

Name data set: MAB_Demo1_t2_t1
 Name lis-file: MAB_Demo_2_mod_cleaned
 Name sequence file: MAB_Demo_LC

Min. relative intensity [%]: 0

Path res_summary-file: C:\massmap\web_site\reports\pepmap\final_evaluations\MAB_Demo1_t2...
 ..._t1_MAB_Demo_2_mod_cleaned\MAB_Demo1_t2_t1_MAB_Demo_2_mod_clea...
 ...ned.res_summary

Path sequence file: C:\massmap\web_site\reports\pepmap\lis_etc\MAB_Demo_LC.txt

AA position	10	20	30	40	50	60	70	80
Protein							
LC01	DIVLTQSPATLSVTPGDSVSLSCRASQISNNLHWYQQKSHESPRLLIKYASQISIGIPSR FSGSGSGTDF TL SINSVET							
LC02ASQISNNLHWYQQK							
LC02_deamidASQISNNLHWYQQK							
LC03SHESPR							
LC03-04SHESPRLLIK							
LC04LLIK							
LC05YASQISIGIPSR							

AA position	90	100	110	120	130	140	150	160
Protein							
LC07	EDFGMYFCQ QNSW PLTFGAGTK LELKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINV KWK IDGSERQNGVL							
LC07-08LELKR							
LC08-09RADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPK							
LC08-09_deamidRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPK							
LC09ADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPK							
LC09_deamidADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPK							
LC10DINVK							
LC12IDGSER							
LC13QNGVL							
LC13_deamidQNGVL							

AA position	90	100	110	120	130	140	150	160
LC13_pyEQNGVL							
LC13_deamid_pyEQNGVL							
LC13-14_deamidQNGVL							
LC13-14_pyEQNGVL							

AA position	170	180	190	200	210
Protein				
LC13	NSWTDQDSKDYSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC				
LC13_deamid	NSWTDQDSK				
LC13_pyE	NSWTDQDSK				
LC13_deamid_pyE	NSWTDQDSK				
LC13-14_deamid	NSWTDQDSKDYSTYSMSSTLTLTK				
LC13-14_pyE	NSWTDQDSKDYSTYSMSSTLTLTK				
LC14DSTYSMSSTLTLTK				
LC14_oxDSTYSMSSTLTLTK				
LC15DEYER				
LC16HNSYTCEATHK				

Length of protein sequence: 214
 Number of AA covered by peptides: 170
 Sequence coverage [%]: 79.43

Name data set: MAB_Demo1_t2_t1
 Name lis-file: MAB_Demo_2_mod_cleaned
 Name sequence file: MAB_Demo_HC

Min. relative intensity [%]: 0

Path res_summary-file: C:\massmap\web_site\reports\pepmap\final_evaluations\MAB_Demo1_t2_t...
 ...1_MAB_Demo_2_mod_cleaned\MAB_Demo1_t2_t1_MAB_Demo_2_mod_cleaned...
 ...res_summary

Path sequence file: C:\massmap\web_site\reports\pepmap\lis_etc\MAB_Demo_HC.txt

AA position	10	20	30	40	50	60	70	80
Protein	EVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNNLY						
HC01	EVQGVESGGGLVKPGGSLK						
HC02LSCAASGFTFSDYYMYWVR						
HC03QTPEK						
HC03_pyEQTPEK						
HC04-05RLEWVATISDGGSYTYYPDSVK						
HC05LEWVATISDGGSYTYYPDSVK						
HC07FTISR						
HC07-08_deamidFTISRDNAK						
HC08DNAK						
HC08-09_deamidDNAKNNLY						
	10	20	30	40	50	60	70	80
HC09NNLY						
HC09_oxNNLY						
HC09_deamidNNLY						

AA position	90	100	110	120	130	140	150	160
Protein	LQMSSLKSEDTAMYYCARDKAYYGNYGDAMDYWGQTSVTVSSAKTTPPSVYPLAPGSAAQTNMVMTLGCLVKGYFPEPV						
HC08-09_deamid	LQMSSLK						
HC09	LQMSSLK						
HC09_ox	LQMSSLK						
HC09_deamid	LQMSSLK						
HC10SEDTAMYYCAR						
HC10_oxSEDTAMYYCAR						
HC12	AYYGNYGDAMDYWGQTSVTVSSAK					
HC12_ox	AYYGNYGDAMDYWGQTSVTVSSAK					
HC13TTPPSVYPLAPGSAAQTNMVMTLGCLVK					
HC13_oxTTPPSVYPLAPGSAAQTNMVMTLGCLVK					
	90	100	110	120	130	140	150	160
HC13_deamidTTPPSVYPLAPGSAAQTNMVMTLGCLVK					
HC13_ox_deamidTTPPSVYPLAPGSAAQTNMVMTLGCLVK					
HC14GYFPEPV					

AA position	170	180	190	200	210	220	230	240
Protein	TVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVIVPSSVTPSEIVTCDVAHPASSTKVDKDKIVPRDCGCKPCICTVPEVSSV						
HC14	TVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVIVPSSVTPSEIVTCDVAHPASSTK						
HC15VDK						
HC15-16VDKK						
HC17IVPR						
HC18DCGCKPCICTVPEVSSV						

AA position	250	260	270	280	290	300	310	320
Protein	FIFPPKPKDVLITITLTPKVTVCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFK						
HC18	FIFPPKPK						
HC19DVLITITLTPK						
HC20VTCVVVDISK						
HC20-21VTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPR						
HC21DDPEVQFSWFVDDVEVHTAQTQPR						
HC22EEQFNSTFR						
HC22_A2G0EEQFNSTFR						
HC22_A2G0-GlcNAcEEQFNSTFR						
HC22_A2G1EEQFNSTFR						
HC22_A2G1-GlcNAcEEQFNSTFR						

AA position	250	260	270	280	290	300	310	320
Protein	FIFPPKPKDVLITITLTPKVT	CVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFK						
	250	260	270	280	290	300	310	320
HC22_A2G2S1						..EEQFNSTFR		
HC22_A2FG0						..EEQFNSTFR		
HC22_A2FG0-GlcNAc						..EEQFNSTFR		
HC22_A2FG1						..EEQFNSTFR		
HC22_A2FG1-GlcNAc						..EEQFNSTFR		
HC22_A2FG2						..EEQFNSTFR		
HC22_Man5						..EEQFNSTFR		
HC23							.SVSELPIMHQDWLNGK	
HC23_ox							.SVSELPIMHQDWLNGK	
HC23_deamid							.SVSELPIMHQDWLNGK	
	250	260	270	280	290	300	310	320
HC23_ox_deamid							.SVSELPIMHQDWLNGK	
HC24								..EFK

AA position	330	340	350	360	370	380	390	400
Protein	CRVNSAAFPAPIEKTISK TK GRPKAPQVYTI	PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPI						
HC25-26	CRVNSAAFPAPIEK							
HC25-26_deamid	CRVNSAAFPAPIEK							
HC26	..VNSAAFPAPIEK							
HC26_deamid	..VNSAAFPAPIEK							
HC27TISK							
HC29 GRPK							
HC30APQVYTI	PPPK						
HC30-31APQVYTI	PPPKEQMAK						
HC31EQMAK							
HC32-33DKVSLTCMITDFFPEDITVEWQWNGQPAENYK							
	330	340	350	360	370	380	390	400
HC32-33_deamidDKVSLTCMITDFFPEDITVEWQWNGQPAENYK							
HC33VSLTCMITDFFPEDITVEWQWNGQPAENYK							
HC33_deamidVSLTCMITDFFPEDITVEWQWNGQPAENYK							
HC34NTQPI	MDT						
HC34_oxNTQPI	MDT						
HC34_deamidNTQPI	MDT						
HC34-35NTQPI	MDT						

AA position	410	420	430	440
Protein	DGSYFVYSKLN	VQKSNWEAGNTFTCSVLHEGLHNNHTEKSLSHSPGK		
HC34	DGSYFVYSK			
HC34_ox	DGSYFVYSK			
HC34_deamid	DGSYFVYSK			
HC34-35	DGSYFVYSKLN	VQK		
HC35LNVQK			
HC36SNWEAGNTFTCSVLHEGLHNNHTEK			
HC36_deamidSNWEAGNTFTCSVLHEGLHNNHTEK			
HC37SLSHSPGK			

Length of protein sequence: 447
 Number of AA covered by peptides: 441
 Sequence coverage [%]: 98.65