0F glycosylation.

**6867.2164 is the monoisotopic mass for H266-310 with G1F glycosylation.

***7029.2668 is the monoisotopic mass for H266-310 with G2F glycosylation.

Table S-7. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) peptic digest of **Vectibix**.

m/z of [M+H]+	Peptide Sequence	Amino Acids
1206.5671	(-)DIQMTQSPSSL(S)	L1-11
2524.2018	(-)DIQMTQSPSSLSASVGDRVTITCQ(A)	L1-24
3239.5155	(-)DIQMTQSPSSLSASVGDRVTITCQASQDISN(Y)	L1-31
5054.4986	(-)DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKL(L)	L1-46
5830.8691	(-)DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN(L)	L1-53
5943.9532	(-)DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNL(E)	L1-54

9116.4368	(-)DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIAT(Y)	L1-85
1336.6525	(L)SASVGDRVTITCQ(A)	L12-24
2051.9662	(L)SASVGDRVTITCQASQDISN(Y)	L12-31
4643.3199	(L)SASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN(L)	L12-53
2549.3147	(Q)ASQDISNYLNWYQQKPGKAPKL(L)	L25-46
3325.6852	(Q)ASQDISNYLNWYQQKPGKAPKLLIYDASN(L)	L25-53
1834.001	(N)YLNWYQQKPGKAPKL(L)	L32-46
2723.4555	(N)YLNWYQQKPGKAPKLLIYDASNL(E)	L32-54
3288.6986	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSV(F)	L86-115
3435.7671	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSVF(I)	L86-116
5092.603	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV(V)	L86-132
5407.7646	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL(L)	L86-135
3125.6353	(Y)FCQHFDHLPLAFGGGTKVEIKRTVAAPSV(F)	L87-115
3272.7037	(Y)FCQHFDHLPLAFGGGTKVEIKRTVAAPSVF(I)	L87-116
1822.9222	(V)FIFPPSDEQLKSGTASV(V)	L116-132
2138.0838	(V)FIFPPSDEQLKSGTASVVCL(L)	L116-135
1675.8537	(F)IFPPSDEQLKSGTASV(V)	L117-132
1991.0154	(F)IFPPSDEQLKSGTASVVCL(L)	L117-135
1877.9313	(I)FPPSDEQLKSGTASVVCL(L)	L118-135
9173.4266	(V)VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L133-214
6830.2803	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE(V)	L136-195
8858.265	(L)LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC(-)	L136-214
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
2093.1114	(-)QVQLQESGPGLVKPSETLSL(T)	H1-20
1641.8694	(L)QESGPGLVKPSETLSL(T)	H5-20
5485.6335	(L)TCTVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTNYNPSLKSRL(T)	H21-69
1240.642	(L)TISIDTSKTQF(S)	H70-80
1702.8898	(F)SLKLSSVTAADTAIYY(C)	H81-96
1123.5677	(Y)CVRDRVTGAF(D)	H97-106
2011.9477	(Y)CVRDRVTGAFDIWGQGTM(V)	H97-114
2683.3243	(M)VTVSSASTKGPSVFPLAPCSRSTSEST(A)	H115-141
3211.5973	(M)VTVSSASTKGPSVFPLAPCSRSTSESTAALGCL(V)	H115-147
1194.6041	(L)VKDYFPEPVT(V)	H148-157

3118.5884	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVL(Q)	H148-176
3590.8166	(L)VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H148-181
2938.4945	(F)PEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H153-181
1873.9178	(L)YSLSSVVTVPSSNFGTQT(Y)	H182-199
6023.8745	(L)YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSV(F)	H182-238
6170.9429	(L)YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF(L)	H182-239
7307.6023	(L)YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL(M)	H182-249
7438.6427	(L)YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM(I)	H182-250
4703.2183	(F)GTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF(L)	H196-239
5970.9182	(F)GTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM(I)	H196-250
4168.9745	(T)YTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSV(F)	H200-238
4316.0429	(T)YTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF(L)	H200-239
5583.7428	(T)YTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM(I)	H200-250
3948.9227	(C)NVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF(L)	H203-239
5216.6226	(C)NVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM(I)	H203-250
1433.7861	(V)FLFPPKPKDTLM(I)	H239-250
1286.7177	(F)LFPPKPKDTLM(I)	H240-250
2273.2032	(F)LFPPKPKDTLMISRTPEVTC(V)	H240-259
1173.6336	(L)FPPKPKDTLM(I)	H241-250
1136.5438	(L)MISRTPEVTC(V)	H250-259
1005.5034	(M)ISRTPEVTC(V)	H251-259
1598.7697	(C)VVVDVSHEDPEVQF(N)	H260-273
1898.8919	(C)VVVDVSHEDPEVQFNW(Y)	H260-275
6019.7183	(C)VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF(R)*	H260-298
6181.7644	(C)VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF(R)**	H260-298
6673.1343	(C)VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVL(T)***	H260-304
6835.1836	(C)VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVL(T)****	H260-304

4139.8438	(W)YVDGVEVHNAKTKPREEQFNSTF(R)*****	H276-298
4301.8954	(W)YVDGVEVHNAKTKPREEQFNSTF(R)******	H276-298
4793.2674	(W)YVDGVEVHNAKTKPREEQFNSTFRVVSVL(T)*******	H276-304
4955.3153	(W)YVDGVEVHNAKTKPREEQFNSTFRVVSVL(T)********	H276-304
6705.5284	(L)TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSL(T)	H305-363
6909.5852	(L)TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC(L)	H305-365
7022.6693	(L)TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCL(V)	H305-366
1229.5871	(L)TCLVKGFYPSD(I)	H364-374
1025.5302	(C)LVKGFYPSD(I)	H366-374
912.4462	(L)VKGFYPSD(I)	H367-374
2518.1919	(D)IAVEWESNGQPENNYKTTPPML(D)	H375-396
3126.3997	(D)IAVEWESNGQPENNYKTTPPMLDSDGSF(F)	H375-402
2316.2135	(F)FLYSKLTVDKSRWQQGNVF(S)	H403-421
2506.2547	(F)FLYSKLTVDKSRWQQGNVFSC(S)	H403-423
4823.3821	(F)FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H403-444
2056.061	(L)YSKLTVDKSRWQQGNVF(S)	H405-421
4563.2296	(L)YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H405-444
4071.9552	(L)TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG(K)	H409-444
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H422-444
2336.1452	(C)SVMHEALHNHYTQKSLSLSPG(K)	H424-444

*6019.7183 is the monoisotopic mass for H260-298 with G0F glycosylation.

**6181.7644 is the monoisotopic mass for H260-298 with G1F glycosylation.

***6673.1343 is the monoisotopic mass for H260-304 with G0F glycosylation.

****6835.1836 is the monoisotopic mass for H260-304 with G1F glycosylation.

*****4139.8438 is the monoisotopic mass for H276-298 with G0F glycosylation.

******4301.8954 is the monoisotopic mass for H276-298 with G1F glycosylation.

*******4793.2674 is the monoisotopic mass for H276-304 with G0F glycosylation.

********4955.3153 is the monoisotopic mass for H276-304 with G1F glycosylation.

Table S-8. Yields of peptides from spin-membrane and in-solution digestion as determined using tryptophan fluorescence.

	Avastin (%)	Rituxumab (%)
Pepsin spin membrane	80 ± 16	88 ± 5
Trypsin spin membrane	60 ± 8	61 ± 9
Pepsin in-solution digests	65 ± 1	69 ± 2
Trypsin in-solution digests	37 ± 1	24 ± 2

Table S-9. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) tryptic digest of **Herceptin**.

m/z of [M+H]+	Peptide Sequence	Amino Acids	Missed cleavages
2609.2658	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamido methyl)R(A)	L1-24	1
7165.6262	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamido methyl)RASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR(S)	L1-66	5
11959.9174	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamido methyl)RASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQHYTTPPTFGQGTKVEIKR(T)	L1-108	8
2287.183	(R)ASQDVNTAVAWYQQKPGKAPK(L)	L25-45	1
4575.3783	(R)ASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR(S)	L25-66	3
9369.6695	(R)ASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYC(Carbamido methyl)QQHYTTPPTFGQGTKVEIKR(T)	L25-108	6
1772.9581	(K)LLIYSASFLYSGVPSR(F)	L46-61	0
2307.2132	(K)LLIYSASFLYSGVPSRFSGSR(S)	L46-66	1
4657.2079	(R)SGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQHYTTPPTFGQGTKVEIK(R)	L67-107	1

4813.309	(R)SGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQHYTTPPTFGQGTKVEIKR(T)	L67-108	2
7336.7223	(K)VEIKRTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK(D)	L104-169	6
3881.0055	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L108-142	2
4209.1801	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L108-145	3
1946.027	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
3724.9043	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L109-142	1
4053.079	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L109-145	2
4594.3803	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWK(V)	L109-149	3
10923.3997	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L109-207	8
11773.7389	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L109-214	10
2126.0699	(K)SGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L127-145	1
7739.6777	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L146-214	7
1502.7584	(K)DSTYSLSSTLTLSK(A)	L170-183	0
2747.3457	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L184-207	2

3597.6849	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L184-214	4
2141.0808	(K)HKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L189-207	1
1875.9269	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L191-207	0
2726.2661	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L191-214	2
1882.0029	(-)EVQLVESGGGLVQPGGSLR(L)	H1-19	0
4101.0975	(-)EVQLVESGGGLVQPGGSLRLSC(Carbamidomethyl)AASGFNIKDTYIHWVR(Q)	H1-38	2
5393.7964	(-)EVQLVESGGGLVQPGGSLRLSC(Carbamidomethyl)AASGFNIKDTYIHWVRQAPGKGLEWVAR(I)	H1-50	4
6459.3208	(-)EVQLVESGGGLVQPGGSLRLSC(Carbamidomethyl)AASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTR(Y)	H1-59	5
2238.1124	(R)LSC(Carbamidomethyl)AASGFNIKDTYIHWVR(Q)	H20-38	1
3530.8114	(R)LSC(Carbamidomethyl)AASGFNIKDTYIHWVRQAPGKGLEWVAR(I)	H20-50	3
5472.7811	(R)LSC(Carbamidomethyl)AASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGR(F)	H20-67	6
1089.5476	(K)DTYIHWVR(Q)	H31-38	0
2377.2411	(R)QAPGKGLEWVARIYPTNGYTR(Y)	H39-59	2
895.4632	(R)YADSVKGR(F)	H60-67	1
3576.6734	(R)FTISADTSKNTAYLQMNSLRAEDTAVYYC(Carbamidomethyl)SR(W)	H68-98	2
3951.8898	(R)WGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSK(S)	H99-136	1
1186.6467	(K)GPSVFPLAPSSK(S)	H125-136	0
1321.678	(K)STSGGTAALGC(Carbamidomethyl)LVK(D)	H137-150	0
8939.5187	(K)STSGGTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDKKVEPK(S)	H137-221	4

7636.8585	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDKKVEPK(S)	H151-221	3
3334.6421	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H222-251	1
4151.0585	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISR(T)	H222-258	2
7929.8522	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H222-291	4
3797.8116	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H259-291	1
501.3144	(K)TKPR(E)	H292-295	0
2634.238	(R)EEQYNSTYR(V)*	H296-304	0
2516.333	(R)VVSVLTVLHQDWLNGKEYKC(Carbamidomethyl)K(V)	H305-325	2
1895.1324	(K)VSNKALPAPIEKTISKAK(G)	H326-343	3
838.5033	(K)ALPAPIEK(T)	H330-337	0
1267.762	(K)ALPAPIEKTISK(A)	H330-341	1
1466.8941	(K)ALPAPIEKTISKAK(G)	H330-343	2
4933.6642	(K)ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H330-373	6
4114.1787	(K)TISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H338-373	5
3684.92	(K)AKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H342-373	4
2343.1762	(K)GQPREPQVYTLPPSREEMTK(N)	H344-363	2
3485.7879	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H344-373	3
12088.8484	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H344-449	9

3047.554	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H348-373	2
1161.6296	(K)NQVSLTC(Carbamidomethyl)LVK(G)	H364-373	0
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H374-395	0
4399.0354	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK(L)	H374-412	1
5198.4906	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR(W)	H374-419	3
7980.7398	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H374-442	4
8622.0783	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H374-449	5
6096.9647	(K)TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H396-449	4
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H420-442	0
3442.6056	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H420-449	1

*2634.238 is the monoisotopic mass for H296-304 with G0F glycosylation.

Table S-10. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) tryptic digest of **Avastin**.

m/z of [M+H]+	Peptide Sequence	Amino Acids	Missed cleavages
1878.8862	(-)DIQMTQSPSSLSASVGDR(V)	L1-18	0
4957.4095	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGKAPK(V)	L1-45	2
6701.3403	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSR(F)	L1-61	3

2801.3563	(R)VTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGK(A)	L19-42	0
3097.5411	(R)VTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGKAPK(V)	L19-45	1
1762.9486	(K)VLIYFTSSLHSGVPSR(F)	L46-61	0
5285.5048	(R)FSGSGSGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQYSTVPWTFGQGTKVEIKR(T)	L62-108	2
3881.0055	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L108-142	2
4209.1801	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L108-145	3
1946.027	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
3724.9043	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L109-142	1
4053.079	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L109-145	2
4594.3803	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWK(V)	L109-149	3
1797.8952	(K)SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L127-142	0
2126.0699	(K)SGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L127-145	1
4489.1853	(R)EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L143-183	3
7217.5132	(R)EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L143-207	6
4161.0106	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L146-183	2
5032.4294	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK(V)	L146-190	4
6889.3385	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L146-207	5
7739.6777	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L146-214	7
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L150-183	1

6348.0372	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L150-207	4
1502.7584	(K)DSTYSLSSTLTLSK(A)	L170-183	0
2747.3457	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L184-207	2
3597.6849	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L184-214	4
2141.0808	(K)HKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L189-207	1
2991.42	(K)HKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L189-214	3
1875.9269	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L191-207	0
2726.2661	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L191-214	2
1882.0029	(-)EVQLVESGGGLVQPGGSLR(L)	H1-19	0
2197.9794	(R)LSC(Carbamidomethyl)AASGYTFTNYGMNWVR(Q)	H20-38	0
5178.4189	(R)LSC(Carbamidomethyl)AASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFK(R)	H20-65	2
5334.52	(R)LSC(Carbamidomethyl)AASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFKR(R)	H20-66	3
2999.4574	(R)QAPGKGLEWVGWINTYTGEPTYAADFK(R)	H39-65	1
3155.5585	(R)QAPGKGLEWVGWINTYTGEPTYAADFKR(R)	H39-66	2
2674.2936	(K)GLEWVGWINTYTGEPTYAADFKR(R)	H44-66	1
1201.6212	(R)RFTFSLDTSK(S)	H67-76	1
1045.5201	(R)FTFSLDTSK(S)	H68-76	0
1283.6412	(K)STAYLQMNSLR(A)	H77-87	0
5762.7213	(R)AEDTAVYYC(Carbamidomethyl)AKYPHYYGSSHWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSK(S)	H88-139	2
1186.6467	(K)GPSVFPLAPSSK(S)	H128-139	0
1321.678	(K)STSGGTAALGC(Carbamidomethyl)LVK(D)	H140-153	0
8015.9746	(K)STSGGTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT	H140-216	1

	QTYIC(Carbamidomethyl)NVNHKPSNTK(V)		
8358.165	(K)STSGGTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDK(K)	H140-219	2
8486.2599	(K)STSGGTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDKK(V)	H140-210	3
8939.5187	(K)STSGGTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDKKVEPK(S)	H140-224	4
6713.3145	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTK(V)	H154-216	0
7055.5048	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDK(K)	H154-219	1
7636.8585	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDKKVEPK(S)	H154-224	3
3334.6421	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H225-254	1
4151.0585	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISR(T)	H225-261	2
6271.0681	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H225-280	3
7929.8522	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H225-294	4

2844.4575	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H229-254	0
4614.2279	(K)DTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H255-294	2
2139.0274	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H262-280	0
3797.8116	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H262-294	1
1677.802	(K)FNWYVDGVEVHNAK(T)	H281-294	0
5325.5188	(K)TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK(C)*	H295-326	3
5613.679	(K)TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC(Carbamidomethyl)K(V)**	H295-328	4
6042.0424	(K)TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC(Carbamidomethyl)KVSNK(A)***	H295-332	5
2228.2074	(R)VVSVLTVLHQDWLNGKEYK(C)	H308-326	1
2516.333	(R)VVSVLTVLHQDWLNGKEYKC(Carbamidomethyl)K(V)	H308-328	2
735.3818	(K)C(Carbamidomethyl)KVSNK(A)	H327-332	1
1696.0003	(K)VSNKALPAPIEKTISK(A)	H329-344	2
1895.1324	(K)VSNKALPAPIEKTISKAK(G)	H329-346	3
838.5033	(K)ALPAPIEK(T)	H333-340	0
1267.762	(K)ALPAPIEKTISK(A)	H333-344	1
1466.8941	(K)ALPAPIEKTISKAK(G)	H333-346	2
4933.6642	(K)ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H333-376	6
2971.567	(K)TISKAKGQPREPQVYTLPPSREEMTK(N)	H341-366	4
4114.1787	(K)TISKAKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H341-376	5
2542.3082	(K)AKGQPREPQVYTLPPSREEMTK(N)	H346-366	3
3684.92	(K)AKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H345-376	4
6210.0335	(K)AKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H345-398	5
8621.2596	(K)AKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYP	H345-420	7

	SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK(S)		
2343.1762	(K)GQPREPQVYTLPPSREEMTK(N)	H347-366	2
3485.7879	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H347-376	3
6010.9015	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H347-398	4
8665.2607	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR(W)	H347-422	7
12091.8591	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H347-452	9
3047.554	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H351-376	2
5572.6676	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H351-398	3
1161.6296	(K)NQVSLTC(Carbamidomethyl)LVK(G)	H367-376	0
6097.9692	(K)NQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK(S)	H367-420	3
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H377-398	0
4399.0354	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK(L)	H377-415	1
5198.4906	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR(W)	H377-422	3
7980.7398	(K)GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H377-445	4
2673.377	(K)TTPPVLDSDGSFFLYSKLTVDKSR(W)	H399-422	2
5455.6263	(K)TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H399-445	3
3442.6043	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H423-452	1

*5325.5188 is the monoisotopic mass for H295-326 with G0F glycosylation.

**5613.679 is the monoisotopic mass for H295-328 with G0F glycosylation.

***6042.0424 is the monoisotopic mass for H295-332 with G0F glycosylation.

Table S-11. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) tryptic digest of **Rituxan**.

m/z of [M+H]+	Peptide Sequence	Amino Acids	Missed cleavages
1808.0248	(-) QIVLSQSPAILSASPGEK(V)	L1-18	0
2556.3486	(-)QIVLSQSPAILSASPGEKVTMTC(Carbamidomethyl)R(A)	L1-24	1
3933.0082	(R) ASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVR(F)	L25-60	0
1606.7707	(R) FSGSGSGTSYSLTISR(V)	L61-76	0
4466.0154	(R) FSGSGSGTSYSLTISRVEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTK(L)	L61-102	1
4949.321	(R) FSGSGSGTSYSLTISRVEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTKLEIK(R)	L61-106	2
5105.4222	(R) FSGSGSGTSYSLTISRVEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTKLEIKR(T)	L61-107	3
2878.2625	(R) VEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTK(L)	L77-102	0
3361.5681	(R) VEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTKLEIK(R)	L77-106	1
3517.6693	(R) VEAEDAATYYC(Carbamidomethyl)QQWTSNP	L77-107	2

	PTFGGGTKLEIKR(T)		
2102.1281	(K) RTVAAPSVFIFPPSDEQLK(S)	L107-125	1
1946.027	(R) TVAAPSVFIFPPSDEQLK(S)	L108-125	0
3724.9043	(R) TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L108-141	1
4053.079	(R) TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L108-144	2
1797.8952	(K) SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L126-141	0
2126.0699	(K) SGTASVVC(Carbamidomethyl)LLNNFYPREAK (V)	L126-144	1
4161.0106	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L145-182	2
4767.2755	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEK(H)	L145-187	3
5032.4294	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK(V)	L145-189	4
6889.3385	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L145-206	5
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L149-182	1
4225.9743	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK(H)	L149-187	2
4491.1281	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK(V)	L149-189	3
6348.0372	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L149-206	4
1502.7584	(K) DSTYSLSSTLTLSK(A)	L169-182	0
4231.0863	(K)DSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L169-206	3
2747.3457	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L183-206	2

2141.0808	(K)HKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L188-206	1
1875.9269	(K) VYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L190-206	0
1960.1098	(-) QVQLQQPGAELVKPGASVK(M)	H1-19	0
1791.8159	(K) ASGYTFTSYNMHWVK(Q)	H24-38	0
2183.0404	(R) GLEWIGAIYPGNGDTSYNQK(F)	H44-63	0
2458.2038	(R) GLEWIGAIYPGNGDTSYNQKFK(G)	H44-65	1
3562.6676	(K)GKATLTADKSSSTAYMQLSSLTSEDSAVYYC(Carbamidomethyl)AR(S)	H66-98	2
3377.5512	(K)ATLTADKSSSTAYMQLSSLTSEDSAVYYC(Carbamidomethyl)AR(S)	H68-98	1
2677.1756	(K)SSSTAYMQLSSLTSEDSAVYYC(Carbamidomethyl)AR(S)	H75-98	0
2889.3366	(R) STYYGGDWYFNVWGAGTTVTVSAASTK(G)	H99-125	0
1186.6467	(K) GPSVFPLAPSSK(S)	H126-137	0
1321.678	(K) STSGGTAALGC(Carbamidomethyl)LVK(D)	H138-151	0
6713.3145	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTK(V)	H152-214	0
7055.5048	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTKVDK(K)	H152-217	1
3334.6421	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H223-252	1
4151.0585	(K)SC(Carbamidomethyl)DKTHTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISR(T)	H223-259	2
2844.4575	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H227-252	0
3660.8739	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPKDTLMISR(T)	H227-259	1
835.4342	(K) DTLMISR(T)	H253-259	0

4614.2279	(K)DTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H253-292	2
2139.0274	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H260-278	0
3797.8116	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVKFNWYVDGVEVHNAK(T)	H260-292	1
1677.802	(K) FNWYVDGVEVHNAK(T)	H279-292	0
4843.2928	(R) EEQYNSTYRVVSVLTVLHQDWLNGKEYK(C)*	H297-324	2
5005.3526	(R) EEQYNSTYRVVSVLTVLHQDWLNGKEYK(C)**	H297-324	2
5167.3993	(R) EEQYNSTYRVVSVLTVLHQDWLNGKEYK(C)***	H297-324	2
2228.2074	(R) VVSVLTVLHQDWLNGKEYK(C)	H306-324	1
838.5033	(K) ALPAPIEK(T)	H331-338	0
1267.762	(K) ALPAPIEKTISK(A)	H331-342	1
2311.2041	(K) GQPREPQVYTLPPSRDELTK(N)	H345-364	2
1872.9702	(R) EPQVYTLPPSRDELTK(N)	H349-364	1
3015.5819	(R)EPQVYTLPPSRDELTKNQVSLTC(Carbamidomethyl)LVK(G)	H349-374	2
5540.6955	(R)EPQVYTLPPSRDELTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H349-396	3
1161.6296	(K) NQVSLTC(Carbamidomethyl)LVK(G)	H365-374	0
2544.1314	(K) GFYPSDIAVEWESNGQPENNYK(T)	H375-396	0
2430.2439	(K) TTPPVLDSDGSFFLYSKLTVDK(S)	H397-418	1
2673.377	(K) TTPPVLDSDGSFFLYSKLTVDKSR(W)	H397-420	2
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H421-443	0

*4843.2928 is the monoisotopic mass for H297-324 with G0F glycosylation.

**5005.3526 is the monoisotopic mass for H297-324 with G1F glycosylation.

***5167.3993 is the monoisotopic mass for H297-324 with G2F glycosylation.

Table S-12. Light- and heavy-chain peptides identified from a spin-membrane (spun at 500 *g*) tryptic digest of **Vectibix**.

m/z of [M+H]+	Peptide Sequence	Amino Acids	Missed cleavages
4998.436	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamidomethyl)QASQDISNYLNWYQQKPGKAPK(L)	L1-45	2
6727.3407	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamidomethyl)QASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSR(F)	L1-61	3
11874.817	(-)DIQMTQSPSSLSASVGDRVTITC(Carbamidomethyl)QASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYFC(Carbamidomethyl)QHFDHLPLAFGGGTKVEIKR(T)	L1-108	6
3138.5677	(R)VTITC(Carbamidomethyl)QASQDISNYLNWYQQKPGKAPK(L)	L19-45	1
1747.9225	(K)LLIYDASNLETGVPSR(F)	L46-61	0
6895.3989	(K)LLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYFC(Carbamidomethyl)QHFDHLPLAFGGGTKVEIKR(T)	L46-108	3
5166.4942	(R)FSGSGSGTDFTFTISSLQPEDIATYFC(Carbamidomethyl)QHFDHLPLAFGGGTKVEIKR(T)	L62-108	2
2102.1281	(K)RTVAAPSVFIFPPSDEQLK(S)	L108-126	1
3881.0055	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L108-142	2
4209.1801	(K)RTVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L108-145	3
1946.027	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
3724.9043	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L109-142	1
4053.079	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L109-145	2

4594.3803	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWK(V)	L109-149	3
10923.3997	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L109-207	8
11773.7389	(R)TVAAPSVFIFPPSDEQLKSGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L109-214	10
2126.0699	(K)SGTASVVC(Carbamidomethyl)LLNNFYPREAK(V)	L127-145	1
8996.3906	(K)SGTASVVC(Carbamidomethyl)LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L127-207	7
7217.5132	(R)EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L143-207	6
8067.8524	(R)EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L143-214	8
4161.0106	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L146-183	2
6889.3385	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L146-207	5
7739.6777	(K)VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L146-214	7
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L150-183	1

6348.0372	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L150-207	4
2747.3457	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L184-207	2
3597.6849	(K)ADYEKHKVYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L184-214	4
2141.0808	(K)HKVYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L189-207	1
1875.9269	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L191-207	0
2726.2661	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTKSFNRGEC(Carbamidomethyl)(-)	L191-214	2
7260.539	(-)QVQLQESGPGLVKPSETLSLTC(Carbamidomethyl)TVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTNYNPSLK(S)	H1-66	2
14701.312	(-)QVQLQESGPGLVKPSETLSLTC(Carbamidomethyl)TVSGGSVSSGDYYWTWIRQSPGKGLEWIGHIYYSGNTNYNPSLKSRLTISIDTSKTQFSLKLSSVTAADTAIYYC(Carbamidomethyl)VRDRVTGAFDIWGQGTMVTVSSASTKGPSVFPLAPC(Carbamidomethyl)SR(S)	H1-135	9
2514.2293	(R)DRVTGAFDIWGQGTMVTVSSASTK(G)	H100-123	1
3782.8629	(R)DRVTGAFDIWGQGTMVTVSSASTKGPSVFPLAPC(Carbamidomethyl)SR(S)	H100-135	2
1287.6514	(K)GPSVFPLAPC(Carbamidomethyl)SR(S)	H124-135	0
1423.7097	(R)STSESTAALGC(Carbamidomethyl)LVK(D)	H136-149	0
8167.9492	(R)STSESTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC(Carbamidomethyl)NVDHKPSNTK(V)	H136-212	1
8510.1395	(R)STSESTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN	H136-215	2

	FGTQTYTC(Carbamidomethyl)NVDHKPSNTKVDK(T)		
9123.4943	(R)STSESTAALGC(Carbamidomethyl)LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC(Carbamidomethyl)NVDHKPSNTKVDKTVERK(C)	H136-220	4
6763.2573	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC(Carbamidomethyl)NVDHKPSNTK(V)	H150-212	0
7105.4477	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC(Carbamidomethyl)NVDHKPSNTKVDK(T)	H150-215	1
3036.4966	(R)KC(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPK(D)	H220-246	1
3852.913	(R)KC(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPKDTLMISR(T)	H220-253	2
7631.6704	(R)KC(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPKDTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVQFNWYVDGVEVHNAK(T)	H220-286	3
2908.4017	(K)C(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPK(D)	H221-246	0
3724.8181	(K)C(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPKDTLMISR(T)	H221-253	1
7503.5754	(K)C(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPKDTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVQFNWYVDGVEVHNAK(T)	H221-286	2
4614.1916	(K)DTLMISRTPEVTC(Carbamidomethyl)VVVDVSHEDPEVQFNWYVDGVEVHNAK(T)	H247-286	1

3797.7752	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVQFNWYVDGVEVHNAK(T)	H254-286	0
5279.5233	(K)TKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK(C)*	H287-318	3
5567.649	(K)TKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC(Carbamidomethyl)K(V)**	H287-320	4
9301.4297	(R)EEQFNSTFRVVSVLTVVHQDWLNGKEYKC(Carbamidomethyl)KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTK(N)***	H291-358	10
2214.1917	(R)VVSVLTVVHQDWLNGKEYK(C)	H300-318	1
2502.3173	(R)VVSVLTVVHQDWLNGKEYKC(Carbamidomethyl)K(V)	H300-320	2
2930.5557	(R)VVSVLTVVHQDWLNGKEYKC(Carbamidomethyl)KVSNK(G)	H300-324	3
3736.0255	(R)VVSVLTVVHQDWLNGKEYKC(Carbamidomethyl)KVSNKGLPAPIEK(T)	H300-332	4
1540.8516	(K)C(Carbamidomethyl)KVSNKGLPAPIEK(T)	H319-332	2
1252.726	(K)VSNKGLPAPIEK(T)	H321-332	1
1681.9847	(K)VSNKGLPAPIEKTISK(T)	H321-336	2
1911.1273	(K)VSNKGLPAPIEKTISKTK(G)	H321-338	3
1253.7464	(K)GLPAPIEKTISK(T)	H325-336	1
1482.889	(K)GLPAPIEKTISKTK(G)	H325-338	2
3807.0473	(K)GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTK(N)	H325-358	5
4949.6591	(K)GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H325-368	6
3001.5775	(K)TISKTKGQPREPQVYTLPPSREEMTK(N)	H333-358	4
4144.1893	(K)TISKTKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H333-368	5
2572.3188	(K)TKGQPREPQVYTLPPSREEMTK(N)	H337-358	3
3714.9306	(K)TKGQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H337-368	4
2343.1762	(K)GQPREPQVYTLPPSREEMTK(N)	H339-358	2
3485.7879	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H339-368	3

6010.9015	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H339-390	4
11479.482	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H339-437	8
12120.8204	(K)GQPREPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H339-444	9
1904.9422	(R)EPQVYTLPPSREEMTK(N)	H343-358	1
3047.554	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H343-368	2
5572.6676	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYK(T)	H343-390	3
1161.6296	(K)NQVSLTC(Carbamidomethyl)LVK(G)	H359-368	0
6129.9413	(K)NQVSLTC(Carbamidomethyl)LVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDK(S)	H359-412	3
5230.4626	(K)GFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR(W)	H369-414	3
8012.7119	(K)GFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H369-437	4
8654.0503	(K)GFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H369-444	5
5487.5984	(K)TTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H391-437	3
4242.0608	(K)LTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H408-444	3
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H415-437	0

3442.6056	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPG(-)	H415-444	1

*5279.5233 is the monoisotopic mass for H287-318 with G0F glycosylation.

**5567.649 is the monoisotopic mass for H287-320 with G0F glycosylation.

***9301.4297 is the monoisotopic mass for H291-358 with G0F glycosylation.

Table S-13. Light- and heavy-chain peptides identified from an overnight in-solution peptic digest of **Herceptin**.

m/z of [M+H]$^+$	Peptide Sequence	Amino Acids
1105.5848	(L)SASVGDRVTIT(C)	L12-22
1257.7314	(W)YQQKPGKAPKL(L)	L36-46
1919.9246	(F)LYSGVPSRFSGSRSGTDF(T)	L54-71
1659.7721	(L)YSGVPSRFSGSRSGTD(F)	L55-70
1806.8406	(L)YSGVPSRFSGSRSGTDF(T)	L55-71
1136.547	(L)TISSLQPEDF(A)	L74-83
3517.7573	(T)YYCQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L86-116
3207.6255	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSV(F)	L87-115
3354.694	(Y)YCQQHYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L87-116
2832.5043	(Q)HYTTPPTFGQGTKVEIKRTVAAPSVF(I)	L91-116
1192.5885	(V)FIFPPSDEQL(K)	L116-125
1675.8537	(F)IFPPSDEQLKSGTASV(V)	L117-132
1843.947	(F)PPSDEQLKSGTASVVCLL(N)	L119-136
1998.0113	(L)KSGTASVVCLLNNFYPRE(A)	L126-143
1052.516	(L)LNNFYPRE(A)	L136-143
2305.2088	(L)LNNFYPREAKVQWKVDNAL(Q)	L136-154
3035.497	(L)LNNFYPREAKVQWKVDNALQSGNSQE(S)	L136-161
2001.9988	(E)AKVQWKVDNALQSGNSQE(S)	L144-161
1271.7106	(E)AKVQWKVDNAL(Q)	L144-154
1559.7071	(E)SVTEQDSKDSTYSL(S)	L162-175
1834.8189	(E)SVTEQDSKDSTYSLSST(L)	L162-178
1998.0001	(T)LTLSKADYEKHKVYACE(V)	L179-195
1884.916	(L)TLSKADYEKHKVYACE(V)	L180-195
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
1411.6634	(L)SSPVTKSFNRGEC(-)	L202-214

2002.0022	(L)VESGGGLVQPGGSLRLSCAASG(F)	H5-26
1189.6000	(F)NIKDTYIHW(V)	H28-36
2225.1826	(F)NIKDTYIHWVRQAPGKGLE(W)	H28-46
2411.2619	(F)NIKDTYIHWVRQAPGKGLEW(V)	H28-47
1054.6004	(W)VRQAPGKGLE(W)	H37-46
1240.6797	(W)VRQAPGKGLEW(V)	H37-47
1176.6160	(E)WVARIYPTNG(Y)	H47-56
1462.7437	(G)YTRYADSVKGRF(T)	H57-68
1299.6804	(Y)TRYADSVKGRF(T)	H58-68
1271.6114	(F)TISADTSKNTAY(L)	H69-80
1075.5378	(M)NSLRAEDTAV(Y)	H84-93
1310.5259	(V)YYCSRWGGDGF(Y)	H94-104
1147.4626	(Y)YCSRWGGDGF(Y)	H95-104
2952.4983	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAALGC(L)	H116-147
2792.4676	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAAL(G)	H116-145
1366.7213	(L)VTVSSASTKGPSVF(P)	H116-129
2679.3836	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAA(L)	H116-144
1444.7642	(F)PLAPSSKSTSGGTAAL(G)	H130-145
1307.6882	(C)LVKDYFPEPVT(V)	H148-158
1194.6041	(L)VKDYFPEPVT(V)	H149-158
1293.6725	(L)VKDYFPEPVTV(S)	H149-159
1943.0021	(T)VSWNSGALTSGVHTFPAVL(Q)	H159-177
1562.7598	(T)VSWNSGALTSGVHTF(P)	H159-173
1843.9337	(V)SWNSGALTSGVHTFPAVL(Q)	H160-177
676.3665	(L)LGGPSVF(L)	H238-244
1433.7861	(V)FLFPPKPKDTLM(I)	H244-255
2832.5038	(V)FLFPPKPKDTLMISRTPEVTCVVVD(V)	H244-268
1286.7177	(F)LFPPKPKDTLM(I)	H245-255
1026.5652	(F)PPKPKDTLM(I)	H247-255
1136.5438	(L)MISRTPEVTC(V)	H255-264
1005.5034	(M)ISRTPEVTC(V)	H256-264
902.4942	(M)ISRTPEVT(C)	H256-263
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H265-280
1700.7915	(V)VDVSHEDPEVKFNW(Y)	H267-280
1486.6961	(D)VSHEDPEVKFNW(Y)	H269-280
4171.8209	(W)YVDGVEVHNAKTKPREEQYNSTY(R)*	H281-303
672.4403	(Y)RVVSVL(T)	H304-309
1439.7278	(L)TVLHQDWLNGKE(Y)	H310-321
3081.6190	(L)TVLHQDWLNGKEYKCKVSNKALPAPIE(K)	H310-336
4729.5610	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV(Y)	H310-351
1239.6117	(V)LHQDWLNGKE(Y)	H312-321

3308.8511	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQV(Y)	H322-351
4252.3275	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE(E)	H322-359
2610.4362	(E)KTISKAKGQPREPQVYTLPPSRE(E)	H337-359
1666.9599	(E)KTISKAKGQPREPQV(Y)	H337-351
962.4942	(V)YTLPPSRE(E)	H352-359
1049.5296	(E)EMTKNQVSL(T)	H360-368
1106.5874	(M)TKNQVSLTCL(V)	H362-371
912.4462	(L)VKGFYPSD(I)	H372-379
431.2500	(D)IAVE(W)	H380-383
2302.0986	(A)VEWESNGQPENNYKTTPPVL(D)	H382-401
2073.9876	(E)WESNGQPENNYKTTPPVL(D)	H384-401
1174.4760	(E)WESNGQPENN(Y)	H384-393
918.5295	(N)YKTTPPVL(D)	H394-401
770.4447	(F)FLYSKL(T)	H408-413
1564.7867	(L)TVDKSRWQQGNVF(S)	H414-426
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(-)	H427-449
2336.1452	(C)SVMHEALHNHYTQKSLSLSPG(-)	H429-449
2249.1132	(S)VMHEALHNHYTQKSLSLSPG(-)	H430-449

* 4171.8209 is the monoisotopic mass for H281-303 with G0F glycosylation.

Table S-14. Light- and heavy-chain peptides identified from an overnight in-solution peptic digest of **Avastin**.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids
1105.5848	(L)SASVGDRVTIT(C)	L12-22
1208.5940	(L)SASVGDRVTITC(S)	L12-23
1295.6260	(L)SASVGDRVTITCS(A)	L12-24
1933.0694	(L)NWYQQKPGKAPKVLIY(F)	L34-49
1356.7998	(W)YQQKPGKAPKVL(I)	L36-47
1632.9472	(W)YQQKPGKAPKVLIY(F)	L36-49
1562.7558	(F)TSSLHSGVPSRFSGSG(S)	L51-66
1681.7565	(L)HSGVPSRFSGSGSGTDF(T)	L55-71
886.4530	(L)HSGVPSRF(S)	L55-62
1534.6881	(L)HSGVPSRFSGSGSGTD(F)	L55-70
2439.3031	(Q)YSTVPWTFGQGTKVEIKRTVAA(P)	L91-112
2722.4563	(Q)YSTVPWTFGQGTKVEIKRTVAAPSV(F)	L91-115
2869.5247	(Q)YSTVPWTFGQGTKVEIKRTVAAPSVF(I)	L91-116

1192.5885	(V)FIFPPSDEQL(K)	L116-125
1045.5201	(F)IFPPSDEQL(K)	L117-125
649.3515	(L)KSGTASV(V)	L126-132
1052.5160	(L)LNNFYPRE(A)	L136-143
3035.4970	(L)LNNFYPREAKVQWKVDNALQSGNSQE(S)	L136-161
1271.7106	(E)AKVQWKVDNAL(Q)	L144-154
2001.9988	(E)AKVQWKVDNALQSGNSQE(S)	L144-161
1834.8189	(E)SVTEQDSKDSTYSLSST(L)	L162-178
1998.0001	(T)LTLSKADYEKHKVYACE(V)	L179-195
1884.9160	(L)TLSKADYEKHKVYACE(V)	L180-195
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
1237.5994	(S)PVTKSFNRGEC(-)	L204-214
2002.0022	(L)VESGGGLVQPGGSLRLSCAASG(Y)	H5-26
1240.6797	(N)WVRQAPGKGLE(W)	H36-46
1426.7590	(N)WVRQAPGKGLEW(V)	H36-47
1768.9282	(N)WVRQAPGKGLEWVGW(I)	H36-50
1582.8489	(W)VRQAPGKGLEWVGW(I)	H37-50
1240.6797	(W)VRQAPGKGLEW(V)	H37-47
2336.1458	(G)WINTYTGEPTYAADFKRRF(T)	H50-68
1001.5679	(D)FKRRFTF(S)	H64-70
1316.7110	(D)FKRRFTFSLD(T)	H64-73
1201.6840	(D)FKRRFTFSL(D)	H64-72
1054.6156	(F)KRRFTFSL(D)	H65-72
1075.5378	(M)NSLRAEDTAV(Y)	H84-93
2234.9429	(V)YYCAKYPHYYGSSHWYF(D)	H94-110
1075.5419	(F)DVWGQGTLVT(V)	H111-120
2792.4676	(L)VTVSSASTKGPSVFPLAPSSKSTSGGTAAL(G)	H119-148
1366.7213	(L)VTVSSASTKGPSVF(P)	H119-132
1444.7642	(F)PLAPSSKSTSGGTAAL(G)	H133-148
1604.7948	(F)PLAPSSKSTSGGTAALGC(L)	H133-150
1307.6882	(C)LVKDYFPEPVT(V)	H151-161
1194.6041	(L)VKDYFPEPVT(V)	H152-161
1604.7955	(Y)FPEPVTVSWNSGALT(S)	H156-170
1278.6325	(V)TVSWNSGALTSGV(H)	H161-173
1562.7598	(T)VSWNSGALTSGVHTF(P)	H162-176
1943.0021	(T)VSWNSGALTSGVHTFPAVL(Q)	H162-180
1843.9337	(V)SWNSGALTSGVHTFPAVL(Q)	H163-180
1176.6107	(V)VTVPSSSLGTQT(Y)	H192-203

1433.7861	(V)FLFPPKPKDTLM(I)	H247-258
1286.7177	(F)LFPPKPKDTLM(I)	H248-258
1173.6336	(L)FPPKPKDTLM(I)	H249-258
1026.5652	(F)PPKPKDTLM(I)	H250-258
1005.5034	(M)ISRTPEVTC(V)	H259-267
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H268-283
1799.8599	(V)VVDVSHEDPEVKFNW(Y)	H269-283
1601.7231	(V)DVSHEDPEVKFNW(Y)	H271-283
1486.6961	(D)VSHEDPEVKFNW(Y)	H272-283
4171.8209	(W)YVDGVEVHNAKTKPREEQYNSTY(R)*	H284-306
3737.6407	(G)VEVHNAKTKPREEQYNSTY(R)**	H288-306
672.4403	(Y)RVVSVL(T)	H307-312
1439.7278	(L)TVLHQDWLNGKE(Y)	H313-324
3081.6190	(L)TVLHQDWLNGKEYKCKVSNKALPAPIE(K)	H313-339
1239.6117	(V)LHQDWLNGKE(Y)	H315-324
3308.8511	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQV(Y)	H325-354
4252.3275	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE(E)	H325-362
1666.9599	(E)KTISKAKGQPREPQV(Y)	H340-354
2610.4362	(E)KTISKAKGQPREPQVYTLPPSRE(E)	H340-362
962.4942	(V)YTLPPSRE(E)	H355-362
1049.5296	(E)EMTKNQVSL(T)	H363-371
912.4462	(L)VKGFYPSD(I)	H375-382
2302.0986	(A)VEWESNGQPENNYKTTPPVL(D)	H385-404
2073.9876	(E)WESNGQPENNYKTTPPVL(D)	H387-404
770.4447	(F)FLYSKL(T)	H411-416
1564.7867	(L)TVDKSRWQQGNVF(S)	H417-429
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H430-452
2336.1452	(C)SVMHEALHNHYTQKSLSLSPG(K)	H432-452

*4171.8209 is the monoisotopic mass for H284-306 with G0F glycosylation.

**3737.6407 is the monoisotopic mass for H288-306 with G0F glycosylation.

Table S-15. Light- and heavy-chain peptides identified from an overnight in-solution peptic digest of **Rituxan**.

m/z of [M+H]$^+$	Peptide Sequence	Amino Acids
715.3985	(L)SQSPAIL(S)	L5-11
2099.0861	(Y)IHWFQQKPGSSPKPWIY(A)	L32-48
1452.7077	(L)ASGVPVRFSGSGSGTS(Y)	L54-69
1615.7711	(L)ASGVPVRFSGSGSGTSY(S)	L54-70
1815.8872	(L)ASGVPVRFSGSGSGTSYSL(T)	L54-72
1916.9348	(L)ASGVPVRFSGSGSGTSYSLT(I)	L54-73
1462.7384	(Y)SLTISRVEAEDAAT(Y)	L71-84
1219.6165	(Y)SLTISRVEAED(A)	L71-81
1462.7325	(Q)WTSNPPTFGGGTKL(E)	L90-103
1317.7525	(L)EIKRTVAAPSVF(I)	L104-115
1045.5201	(F)IFPPSDEQL(K)	L116-124
1998.0113	(L)KSGTASVVCLLNNFYPRE(A)	L125-142
1052.516	(L)LNNFYPRE(A)	L135-142
3035.497	(L)LNNFYPREAKVQWKVDNALQSGNSQE(S)	L135-160
2001.9988	(E)AKVQWKVDNALQSGNSQE(S)	L143-160
2089.0309	(E)AKVQWKVDNALQSGNSQES(V)	L143-161
1559.7071	(E)SVTEQDSKDSTYSL(S)	L161-174
1834.8189	(E)SVTEQDSKDSTYSLSST(L)	L161-177
1998.0001	(T)LTLSKADYEKHKVYACE(V)	L178-194
1694.9112	(T)LTLSKADYEKHKVY(A)	L178-191
1884.916	(L)TLSKADYEKHKVYACE(V)	L179-194
1670.7843	(L)SKADYEKHKVYACE(V)	L181-194
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L195-213
1943.0089	(Q)LQQPGAELVKPGASVKMSC(K)	H4-22
4089.9552	(C)KASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTS(Y)	H23-59
773.3828	(C)KASGYTF(T)	H23-29
2360.1604	(F)TSYNMHWVKQTPGRGLEWIG(A)	H30-49
1874.9330	(F)TSYNMHWVKQTPGRGL(E)	H30-45
2009.0174	(Y)NMHWVKQTPGRGLEWIG(A)	H33-49
1005.5040	(L)EWIGAIYPG(N)	H46-54
2273.1561	(G)AIYPGNGDTSYNQKFKGKATL(T)	H50-70
1925.9716	(Y)PGNGDTSYNQKFKGKATL(T)	H53-70
1134.6630	(Y)NQKFKGKATL(T)	H61-70
1030.4687	(L)TADKSSSTAY(M)	H71-80

1092.4415	(Y)CARSTYYGGD(W)	H96-105
1005.5000	(F)NVWGAGTTVT(V)	H109-118
2776.4727	(T)VTVSAASTKGPSVFPLAPSSKSTSGGTAAL(G)	H117-146
2736.3873	(T)VSAASTKGPSVFPLAPSSKSTSGGTAALGC(L)	H119-148
2576.3566	(T)VSAASTKGPSVFPLAPSSKSTSGGTAAL(G)	H119-146
2319.2191	(A)ASTKGPSVFPLAPSSKSTSGGTAAL(G)	H122-146
1444.7642	(F)PLAPSSKSTSGGTAAL(G)	H131-146
1604.7948	(F)PLAPSSKSTSGGTAALGC(L)	H131-148
2009.0015	(C)LVKDYFPEPVTVSWNSGA(L)	H149-166
1194.6041	(L)VKDYFPEPVT(V)	H150-159
1293.6725	(L)VKDYFPEPVTV(S)	H150-160
1943.0021	(T)VSWNSGALTSGVHTFPAVL(Q)	H160-178
1562.7598	(T)VSWNSGALTSGVHTF(P)	H160-174
1843.9337	(V)SWNSGALTSGVHTFPAVL(Q)	H161-178
1241.6888	(A)LTSGVHTFPAVL(Q)	H167-178
1275.6791	(S)VVTVPSSSLGTQT(Y)	H189-201
1176.6107	(V)VTVPSSSLGTQT(Y)	H190-201
1005.5034	(D)KKAEPKSCD(K)	H217-225
2267.0617	(D)KKAEPKSCDKTHTCPPCPAPE(L)	H217-237
676.3665	(L)LGGPSVF(L)	H239-245
1433.7861	(V)FLFPPKPKDTLM(I)	H245-256
1286.7177	(F)LFPPKPKDTLM(I)	H246-256
929.5091	(L)FPPKPKDT(L)	H247-254
1026.5652	(F)PPKPKDTLM(I)	H248-256
1005.5034	(M)ISRTPEVTC(V)	H257-265
1302.7086	(M)ISRTPEVTCVVV(D)	H257-268
1898.9283	(C)VVVDVSHEDPEVKFNW(Y)	H266-281
1601.7231	(V)DVSHEDPEVKFNW(Y)	H269-281
1486.6961	(D)VSHEDPEVKFNW(Y)	H270-281
4171.8209	(W)YVDGVEVHNAKTKPREEQYNSTY(R)*	H282-304
3737.6407	(G)VEVHNAKTKPREEQYNSTY(R)**	H286-304
672.4403	(Y)RVVSVL(T)	H305-310
4729.5610	(L)TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV(Y)	H311-352
1439.7278	(L)TVLHQDWLNGKE(Y)	H311-322
3081.6190	(L)TVLHQDWLNGKEYKCKVSNKALPAPIE(K)	H311-337
1239.6117	(V)LHQDWLNGKE(Y)	H313-322

1660.9091	(E)YKCKVSNKALPAPIE(K)	H323-337
3308.8511	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQV(Y)	H323-352
5250.8671	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL(T)	H323-369
4480.4385	(E)YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL(T)	H323-362
3608.9759	(E)KTISKAKGQPREPQVYTLPPSRDELTKNQVSL(T)	H338-369
2838.5472	(E)KTISKAKGQPREPQVYTLPPSRDEL(T)	H338-362
1666.9599	(E)KTISKAKGQPREPQV(Y)	H338-352
1961.0338	(V)YTLPPSRDELTKNQVSL(T)	H353-369
1583.8388	(L)PPSRDELTKNQVSL(T)	H356-369
2598.3272	(L)TKNQVSLTCLVKGFYPSDIAVEW(E)	H363-385
2302.0986	(A)VEWESNGQPENNYKTTPPVL(D)	H383-402
2073.9876	(E)WESNGQPENNYKTTPPVL(D)	H385-402
770.4447	(F)FLYSKL(T)	H409-414
1564.7867	(L)TVDKSRWQQGNVF(S)	H415-427
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H428-450

*4171.8209 is the monoisotopic mass for H282-304 with G0F glycosylation.

**3737.6407 is the monoisotopic mass for H286-304 with G0F glycosylation.

Table S-16. Light- and heavy-chain peptides identified from an overnight in-solution peptic digest of **Vectibix**.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids
1336.6525	(L)SASVGDRVTITCQ(A)	L12-24
1407.6897	(L)SASVGDRVTITCQA(S)	L12-25
1834.0010	(N)YLNWYQQKPGKAPKL(L)	L32-46
1670.9377	(L)NWYQQKPGKAPKLL(I)	L34-47
1257.7314	(W)YQQKPGKAPKL(L)	L36-46
1483.8995	(W)YQQKPGKAPKLLI(Y)	L36-48
1669.9636	(Y)QQKPGKAPKLLIYDA(S)	L37-51
1653.7715	(N)LETGVPSRFSGSGSGTD(F)	L54-70
1979.9637	(D)FTFTISSLQPEDIATYF(C)	L71-87
3288.5710	(D)FTFTISSLQPEDIATYFCQHFDHLPLAF(G)	L71-98

1490.6885	(T)YFCQHFDHLPLA(F)	L86-97
2266.0750	(T)YFCQHFDHLPLAFGGGTKVE(I)	L86-105
3005.5454	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAA(P)	L86-112
3288.6986	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSV(F)	L86-115
3435.7671	(T)YFCQHFDHLPLAFGGGTKVEIKRTVAAPSVF(I)	L86-116
2842.4821	(Y)FCQHFDHLPLAFGGGTKVEIKRTVAA(P)	L87-112
1386.8063	(F)GGGTKVEIKRTVAA(P)	L99-112
1669.9595	(F)GGGTKVEIKRTVAAPSV(F)	L99-115
1817.0280	(F)GGGTKVEIKRTVAAPSVF(I)	L99-116
1045.5201	(F)IFPPSDEQL(K)	L117-125
1165.6000	(C)LLNNFYPRE(A)	L135-143
1052.5160	(L)LNNFYPRE(A)	L136-143
3035.4970	(L)LNNFYPREAKVQWKVDNALQSGNSQE(S)	L136-161
2001.9988	(E)AKVQWKVDNALQSGNSQE(S)	L144-161
1389.6605	(W)KVDNALQSGNSQE(S)	L149-161
1463.6609	(D)NALQSGNSQESVTE(Q)	L152-165
1559.7071	(E)SVTEQDSKDSTYSL(S)	L162-175
1694.9112	(T)LTLSKADYEKHKVY(A)	L179-192
1998.0001	(T)LTLSKADYEKHKVYACE(V)	L179-195
1581.8271	(L)TLSKADYEKHKVY(A)	L180-192
1884.9160	(L)TLSKADYEKHKVYACE(V)	L180-195
1490.6944	(V)YACEVTHQGLSSPV(T)	L192-205
2047.0025	(E)VTHQGLSSPVTKSFNRGEC(-)	L196-214
1328.6692	(L)QESGPGLVKPSET(L)	H5-17
1456.7696	(T)WIRQSPGKGLEW(I)	H38-49
3250.6069	(T)WIRQSPGKGLEWIGHIYYSGNTNYNPSL(K)	H38-65
1854.0021	(W)IRQSPGKGLEWIGHIY(Y)	H39-54
3064.5275	(W)IRQSPGKGLEWIGHIYYSGNTNYNPSL(K)	H39-65
3435.7556	(I)RQSPGKGLEWIGHIYYSGNTNYNPSLKSRL(T)	H40-69
2127.9770	(L)EWIGHIYYSGNTNYNPSL(K)	H48-65
1812.8551	(W)IGHIYYSGNTNYNPSL(K)	H50-65
1240.6420	(L)TISIDTSKTQF(S)	H70-80
834.4931	(F)SLKLSSVT(A)	H81-88
2035.9542	(A)ADTAIYYCVRDRVTGAFD(I)	H90-107

3256.6419	(C)VRDRVTGAFDIWGQGTMVTVSSASTKGPSVF(P)	H98-128
1336.6566	(D)IWGQGTMVTVSSA(S)	H108-120
1366.7213	(M)VTVSSASTKGPSVF(P)	H115-128
2495.2446	(M)VTVSSASTKGPSVFPLAPCSRSTSE(S)	H115-139
2683.3243	(M)VTVSSASTKGPSVFPLAPCSRSTSEST(A)	H115-141
2938.4826	(M)VTVSSASTKGPSVFPLAPCSRSTSESTAAL(G)	H115-144
1166.6052	(T)VSSASTKGPSVF(P)	H117-128
2483.2082	(T)VSSASTKGPSVFPLAPCSRSTSEST(A)	H117-141
1307.6882	(C)LVKDYFPEPVT(V)	H147-157
1194.6041	(L)VKDYFPEPVT(V)	H148-157
2938.4945	(F)PEPVTVSWNSGALTSGVHTFPAVLQSSGL(Y)	H153-181
1562.7598	(T)VSWNSGALTSGVHTF(P)	H158-172
1943.0021	(T)VSWNSGALTSGVHTFPAVL(Q)	H158-176
1128.6048	(L)TSGVHTFPAVL(Q)	H166-176
1240.6420	(V)LQSSGLYSLSSV(V)	H176-187
850.4305	(V)VTVPSSNF(G)	H188-195
2178.0496	(T)YTCNVDHKPSNTKVDKTVE(R)	H200-218
1194.5969	(D)KTVERKCCVE(C)	H215-224
1433.7861	(V)FLFPPKPKDTLM(I)	H239-250
1286.7177	(F)LFPPKPKDTLM(I)	H240-250
1173.6336	(L)FPPKPKDTLM(I)	H241-250
1026.5652	(F)PPKPKDTLM(I)	H242-250
1005.5034	(M)ISRTPEVTC(V)	H251-259
1104.5718	(M)ISRTPEVTCV(V)	H251-260
3646.7370	(M)ISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV(H)	H251-282
1598.7697	(C)VVVDVSHEDPEVQF(N)	H260-273
1499.7013	(V)VVDVSHEDPEVQF(N)	H261-273
1186.5375	(D)VSHEDPEVQF(N)	H264-273
4139.8311	(W)YVDGVEVHNAKTKPREEQFNSTF(R)*	H276-298
672.4403	(F)RVVSVL(T)	H299-304
1425.7121	(L)TVVHQDWLNGKE(Y)	H305-316
3053.5877	(L)TVVHQDWLNGKEYKCKVSNKGLPAPIE(K)	H305-331
4731.5403	(L)TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV(Y)	H305-346
1646.8934	(E)YKCKVSNKGLPAPIE(K)	H317-331

3324.8460	(E)YKCKVSNKGLPAPIEKTISKTKGQPREPQV(Y)	H317-346
4268.3224	(E)YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE(E)	H317-354
2930.6786	(C)KVSNKGLPAPIEKTISKTKGQPREPQV(Y)	H320-346
1696.9704	(E)KTISKTKGQPREPQV(Y)	H332-346
2640.4468	(E)KTISKTKGQPREPQVYTLPPSRE(E)	H332-354
962.4942	(V)YTLPPSRE(E)	H347-354
1049.5296	(E)EMTKNQVSL(T)	H355-363
912.4462	(L)VKGFYPSD(I)	H367-374
431.2500	(D)IAVE(W)	H375-378
2105.9597	(E)WESNGQPENNYKTTPPML(D)	H379-396
770.4447	(F)FLYSKL(T)	H403-408
1564.7867	(L)TVDKSRWQQGNVF(S)	H409-421
2526.1864	(F)SCSVMHEALHNHYTQKSLSLSPG(K)	H422-444
2336.1452	(C)SVMHEALHNHYTQKSLSLSPG(K)	H424-444

*4139.8311 is the monoisotopic mass for H276-298 with G0F glycosylation.

Table S-17. Light- and heavy-chain peptides identified from an overnight in-solution tryptic digest of **Herceptin**.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids	Missed cleavages
1878.8862	(-)DIQMTQSPSSLSASVGDR(V)	L1-18	0
1990.9981	(R)ASQDVNTAVAWYQQKPGK(A)	L25-42	0
1772.9581	(K)LLIYSASFLYSGVPSR(F)	L46-61	0
4187.9179	(R)SGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQHYTTPPTFGQGTK(V)	L67-103	0
1946.0270	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
1797.8952	(K)SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L127-142	0
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L150-183	1
1502.7584	(K)DSTYSLSSTLTLSK(A)	L170-183	0
1882.0029	(-)EVQLVESGGGLVQPGGSLR(L)	H1-19	0
1895.9763	(K)GLEWVARIYPTNGYTR(Y)	H44-69	1
1845.9341	(R)YADSVKGRFTISADTSK(N)	H60-76	1
2784.2610	(R)WGGDGFYAMDYWGQGTLVTVSSASTK(G)	H99-124	0

6713.3145	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTK(V)	H151-213	0
2844.4575	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H226-251	0
2139.0274	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H259-277	0
1677.8020	(K)FNWYVDGVEVHNAK(T)	H278-291	0
1808.0065	(R)VVSVLTVLHQDWLNGK(E)	H305-320	0
1161.6296	(K)NQVSLTC(Carbamidomethyl)LVK(G)	H364-373	0
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H374-395	0
1873.9218	(K)TTPPVLDSDGSFFLYSK(L)	H396-412	0
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H420-442	0

Table S-18. Light- and heavy-chain peptides identified from an overnight in-solution tryptic digest of **Avastin**.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids	Missed cleavages
1878.8862	(-)DIQMTQSPSSLSASVGDR(V)	L1-18	0
2801.3563	(R)VTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGK(A)	L19-42	0
1762.9486	(K)VLIYFTSSLHSGVPSR(F)	L46-61	0
4660.1137	(R)FSGSGSGTDFTLTISSLQPEDFATYYC(Carbamidomethyl)QQYSTVPWTFGQGTK(V)	L62-103	0
1946.0270	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
1797.8952	(K)SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L127-142	0
1502.7584	(K)DSTYSLSSTLTLSK(A)	L170-183	0
1882.0029	(-)EVQLVESGGGLVQPGGSLR(L)	H1-19	0
2197.9794	(R)LSC(Carbamidomethyl)AASGYTFTNYGMNWVR(Q)	H20-38	0
2518.1925	(K)GLEWVGWINTYTGEPTYAADFK(R)	H44-65	0
2674.2936	(K)GLEWVGWINTYTGEPTYAADFKR(R)	H44-66	1
1045.5201	(R)FTFSLDTSK(S)	H68-76	0
3323.5433	(K)YPHYYGSSHWYFDVWGQGTLVTVSSASTK(G)	H99-127	0

6713.3145	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTK(V)	H154-216	0
2844.4575	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H229-254	0
2139.0274	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H262-280	0
1677.8020	(K)FNWYVDGVEVHNAK(T)	H281-294	0
1808.0065	(R)VVSVLTVLHQDWLNGK(E)	H308-323	0
1161.6296	(K)NQVSLTC(Carbamidomethyl)LVK(G)	H367-376	0
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H377-398	0
1873.9218	(K)TTPPVLDSDGSFFLYSK(L)	H399-415	0
2801.2671	(R)VTITC(Carbamidomethyl)SASQDISNYLNWYQQKPGK(A)	H423-445	0

Table S-19. Light- and heavy-chain peptides identified from an overnight in-solution tryptic digest of **Rituxan**.

m/z of $[M+H]^+$	Peptide Sequence	Amino Acids	Missed cleavages
3933.0082	(R)ASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVR(F)	L25-60	0
1606.7707	(R)FSGSGSGTSYSLTISR(V)	L61-76	0
2878.2625	(R)VEAEDAATYYC(Carbamidomethyl)QQWTSNPPTFGGGTK(L)	L77-102	0
2102.1281	(K)RTVAAPSVFIFPPSDEQLK(S)	L107-125	1
1946.0270	(R)TVAAPSVFIFPPSDEQLK(S)	L108-125	0
1797.8952	(K)SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L126-141	0
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L149-182	1
1502.7584	(K)DSTYSLSSTLTLSK(A)	L169-182	0
1875.9269	(K)VYAC(Carbamidomethyl)EVTHQGLSSPVTK(S)	L190-206	0
1960.0862	(-)QVQLQQPGAELVKPGASVK(M)	H1-19	0
1791.8159	(K)ASGYTFTSYNMHWVK(Q)	H24-38	0
2183.0404	(R)GLEWIGAIYPGNGDTSYNQK(F)	H44-63	0
2677.1756	(K)SSSTAYMQLSSLTSEDSAVYYC(Carbamidomethyl)AR(S)	H75-98	0

2889.3366	(R)STYYGGDWYFNVWGAGTTVTVSAASTK(G)	H99-125	0
1186.6467	(K)GPSVFPLAPSSK(S)	H126-137	0
6713.3145	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC(Carbamidomethyl)NVNHKPSNTK(V)	H152-214	0
2844.4575	(K)THTC(Carbamidomethyl)PPC(Carbamidomethyl)PAPELLGGPSVFLFPPKPK(D)	H227-252	0
2139.0274	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVK(F)	H260-278	0
1677.8020	(K)FNWYVDGVEVHNAK(T)	H279-292	0
1808.0065	(R)VVSVLTVLHQDWLNGK(E)	H306-321	0
1872.9702	(R)EPQVYTLPPSRDELTK(N)	H349-364	1
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H375-396	0
1873.9218	(K)TTPPVLDSDGSFFLYSK(L)	H397-413	0
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H421-433	0

Table S-20. Light- and heavy-chain peptides identified from an overnight in-solution tryptic digest of **Vectibix**.

m/z of [M+H]$^+$	Peptide Sequence	Amino Acids	Missed cleavages
2842.3829	(R)VTITC(Carbamidomethyl)QASQDISNYLNWYQQKPGK(A)	L19-42	0
1747.9225	(K)LLIYDASNLETGVPSR(F)	L46-61	0
4541.1031	(R)FSGSGSGTDFTFTISSLQPEDIATYFC(Carbamidomethyl)QHFDHLPLAFGGGTK(V)	L62-103	0
1946.0270	(R)TVAAPSVFIFPPSDEQLK(S)	L109-126	0
1797.8952	(K)SGTASVVC(Carbamidomethyl)LLNNFYPR(E)	L127-142	0
3619.7093	(K)VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK(A)	L150-183	1
1502.7584	(K)DSTYSLSSTLTLSK(A)	L170-183	0
4373.1394	(-)QVQLQESGPGLVKPSETLSLTC(Carbamidomethyl)TVSGGSVSSGDYYWTWIR(Q)	H1-40	0
2426.1775	(K)GLEWIGHIYYSGNTNYNPSLK(S)	H46-66	0
977.5514	(R)LTISIDTSK(T)	H69-77	0

1789.8789	(K)LSSVTAADTAIYYC(Carbamidomethyl)VR(D)	H84-99	0
2514.2293	(R)DRVTGAFDIWGQGTMVTVSSASTK(G)	H100-123	0
2243.1013	(R)VTGAFDIWGQGTMVTVSSASTK(G)	H102-123	0
6763.2573	(K)DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC(Carbamidomethyl)NVDHKPSNTK(V)	H150-212	0
3036.4966	(R)KC(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPK(D)	H220-246	1
2908.4017	(K)C(Carbamidomethyl)C(Carbamidomethyl)VEC(Carbamidomethyl)PPC(Carbamidomethyl)PAPPVAGPSVFLFPPKPK(D)	H221-246	0
3797.7752	(R)TPEVTC(Carbamidomethyl)VVVDVSHEDPEVQFNWYVDGVEVHNAK(T)	H254-286	0
1793.9908	(R)VVSVLTVVHQDWLNGK(E)	H300-315	0
3047.5540	(R)EPQVYTLPPSREEMTKNQVSLTC(Carbamidomethyl)LVK(G)	H343-368	1
2544.1314	(K)GFYPSDIAVEWESNGQPENNYK(T)	H369-390	0
4370.1557	(K)LTVDKSRWQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQKSLSLSPGK(-)	H408-445	2
2801.2671	(R)WQQGNVFSC(Carbamidomethyl)SVMHEALHNHYTQK(S)	H415-437	0

Table S-21. Herceptin sequence coverage from tryptic spin digestion of 0.1-mL solutions containing different amounts of antibody. Analysis employed nanoLC-MS/MS.

ng	fmol	Coverage/%	Unique peptides
1	6.7	15	9
5	33.3	34	20
10	66.7	37	24
25	166.7	43	26
50	333.3	49	33
100	666.7	73	47