

Table S1A**MS/MS results of 7 spots from Avastin (MASCOT) Identified by HCT**

Avastin was separated by 2-DE and identified by nano-LC-ESI-CID/ETD-MS/MS using the MASCOT search engine.

Spot	Coverage	Identified Peptide (enzyme/ion score/mass error)
1	64%	1 -.EVQLVESGGGLVQPGGSLR.L 19 (Try/122/-0.1042) 3 V.QLVESGGGLVQPGGSLR.L 19 (Try/101/0.0307) 20 R.LSCAASGYTF.T 29 (Try/30/-0.0457) 20 R.LSCAASGYTFTNYGM.N 34 (Try/79/0.0857) 20 R.LSCAASGYTFTNYGM*N.W Oxidation(M) 35 (Try/69/0.0151) 20 R.LSCAASGYTFTNYGMNWVR.Q 38 (Try/108/0.0564) 28 Y.TFTNYGMNWVR.Q 38 (Try/37/0.1675) 51 W.INTYTGEPTYAADFK.R 65 (Try/73/-0.1062) 53 N.TYTGEPTYAADFK.R 65 (Try/69/0.0056) 77 K.STAYLQMNSLR.A 87 (Try/39/0.0311) 77 K.STAYLQM*NSLR.A Oxidation(M) 87 (Try/63/0.077) 80 A.YLQMNSLR.A 87 (Try/30/0.1719) 88 R.AEDTAVYYCAK.Y 98 (Try/79/0.0829) 128 K.GPSVFPLAPSSK.S 139 (Try/44/-0.0045) 129 G.PSVFPLAPSSK.S 139 (Try/34/0.1217) 140 K.STSGGTAALGCLVK.D 153 (Try/63/0.0663) 142 T.SGGTAALGCLVK.D 153 (Try/56/0.1502) 154 K.DYFPEPVTVSWN.S 165 (Try/64/0.1589) 154 K.DYFPEPVTVSWNSGAL.T 169 (Try/41/-0.0076) 154 K.DYFPEPVTVSWNSGALTS.G 171 (Try/62/-0.0731) 187 Y.SLSSVVTVPSSSLGTQTY.I 204 (Try/38/0.0799) 189 L.SSVVTVPSSSLGTQTY.I 204 (Try/41/0.0204) 189 L.SSVVTVPSSSLGTQTYICNVN.H 209 (Try/54/-0.0827) 190 S.SVVTVPSSSLGTQTYICNVN.H 209 (Try/78/-0.0301) 229 K.THTCPPCPAPELLGGPS.V 245 (Try/66/0.0887) 229 K.THTCPPCPAPELLGGPSVF.L 247 (Try/36/-0.021) 238 A.PELLGGPSVFLFPPKPK.D 254 (Try/57/-0.012) 262 R.TPEVTCVVVDVSHED.P 276 (Try/70/-0.0124) 262 R.TPEVTCVVVDVSHEDPEVK.F 280 (Try/69/0.1366) 281 K.FNWYVDGVEVHNAK.T 294 (Try/92/0.0217) 308 R.VVSVLTVLHQDWLNGK.E 323 (Try/69/0.0032) 351 R.EPQVYTLPPSR.E 361 (Try/50/0.0428) 352 E.PQVYTLPPSR.E 361 (Try/68/0.0596) 367 K.NQVSLTCLVK.G 376 (Try/43/-0.0621) 377 K.GFYPSDIAVEWESNGQPENNYK.T 398 (Try/37/0.1155) 399 K.TTPPVLDSDGSFFLY.S 413 (Try/62/0.0637) 401 T.PPVLDSDGSFFLYSK.L 415 (Try/103/0.0856) 430 F.SCSVMHEALHNHYTQK.S 445 (Try/53/-0.0259)
2	96%	1 -.EVQLVESGGGLVQPGGSLRLSCAASGY.T 27 (Chy/35/0.019)

	1 -.EVQLVESGGGLVQPGGSLR.L 19 (Try/94/-0.1454) 4 Q.LVESGGGLVQPGGSLR.L 19 (Try/41/0.011) 4 Q.LVESGGGLVQPGGSL.L 17 (Pep/40/-0.0176) 4 Q.LVESGGGLVQPGGSL.R 18 (Pep/39/0.1023) 5 L.VESGGGLVQPGGSLRL.S 20 (Pep/44/0.1566) 14 Q.PGGSL.R 18 (ProK/32/0.0536) 20 R.LSCAASGYTFTNYGMNWVR.Q 38 (Chy/104/-0.1228) 20 R.LSCAASGYTFTNYGMNWVR.Q 38 (Try/129/-0.1398) 20 R.LSCAASGYTFTNYGM*NWVR.Q Oxidation(M) 38 (Try/98/-0.1966) 21 L.SCAASGY.T 27 (Chy/31/0.0629) 23 C.AASGYTFTNYGMNWVR.Q 38 (Try/72/0.0049) 25 A.SGYTFTNYGMNWVR.Q 38 (Try/44/0.0155) 28 Y.TFTNYGMNWVR.Q 38 (Try/57/0.0823) 36 N.WVRQAPGKGLE.W 46 (Pep/44/0.0977) 36 N.WVRQAPGKGLEW.V 47 (Pep/42/0.0867) 36 N.WVRQAPGKGLEWVG.W 49 (Pep/45/0.1176) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65 (Chy/64/-0.0982) 44 K.GLEWVGWINTY.T 54 (Try/67/0.0785) 44 K.GLEWVGWINTYTGEPT.Y 59 (Try/38/-0.0413) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65 (Try/142/-0.172) 53 N.TYTGEPTYAADFK.R 65 (Try/37/0.1066) 55 Y.TGEPTYAADF.K 64 (Chy/31/-0.0055) 55 Y.TGEPTYAADFK.R 65 (Try/33/0.0288) 56 T.GEPTYAADFK.R 65 (Try/40/-0.1127) 67 R.RFTFSLDTSK.S 76 (Try/42/0.097) 71 F.SLDTSKSTAY.L 80 (Chy/43/0.18) 73 L.DTSKSTAY.L 80 (Chy/40/0.0273) 74 D.TSKSTAY.L 80 (Chy/37/0.0948) 77 K.STAYLQMNSLR.A 87 (Try/46/0.0563) 77 K.STAYLQM*NSLR.A Oxidation(M) 87 (Try/58/0.086) 81 Y.LQMNSLRAEDTAVY.Y 94 (Chy/42/0.0267) 87 L.RAEDTAVY.Y 94 (Pep/48/-0.0209) 88 R.AEDTAVYYCAK.Y 98 (Try/80/0.1271) 94 V.YYCAKYPHY.Y 102 (Pep/34/0.0194) 94 V.YYCAKYPHYYGSS.H 106 (Pep/37/-0.0309) 95 Y.YCAKYPHYYGSS.H 106 (Pep/42/0.0653) 95 Y.YCAKYPHYYGSSHW.Y 108 (Pep/40/-0.0978) 109 W.YFDVWGQGT.L.V 118 (Chy/35/-0.0471) 119 L.VTVSSASTKGPSVF.P 132 (Pep/55/0.1004) 119 L.VTVSSASTKGPSVFPLAPSSKSTSGGTAAL.G 148 (Pep/41/0.0643) 121 T.VSSASTKGPSVFPLAPSSKSTSGGTAAL.G 148 (Pep/39/-0.117) 122 V.SSASTKGPSVFPLAPSSKSTSGGTAAL.G 148 (Chy/38/0.0429) 125 A.STKGPSVFPLAPS.S 137 (Pep/31/0.1378) 127 T.KGPSVFPLAPS.S 137 (Pep/34/0.02) 128 K.GPSVFPLAPSSK.S 139 (Try/49/-0.0171) 133 F.PLAPSSKSTSGGTAAL.G 148 (Pep/81/-0.0551) 140 K.STSGGTAALGCLVK.D 153 (Try/67/0.1415) 142 T.SGGTAALGCLVK.D 153 (Try/52/0.0668)
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	149 L.GCLVKDYFPEPVTVSW.N 164 (Chy/95/-0.0597)
	149 L.GCLVKDYFPEPVTVSWNSGAL.T 169 (Chy/52/-0.1971)
	149 L.GCLVKDYFPEPVTVSWNSGALTSGVH.T 174 (Chy/65/-0.158)
	151 C.LVKDYFPEPVTVS.W 163 (Pep/59/0.1083)
	152 L.VKDYFPEPVT.V 161 (Pep/33/0.0624)
	154 K.DYFPEPVTVS.W 163 (ProK/56/-0.0063)
	154 K.DYFPEPVTVSWN.S 165 (Try/63/-0.0503)
	154 K.DYFPEPVTVSWNSGAL.T 169 (Try/77/0.0598)
	154 K.DYFPEPVTVSWN*SGALTSGVHTFPAVLQ.S Deamidation(N) 181 (Try/61/0.0427)
	162 T.VSWNSGALTSGVHTF.P 176 (Pep/59/0.1051)
	163 V.SWNSGALTSGVHTF.P 176 (Pep/61/0.0795)
	166 N.SGALTSGVHTFPAVLQSSGLY.S 186 (Chy/44/-0.032)
	166 N.SGALTSGVHTFPAVLQ.S 181 (Try/29/0.0649)
	166 N.SGALTSGVHTFPAVLQSS.G 183 (Try/58/0.0458)
	166 N.SGALTSGVHTFPAVLQSSGLY.S 186 (Try/52/-0.044)
	170 L.TSGVHTFPAVLQSSGLY.S 186 (Chy/93/0.0826)
	171 T.SGVHTFPAVLQSSGLY.S 186 (Chy/63/0.1327)
	175 H.TFPAVLQSSGLY.S 186 (Chy/64/-0.0163)
	177 F.PAVLQ.S 181 (ProK/27/0.0383)
	187 Y.SLSSVVTVPSSSLGTQTY.I 204 (Chy/41/-0.0127)
	189 L.SSVVTVPSSSL.G 199 (ProK/39/0.0134)
	189 L.SSVVTVPSSSLGTQTYICNVNHKPSNTK.V 216 (Try/46/-0.1276)
	191 S.VVTVPSSSLGTQT.Y 203 (Pep/31/0.0194)
	195 V.PSSSLGTQTY.I 204 (Chy/39/-0.0363)
	197 S.SSLGTQTYICNVNHKPSNTK.V 216 (Try/54/-0.103)
	205 Y.ICNVNHKPSNTK.V 216 (Try/39/0.0833)
	216 T.KVDKKVEPK.S 224 (ProK/28/0.1511)
	216 T.KVDKKVEPKSCDKTHTCPPCPAPEL.L 240 (Pep/51/-0.0807)
	225 K.SCDKTHTCPPCPAPEL.L 240 (Pep/40/-0.1417)
	225 K.SCDKTHTCPPCPAPEL.G 241 (Pep/42/-0.1744)
	225 K.SCDKTHTCPPCPAPELLGGPS.V 245 (Pep/60/-0.1585)
	229 K.THTCPPCPAPELLGGPSVF.L 247 (Try/52/-0.1036)
	231 H.TCPPCPAPELLGGPSVF.L 247 (Chy/35/0.0504)
	236 C.PAPELLGGPSVFLFPPKPK.D 254 (Try/63/-0.1237)
	238 A.PELLGGPSVFLFPPK.P 252 (Try/56/0.1645)
	238 A.PELLGGPSVFLFPPKPK.D 254 (Try/80/0.0116)
	240 E.LLGGPSVFLFPPKPK.D 254 (Try/64/-0.0551)
	241 L.LGGPSVFLFPPKPK.D 254 (Try/41/0.0216)
	250 F.PPKPKDTLM.I 258 (Pep/37/0.0067)
	259 M.ISRTPEVTC.V 267 (Pep/33/-0.0021)
	262 R.TPEVTCVVVDVSHEDPEVK.F 280 (Try/85/-0.1463)
	266 V.TCVVDVSHEDPEVK.F 280 (Try/90/0.0559)
	267 T.CVVVDVSHEDPEVK.F 280 (Try/49/-0.0474)
	267 T.CVVVDVSHEDPEVK.F 280 (Pep/85/0.0492)
	267 T.CVVVDVSHEDPEVKFN.W 282 (Pep/52/0.0159)
	268 C.VVVDVSHEDPEVKF.N 281 (Pep/36/0.0336)
	268 C.VVVDVSHEDPEVKFNW.Y 283 (Pep/68/-0.037)
	270 V.VDVSHEDPEVKFNW.Y 283 (Pep/36/0.0482)

	271 V.DVSHEDPEVKFNW.Y 283 (Pep/46/0.1857)
	272 D.VSHEDPEVKFNW.Y 283 (Pep/52/0.0838)
	281 K.FNWYVDGVEVHNAK.T 294 (Try/79/0.0193)
	282 F.NWYVDGVEVH.N 291 (Chy/34/-0.0635)
	283 N.WYVDGV.E 288 (Pep/37/0.1192)
	283 N.WYVDGVEVH.N 291 (Pep/40/0.0177)
	284 W.YVDGVEVHNAK.T 294 (Try/43/0.0646)
	287 D.GVEVHNAK.T 294 (Try/31/-0.0422)
	307 Y.RVVSVLTVLHQDWLNGKEY.K 325 (Chy/53/-0.158)
	307 Y.RVVSVLTVLHQ*DWLNGKEY.K Deamidation(Q) 325 (Chy/48/0.1911)
	308 R.VVSVLTVLHQDWLNGK.E 323 (Chy/41/0.1726)
	308 R.VVSVLTVLHQDWL.N 320 (Try/25/0.1658)
	308 R.VVSVLTVLHQDWLN.G 321 (Try/26/0.0728)
	308 R.VVSVLTVLHQDWLNGK.E 323 (Try/93/-0.0046)
	308 R.VVSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/107/0.106)
	309 V.VSVLTVLHQDWLNGK.E 323 (Try/61/0.051)
	309 V.VSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/80/0.0094)
	310 V.SVLTVLHQDWLNGK.E 323 (Chy/45/0.1481)
	310 V.SVLTVLHQDWLNGK.E 323 (Try/88/0.1091)
	310 V.SVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/80/0.048)
	311 S.VLTVLHQDWLNGK.E 323 (Try/100/0.1773)
	312 V.LTVLHQDWLNGK.E 323 (Try/34/0.0815)
	313 L.TVLHQDWLN*GKEY.K Deamidation(N) 325 (Chy/43/0.1788)
	313 L.TVLHQDWLNGK.E 323 (Try/49/0.119)
	313 L.TVLHQDWLNGKE.Y 324 (Pep/61/0.069)
	313 L.TVLHQDWLN*GKE.Y Deamidation(N) 324 (Pep/53/-0.0272)
	314 T.VLHQDWLNGKEY.K 325 (Chy/40/0.1617)
	315 V.LHQDWLNGKEY.K 325 (Chy/45/0.1616)
	316 L.HQDWLNGKE.Y 324 (Pep/34/0.1073)
	325 E.YKCKVSNKALPAPIE.K 339 (Pep/64/-0.0882)
	325 E.YKCKVSNKALPAPIEKT.I 341 (Pep/48/-0.1174)
	331 S.NKALPAPIEKTIS.K 343 (Pep/22/0.0924)
	333 K.ALPAPIEKTISKAKGQPREPQVY.T 355 (Chy/37/0.0839)
	333 K.ALPAPIEKTISK.A 344 (Pep/41/0.1793)
	333 K.ALPAPIEKTISKAK.G 346 (Pep/31/0.1321)
	337 A.PIEKTISKA.K 345 (Chy/48/-0.1023)
	340 E.KTISKAKGQPREPQV.Y 354 (Pep/91/-0.0449)
	341 K.TISKAKGQPREPQV.Y 354 (Pep/69/0.0068)
	342 T.ISKAKGQPREPQVY.T 355 (Chy/32/0.0032)
	342 T.ISKAKGQPREPQV.Y 354 (Pep/62/0.1569)
	349 Q.PREPQVY.T 355 (Chy/31/-0.0012)
	351 R.EPQVYTLPPSR.E 361 (Try/39/0.1076)
	352 E.PQVYTLPPSR.E 361 (Try/50/0.0198)
	366 T.KNQ*VSLTCLVKGFYPSDIAVEWESN*GQPENNYK.T Deamidation(NQ) 398 (Try/50/-0.0025)
	367 K.NQVSLTCLVK.G 376 (Try/40/0.0019)
	372 L.TCLVKGFYPSDIAVEW.E 387 (Chy/71/0.0529)
	372 L.TCLVKGFYPSDIAVEWESNGQPENNY.K 397 (Chy/48/-0.0804)

		372 L.TCLVKGFYPSD.I 382 (Pep/35/0.1552) 373 T.CLVKGFYPSDIAVEW.E 387 (Chy/70/0.0144) 373 T.CLVKGFYPSDIAVEWESN*GQPENNY.K Deamidation(N) 397 (Chy/49/-0.0676) 377 K.GFYPSDIAVEWESNGQ*PENNYK.T Deamidation(Q) 398 (Chy/82/0.0324) 377 K.GFYPSDIAVEWESNGQPENNYK.T 398 (Try/75/-0.1596) 379 F.YPSDIAVE.W 386 (ProK/31/-0.0349) 380 Y.PSDIAVEWESNGQPENNYK.T 398 (Try/118/-0.1572) 385 A.VEWESN.G 390 (ProK/37/-0.0381) 387 E.WESNGQPENNYKTTTPVL.D 404 (Pep/39/-0.0871) 387 E.WESN*GQPENNYKTTTPVL.D Deamidation(N) 404 (Pep/51/-0.0429) 391 N.GQPENNYKTTTPVLDSGSF.F 410 (Pep/46/-0.1065) 395 E.NNYKTTTPVLDSGSF.F 410 (Pep/96/-0.0241) 397 N.YKTTTPVLDSGSF.F 410 (Pep/94/-0.074) 398 Y.KTTTPVLDSGSFF.L 411 (Chy/84/0.0015) 398 Y.KTTTPVLDSGSF.F 410 (Pep/38/-0.0029) 399 K.TTPPVLDSDGSFFLYSK.L 415 (Chy/71/0.0073) 399 K.TTPPVLDSDGSF.F 410 (ProK/49/0.1227) 399 K.TTPPVLDSDGSFFLY.S 413 (Try/56/0.0249) 399 K.TTPPVLDSDGSFFLYSK.L 415 (Try/68/-0.1105) 401 T.PPVLDSDGSFFLYSK.L 415 (Chy/32/0.1658) 401 T.PPVLDSDGSFFLYSK.L 415 (Try/110/0.009) 402 P.PVLDSGSFFLYSK.L 415 (Try/81/-0.0244) 414 Y.SKLTVDKSRWQQGNVF.S 429 (Chy/52/0.1544) 417 L.TVDKSRWQQGNVF.S 429 (Pep/33/0.0226) 428 N.VFSCSVM*HEALHNHYTQK.S Oxidation(M) 445 (Try/59/0.0367) 429 V.FSCSVMHEALHNHYTQK.S 445 (Try/43/0.1115) 430 F.SCSVMHEALHNHYTQK.S 445 (Try/54/-0.1437) 432 C.SVMHEALHNHY.T 442 (Chy/42/0.179) 432 C.SVMHEALHNHYTQK.S 445 (Try/61/-0.0604) 434 V.MHEALHNHYTQK.S 445 (Try/69/-0.0616) 435 M.HEALHNHYTQK.S 445 (Try/84/0.0645) 435 M.HEALHNHYTQKS.L 446 (Pep/46/0.1187) 435 M.HEALHNHYTQKSLSLSPG.K 452 (Pep/41/-0.0843) 439 L.HNHYTQKSLSLSPG.K 452 (Pep/47/-0.0516)
3	95%	1 -.EVQLVESGGGLVQPGGSLR.L 19 (Try/62/-0.0096) 1 -.EVQLVESGGGLVQPGGSL.R 18 (Chy/98/0.1397) 1 -.EVQLVESGGGLVQPGGSLRLSCAASGY.T 27 (Chy/90/-0.1479) 1 -.EVQLVESGGGLVQ*PGGSLRLSCAASGY.T Deamidation(Q) 27 (Chy/67/0.0922) 3 V.QLVESGGGLVQPGGSLR.L 19 (Try/112/0.015) 4 Q.LVESGGGLVQPGGSLRL.S 20 (Pep/88/0.1036) 5 L.VESGGGLVQPGGSLR.L 19 (Try/43/0.1025) 14 Q.PGGSLRLSCAASGY.T 27 (Chy/41/0.039) 14 Q.PGGSL.R 18 (Pep/31/0.0488) 19 L.RLSCAASGY.T 27 (Chy/42/-0.0058) 20 R.LSCAASGYTFTNYGMNWVR.Q 38 (Try/128/-0.1446) 20 R.LSCAASGYTFTNYGM*NWVR.Q Oxidation(M) 38 (Try/118/-0.1644) 21 L.SCAASGY.T 27 (Chy/35/0.009) 23 C.AASGYTFTNYGMNWVR.Q 38 (Try/87/-0.0029)

	28 Y.TFTNYGMNWVR.Q 38 (Try/57/0.1813) 36 N.WVRQAPGKGLE.W 46 (Pep/36/0.1401) 36 N.WVRQAPGKGLEW.V 47 (Pep/54/0.1163) 36 N.WVRQAPGKGLEWVG.W 49 (Pep/48/0.0586) 44 K.GLEWVGWINTY.T 54 (Try/69/-0.0187) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65 (Try/136/-0.1948) 44 K.GLEWVGWINTYTGEPTYAADFKR.R 66 (Try/52/0.0908) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65 (Chy/150/-0.1842) 48 W.VGWINTYTGEPTYAADFK.R 65 (Try/113/-0.1374) 49 V.GWINTYTGEPTYAADFK.R 65 (Try/113/-0.0665) 52 I.NTYTGEPTYAADFK.R 65 (Try/74/0.1411) 55 Y.TGEPTYAADFK.R 65 (Try/73/0.1614) 55 Y.TGEPTYAADF.K 64 (Chy/44/-0.0647) 55 Y.TGEPTYAADFKRRFTF.S 70 (Chy/36/0.0059) 58 E.PTYAADFK.R 65 (Try/43/0.0286) 67 R.RFTFSLDTSK.S 76 (Try/51/0.0282) 71 F.SLDTSKSTAY.L 80 (Chy/49/0.05) 73 L.DTSKSTAY.L 80 (Chy/37/0.0065) 77 K.STAYLQMN.S 84 (Try/29/-0.0153) 77 K.STAYLQMNSLR.A 87 (Try/69/-0.0075) 77 K.STAYLQM*NSLR.A Oxidation(M) 87 (Try/62/0.138) 81 Y.LQMNSLRAEDTAVYY.C 95 (Chy/53/0.0071) 87 L.RAEDTAVY.Y 94 (Chy/43/-0.0053) 88 R.AEDTAVYYCAK.Y 98 (Try/69/0.0533) 94 V.YYCAKYPHYYGSS.H 106 (Pep/34/0.0305) 95 Y.YCAKYPHYYGSS.H 106 (Pep/37/0.0899) 109 W.YFDVWGQGTL.V 118 (Chy/35/-0.0894) 114 W.GQGTLVTVSSASTKGPSVFPL.A 134 (Chy/34/-0.0711) 119 L.VTVSSASTKGPSVF.P 132 (Pep/75/0.1456) 119 L.VTVSSASTKGPSVFPLAPSS.K 138 (Pep/32/-0.0295) 121 T.VSSASTKGPSVFPLAPSSKSTSGGTAAL.G 148 (Chy/43/-0.0294) 121 T.VSSASTKGPSVFPLAPSSKSTSGGTAAL.G 148 (Pep/48/-0.0675) 125 A.STKGPSVFPLAPSSKSTSGGTAAL.G 148 (Pep/70/-0.0982) 127 T.KGPSVFPLAPSSKSTSGGTAAL.G 148 (Chy/73/-0.0291) 128 K.GPSVFPLAPSSK.S 139 (Try/59/-0.0321) 133 F.PLAPSSKSTSGGTAAL.G 148 (Pep/63/0.0703) 140 K.STSGGTAALGCLVK.D 153 (Try/87/0.0941) 141 S.TSGGTAALGCLVK.D 153 (Try/89/0.1919) 142 T.SGGTAALGCLVK.D 153 (Try/52/-0.0676) 146 T.AALGCLVKDYFPEPVTVSW.N 164 (Chy/36/0.0644) 149 L.GCLVKDYFPEPVTVSW.N 164 (Chy/89/-0.0555) 149 L.GCLVKDYFPEPVTVSWNSGAL.T 169 (Chy/68/-0.0361) 149 L.GCLVKDYFPEPVTVSWNSGALTSGVH.T 174 (Chy/65/-0.1676) 149 L.GCLVKDYFPEPVT.V 161 (Pep/51/0.1526) 150 G.CLVKDYFPEPVTVSW.N 164 (Chy/55/-0.0745) 154 K.DYFPEPVTVSWN.S 165 (Try/58/-0.0819) 154 K.DYFPEPVTVSWNSGAL.T 169 (Try/76/0.0338) 157 F.PEPVTVSW.N 164 (Chy/42/-0.04)
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	162 T.VSWNSGALTSGVHTF.P 176 (Pep/54/0.1091)
	165 W.N*SGALTSGVHTFPAVLQSSGLY.S Deamidation(N) 186 (Chy/55/-0.113)
	166 N.SGALTSGVHTFPAVLQS.S 182 (Try/78/-0.0236)
	166 N.SGALTSGVHTFPAVLQSS.G 183 (Try/49/-0.073)
	166 N.SGALTSGVHTFPAVLQSSGLY.S 186 (Try/82/-0.1222)
	166 N.SGALTSGVHTFPAVLQSSGLYSL.S 188 (Try/85/-0.1999)
	166 N.SGALTSGVHTFPAVLQ*SSGLYSLSSVTVPS.S Deamidation(Q) 196 (Try/41/-0.0192)
	170 L.TSGVHTFPAVLQSSGLY.S 186 (Chy/68/0.0678)
	170 L.TSGVHTFPAVL.Q 180 (Pep/38/-0.0174)
	171 T.SGVHTFPAVLQSSGLY.S 186 (Chy/70/0.1587)
	175 H.TFPAVLQSSGLY.S 186 (Chy/56/0.0225)
	191 S.VVTVPSSSL.G 199 (Pep/26/0.162)
	195 V.PSSSLGTQTY.I 204 (Chy/37/-0.0448)
	197 S.SSLGTQTYICNVNHKPSNTK.V 216 (Try/48/-0.0984)
	203 Q.TYICNVNHKPSNTK.V 216 (Try/46/-0.0109)
	205 Y.ICNVNHKPSNTK.V 216 (Try/34/0.0377)
	229 K.THTCPPCPAPELLGGPSVF.L 247 (Try/42/-0.1168)
	229 K.THTCPPCPAPELLGGPSVFLFPPKPK.D 254 (Try/44/-0.1876)
	231 H.TCPPCPAPELLGGPSVF.L 247 (Chy/42/0.13)
	238 A.PELLGGPSVFLFPPKPK.D 254 (Try/72/0.0074)
	239 P.ELLGGPSVFLFPPKPK.D 254 (Try/39/0.1143)
	240 E.LLGGPSVFLFPPKPK.D 254 (Try/67/-0.0001)
	241 L.LGGPSVFLFPPKPK.D 254 (Try/38/-0.0032)
	247 V.FLFPKPKDTLM.I 258 (Pep/24/0.185)
	248 F.LFPKPKDTLM.I 258 (Pep/27/0.0962)
	250 F.PPKPKDTLM.I 258 (Pep/36/0.1305)
	255 K.DTLMISR.T 261 (Try/34/0.0045)
	259 M.ISRTPEVTC.V 267 (Pep/50/0.1281)
	262 R.TPEVTCVVVDVSHEDPEVK.F 280 (Try/92/-0.1743)
	263 T.PEVTCVVVDVSHEDPEVK.F 280 (Try/103/-0.1929)
	264 P.EVTCVVVDVSHEDPEVK.F 280 (Try/82/-0.1505)
	266 V.TCVVDVSHEDPEVK.F 280 (Try/96/-0.1105)
	268 C.VVVDVSHEDPEVKF.N 281 (Pep/51/0.038)
	268 C.VVVDVSHEDPEVKFNW.Y 283 (Pep/53/-0.0536)
	269 V.VVDVSHEDPEVKFNW.Y 283 (Pep/51/0.1162)
	272 D.VSHEDPEVKFNW.Y 283 (Pep/76/0.0422)
	281 K.FNWWYVDGVEVH.N 291 (Try/49/0.1653)
	281 K.FNWWYVDGVEVHNAK.T 294 (Try/100/0.1483)
	282 F.NWWYVDGVEVHNAK.T 294 (Try/82/-0.005)
	282 F.NWWYVDGVEVH.N 291 (Chy/34/0.1837)
	284 W.YVDGVEVHNAK.T 294 (Try/53/0.0328)
	307 Y.RVVSVLTVLHQDW.L 319 (Chy/71/-0.0385)
	307 Y.RVVSVLTVLHQDWLNGKEY.K 325 (Chy/63/-0.1678)
	307 Y.RVVSVLTVLHQ*DWLNGKEY.K Deamidation(Q) 325 (Chy/51/0.1698)
	308 R.VVSVLTVLHQDWLN.G 321 (Try/28/0.0896)
	308 R.VVSVLTVLHQDWLNGK.E 323 (Try/93/-0.0438)
	308 R.VVSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/97/-0.0126)
	309 V.VSVLTVLHQDWLNGK.E 323 (Try/68/0.0384)

	309 V.VSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/71/0.0182) 310 V.SVLTVLHQDWLNGK.E 323 (Try/104/0.0523) 310 V.SVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/79/0.0502) 311 S.VLTVLHQDWLNGK.E 323 (Try/87/0.1035) 311 S.VLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/88/-0.0109) 312 V.LTVLHQDWLNGK.E 323 (Try/74/0.1825) 312 V.LTVLHQDWLN*GK.E Deamidation(N) 323 (Try/86/0.0467) 313 L.TVLHQDWLN*GK.E Deamidation(N) 323 (Try/47/0.0364) 313 L.TVLHQDWLNGKEY.K 325 (Chy/79/0.0144) 313 L.TVLHQDWLN*GKEY.K Deamidation(N) 325 (Chy/47/0.1744) 314 T.VLHQDWLNGKEY.K 325 (Chy/40/0.1489) 315 V.LHQDWLNGKEY.K 325 (Chy/54/0.0554) 325 E.YKCKVSNKALPAPIE.K 339 (Pep/93/-0.0124) 338 P.IEKTISKAKGQPREPQV.Y 354 (Pep/56/-0.1994) 340 E.KTISKAKGQPREPQV.Y 354 (Pep/58/-0.1253) 344 S.KAKGQPREPVY.T 355 (Chy/36/0.1083) 351 R.EPQVYTLPPSR.E 361 (Try/44/0.0214) 352 E.PQVYTLPPSR.E 361 (Try/53/0.081) 366 T.KNQ*VSLTCLVKGFYPSDIAVEWESN*GPENNYK.T 2 Deamidation(NQ) 398 (Try/52/-0.064) 367 K.NQVSLTCLVK.G 376 (Try/44/0.0199) 372 L.TCLVKGFYPSDIAVEW.E 387 (Chy/59/0.0845) 372 L.TCLVKGFYPSDIAVEWESN*GPENNY.K Deamidation(N) 397 (Chy/56/-0.1137) 373 T.CLVKGFYPSDIAVEW.E 387 (Chy/65/0.03) 373 T.CLVKGFYPSDIAVEWESNGQPENNY.K 397 (Chy/64/-0.0304) 375 L.VKGFYPSDIAVEWESNGQPENNY.K 397 (Chy/37/0.0732) 377 K.GFYPSDIAVEWESNGQPENNYK.T 398 (Try/86/-0.1938) 377 K.GFYPSDIAVEWESNGQ*PENNYK.T Deamidation(Q) 398 (Try/50/0.1353) 380 Y.PSDIAVEWESNGQPENNYK.T 398 (Try/111/-0.0606) 387 E.WESNGQPENNYKTTTPVL.D 404 (Pep/44/-0.1409) 397 N.YKTTTPVL.D 404 (Pep/29/0.0063) 398 Y.KTTTPVLDSGDSFFLY.S 413 (Chy/64/0.1625) 399 K.TTPPVLDSDGSFFLY.S 413 (Try/62/0.0751) 399 K.TTPPVLDSDGSFFLYSK.L 415 (Try/88/-0.1527) 400 T.TPPVLDSGDSFFLYSK.L 415 (Try/118/-0.0392) 401 T.PPVLDSDGSFFLYSK.L 415 (Try/123/0.0534) 402 P.PVLDSGDSFFLYSK.L 415 (Try/68/0.0058) 412 F.LYSKL.T 416 (Chy/17/0.1468) 414 Y.SKLTVDKSRWQQGNVF.S 429 (Chy/60/-0.0482) 417 L.TVDKSRWQQGNVF.S 429 (Pep/33/0.0938) 423 R.WQQGNVFSCSVMHEALHN*HYTQK.S Deamidation(N) 445 (Try/64/0.164) 423 R.WQQGNVFSCSVM*HEALHNHYTQK.S Oxidation(M) 445 (Try/44/-0.1766) 428 N.VFSCSVMHEALHNHYTQK.S 445 (Try/53/0.1226) 429 V.FSCSVMHEALHNHYTQK.S 445 (Try/39/0.1199) 430 F.SCSVMHEALHNHYTQK.S 445 (Try/59/-0.1117) 430 F.SCSVMHEALHNHY.T 442 (Chy/54/0.0631) 430 F.SCSVMHEALHNHYTQKS.L 448 (Pep/36/-0.1638) 431 S.CSVMHEALHNHYTQK.S 445 (Try/34/0.011) 432 C.SVMHEALHNHYTQK.S 445 (Try/71/0.0082)
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		432 C.SVMHEALHNHY.T 442 (Chy/32/0.1812) 434 V.MHEALHNHYTQK.S 445 (Try/80/0.0058) 435 M.HEALHNHYTQK.S 445 (Try/85/0.0741) 435 M.HEALHNHYTQKSLSLSPG.K 452 (Pep/41/-0.1197)
4	83%	20 R.LSCAASGYTFTNYGMNWVR.Q 38 (Try/124/-0.1662) 20 R.LSCAASGYTFTNYGM*NWVR.Q Oxidation(M) 38 (Try/102/-0.1352) 23 C.AASGYTFTNYGMNWVR.Q 38 (Try/89/-0.0181) 28 Y.TFTNYGMNWVR.Q 38 (Try/41/0.1049) 28 Y.TFTNYGM*NWVR.Q Oxidation(M) 38 (Try/38/0.0296) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65 (Try/98/-0.1764) 48 W.VGWINTYTGEPTYAADFK.R 65 (Try/77/0.0264) 49 V.GWINTYTGEPTYAADFK.R 65 (Try/114/0.0147) 51 W.INTYTGEPTYAADFK.R 65 (Try/98/0.0346) 51 W.IN*TYTGEPTYAADFK.R Deamidation(N) 65 (Try/56/0.0174) 52 I.NTYTGEPTYAADFK.R 65 (Try/64/0.0995) 53 N.TYTGEPTYAADFK.R 65 (Try/75/0.0894) 55 Y.TGEPTYAADFK.R 65 (Try/35/0.0404) 58 E.PTYAADFK.R 65 (Try/31/0.0194) 67 R.RFTFSLDTSK.S 76 (Try/49/0.1258) 77 K.STAYLQMNSLR.A 87 (Try/62/0.1127) 77 K.STAYLQM*NSLR.A Oxidation(M) 87 (Try/62/0.1134) 88 R.AEDTAVYYCAK.Y 98 (Try/70/0.1203) 128 K.GPSVFPLAPSSK.S 139 (Try/39/0.1917) 140 K.STSGGTAALGCLVK.D 153 (Try/81/0.0469) 141 S.TSGGTAALGCLVK.D 153 (Try/61/0.0887) 142 T.SGGTAALGCLVK.D 153 (Try/55/-0.0694) 154 K.DYFPEPVTVSWNSGAL.T 169 (Try/68/0.1052) 166 N.SGALTSGVHTFPAVLQ*SSGLYSLSSVTVPSSSLGTQTY.I Deamidation(Q) 204 (Try/45/-0.003) 195 V.PSSSLGTQTYICNVNHNK.P 211 (Try/39/-0.1594) 195 V.PSSSLGTQTYICNVNHNKPSNTK.V 216 (Try/37/0.1593) 229 K.THTCPPCPAPELLGGPSVF.L 247 (Try/63/-0.0846) 236 C.PAPELLGGPSVFLFPPKPK.D 254 (Try/80/-0.1109) 238 A.PELLGGPSVFLFPPKPK.D 254 (Try/77/0.0444) 262 R.TPEVTCVVVDVSHEDPEVK.F 280 (Try/80/-0.1967) 263 T.PEVTCVVVDVSHEDPEVK.F 280 (Try/72/0.0171) 265 E.VTCVVVDVSHEDPEVK.F 280 (Try/99/-0.1617) 266 V.TCVVVDVSHEDPEVK.F 280 (Try/66/-0.1179) 267 T.CVVVDVSHEDPEVK.F 280 (Try/84/-0.1344) 281 K.FNWWYVDGVEVHNAK.T 294 (Try/78/0.0063) 282 F.NWWYVDGVEVHNAK.T 294 (Try/64/0.039) 308 R.VVSVLTVLHQDWLNGK.E 323 (Try/93/0.0166) 308 R.VVSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/91/0.0072) 309 V.VSVLTVLHQDWLNGK.E 323 (Try/71/0.0766) 309 V.VSVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/70/0.071) 310 V.SVLTVLHQDWLNGK.E 323 (Try/94/0.0847) 310 V.SVLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/73/0.0874) 311 S.VLTVLHQDWLN*GK.E Deamidation(N) 323 (Try/81/0.1077) 313 L.TVLHQDWLN*GK.E Deamidation(N) 323 (Try/61/0.078)

		351 R.EPQVYTLPPSR.E 361 (Try/50/0.0754) 352 E.PQVYTLPPSR.E 361 (Try/56/0.0752) 367 K.NQVSLTCLVK.G 376 (Try/41/0.1271) 377 K.GFYPSDIAVEWESNGQPENNYK.T 398 (Try/87/-0.1406) 380 Y.PSDIAVEWESN*GQPENNYK.T Deamidation(N) 398 (Try/42/-0.1548) 399 K.TTPPVLDSDGSFFLYSK.L 415 (Try/74/0.0839) 401 T.PPVLDSDGSFFLYSK.L 415 (Try/106/0.0226) 423 R.WQQGNVFSCSVM*HEALHNHYTQK.S Oxidation(M) 445 (Try/61/-0.1154) 428 N.VFSCSVMHEALHNHYTQK.S 445 (Try/45/0.1628) 430 F.SCSVMHEALHNHYTQK.S 445 (Try/43/-0.1353) 432 C.SVMHEALHNHYTQK.S 445 (Try/60/0.0138) 434 V.MHEALHNHYTQK.S 445 (Try/45/-0.0584) 435 M.HEALHNHYTQK.S 445 (Try/47/0.0269)
5	100%	1 -.DIQMTQSPSSLSASVGDR.V 18 (Try/147/-0.1515) 1 -.DIQMTQSPSSLSASVGDR.V 18 (Try/69/-0.104) 1 -.DIQMTQSPSSLSASVGDRVTITCSASQDISNY.L 32 (Chy/47/-0.1008) 1 -.DIQM*TQSPSSL.S Oxidation(M) 11 (Pep/33/-0.0369) 2 D.IQMTQSPSSLSASVGDR.V 18 (Try/95/0.0565) 3 I.QMTQSPSSLSASVGDR.V 18 (Try/80/-0.0013) 4 Q.MTQSPSSLSASVGDR.V 18 (Try/63/-0.1073) 5 M.TQSPSSLSASVGDRVTIT.C 22 (Pep/43/-0.102) 6 T.QSPSSLSASVGDRVT.I 20 (ProK/38/-0.0624) 12 L.SASVGDRVTITCSASQDISNYLNW.Y 35 (Chy/64/0.0862) 12 L.SASVGDRVTIT.C 22 (ProK/30/-0.0379) 12 L.SASVGDRVTIT.C 22 (Pep/31/-0.0379) 12 L.SASVGDRVTITCSASQ.D 27 (Pep/67/-0.0905) 12 L.SASVGDRVTITCSASQD.I 28 (Pep/53/-0.1008) 12 L.SASVGDRVTITCSASQDISN.Y 31 (Pep/90/-0.1428) 12 L.SASVGDRVTITCSASQDISNY.L 32 (Pep/65/-0.0971) 14 A.SVGDRVTITCSASQDISN.Y 31 (Pep/71/-0.1137) 19 R.VTITCSASQDISNY.L 32 (Try/74/0.1292) 19 R.VTITCSASQDISNYLNWY.Q 36 (Try/114/-0.1615) 19 R.VTITCSASQDISNYLNWYQQKPGK.A 42 (Try/77/-0.0286) 19 R.VTITCSASQDISN*YLNWYQQKPGK.A Deamidation(N) 42 (Try/137/0.1189) 20 V.TITCSASQDISNYLNWYQQKPGK.A 42 (Try/57/-0.0628) 21 T.ITCSASQDISNYLNWYQQKPGK.A 42 (Try/66/-0.1469) 24 C.SASQDISNYLNWYQQK.P 39 (Try/74/-0.0707) 24 C.SASQDISNYLNWYQQKPGK.A 42 (Try/85/-0.1355) 24 C.SASQDISNY.L 32 (Chy/33/-0.0489) 26 A.SQDISNY.L 32 (ProK/36/-0.0669) 33 Y.LNWYQQKPGKAPK.V 45 (ProK/30/0.0135) 33 Y.LNWYQQKPGKAPK.V 45 (Pep/36/0.0349) 35 N.WYQQKPGKAPK.V 45 (ProK/46/0.1213) 36 W.YQQKPGKAPKVL.I 47 (Chy/26/0.0758) 36 W.YQQKPGKAPKV.L 46 (ProK/28/0.1344) 36 W.YQQKPGKAPKVL.I 47 (Pep/39/-0.0118) 36 W.YQQKPGKAPKVL.I.Y 48 (Pep/28/0.0187) 36 W.YQQKPGKAPKVL.IY.F 49 (Pep/43/0.0572)

		46 K.VLIYFTSSLHSGVPSR.F 61 (Try/85/-0.0187) 47 V.LIYFTSSLHSGVPSR.F 61 (Try/100/-0.0775) 48 L.IYFTSSLHSGVPSR.F 61 (Try/114/0.0524) 48 L.IYFTSSLHSGVPSRF.S 62 (Pep/48/-0.0921) 49 I.YFTSSLHSGVPSR.F 61 (Try/94/0.023) 50 Y.FTSSLHSGVPSR.F 61 (Try/84/0.1433) 51 F.TSSLHSGVPSR.F 61 (Try/63/0.0604) 51 F.TSSLHSGVPSRF.S 62 (Chy/42/0.1207) 55 L.HSGVPSR.F 61 (ProK/28/0.0934) 55 L.HSGVPSRFSGSGSGTD.F 70 (Pep/75/0.0508) 55 L.HSGVPSRFSGSGSGTDF.T 71 (Pep/69/-0.0834) 72 F.TLTISLQPEDFATY.Y 86 (Chy/62/0.0771) 74 L.TISLQPEDFATYY.C 87 (Chy/68/0.1713) 77 S.SLQPEDFAT.Y 85 (ProK/37/-0.0297) 80 Q.PEDFAT.Y 85 (ProK/42/-0.097) 87 Y.YCQQYSTVPWTFGQGTK.V 103 (Pep/55/-0.117) 88 Y.CQQYSTVPWTFGQGTK.V 103 (Try/62/-0.1047) 91 Q.YSTVPWTFGQGTKVE.I 105 (Pep/41/0.0863) 91 Q.YSTVPWTFGQGTKVEIKRTVAA.P 112 (Pep/54/-0.12) 92 Y.STVPWTFGQGTK.V 103 (Try/45/0.008) 94 T.VPWTFGQGTK.V 103 (Try/38/0.1685) 95 V.PWTFGQGTK.V 103 (Try/36/0.0199) 97 W.TFGQGTKVEIKRT.V 109 (Chy/31/0.1204) 97 W.TFGQGTKVEIKRTVAAPSVF.I 116 (Chy/57/-0.0983) 99 F.GQGTKVEIKRTVAAPSVF.I 116 (Chy/68/-0.143) 99 F.GQGTKVEIKRTVAA.P 112 (Pep/53/-0.0565) 103 T.KVEIKRTVAAPSVF.I 116 (Chy/44/0.1602) 108 K.RTVAAPSVFIFPPSDEQLK.S 126 (Try/68/-0.1517) 109 R.TVAAPSVFIFPPSDEQLK.S 126 (Try/79/0.1036) 111 V.AAPSVFIFPPSDEQLK.S 126 (Try/69/-0.0865) 112 A.APSVFIFPPSDEQLK.S 126 (Try/60/-0.1932) 113 A.PSVFIFPPSDEQLK.S 126 (Try/85/0.0521) 115 S.VFIFPPSDEQLKSG.T 128 (ProK/47/0.0374) 115 S.VFIFPPSDEQLK.S 126 (Pep/43/0.0741) 115 S.VFIFPPSDEQLKSG.T 128 (Pep/48/-0.0088) 116 V.FIFPPSD.E 122 (Pep/29/0.0299) 117 F.IFPPSDEQLKSGTASVVCL.L 135 (Chy/37/0.0454) 117 F.IFPPSDEQLKSGTASVVCLL.N 136 (Chy/63/-0.0764) 118 I.FPPSDEQLK.S 126 (Try/35/-0.0717) 119 F.PPSDEQLK.S 126 (Try/55/0.0024) 119 F.PPSDEQLKSGTASVVCLL.N 136 (Chy/93/0.1479) 119 F.PPSDEQLK.S 126 (ProK/51/0.052) 119 F.PPSDEQLKS.G 127 (ProK/38/0.038) 119 F.PPSDEQLKSG.T 128 (ProK/42/0.1317) 119 F.PPSDEQLKSGT.A 129 (ProK/29/0.1394) 119 F.PPSDEQLKSGT.A.S 130 (ProK/48/0.1607) 120 P.PSDEQLKS.G 127 (ProK/47/0.0105) 120 P.PSDEQLKSG.T 128 (ProK/52/-0.006)
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		126 L.KSGTASVVCLLNNFYPREAKVQ*W.K Deamidation(Q) 148 (Chy/48/-0.0673) 127 K.SGTASVVCLLNNFYPR.E 142 (Try/59/-0.0103) 127 K.SGTASVVCLLN*NFYPR.E Deamidation(N) 142 (Try/65/0.0651) 130 T.ASVVCLLNNFYPR.E 142 (Try/40/-0.1147) 133 V.VCLLNNFYPRE.A 143 (Pep/35/0.1084) 133 V.VCLLN*NFYPRE.A Deamidation(N) 143 (Pep/36/0.0156) 134 V.CLLNNFYPREAKVQW.K 148 (Chy/27/0.198) 137 L.NNFYPREAKVQW.K 148 (Chy/65/-0.0407) 140 F.YPREAKVQWKVDNALQSGNSQE.S 161 (Pep/65/-0.1336) 144 E.AKVQWKVDNALQSGNSQE.S 161 (Pep/78/-0.1415) 148 Q.WKVDNA.L 153 (ProK/28/-0.0778) 149 W.KVDNALQSGNSQE.S 161 (Pep/92/0.1469) 150 K.VDNALQSGNSQESVTEQDSK.D 169 (Try/135/-0.134) 150 K.VDN*ALQSGNSQESVTEQDSK.D Deamidation(N) 169 (Try/76/-0.1906) 153 N.ALQSGNSQESVTEQDSK.D 169 (Try/37/-0.1403) 159 N.SQESVTEQDSKDST.Y 172 (ProK/34/-0.0624) 161 Q.ESVTEQDSKDSTY.S 173 (ProK/68/-0.0855) 162 E.SVTEQDSKDST.Y 172 (Pep/35/0.1966) 162 E.SVTEQDSKDSTY.S 173 (Pep/32/0.1839) 162 E.SVTEQDSKDSTYSL.S 175 (Pep/46/-0.0434) 162 E.SVTEQDSKDSTYSLSST.L 178 (Pep/42/-0.053) 162 E.SVTEQDSKDSTYSLSSTL.T 179 (Pep/79/-0.1178) 170 K.DSTYSLSSTLTLSK.A 183 (Try/96/0.0193) 179 T.LTLSKADYEKHKVY.A 192 (Pep/32/0.0332) 179 T.LTLSKADYEKHKVYACE.V 195 (Pep/32/0.0795) 180 L.TLSKADYEKHKVY.A 192 (Chy/58/-0.1384) 180 L.TLSKADYEKHKVY.A 192 (Pep/40/-0.1048) 180 L.TLSKADYEKHKVYACE.V 195 (Pep/88/0.0043) 182 L.SKADYEKHKVY.A 192 (Chy/38/0.0716) 182 L.SKADYEKHKVY.A 192 (Pep/41/0.129) 182 L.SKADYEKHKVYACE.V 195 (Pep/84/-0.0276) 191 K.VYACEVTHQGLSSPVT.K.S 207 (Try/84/0.0882) 192 V.YACEVTHQGLSSPVT.K.S 207 (Try/104/0.0096) 193 Y.ACEVTHQGLSSPVT.K.S 207 (Try/106/0.0479) 193 Y.ACEVTHQGL.S 201 (Chy/42/-0.0224) 193 Y.ACEVTHQGLSSPVT.K.S 207 (Chy/89/0.0715) 193 Y.ACEVTHQGLSSPVT.KSF.N 209 (Chy/36/-0.0545) 193 Y.ACEVTHQGLSSPVT.KSFNRGEC.- 214 (Pep/41/-0.052) 194 A.CEVTHQGLSSPVT.K.S 207 (Try/68/0.0116) 194 A.CEVTHQGL.S 201 (Chy/36/-0.0027) 194 A.CEVTHQGLSSPVT.K.S 207 (Chy/53/0.1138) 195 C.EVTHQGLSSPVT.K.S 207 (Try/57/0.0353) 196 E.VTHQGLSSPVT.KS.F 208 (Pep/32/0.1453) 196 E.VTHQGLSSPVT.KSFNRGEC.- 214 (Pep/57/-0.0923) 202 L.SSPVT.KSFNRGEC.- 214 (Chy/62/0.029) 204 S.PVT.KSFNRGEC.- 214 (Chy/39/0.0797) 204 S.PVT.KSFNRGEC.- 214 (Pep/39/0.0877)
6	88%	1 -.DIQMTQSPSSLSASVGDR.V 18 (Try/142/-0.1007)

		1 -.DIQM*TQSPSSLSASVGDR.V Oxidation(M) 18 (Try/111/-0.1384)
		1 -.DIQMTQSPSSLSASVGDRVTITCSASQDISNY.L 32 (Chy/71/-0.1875)
		3 I.QMTQSPSSLSASVGDR.V 18 (Try/103/0.1589)
		3 I.QM*TQSPSSLSASVGDR.V Oxidation(M) 18 (Try/86/0.011)
		4 Q.MTQSPSSLSASVGDR.V 18 (Try/79/0.0483)
		5 M.TQSPSSLSASVGDR.V 18 (Try/32/0.0604)
		8 S.PSSLSASVGDR.V 18 (Try/80/-0.0951)
		12 L.SASVGDRVTITC.S 23 (Chy/25/0.1827)
		12 L.SASVGDRVTITCSASQDISNY.L 32 (Chy/110/-0.1119)
		12 L.SASVGDRVTITCSASQD.I 28 (Pep/54/0.1336)
		12 L.SASVGDRVTITCSASQDISN.Y 31 (Pep/98/-0.0464)
		12 L.SASVGDRVTITCSASQDISNY.L 32 (Pep/86/-0.0339)
		19 R.VTITCSASQDISNYLNWY.Q 36 (Try/104/-0.1217)
		19 R.VTITCSASQDISNYLNWYQQK.P 39 (Try/103/-0.1596)
		19 R.VTITCSASQDISNYLNWYQQKPGK.A 42 (Try/99/-0.1276)
		19 R.VTITCSASQDISNYLN*WYQQKPGK.A Deamidation(N) 42 (Try/107/0.0619)
		20 V.TITCSASQDISNYLNWYQQKPGK.A 42 (Try/77/-0.142)
		21 T.ITCSASQDISNYLNWYQQKPGK.A 42 (Try/77/0.004)
		22 I.TCSASQDISNYLNWYQQKPGK.A 42 (Try/46/0.1779)
		24 C.SASQDISNYLNWYQQKPGK.A 42 (Try/56/-0.1305)
		24 C.SASQDISNYLNWYQQKPGK.A 42 (Try/90/-0.1305)
		24 C.SASQDISNY.L 32 (Chy/30/-0.0786)
		28 Q.DISNYLNWYQQKPGK.A 42 (Try/37/-0.0143)
		28 Q.DISNYLNWYQQKPGK.A 42 (Try/55/-0.0143)
		30 I.SNYLNWYQQKPGK.A 42 (Try/59/0.0881)
		32 N.YLNWYQQKPGKAPKVL.I 47 (Pep/58/0.0971)
		33 Y.LNWYQQKPGKAPKVL.I 47 (Pep/58/0.1201)
		33 Y.LNWYQQKPGKAPKVL.IY.F 49 (Pep/31/0.1113)
		36 W.YQQKPGKAPKVL.I 47 (Chy/17/0.1708)
		36 W.YQQKPGKAPKVL.I 47 (Pep/32/0.1142)
		36 W.YQQKPGKAPKVL.IY.F 49 (Pep/40/0.1656)
		46 K.VLIYFTSSLHSGVPSR.F 61 (Try/102/-0.0613)
		47 V.LIYFTSSLHSGVPSR.F 61 (Try/97/0.0155)
		48 L.IYFTSSLHSGVPSR.F 61 (Try/109/-0.0134)
		48 L.IYFTSSLHSGVPSRF.S 62 (Chy/86/-0.0157)
		48 L.IYFTSSL.H 54 (Pep/32/0.0367)
		49 I.YFTSSLHSGVPSR.F 61 (Try/87/0.0494)
		49 I.YFTSSLHSGVPSRF.S 62 (Chy/54/0.0264)
		50 Y.FTSSLHSGVPSRF.S 62 (Chy/74/0.1183)
		51 F.TSSLHSGVPSR.F 61 (Try/79/-0.0228)
		51 F.TSSLHSGVPSRF.S 62 (Chy/49/0.0451)
		52 T.SSLHSGVPSR.F 61 (Try/37/-0.0368)
		53 S.SLHSGVPSR.F 61 (Try/40/-0.0757)
		55 L.HSGVPSR.F 61 (Try/27/0.0092)
		55 L.HSGVPSRFSGSGSGTD.F 70 (Pep/90/-0.0124)
		55 L.HSGVPSRFSGSGSGTDF.T 71 (Pep/76/0.1618)
		56 H.SGVPSRF.S 62 (Chy/27/-0.0295)
		87 Y.YCQYSTVPWTFGQGTKV.E 104 (Pep/50/0.0433)

	87 Y.YCQQYSTVPWTFGQGGTKVE.I 105 (Pep/81/-0.1527)
	88 Y.CQQYSTVPWTFGQGGTK.V 103 (Try/82/-0.1737)
	91 Q.YSTVPWTFGQGGTKV.E 104 (Pep/35/0.0641)
	91 Q.YSTVPWTFGQGGTKVE.I 105 (Pep/38/0.1031)
	91 Q.YSTVPWTFGQGGTKVEIKRTVAA.P 112 (Pep/54/-0.131)
	92 Y.STVPWTFGQGGTK.V 103 (Try/41/0.0292)
	92 Y.STVPWTFGQ*GTKVEIKRTVAAPSVF.I Deamidation(Q) 116 (Chy/27/0.1082)
	92 Y.STVPWTFGQGGTKVEIKRTVAA.P 112 (Pep/47/-0.0252)
	94 T.VPWTFGQGGTK.V 103 (Try/30/0.0485)
	95 V.PWTFGQGGTK.V 103 (Try/45/-0.0619)
	95 V.PWTFGQGGTKV.E 104 (Pep/30/-0.0407)
	95 V.PWTFGQGGTKVE.I 105 (Pep/52/0.1773)
	95 V.PWTFGQGGTKVEIKRTVA.A 111 (Pep/30/0.013)
	95 V.PWTFGQGGTKVEIKRTVAA.P 112 (Pep/72/0.1271)
	97 W.TFGQGGTKVEIKRT.V 109 (Chy/26/0.0868)
	97 W.TFGQGGTKVEIKRTVAAPSVF.I 116 (Chy/55/-0.1938)
	99 F.GQGGTKVEIKRT.V 109 (Chy/47/0.1589)
	99 F.GQGGTKVEIKRTVAAPSVF.I 116 (Chy/67/-0.0468)
	99 F.GQGGTKVEIKRTVAAPSVF.I 116 (Pep/51/0.1482)
	102 G.TKVEIKRTVAAPSV.F 115 (Pep/60/0.1782)
	102 G.TKVEIKRTVAAPSVF.I 116 (Pep/57/0.18)
	108 K.RTVAAPSVFIFPPSDEQLK.S 126 (Try/74/-0.1079)
	109 R.TVAAPSVFIFPPSDEQLK.S 126 (Try/97/-0.1022)
	111 V.AAPSVFIFPPSDEQLK.S 126 (Try/74/-0.1095)
	112 A.APSVFIFPPSDEQLK.S 126 (Try/64/-0.0996)
	113 A.PSVFIFPPSDEQLK.S 126 (Try/98/0.0081)
	117 F.IFPPSDEQLKSGTASVV.C 133 (Chy/29/0.077)
	117 F.IFPPSDEQLKSGTASVVCL.L 135 (Chy/60/-0.0178)
	117 F.IFPPSDEQ*LKSGTASVVCL.L Deamidation(Q) 135 (Chy/48/-0.1208)
	117 F.IFPPSDEQLKSGTASVVCLL.N 136 (Chy/90/0.0204)
	119 F.PPSDEQLK.S 126 (Try/45/-0.0156)
	119 F.PPSDEQLKSGTASVVCL.L 135 (Chy/75/0.0677)
	119 F.PPSDEQL.K 125 (Pep/32/0.1786)
	127 K.SGTASVVCLLNNFYPR.E 142 (Try/64/0.1039)
	128 S.GTASVVCLLNNFYPR.E 142 (Try/37/-0.0765)
	129 G.TASVVCLLNNFYPR.E 142 (Try/58/0.0566)
	130 T.ASVVCLLNNFYPR.E 142 (Try/47/-0.0063)
	130 T.ASVVCLLNNFYPR.E 142 (Try/33/0.0035)
	131 A.SVVCLLNNFYPR.E 142 (Try/53/-0.1648)
	134 V.CLLNNFYPREAKVQW.K 148 (Chy/52/-0.1399)
	135 C.LLNNFYPR.E 142 (Try/42/0.1633)
	135 C.LLNNFYPREAKVQW.K 148 (Chy/46/0.0419)
	136 L.LNNTFYPREAKVQW.K 148 (Chy/62/0.0754)
	137 L.NNNTFYPREAKVQW.K 148 (Chy/60/0.0667)
	140 F.YPREAKVQWKVDNAL.Q 154 (Pep/30/0.1019)
	140 F.YPREAKVQWKVDNALQSGNSQE.S 161 (Pep/59/-0.1789)
	144 E.AKVQWKVDNALQSGNSQE.S 161 (Pep/114/0.0407)
	144 E.AKVQWKVDNALQSGNSQ*E.S Deamidation(Q) 161 (Pep/45/-0.0619)

		144 E.AKVQWKVDNALQSGNSQESV.T 163 (Pep/36/-0.0621) 149 W.KVDNALQSGNSQESVTEQD.S 167 (Chy/79/-0.0838) 149 W.KVDNALQSGNSQESVTEQDSKDSTY.S 173 (Chy/47/0.1194) 149 W.KVDNALQSGNSQE.S 161 (Pep/113/0.1557) 150 K.VDNALQSGNSQESVTEQD.S 167 (Try/65/-0.1356) 150 K.VDNALQSGNSQESVTEQDSK.D 169 (Try/137/-0.1814) 155 L.QSGNSQESVTEQDSK.D 169 (Try/42/-0.0135) 156 Q.SGNSQESVTEQDSKDSTY.S 173 (Chy/53/-0.1147) 162 E.SVTEQDSKDSTYSL.S 175 (Pep/60/0.1796) 162 E.SVTEQDSKDSTYSLSST.L 178 (Pep/71/0.1154) 162 E.SVTEQDSKDSTYSLSSTL.T 179 (Pep/60/0.0894) 170 K.DSTYSLSSTLTLSK.A 183 (Try/86/-0.0919) 173 T.YLSSTLTLSK.A 183 (Try/48/-0.1599) 174 Y.SLSSTLTLSKADYEKHKVY.A 192 (Chy/53/-0.0671) 179 T.LTLSKADYEKHKVY.A 192 (Pep/41/0.0046) 179 T.LTLSKADYEKHKVYACE.V 195 (Pep/77/0.0028) 180 L.TLSKADYEKHKVY.A 192 (Chy/64/0.0599) 180 L.TLSKADYEKHKVY.A 192 (Pep/52/0.0208) 181 T.LSKADYEKHKVYACE.V 195 (Pep/80/0.0156) 182 L.SKADYEKHKVY.A 192 (Chy/37/0.1494) 182 L.SKADYEKHKVYACE.V 195 (Pep/87/-0.0276) 183 S.KADYEKHKVY.A 192 (Chy/26/0.1834) 191 K.VYACEVTHQGLSSPVT.K.S 207 (Try/96/0.0346) 192 V.YACEVTHQGLSSPVT.K.S 207 (Try/113/0.018) 193 Y.ACEVTHQGLSSPVT.K.S 207 (Try/114/0.0883) 193 Y.ACEVTHQGL.S 201 (Chy/35/-0.0328) 193 Y.ACEVTHQGLSSPVT.K.S 207 (Chy/80/0.1123) 193 Y.ACEVTHQGLSSPVT.KSF.N 209 (Chy/73/-0.0775) 193 Y.ACEVTHQGLSSPVT.KSFNRGEC.- 214 (Pep/47/0.1958) 194 A.CEVTHQGLSSPVT.K.S 207 (Try/75/0.1506) 194 A.CEVTHQGL.S 201 (Chy/35/0.0495) 195 C.EVTHQGLSSPVT.K.S 207 (Try/65/0.0285) 196 E.VTHQ*GLSSPVT.KS.F Deamidation(Q) 208 (Pep/33/0.1336) 196 E.VTHQGLSSPVT.KSF.N 209 (Pep/37/0.0566) 196 E.VTHQGLSSPVT.KSFNRGEC.- 214 (Pep/70/-0.0105) 197 V.THQGLSSPVT.KSFNRGEC.- 214 (Pep/47/0.1699) 202 L.SSPVT.KSFNRGEC.- 214 (Chy/44/0.0046) 204 S.PVT.KSFNRGEC.- 214 (Chy/36/0.0007)
7	78%	1 -.DIQMTQSPSSLSASVGDR.V 18 (Try/133/0.0319) 1 -.DIQ*M*TQSPSSLSASVGDR.V Deamidation(Q) Oxidation(M) 18 (Try/60/-0.129) 2 D.IQMTQSPSSLSASVGDR.V 18 (Try/112/0.0481) 3 I.QMTQSPSSLSASVGDR.V 18 (Try/98/-0.0017) 4 Q.MTQSPSSLSASVGDR.V 18 (Try/32/0.1727) 8 S.PSSLSASVGDR.V 18 (Try/68/0.1433) 19 R.VTITCSASQDISNYLNWYQQKPGK.A 42 (Try/70/-0.1567) 21 T.ITCSASQDISN*YLNWYQQKPGK.A 42 (Try/87/-0.1064) 24 C.SASQDISNYLNWYQQKPGK.A 42 (Try/62/-0.1233) 30 I.SNYLNWYQQKPGK.A 42 (Try/63/-0.0291)

		46 K.VLIYFTSSLHSGVPSR.F 61 (Try/106/-0.0029) 47 V.LIYFTSSLHSGVPSR.F 61 (Try/107/0.0593) 48 L.IYFTSSLHSGVPSR.F 61 (Try/105/0.0844) 49 I.YFTSSLHSGVPSR.F 61 (Try/94/0.1292) 50 Y.FTSSLHSGVPSR.F 61 (Try/85/0.1299) 51 F.TSSLHSGVPSR.F 61 (Try/70/0.0748) 52 T.SSLHSGVPSR.F 61 (Try/34/0.087) 88 Y.CQYSTVPWTFGQGTK.V 103 (Try/59/-0.1649) 95 V.PWTFGQGTK.V 103 (Try/31/0.0133) 108 K.RTVAAPSVFIFPPSDEQLK.S 126 (Try/41/-0.1713) 109 R.TVAAPSVFIFPPSDEQLK.S 126 (Try/78/0.1478) 111 V.AAPSVFIFPPSDEQLK.S 126 (Try/70/0.0311) 112 A.APSVFIFPPSDEQLK.S 126 (Try/52/-0.0592) 113 A.PSVFIFPPSDEQLK.S 126 (Try/64/0.0335) 119 F.PPSDEQLK.S 126 (Try/59/0.0082) 127 K.SGTASVVCLLNNFYPR.E 142 (Try/71/0.0851) 127 K.SGTASVVCLLN*NFYPR.E 142 (Try/55/0.0579) 131 A.SVVCLLNNFYPR.E 142 (Try/43/-0.1028) 150 K.VDNALQSGNSQESVTEQDSK.D 169 (Try/140/-0.0138) 152 D.NALQSGNSQESVTEQDSK.D 169 (Try/63/-0.0478) 155 L.QSGNSQESVTEQDSK.D 169 (Try/53/-0.1219) 159 N.SQESVTEQDSK.D 169 (Try/48/-0.0609) 170 K.DSTYLSSTLTLSK.A 183 (Try/91/0.0805) 191 K.VYACEVTHQGLSPVTK.S 207 (Try/98/0.0832) 192 V.YACEVTHQGLSPVTK.S 207 (Try/98/0.0506) 193 Y.ACEVTHQGLSPVTK.S 207 (Try/100/0.0611) 194 A.CEVTHQGLSPVTK.S 207 (Try/81/0.0826) 195 C.EVTHQGLSPVTK.S 207 (Try/62/0.1543)
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Table S1B

MS/MS results of 4 spots from Avastin (MASCOT) identified by Orbitrap

Avastin was separated by 2-DE and identified by LTQ-Orbitrap Velos ETD MS/MS, using the MASCOT search engine.

spot	coverage	Identified Peptide (enzyme/ion score/mass error[ppm])
2	76%	1 -.EVQLVESGGGLVQPGGSLR.L 19(Trypsin/129/0) 20 R.LSCAASGYFTNYGM*NWVR.Q Oxidation(M) 38(Trypsin/112/0) 44 K.GLEWVGWINTYTGEPTYAADFK.R 65(Trypsin/47/0) 68 R.FTFSLDTSK.S 76(Trypsin/51/0) 68 R.FTFSLDTSKSTAYLQM*NSLR.A Oxidation(M) 87(Trypsin/37/-1) 68 R.FTFSLDTSKSTAYLQM*NSLR.A Oxidation(M) 87(Trypsin/56/0) 77 K.STAYLQM*NSLR.A Oxidation(M) 87(Trypsin/64/0) 88 R.AEDTAVYYCAK.Y 98(Trypsin/69/0) 128 K.GPSVFPLAPSSK.S 139(Trypsin/57/0) 128 K.GPSVFPLAPSSKSTSGGTAALGCLVK.D 153(Trypsin/44/1) 140 K.STSGGTAALGCLVK.D 153(Trypsin/98/-1) 217 K.VDKKVEPK.S 224(Trypsin/26/0) 220 K.KVEPKSCDK.T 228(Trypsin/23/0) 225 K.SCDKTHTCPPCPAPELLGGPSVFLFPPKPK.D 254(Trypsin/64/-1) 229 K.THTCPPCPAPELLGGPSVFLFPPKPK.D 254(Trypsin/59/-1) 255 K.DTLMISR.T 261(Trypsin/34/0) 255 K.DTLM*ISR.T Oxidation(M) 261(Trypsin/45/0) 255 K.DTLM*ISRTPEVTCVVVDVSHEDPEVK.F Oxidation(M) 280(Trypsin/40/-1) 262 R.TPEVTCVVVDVSHEDPEVK.F 280(Trypsin/90/0) 281 K.FNWYVDGVEVHNAK.T 294(Trypsin/73/0) 295 K.TKPREEQYNSTYR.V 307(Trypsin/40/1) 299 R.EEQYNSTYR.V 307(Trypsin/37/0) 308 R.VVSVLTVLHQDWLNGK.E 323(Trypsin/44/1) 308 R.VVSVLTVLHQDWLNGK.E 323(Trypsin/37/1) 329 K.VSNKALPAPIEK.T 340(Trypsin/49/0) 333 K.ALPAPIEK.T 340(Trypsin/26/1) 341 K.TISKAKGQPR.E 350(Trypsin/44/0) 351 R.EPQVYTLPPSREEMTK.N 366(Trypsin/49/-1) 351 R.EPQVYTLPPSREEM*TK.N Oxidation(M) 366(Trypsin/48/-1) 362 R.EEMTKNQVSLTCLVK.G 376(Trypsin/61/0) 362 R.EEM*TKNQVSLTCLVK.G Oxidation(M) 376(Trypsin/46/0) 367 K.NQVSLTCLVK.G 376(Trypsin/51/0) 377 K.GFYPSDIAVEWESNGQPENNYK.T 398(Trypsin/68/0) 399 K.TTPPVLDSDGSFFLYSK.L 415(Trypsin/74/1) 416 K.LTVDKSR.W 422(Trypsin/35/0) 423 R.WQQGNVFSCSVMHEALHNHYTQK.S 445(Trypsin/50/-1)
4	83%	1 -.EVQLVESGGGLVQPGGSLR.L 19(Trypsin/102/-1)

		20 R.LSCAASGYFTFTNYGM*NWVR.Q Oxidation(M) 38(Trypsin/35/0) 67 R.RFTFSLDTSK.S 76(Trypsin/44/0) 68 R.FTFSLDTSK.S 76(Trypsin/50/0) 77 K.STAYLQMNSLR.A 87(Trypsin/51/1) 77 K.STAYLQM*NSLR.A Oxidation(M) 87(Trypsin/59/1) 88 R.AEDTAVYYCAK.Y 98(Trypsin/81/0) 128 K.GPSVFPLAPSSK.S 139(Trypsin/53/0) 140 K.STSGGTAALGCLVK.D 153(Trypsin/80/0) 154 K.DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK.V 216(Trypsin/30/-1) 225 K.SCDKTHTCPPCPAPELLGGPSVFLFPPKPK.D 254(Trypsin/68/-1) 229 K.THTCPPCPAPELLGGPSVFLFPPKPK.D 254(Trypsin/59/0) 255 K.DTLM*ISR.T Oxidation(M) 261(Trypsin/44/0) 262 R.TPEVTCVVVDVSHEDPEVK.F 280(Trypsin/48/1) 281 K.FNWYVDGVEVHNAK.T 294(Trypsin/55/-1) 299 R.EEQYNSTYR.V 307(Trypsin/32/0) 308 R.VVSVLTVLHQDWLNGK.E 323(Trypsin/60/0) 329 K.VSNKALPAPIEK.T 340(Trypsin/44/0) 341 K.TISKAKGQPR.E 350(Trypsin/38/0) 351 R.EPQVYTLPPSR.E 361(Trypsin/41/0) 351 R.EPQVYTLPPSREEM*TK.N Oxidation(M) 366(Trypsin/47/-1) 367 K.NQVSLTCLVK.G 376(Trypsin/53/0) 399 K.TTPPVLDSDGSFFLYSK.L 415(Trypsin/40/-2) 399 K.TTPPVLDSDGSFFLYSK.L 415(Trypsin/48/0) 416 K.LTVDKSR.W 422(Trypsin/34/1) 423 R.WQQGNVFSCSVMHEALHNHYTQK.S 445(Trypsin/32/0) 423 R.WQQGNVFSCSVM*HEALHNHYTQK.S Oxidation(M) 445(Trypsin/34/2)
6	100%	1 -.DIQMTQSPSSLSASVGDR.V 18(Trypsin/Ions/0) 19 R.VTITCSASQDISNYLNWYQQKPGK.A 42(Trypsin/Ions/0) 19 R.VTITCSASQDISNYLNWYQQKPGKAPK.V 45(Trypsin/Ions/-1) 43 K.APKVLIYFTSSLHSGVPSR.F 61(Trypsin/Ions/0) 46 K.VLIYFTSSLHSGVPSR.F 61(Trypsin/Ions/0) 62 R.FSGSGSGTDFTLTISLQPEDFATYYCQQYSTVPWTFGQGTK.V 103(Trypsin/Ions/1) 104 K.VEIKRTVAAPSVFIFPPSDEQLK.S 126(Trypsin/Ions/0) 108 K.RTVAAPSVFIFPPSDEQLK.S 126(Trypsin/Ions/0) 127 K.SGTASVVCLLNNFYPR.E 142(Trypsin/Ions/0) 143 R.EAKVQWK.V 149(Trypsin/Ions/0) 150 K.VDNALQSGNSQESVTEQDSK.D 169(Trypsin/Ions/0) 150 K.VDNALQSGNSQESVTEQDSKDYSLSTLTLSK.A 183(Trypsin/Ions/-1) 170 K.DSTYLSSTLTLSK.A 183(Trypsin/Ions/-1) 170 K.DSTYLSSTLTLSKADYEK.H 188(Trypsin/Ions/-1) 184 K.ADYEKHKVYACEVTHQGLSPVTK.S 207(Trypsin/Ions/1) 189 K.HKVYACEVTHQGLSPVTK.S 207(Trypsin/Ions/-1) 189 K.HKVYACEVTHQGLSPVTKSFNR.G 211(Trypsin/Ions/0) 191 K.VYACEVTHQGLSPVTK.S 207(Trypsin/Ions/1) 191 K.VYACEVTHQGLSPVTK.S 207(Trypsin/Ions/2) 191 K.VYACEVTHQGLSPVTKSFNR.G 211(Trypsin/Ions/0) 208 K.SFNRGEC.- 214(Trypsin/Ions/0)

7	95%	1 -.DIQMTQSPSSLSASVGDR.V 18(Trypsin/114/0) 1 -.DIQM*TQSPSSLSASVGDR.VoxidationM) 18(Trypsin/101/0) 19 R.VTITCSASQDISNYLNWYQQKPGK.A 42(Trypsin/97/-1) 19 R.VTITCSASQDISNYLNWYQQKPGKAPK.V 45(Trypsin/34/-1) 43 K.APKVLIYFTSSLHSGVPSR.F 61(Trypsin/43/-1) 46 K.VLIYFTSSLHSGVPSR.F 61(Trypsin/100/0) 62 R.FSGSGSGTDFTLTISSLQPEDFATYYCQYSTVPWTFGQGTK.V 103(Trypsin/47/1) 108 K.RTVAAPSVFIFPPSDEQLK.S 126(Trypsin/68/0) 127 K.SGTASVVCLLNNFYPR.E 142(Trypsin/85/-1) 150 K.VDNALQSGNSQESVTEQDSK.D 169(Trypsin/112/-1) 150 K.VDNALQSGNSQESVTEQDSK.D 169(Trypsin/126/0) 150 K.VDNALQSGNSQESVTEQDSKDYSLSTLTLSK.A 183(Trypsin/95/0) 170 K.DSTYSLSTLTLSK.A 183(Trypsin/71/0) 170 K.DSTYSLSTLTLSKADYEK.H 188(Trypsin/94/1) 189 K.HKVYACEVTHQGLSPVTK.S 207(Trypsin/83/0) 191 K.VYACEVTHQGLSPVTK.S 207(Trypsin/84/0) 191 K.VYACEVTHQGLSPVTKSFNR.G 211(Trypsin/86/0) 208 K.SFNRGEC.- 214(Trypsin/44/0)
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