

Figure S1

Sequence information of Avastin® identified by A) HCT and B) Orbitrap is shown

A**Avastin heavy chain (sequence coverage 98%)****Spot 1 (sequence coverage 64%) identified by HCT**

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW
 51 INTYTGPEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP
 101 HYYGSSHWYF DVWGQGTILVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
 151 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
 201 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
 251 PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
 301 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
 351 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
 401 PPVLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL
 451 PGK

Spot 3 (sequence coverage 95%) identified by HCT

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW
 51 INTYTGPEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP
 101 HYYGSSHWYF DVWGQGTILVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
 151 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
 201 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
 251 PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
 301 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
 351 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
 401 PPVLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL
 451 PGK

Avastin light chain (sequence coverage 100%)**Spot 5 (sequence coverage 100%) identified by HCT**

1 DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKPK GKAPKVLIIYF
 51 TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ
 101 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
 151 DNALQSGNSQ ESVTEQDSK STYLSLSTLT LSKADYEKHK VYACEVTHQG
 201 LSSPVTKSFN RGEC

Spot 7 (sequence coverage 78%) identified by HCT

1 DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKPK GKAPKVLIIYF
 51 TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ
 101 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
 151 DNALQSGNSQ ESVTEQDSK STYLSLSTLT LSKADYEKHK VYACEVTHQG
 201 LSSPVTKSFN RGEC

Spot 2 (sequence coverage 96%) identified by HCT

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW
 51 INTYTGPEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP
 101 HYYGSSHWYF DVWGQGTILVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
 151 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
 201 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
 251 PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
 301 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
 351 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
 401 PPVLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL
 451 PGK

Spot 4 (sequence coverage 83%) identified by HCT

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW
 51 INTYTGPEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP
 101 HYYGSSHWYF DVWGQGTILVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
 151 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
 201 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
 251 PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
 301 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
 351 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
 401 PPVLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL
 451 PGK

Spot 6 (sequence coverage 88%) identified by HCT

1 DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKPK GKAPKVLIIYF
 51 TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ
 101 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
 151 DNALQSGNSQ ESVTEQDSK STYLSLSTLT LSKADYEKHK VYACEVTHQG
 201 LSSPVTKSFN RGEC

B

Avastin heavy chain (sequence coverage 97%)

Spot 2 (sequence coverage 76%) identified by Orbitrap

1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW
51 INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP
101 HYYGSSHWYF DVWGQGTLLVTVSSASTKGPS VFPLAPSSKS TSGGTAALGC
151 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
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401 PPVLDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL
451 PGK

Avastin heavy chain (sequence coverage 100%)

Spot 6 (sequence coverage 100%) identified by Orbitrap

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51 TSSLHSGVPS RFGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ
101 GTKVEIKRTV AAPSVEFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
151 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG
201 LSSPVTKSFN RGEK

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151 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG
201 LSSPVTKSFN RGEK