Table S1: List of peptide identifications in *Clostridium difficile* exoproteome after SDS-PAGE, tryptic digestion, LC-MS/MS and database search (Mascot)

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
FFNEEEM*NAILTR	44	815.4	2	Oxidation (M)	Aspartyl-tRNA synthetase OS=Clostridium difficile (s	Q183H4|Q183H4_CLOD6
VGQEGVTSPIAK	45	593.3	2		Aspartyl-tRNA synthetase OS=Clostridium difficile (s	Q183H4|Q183H4_CLOD6
QISSLEEHAK	30	571.3	2		Aspartyl-tRNA synthetase OS=Clostridium difficile (s	Q183H4|Q183H4_CLOD6
SGTTTEPALAFR	43	625.8	2		Glucose-6-phosphate isomerase OS=Clostridium dif	Q180C9|G6PI_CLOD6
NITISSEEVDLDGLNYLAGK	69	1076.0	2		Glucose-6-phosphate isomerase OS=Clostridium dif	Q180C9|G6PI_CLOD6
IYATTDASKGALR	48	683.9	2		Glucose-6-phosphate isomerase OS=Clostridium dif	Q180C9|G6PI_CLOD6
SGNFGQVINK	44	532.2	2		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
ANINSSNDIENLDIVK	75	879.9	2		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
IANQNSELNKANINSSNDIENLDIVK	49	957.7	3		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
TNDIQELTIK	52	587.8	2		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
QIESNVMDDSIK	72	689.8	2		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
ELLEDNANKDIEVITK	52	922.5	2		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
QIESNVM*DDSIK	65	697.8	2	Oxidation (M)	Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
SGNFGQVINKNVDMNK	50	588.9	3		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
ANINSSNDIENLDIVKLR	35	676.7	3		Putative flagellar hook-length control protein OS=Cl	Q18CZ6|Q18CZ6_CLOD6
WGATGPNSFDCSGFTSYVYK	68	1122.3	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
NGAGVNLPR	54	449.2	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
IKSVDNVTGWVNGDYLTIQGGNVDAK	32	922.0	3		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
RLITATR	32	415.7	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
SVDNVTGWVNGDYLTIQGGNVDAK	61	841.6	3		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
AELKPGDLVFFGSGGSINHVGLYVGDSK	32	955.4	3		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
VQNVLNLAFK	54	573.3	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
VTSMAPGTNYAR	34	634.2	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
INTGDKVEVLELHSNGWIK	44	718.3	3		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
FIHSPQTGDVVK	47	664.2	2		Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
VTSM*APGTNYAR	59	642.2	2	Oxidation (M)	Putative cell-wall hydrolase OS=Clostridium difficile	Q183K6|Q183K6_CLOD6
GVLKVQDEVELVGLTEAPR	36	684.7	3		Elongation factor Tu OS=Clostridium difficile (strain	Q18CE4|EFTU_CLOD6
DLLTEYDFPGDDTPIVR	91	983.3	2		Elongation factor Tu OS=Clostridium difficile (strain	Q18CE4|EFTU_CLOD6
LLDQAQAGDNIGALLR	80	834.4	2		Elongation factor Tu OS=Clostridium difficile (strain	Q18CE4|EFTU_CLOD6
GITISTAHVEYETPNR	71	894.3	2		Elongation factor Tu OS=Clostridium difficile (strain	Q18CE4|EFTU_CLOD6
TVASGVVATIIE	30	580.3	2		Elongation factor Tu OS=Clostridium difficile (strain	Q18CE4|EFTU_CLOD6
FNLAGDTTFR	37	571.2	2		Proline reductase OS=Clostridium difficile (strain 63	Q17ZY6|Q17ZY6_CLOD6
DTLEQLVAIPSAGK	46	721.8	2		Proline reductase OS=Clostridium difficile (strain 63	Q17ZY6|Q17ZY6_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
AIEEAGIPTIIIAALPPVVR	55	1022.5	2		Proline reductase OS=Clostridium difficile (strain 63	Q17ZY6|Q17ZY6_CLOD6
VFIDEGDVILCESPSYIGAINAFK	73	886.8	3		Putative amino acid aminotransferase OS=Clostridiu	Q181R8|Q181R8_CLOD6
TNVNKDDILVTSGSQQGLDFAGK	40	803.4	3		Putative amino acid aminotransferase OS=Clostridiu	Q181R8|Q181R8_CLOD6
VSVAVLEENGR	43	586.8	2		Putative amino acid aminotransferase OS=Clostridiu	Q181R8|Q181R8_CLOD6
MYQLEYAGLSK	52	651.7	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
VYLIGGENSLSK	50	640.2	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
GAIVVVIDNTANPNREK	39	905.5	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
NVQTQLSNM*GISVER	83	846.3	2	Oxidation (M)	Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
SELQGADEFLNSSK	52	762.8	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
TDSPVVLVGNKLDESQK	42	610.3	3		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
SSVAYNPM*DLGLTTPAK	75	891.0	2	Oxidation (M)	Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
TSSGQATSGESLTGADRYETAVK	63	772.7	3		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
SEAQGATKPSNM*DTAPTQFNVTDVVR	39	927.4	3	Oxidation (M)	Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
VTAANVFDFSR	57	613.8	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
TDSPVVLVGNK	57	564.8	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
SQGDLIDGLAVGALGAK	92	792.8	2		Cell surface protein (Putative cell surface-associate	Q183M1|Q183M1_CLOD6
DTADWLETTDTSLDQLGNLLADIKK	30	926.0	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
KLANPSDANIK	35	585.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
EINKLSDNPYK	52	660.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
EIANALNATHEGK	76	684.2	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
EKNDEGLIQLK	41	643.8	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LFNVSILDYI	56	598.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
AAELTYQASLQTGGK	95	769.8	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LSDNPYKAIK	39	574.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LANPSDANIK	51	521.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
DVLSQNDEIDYGEKLVQLK	63	736.3	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
VSTGMMSSSYLNSLQDNLQR	66	1116.3	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
DVLSQNDEIDYGEK	69	812.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
GLVSSGNGSYSDDEIK	94	814.3	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
ILNSKSEIK	34	516.2	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
NDEGLIQLK	38	515.2	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
M*KEIANALNATHEGK	87	821.8	2	Oxidation (M)	Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
ELTTTCLGDMENLIDNTVNVR	34	803.6	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LANPSDANIKELTTTCLGDM*ENLIDNTVNV	63	1150.1	3	Oxidation (M)	Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
MKEIANALNATHEGK	106	814.3	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LANPSDANIKELTTTCLGDMENLIDNTVNVR	49	1144.7	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
LSSLGFDPTKTDPFEK	34	594.5	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
LSSLGFDPTK	43	532.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
FNTSLNLNK	60	525.7	2		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
GLVSSGNGSYSDDEIKTISNSTNEK	89	867.9	3		Flagellar hook-associated protein OS=Clostridium di	Q18CX5|Q18CX5_CLOD6
APNTAM*LDYLTVGVLPK	58	909.8	2	Oxidation (M)	Oligopeptide ABC transporter, substrate-binding lipo	Q18A51|Q18A51_CLOD6
SGELDLAQITPK	60	636.4	2		Oligopeptide ABC transporter, substrate-binding lipo	Q18A51|Q18A51_CLOD6
TM*TDPIADMLTR	59	690.7	2	Oxidation (M)	30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
ILLEEGFIR	50	545.2	2		30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
VLNGLGISVISTSK	62	694.3	2		30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
TMTDPIADMLTR	55	682.7	2		30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
TM*TDPIADM*LTR	55	699.2	2	2 Oxidation (M)	30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
KENVGGEVICYVW	39	776.7	2		30S ribosomal protein S8 OS=Clostridium difficile (s	Q18CH0|RS8_CLOD6
LVEVISGQLTSK	49	637.2	2		3-hydroxybutyryl-CoA dehydrogenase OS=Clostridiu	Q18AQ7|Q18AQ7_CLOD6
VTFDTVFELSK	80	643.2	2		3-hydroxybutyryl-CoA dehydrogenase OS=Clostridiu	Q18AQ7|Q18AQ7_CLOD6
SINKVPVDVSESPGFVVNR	32	681.9	3		3-hydroxybutyryl-CoA dehydrogenase OS=Clostridiu	Q18AQ7|Q18AQ7_CLOD6
ILIPM*INEAVGIYADGVASKEEIDEAM*K	38	1018.1	3	2 Oxidation (M)	3-hydroxybutyryl-CoA dehydrogenase OS=Clostridiu	Q18AQ7|Q18AQ7_CLOD6
FNVIASEAVLEGTIR	53	809.9	2		Putative peptidase OS=Clostridium difficile (strain 63	Q18AU1|Q18AU1_CLOD6
LFFQPGEEVGKGAR	31	768.4	2		Putative peptidase OS=Clostridium difficile (strain 63	Q18AU1|Q18AU1_CLOD6
M*ASADFFK	34	466.6	2	Oxidation (M)	Putative peptidase OS=Clostridium difficile (strain 63	Q18AU1|Q18AU1_CLOD6
EVSPLEPLVVSVGVLNSGTR	38	685.0	3		Putative peptidase OS=Clostridium difficile (strain 63	Q18AU1|Q18AU1_CLOD6
NITSVGEINEK	57	602.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
NSPMVLVNDGSDKTVLEGAK	34	692.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
SLADGLSVSGLSGATK	38	731.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
NSPM*VLVNDGSDKTVLEGAK	34	697.7	3	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
VIQQCINASK	59	580.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
NVQTTQDAKDLAK	55	716.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
VLPIEVDGFIDTNR	54	794.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N0|Q183N0_CLOD6
GLAEDVKSGDSILIDDGLVGLR	59	748.1	3		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
SSVAGNTDEVIEKAIEAAR	116	980.8	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
SPIIATTNNEKTM*NK	33	839.4	2	Oxidation (M)	Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
SGDSILIDDGLVGLR	67	765.3	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
VHVISEEIVQGIGVGTQTVEGK	44	760.7	3		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
LNKPVAILLDTKGPEIR	68	939.0	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
SSVAGNTDEVIEK	74	674.8	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
RTEETLDYDR	48	649.3	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
SPIIATTNNEK	54	594.3	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
INLPAITPK	46	483.8	2		Pyruvate kinase OS=Clostridium difficile (strain 630)	Q180P2|Q180P2_CLOD6
YVAPAIGQLTFDATDK	103	855.3	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
MASGDKTVDPSDDTYVLTLTK	60	753.4	3		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
M*ASGDKTVDPSDDTYVLTLTK	66	758.3	3	Oxidation (M)	Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
AGAVSETTATDSAANATFEVKK	62	723.7	3		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
TVDPSDDTYVLTLTK	75	834.3	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
AGAVSETTATDSAANATFEVK	116	1020.8	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
VAGLPSGLDYTAVGNR	62	795.3	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
TASQAVQTDLDNVSVLVK	92	944.4	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
YVAPAIGQLTFDATDKQIK	36	693.9	3		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
YVAAPAVGQLTFDATDK	64	884.3	2		Cell surface protein (Putative hemagglutinin/adhesin	Q188W0|Q188W0_CLOD6
EYLEENLDYLR	43	728.8	2		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
TVDLVEIYDEPTHPEATYK	72	740.7	3		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
TAIM*LEPR	31	473.8	2	Oxidation (M)	Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
NVVIFGQGQVDR	69	666.3	2		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
SIQAIDSHTAGEATR	82	778.8	2		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
VADFNAVVPK	52	530.3	2		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
EVSFLNVPAFLYK	43	763.9	2		Proline racemase OS=Clostridium difficile (strain 63	Q17ZY4|PRAC_CLOD6
NQNDAFLLFDKWK	37	546.9	3		Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
M*QQSPPQDIISM*FEK	54	905.8	2	2 Oxidation (M)	Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
IQYDDTPYHWPSNVISLTNSSEK	55	899.3	3		Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
QVTFNDGSVWK	59	640.7	2		Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
EVSNSVLENYYK	54	722.7	2		Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
SFQGKEVSNSVLENYYK	50	996.3	2		Putative membrane protein OS=Clostridium difficile	Q185R5|Q185R5_CLOD6
AFLGLLNR	31	452.2	2		Putative rubrerythrin OS=Clostridium difficile (strain	Q18C45|Q18C45_CLOD6
IGVAQGVDAEIIEGLR	94	820.3	2		Putative rubrerythrin OS=Clostridium difficile (strain	Q18C45|Q18C45_CLOD6
FAELLGEVVVADTKENLR	75	668.3	3		Putative rubrerythrin OS=Clostridium difficile (strain	Q18C45|Q18C45_CLOD6
IGVAALALGIAQGALDEAVK	65	627.3	3		Acyl-CoA dehydrogenase, short-chain specific OS=	Q188I5|Q188I5_CLOD6
IAM*GTLEVGR	47	531.8	2	Oxidation (M)	Acyl-CoA dehydrogenase, short-chain specific OS=	Q188I5|Q188I5_CLOD6
GLVYDAAQKR	53	560.9	2		Acyl-CoA dehydrogenase, short-chain specific OS=	Q188I5|Q188I5_CLOD6
FISSNIPEEYGGGGAGYVSYAIVMEEIARR	45	1079.0	3		Acyl-CoA dehydrogenase, short-chain specific OS=	Q188I5|Q188I5_CLOD6
SITVASSM*GPGVK	64	625.2	2	Oxidation (M)	50S ribosomal protein L1 OS=Clostridium difficile (s	Q18CE9|RL1_CLOD6
AKEAEQAGADFVGAEELVQK	43	697.6	3		50S ribosomal protein L1 OS=Clostridium difficile (s	Q18CE9|RL1_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
GALACQGINYEK	60	662.2	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
DIPILITAVSDPVAAGLVK	82	946.4	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
VQVDALKEYASK	65	675.8	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
KIGITQLVEHPALDATR	60	621.4	3		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
TLEKPGTNVSGTSDFVSVDKGLELLK	32	912.4	3		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
TIGVM*YNTSEVNSK	70	779.8	2	Oxidation (M)	ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
GITTSNEVNQGISSLVGK	68	902.4	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
IATENKIPVIAAESGPVEK	52	655.9	3		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
TIGVMYNTSEVNSK	83	771.8	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
ALGM*EKPSNENISYVK	45	599.2	3	Oxidation (M)	ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
IGITQLVEHPALDATR	53	867.5	2		ABC transporter, substrate-binding lipoprotein OS=C	Q18A65|Q18A65_CLOD6
VTAIGISDK	34	452.1	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
IGGVDRYQTNK	35	417.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
IAGEIEKIK	36	334.5	3		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
IYVIGGENSISKDVEK	49	875.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
IYVIGGENSISK	44	640.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
NAPVVLVSNKSDK	53	685.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
NAPVVLVSNK	42	520.7	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
EFYITSGDDLVYALVASPLAK	79	1136.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q18A40|Q18A40_CLOD6
LKGVSEPEAK	37	529.3	2		GMP synthase [glutamine-hydrolyzing] OS=Clostridi	Q18CT8|GUAA_CLOD6
VNAEDRFLSK	44	589.8	2		GMP synthase [glutamine-hydrolyzing] OS=Clostridi	Q18CT8|GUAA_CLOD6
IIGEEFIR	45	488.8	2		GMP synthase [glutamine-hydrolyzing] OS=Clostridi	Q18CT8|GUAA_CLOD6
YLEEYPDAK	51	564.2	2		Putative uncharacterized protein OS=Clostridium dif	Q183M6|Q183M6_CLOD6
ALGEAALELYR	69	603.2	2		Putative uncharacterized protein OS=Clostridium dif	Q183M6|Q183M6_CLOD6
YLEEYPDAKVK	34	677.8	2		Putative uncharacterized protein OS=Clostridium dif	Q183M6|Q183M6_CLOD6
SHFDELATNKIQYVHAP	35	657.3	3		Putative uncharacterized protein OS=Clostridium dif	Q183M6|Q183M6_CLOD6
EKDYTLNTSLATTEYLR	59	1009.5	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TVM*IDPGHGGSDTGTTGKPLGGIR	46	780.7	3	Oxidation (M)	Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TLSTDPTKDYLYVLR	70	893.0	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
SDVLVDALAAGPLAANLKSPILITPK	34	863.5	3		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
VM*SSIASSLSK	61	563.3	2	Oxidation (M)	Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
SKGFNVIM*TR	52	584.8	2	Oxidation (M)	Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
DVIIIGDENAISKTTANQIK	71	1072.6	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
DVIIIGDENAISK	70	693.9	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TSAPITELTGSDRYETAVK	71	680.4	3		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
LNPRDVIIIGDENAISK	63	934.0	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
VMSSIASSLSK	49	555.3	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TTANQIKSTVNASQTR	56	860.4	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
VYITNANGGEVDALTIAAK	59	960.5	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
FYTDDELEAVLVAK	76	807.0	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TVATNILNR	58	501.3	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
DTDKTLSLGNR	42	610.3	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
SPILITPK	47	434.8	2		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
SDVLVDALAAGPLAANLK	75	579.9	3		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TVMIDPGHGGSDTGTTGKPLGGIR	53	775.3	3		Cell surface protein (Putative N-acetylmuramoyl-L-a	Q18AN5|Q18AN5_CLOD6
TLLYAINGGVDEKSGVQVGPR	38	725.2	3		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
VSIDTSSVQYENDDLM*R	84	994.3	2	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
SGIITGLPDAYGR	47	660.3	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
ATLEDAM*EHPEEYPQLTIR	53	753.6	3	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
M*VENSCEAFGYELDPEIKDIFTK	55	917.6	3	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
EFIQLNYSPYEGNDSFLAGATENTK	41	937.0	3		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
EQQLDVINR	40	557.7	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
LPYEHAQDGISNTFSIVPAALGK	30	810.0	3		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
VALYGVDALIEDKNEQK	36	635.5	3		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
M*AESYGFDISKPATNSK	47	621.5	3	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
DQNGAAM*SLGR	37	568.2	2	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
VSGYAVNFIK	47	549.2	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
TLLYAINGGVDEK	82	696.8	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
KSGIITGLPDAYGR	51	724.3	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
EFIQLNYSPYEGNDSFLAGATENTKK	36	979.7	3		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
TSTFLDIYFER	66	696.3	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
DTNGALASLSSVAK	32	667.9	2		Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
QM*QFFGAR	31	500.6	2	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
YGNNDDRVDSIAVELVESFM*NK	54	844.6	3	Oxidation (M)	Formate acetyltransferase OS=Clostridium difficile (	Q189V5|Q189V5_CLOD6
YNLDIIDVITEDNK	102	832.8	2		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
YVDSNNENEPFSKELVNR	44	718.6	3		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
YVDSNNENEPFSK	86	771.8	2		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
DLEQWYFK	32	564.7	2		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
GNTVSPM*DIIDEYGADTAR	89	1021.4	2	Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
LFVLFAAPPER	36	630.3	2		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
SM*GM*VDFNEPFK	40	717.2	2	2 Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
TAADVEKEGM*FIGR	38	513.8	3	Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
SKGNTVSPM*DIIDEYGADTAR	48	752.6	3	Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6
LVDELADVVKK	35	614.8	2		Leucyl-tRNA synthetase OS=Clostridium difficile (st	Q182K8|SYL_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
DVEFGELNSQDKDM*R	33	600.2	3	Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (str	Q182K8|SYL_CLOD6
NLLTQGM*VLM*DGSK	59	769.7	2	2 Oxidation (M)	Leucyl-tRNA synthetase OS=Clostridium difficile (str	Q182K8|SYL_CLOD6
EDLPVLLPTDVEFTGKGESPLTTSK	31	892.0	3		Leucyl-tRNA synthetase OS=Clostridium difficile (str	Q182K8|SYL_CLOD6
NYSIGDVVAR	38	547.2	2		Leucyl-tRNA synthetase OS=Clostridium difficile (str	Q182K8|SYL_CLOD6
LLNEPYIHNNYTSGDIDTVVPK	55	835.0	3		Signal peptidase I OS=Clostridium difficile (strain 63	Q18BJ6|Q18BJ6_CLOD6
VIATEGDRIK	31	551.2	2		Signal peptidase I OS=Clostridium difficile (strain 63	Q18BJ6|Q18BJ6_CLOD6
KNNIPNATLK	39	556.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q182K4|Q182K4_CLOD6
NNPIVLVDIGSNKDILK	31	926.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q182K4|Q182K4_CLOD6
ILFYNPDGEDFFEYK	66	948.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q182K4|Q182K4_CLOD6
FIHCSGTQTNPNK	34	752.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
VTSAVSLNVR	60	523.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
LNGGDVVELK	44	522.2	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
SGAGTNYSLVGK	62	577.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
VSSSVVGWGSAK	64	582.2	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
HSVGVSIPR	43	476.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
VDNLTSSYWSKVLLGAR	32	637.2	3		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
SGAGTNYSLVGKANNGDVVK	53	651.3	3		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
GTVTASALNIR	77	551.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
SGPGTSYSIIGK	39	583.7	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
VDNLTSSYWSK	64	650.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
YISTSGSSEGTSSQNNSTSSGTTISGNGK	40	933.0	3		Putative cell wall hydrolase OS=Clostridium difficile	Q18AZ7|Q18AZ7_CLOD6
LYHVDIDANK	48	396.5	3		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
IEM*YEGVPCSLINSSINTIKFTSK	43	916.8	3	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
LSQAQLNSVAQATADFM*NKK	47	727.7	3	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
AYPAVGEVVKTQNPTPTVK	51	1000.0	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
NMTTDAKIR	55	525.2	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
SYVAGTNSIYGPK	73	678.9	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
LSQAQLNSVAQATADFM*NK	89	1027.5	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
VEIGETASNSGR	76	610.2	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
LSQAQLNSVAQATADFMNK	66	1019.4	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
LSQAQLNSVAQATADFMNKK	59	722.4	3		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
LYHVDIDANKSAGADIIYK	58	702.7	3		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
SLTHPLPFDKK	33	428.5	3		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
KAYPAVGEVVK	36	580.8	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
FEDGRLYHVDIDANK	37	598.0	3		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
SAGADIIYK	67	469.2	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
AYPAVGEVVK	42	516.7	2		Putative exported protein OS=Clostridium difficile (st	Q18B20|Q18B20_CLOD6
EVANVIFTVWK	52	653.3	2		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
GKEPLQVSENLQGMANYWSK	47	760.2	3		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
APILLSQR	31	449.3	2		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
M*VSSEM*YSLVNSYRK	32	609.2	3	2 Oxidation (M)	Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
SEENIAFVPLTTK	51	724.8	2		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
TTSISVEVNVLEYK	55	791.3	2		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
M*VSSEM*YSLVNSYR	90	849.3	2	2 Oxidation (M)	Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
M*VSSEMYSLVNSYRK	49	603.9	3	Oxidation (M)	Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
SDKYNENM*LSSK	36	716.2	2	Oxidation (M)	Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
DSNGNDLTPELIGNINTDKVGK	40	771.9	3		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
NAAEVFSGGIRSEENIAFVPLTTK	49	851.0	3		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
DAREVANVIFTVWK	32	549.8	3		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
GKEPLQVSENLQGM*ANYWSK	46	765.6	3	Oxidation (M)	Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
NAAEVFSGGIR	69	560.7	2		Surface surface protein OS=Clostridium difficile (stra	Q183N1|Q183N1_CLOD6
VGAATEVELKER	67	651.4	2		60 kDa chaperonin OS=Clostridium difficile (strain 6	Q18CT5|CH60_CLOD6
LLIIAEDVEGEALSTLVVNKLR	39	799.1	3		60 kDa chaperonin OS=Clostridium difficile (strain 6	Q18CT5|CH60_CLOD6
AVTVAVEELKNQSR	55	772.4	2		60 kDa chaperonin OS=Clostridium difficile (strain 6	Q18CT5|CH60_CLOD6
ISNIQELLPVLEQIVQQGKK	32	760.1	3		60 kDa chaperonin OS=Clostridium difficile (strain 6	Q18CT5|CH60_CLOD6
GFFLVSDAAGNQFYTR	91	896.8	2		Flagellar basal-body rod protein FlgG OS=Clostridiu	Q18D05|Q18D05_CLOD6
EYEANQKIIQAMDSK	36	884.3	2		Flagellar basal-body rod protein FlgG OS=Clostridiu	Q18D05|Q18D05_CLOD6
TTDNKMDVAIQGK	66	474.1	3		Flagellar basal-body rod protein FlgG OS=Clostridiu	Q18D05|Q18D05_CLOD6
IASEIGSVR	67	466.2	2		Flagellar basal-body rod protein FlgG OS=Clostridiu	Q18D05|Q18D05_CLOD6
LGSISDSVYNK	73	591.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
ETGFCNFGGVLDASFKNPCGLK	56	806.6	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
IYIIGKELSISK	45	682.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
VIKEFYPDASEFYLSDGYDLVNALTGSTIAK	61	1143.1	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
SILAGADKITR	55	572.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
MMGEIEATK	46	505.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
EFYPDASEFYLSDGYDLVNALTGSTIAK	34	1029.3	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
GEADTISAAPVSVR	58	686.7	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
AKTVESLSNNWAGGQYGQDLVR	59	798.6	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
ENPIVLVSESSDK	57	708.7	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
ENPIVLVSESSDKSILAGADK	36	724.6	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
M*MGEIEATK	48	513.1	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
MM*GEIEATK	43	513.1	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
TVESLSNNWAGGQYGQDLVR	96	731.9	3		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
TYAVGGSISM*STSLVNK	84	866.3	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
DIAPIVLTDGK	63	571.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
SVETELKNTGAQVTR	58	816.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
ETGFCNFGGVLDASFK	42	874.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q185Y1|Q185Y1_CLOD6
EVDLTLATGGPGMVK	58	744.8	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
TCGVIEKDEAFGM*TK	57	567.8	3	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
ETGM*GIAEDKVIK	46	703.8	2	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
EVDLTLATGGPGM*VK	66	752.3	2	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
LAGFEVPVDTK	43	588.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
ANFVAIPTSAGTGSEVTPFAVITDQDTGVK	45	998.7	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
AVTDLLDEM*NIK	67	689.2	2	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
NGIIFSPHPR	34	380.1	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
SIFEYLPR	35	512.7	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
LVEDGGFGHTSSLYIDDVNQR	52	774.6	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
LAPSLTLGCGSWGGNSVSENVGVK	52	797.3	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
IAEPIGVIAAVVPTTNPTSTAIFK	42	804.3	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
NIILVNGGLNSK	56	621.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
HTTFFEVEPDPTLECAK	33	674.2	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
IFATYSQEQVDK	72	714.8	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
ASDFDDAVR	46	498.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
AVTDLLDEMNIK	74	681.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
SAYSSGKPAIGVGAGNTPAIIDDSADIK	63	892.6	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
AM*REFNPDVIISIGGGSAM*DAGK	87	790.3	3	2 Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
LKVGIPK	32	377.7	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
YAGIASFLGLK	52	570.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
EFNPDVIISIGGGSAM*DAGK	74	997.4	2	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
LVEDGGFGHTSSLYIDDVNQREK	78	860.6	3		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
VPLAIMAQK	39	485.7	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
VLIGEVESVEIEEAFAHEK	100	1064.9	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
TAVNSILVSK	44	516.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
ILINTPSSQGGIGDLYNFK	97	1018.9	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
VPLAIM*AQK	33	493.7	2	Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
IVGQTACTIAK	46	581.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
GAYLLDKDETEK	52	691.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
YPLM*NEIKDM*YLNSYYGR	56	767.9	3	2 Oxidation (M)	Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
AFIVTDTFLYNNGYTK	77	933.9	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6
ASDFDDAVRK	33	562.2	2		Aldehyde-alcohol dehydrogenase [includes: alcohol	Q184F6|Q184F6_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
DLGLVTSLETESAELELQTLQNTQK	79	921.1	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
VGGSVDSYMEGK	70	614.7	2		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
LQELKNNQDYFK	51	770.4	2		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
EAVSAALKNSEK	37	416.2	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
GLIDSYAQLLALEDTIQITKK	55	778.7	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
GLIDSYAQLLALEDTIQITK	52	735.7	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
TSEKEILTAR	35	574.3	2		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
YEKEVEAYNLER	45	514.9	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
FNTENGLVTLEDSKK	35	565.9	3		Putative multidrug efflux pump, outer membrane pro	Q181Z3|Q181Z3_CLOD6
SVELVSQGK	39	473.7	2		Phosphate butyryltransferase OS=Clostridium difficil	Q18CK4|Q18CK4_CLOD6
SIDM*DIENYELIDIKDLAEASLK	57	885.7	3	Oxidation (M)	Phosphate butyryltransferase OS=Clostridium difficil	Q18CK4|Q18CK4_CLOD6
ADILLAPDIEGGNILYK	54	907.9	2		Phosphate butyryltransferase OS=Clostridium difficil	Q18CK4|Q18CK4_CLOD6
IANAILVGDIEK	52	628.3	2		Phosphate butyryltransferase OS=Clostridium difficil	Q18CK4|Q18CK4_CLOD6
GVVDVYPNKPEPK	33	721.3	2		Phenylalanyl-tRNA synthetase beta chain OS=Clost	Q189P6|Q189P6_CLOD6
AAQLVEM*LGAGK	46	602.2	2	Oxidation (M)	Phenylalanyl-tRNA synthetase beta chain OS=Clost	Q189P6|Q189P6_CLOD6
LLNPLGEETSVM*R	72	737.8	2	Oxidation (M)	Phenylalanyl-tRNA synthetase beta chain OS=Clost	Q189P6|Q189P6_CLOD6
LVTLDDVER	32	530.2	2		Phenylalanyl-tRNA synthetase beta chain OS=Clost	Q189P6|Q189P6_CLOD6
SLGLAGVM*GGANSEITSNTK	68	961.9	2	Oxidation (M)	Phenylalanyl-tRNA synthetase beta chain OS=Clost	Q189P6|Q189P6_CLOD6
VNTNVSALIANNQMGR	74	851.4	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
MRVNTNVSALIANNQMGR	52	663.9	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
M*NILVQASQSM*LAQANQQPQGVLQLLG	52	971.7	3	2 Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
AADDAAGLAISEKMR	82	507.2	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
MNILVQASQSM*LAQANQQPQGVLQLLG	49	966.4	3	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
LESTQNNLNNTLENVTAAESR	106	1159.4	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
M*RTLSLQSANEINNTEER	33	707.8	3	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
TM*VSSLDAALK	35	576.2	2	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
M*RVNTNVSALIANNQM*GR	56	674.6	3	2 Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
AADDAAGLAISEK	87	616.2	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
AADDAAGLAISEKM*R	66	767.7	2	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
SMEKLSSGVR	58	547.3	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
ISSSTEFNGK	38	535.2	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
TLSLQSANEINNTEEREK	82	1038.4	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
AQIKGLDQAGR	62	578.8	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
IADELTQLKDEIER	74	836.8	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
IRDTDVASEMVNLSK	92	839.3	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
TMVSSLDAALK	62	568.2	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
SM*EKLSSGVR	53	555.2	2	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
NVQDGISVVQTAEGSLEETGNILQR	100	1329.1	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
MRTLSLQSANEINNTEER	51	702.9	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
LLDGTSSTIR	30	531.7	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
M*NILVQASQSMLAQANQQPQGVLQLLG	53	966.3	3	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
DTDVASEMVNLSK	69	704.7	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
TLSLQSANEINNTEER	92	909.9	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
LGAQQNRLESTQNNLNNTLENVTAAESR	74	1029.4	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
VNTNVSALIANNQM*GR	93	859.4	2	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
GLDQAGRNVQDGISVVQTAEGSLEETGNIL	57	1118.9	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
RAADDAAGLAISEK	76	694.3	2		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
IRDTDVASEM*VNLSK	63	565.3	3	Oxidation (M)	Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
MNILVQASQSMLAQANQQPQGVLQLLG	34	961.0	3		Flagellin subunit OS=Clostridium difficile (strain 630	Q18CX7|Q18CX7_CLOD6
YIGLVLDNAQNINK	87	788.3	2		Putative uncharacterized protein OS=Clostridium dif	Q189L6|Q189L6_CLOD6
NLGLESEFLQGK	78	667.7	2		Putative uncharacterized protein OS=Clostridium dif	Q189L6|Q189L6_CLOD6
QALGILSILM*DR	33	673.7	2	Oxidation (M)	Glycyl-tRNA synthetase beta subunit OS=Clostridiu	Q182B8|SYGB_CLOD6
LSADILDSLGLVDEKTDTIR	98	725.3	3		Glycyl-tRNA synthetase beta subunit OS=Clostridiu	Q182B8|SYGB_CLOD6
IAVDAENNLTKPALGFIK	40	638.6	3		Glycyl-tRNA synthetase beta subunit OS=Clostridiu	Q182B8|SYGB_CLOD6
STLAQGQTLTSYK	72	699.3	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
SGPNTSYGLLGKLPK	44	511.3	3		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
VYNFFGIGAIDK	58	672.3	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
QVISNSLNMR	47	581.7	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
GSKVEVISESNGWSK	43	803.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
GGSSLVFEVPQYK	48	705.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
YNQNTIYK	41	522.2	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
TKQVNTTSLNVR	60	680.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
NQGAAFINAAK	49	552.7	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
QVISNSLNM*R	53	589.2	2	Oxidation (M)	Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
TSSFVNASSSDIEYYLNPK	48	1061.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
NTDKVVNTASLNVR	64	765.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
LGYVSSSYLGDVSNSTNK	97	945.8	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
WISQNYVNSSK	45	663.2	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
QVNTTSLNVR	45	566.2	2		Acd OS=Clostridium difficile (strain 630) GN=acd	Q5S4P9|Q5S4P9_CLOD6
VGDTPAGIDKLK	54	405.2	3		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
VGDTPAGIDK	35	486.6	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
GKEPIVIPLQSISPK	41	803.4	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
LDVIGNNVANAGTTSFKK	31	617.2	3		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
AMYSGVSGMK	39	515.7	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
DGTVQNVLEYNISKDGTVEFLLSDGQR	39	1000.0	3		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
DGTVQNVLEYNISK	58	790.3	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
TQFVYDIPDGAK	54	677.2	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
DGTVEFLLSDGQR	63	718.8	2		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
ITDSFYQTVLYASAPTAALGGTNLGQVGVG	33	1063.0	3		Flagellar hook protein OS=Clostridium difficile (strai	Q18CZ4|Q18CZ4_CLOD6
HSSDEEPFSALAFK	51	782.8	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
GILADGEEAERHSSDEEPFSALAFK	48	902.3	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
EKLVESVAETDEELM*M*K	51	671.5	3	2 Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
SGAQVINAFVPLSEMFGYSTDLR	58	834.6	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
VYAGDIAAAVGLK	61	624.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
LNSNAVPM*QLPIGKEDSFIGIIDLLK	75	947.7	3	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
YLEGEELTIDELKVAIR	70	664.3	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
VLDGSVAVFCAK	63	633.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
QAETYGVPR	45	510.8	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
INIIDTPGHVDFTVEVER	67	685.3	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
ETITQPVDVEYKYSK	37	600.6	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
GLIQGM*EAR	33	495.6	2	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
ETITQPVDVEYK	44	711.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
LVESVAETDEELM*M*K	57	878.3	2	2 Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
LAEEDPTFTVK	55	625.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
GILADGEEAER	55	580.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
VYSGTLESGSYVLNATK	112	894.8	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
IM*TDPFVGK	44	512.2	2	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
ATYTM*IFDHYEQVPASVAK	41	729.9	3	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
ATYTMIFDHYEQVPASVAK	43	724.6	3		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
GITITSAATTASWK	84	704.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
ILQM*HANTREEITK	36	567.2	3	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
VGAPQVAYR	66	480.8	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
SGAQVINAFVPLSEM*FGYSTDLR	35	840.3	3	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
YLEGEELTIDELK	77	776.4	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
IAFVNKM*DILGADFYNVVSM*M*K	58	852.3	3	3 Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
AAQEKM*GIALQK	35	652.3	2	Oxidation (M)	Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
GGVEPQSENVWR	55	679.2	2		Elongation factor G OS=Clostridium difficile (strain 6	Q18CF4|EFG_CLOD6
AVELLLDGK	41	479.1	2		6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6
VTVLGHVQR	39	504.7	2		6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6
GLLEEDLTEMNLSSVGDIIHR	66	781.3	3		6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6
IIDLEISEALAQK	47	721.8	2		6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
VNIVEVM*GR	32	516.7	2	Oxidation (M)	6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6
GLLEEDLTEM*NLSSVGDIIHR	90	786.6	3	Oxidation (M)	6-phosphofructokinase OS=Clostridium difficile (stra	Q180P4|K6PF_CLOD6
SGKDVNVFEM*AQSQVK	40	594.8	3	Oxidation (M)	NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
GGIIVDPSTLSQGELER	84	885.9	2		NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
LVCEAANGPTTPEADEVFAER	68	759.3	3		NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
TAATGFGVAVTAR	88	611.3	2		NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
VIEVSIPVKM*DDGSIK	31	582.9	3	Oxidation (M)	NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
GGIIVDPSTLSQGELERLSR	35	709.7	3		NAD-specific glutamate dehydrogenase OS=Clostri	Q18CS0|Q18CS0_CLOD6
FGNAAYATK	31	472.2	2		Putative O-acetylhomoserine sulfhydrylase OS=Clos	Q187D4|Q187D4_CLOD6
QLTEEQLIASGVLPSLIR	43	656.3	3		Putative O-acetylhomoserine sulfhydrylase OS=Clos	Q187D4|Q187D4_CLOD6
HVPVIEVDGNNVTVK	43	540.5	3		Rubredoxin oxidoreductase (Desulfoferrodoxin) OS=	Q18A22|Q18A22_CLOD6
ELVPNTTDAAVEK	66	693.7	2		Rubredoxin oxidoreductase (Desulfoferrodoxin) OS=	Q18A22|Q18A22_CLOD6
CLAVDGEPVVK	38	594.2	2		Rubredoxin oxidoreductase (Desulfoferrodoxin) OS=	Q18A22|Q18A22_CLOD6
VGDSTAGIAINLPSTGLEYAGKGTTIDFNK	61	1004.5	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
MKDLLDM	45	433.2	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VYLAGGVNSISK	48	604.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
TYNNTYSNVVTVAGEDRIETAIELSSK	36	992.4	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VMNLKSDTGINTSK	64	754.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
EESIDIDASSYTSAENLAK	95	1021.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
YYNSDDKNAITDK	81	773.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
LSGEDRYETSLAIADEIGLDNDK	53	842.0	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VM*NLKSDTGINTSK	61	508.5	3	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
AIVALQNDGIESNLVQLVNGKYQVIFYPEGK	52	1140.9	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VINAKEESIDIDASSYTSAENLAK	102	1284.6	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
AFVVGGTGLADAM*SIAPVASQLK	31	740.5	3	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
TAPLLLTSK	32	472.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DGGTNLVQVGK	55	544.2	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
EISDDAKSFLGTSDVDIIGGK	38	723.2	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DVATFGLK	34	425.7	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SGGSEDTGYVVEMK	83	729.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
MKDLLDM*	43	441.2	2	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
IITNQADAEAIVTK	117	743.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SFLGTSDVDIIGGK	82	704.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DGDATPIVVVDGK	68	643.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DGDATPIVVVDGKAK	38	495.6	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
AVPKDGGTNLVQVGK	33	741.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
VYLAGGVNSISKDVENELK	58	1018.0	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DVENELKNM*GLK	35	703.4	2	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
NSVSKEIEESIDSATGK	50	598.6	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VGDSTAGIAINLPSTGLEYAGK	79	1067.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DGGTNLVQVGKGIASSVINK	67	653.1	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
M*KDLLDM*	32	449.2	2	2 Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
TLIDIATKDTFGM*VSK	65	586.0	3	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
TLIDIATKDTFGMVSK	71	870.5	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
AVNDIVLVGSTSIVDGLVASPLASEK	53	852.5	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
YVFDPDEISEAYKAIVALQNDGIESNLVQLV	35	1251.2	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
IITNQADAEAIVTKLNSLNEK	99	1143.1	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
LYNLVNTQLDK	67	660.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
AIVALQNDGIESNLVQLVNGK	89	1098.1	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
RYVFDPDEISEAYK	39	578.3	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
EIEESIDSATGK	60	639.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
QATNAEVLKEDDYFTDGEVVNYFVAK	67	989.4	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
QLQDGLKDNSIGK	38	473.0	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
ESPAPIILATDTLSSDQNVAVSK	57	786.1	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
FKESPAPIILATDTLSSDQNVAVSK	71	878.1	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SFLGTSDVDIIGGKNSVSK	57	962.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SANDTIASQDTPAKVVIK	69	620.0	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DTFGM*VSKTQDSEGK	36	549.5	3	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
KVYLAGGVNSISK	74	668.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DGSTKEDQLVDALAAAPIAGR	81	1049.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
IETAIELSSK	64	545.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
YVFDPDEISEAYK	72	788.2	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VKDVATFGLK	42	539.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VDVTGGSTPSAVAVSGFVTK	76	939.9	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
DTFGMVSK	39	442.7	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
YQVIFYPEGK	48	622.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
ITVSFNDGVVGEVAPK	114	816.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
GTTIDFNKTLK	42	619.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
VDVTGGSTPSAVAVSGFVTKDDTDLAK	64	880.0	3		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
EIEESIDSATGKTPDR	73	874.3	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
LNSLNEKTLIDIATK	64	837.0	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SGGSEDTGYVVEM*K	83	737.7	2	Oxidation (M)	Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
TAPLLLTSKDK	47	593.8	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
EDQLVDALAAAPIAGR	40	805.4	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
SANDTIASQDTPAK	69	709.7	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6
GIASSVINK	61	444.7	2		Cell surface protein (S-layer protein) OS=Clostridiu	Q183M8|Q183M8_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
EMTTYYDAK	38	561.2	2		Putative exported protein OS=Clostridium difficile (st	Q180L0|Q180L0_CLOD6
GMEGLGFYAAALSGGSYQR	56	968.3	2		Putative exported protein OS=Clostridium difficile (st	Q180L0|Q180L0_CLOD6
TYNAVVSFQK	55	578.7	2		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
KYGLSADGIIGPATWDK	41	597.8	3		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
TITIM*SNEYLTISTTK	70	916.3	2	Oxidation (M)	Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
GVYASYTVSYNIGAK	61	796.8	2		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
TITIMSNEYLTISTTK	45	908.4	2		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
YGLSADGIIGPATWDKLGR	73	663.9	3		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
TYNAVVSFQKK	56	642.7	2		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
YGLSADGIIGPATWDK	81	832.3	2		Putative peptidoglycan-binding/hydrolysing protein C	Q181X4|Q181X4_CLOD6
NADYFGGEPK	43	549.2	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
IIPNEASQEAALNNGEISLM*K	42	753.4	3	Oxidation (M)	Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
IIPNEASQEAALNNGEISLMK	42	748.4	3		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
GM*FETGQYCNQTK	34	790.3	2	Oxidation (M)	Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
KGESIVFEK	43	518.8	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
QIQQDISKDAPIYTIDYEQNLMAAQK	31	1009.1	3		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
NADYFGGEPKADSIALK	60	599.3	3		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
SNSNLQTYTYSEER	61	846.3	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
HVFEGESNIAKSEK	46	525.6	3		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
ITLPTASESFLYGISK	63	863.9	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
HVFEGESNIAK	48	615.8	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
IGIEAEIVPYESK	44	724.4	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
GMFETGQYCNQTK	45	782.3	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
NNNPVGSGAFK	55	552.7	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
SEKNNNPVGSGAFK	63	724.8	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
QALSYALNR	46	518.3	2		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
FGHKNYALVAQQELK	36	582.6	3		Oligopeptide ABC transporter, substrate-binding pro	Q183A6|Q183A6_CLOD6
GAYHGAGIGGGYYTTTK	37	558.6	3		Putative serine-aspartate-rich surface anchored fibri	Q184Y2|Q184Y2_CLOD6
AEIIPADTETSLVVEESK	71	965.9	2		Putative serine-aspartate-rich surface anchored fibri	Q184Y2|Q184Y2_CLOD6
M*VLGFLTDIGGR	87	647.8	2	Oxidation (M)	Phosphoenolpyruvate-protein phosphotransferase C	Q183J1|Q183J1_CLOD6
AYKGIGASPGVALGK	50	694.9	2		Phosphoenolpyruvate-protein phosphotransferase C	Q183J1|Q183J1_CLOD6
AVLEGM*DGKPIVIR	41	757.4	2	Oxidation (M)	Phosphoenolpyruvate-protein phosphotransferase C	Q183J1|Q183J1_CLOD6
ALVVEHSELVIEKK	48	797.5	2		Phosphoenolpyruvate-protein phosphotransferase C	Q183J1|Q183J1_CLOD6
LNNIEAIEK	32	522.2	2		Proline reductase subunit proprotein OS=Clostridiun	Q17ZY9|Q17ZY9_CLOD6
AGTNM*ERPGPLAAHR	33	531.9	3	Oxidation (M)	Proline reductase subunit proprotein OS=Clostridiun	Q17ZY9|Q17ZY9_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
IVLEENEQSLPM*SK	49	816.8	2	Oxidation (M)	Proline reductase subunit proprotein OS=Clostridiun	Q17ZY9|Q17ZY9_CLOD6
LNNIEAIEKVTGEK	31	519.8	3		Proline reductase subunit proprotein OS=Clostridiun	Q17ZY9|Q17ZY9_CLOD6
AM*EDEEIDLVGVVFVGSPQVNAEK	43	864.6	3	Oxidation (M)	Proline reductase subunit proprotein OS=Clostridiun	Q17ZY9|Q17ZY9_CLOD6
M*LLTTEQQTIPR	39	723.8	2	Oxidation (M)	Penicillin-binding protein OS=Clostridium difficile (st	Q189X7|Q189X7_CLOD6
SAADLTLAESALLAGSTKNPSR	42	725.6	3		Penicillin-binding protein OS=Clostridium difficile (st	Q189X7|Q189X7_CLOD6
TADEMWQIANNLR	70	781.3	2		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
SNLAIDGEGFFR	68	663.2	2		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
NYEQGALAPTDSKSNLAIDGEGFFR	43	900.6	3		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
NGELFVDNKK	35	388.8	3		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
SNVSLQEEFVDLIATQR	46	974.9	2		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
INLYQPIGTQNFISEGDSLFVATDAAQIK	42	1051.7	3		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
NGGFNVDALGK	50	546.7	2		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
NYEQGALAPTDSK	58	697.2	2		Putative flagellar basal-body rod protein OS=Clostric	Q18D04|Q18D04_CLOD6
VLNSSDNQIVK	39	608.8	2		Putative collagen-binding protein OS=Clostridium dif	Q183R6|Q183R6_CLOD6
ISFNLTYTPTSK	43	686.3	2		Putative collagen-binding protein OS=Clostridium dif	Q183R6|Q183R6_CLOD6
ISGM*PEISR	41	503.3	2	Oxidation (M)	Butyrate kinase OS=Clostridium difficile (strain 630)	Q18CK3|Q18CK3_CLOD6
IVDVANALDGEGPFSPER	65	943.4	2		Butyrate kinase OS=Clostridium difficile (strain 630)	Q18CK3|Q18CK3_CLOD6
NAQELFEHAKK	36	657.7	2		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
SLNLDTFVNELNKTDEAM*K	38	733.3	3	Oxidation (M)	Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
NM*EPLGNYLK	34	597.7	2	Oxidation (M)	Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
IVFLTFDDGPSTTNTPQVLDILK	46	845.7	3		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
IVFLTFDDGPSTTNTPQVLDILKR	90	897.7	3		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
GTFFIKGDSLER	48	685.3	2		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
SLNLDTFVNELNK	73	753.8	2		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
NAQELFEHAK	56	593.7	2		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
SLNLDTFVNELNKTDEAMK	34	727.9	3		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
NM*ASIDWNALNADAEGK	109	918.3	2	Oxidation (M)	Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
QETVNALDQIITYFKDNGYQFK	59	879.3	3		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
EAVKEYGYDAK	42	636.7	2		Putative polysaccharide deacetylase OS=Clostridiur	Q18C42|Q18C42_CLOD6
VM*SEANTLVK	58	554.2	2	Oxidation (M)	Putative lipoprotein OS=Clostridium difficile (strain 6	Q188Y7|Q188Y7_CLOD6
ALDTSKVM*SEANTLVK	34	574.9	3	Oxidation (M)	Putative lipoprotein OS=Clostridium difficile (strain 6	Q188Y7|Q188Y7_CLOD6
LSEM*LGKEVVFAADDNVVGENAK	58	818.0	3	Oxidation (M)	Phosphoglycerate kinase OS=Clostridium difficile (s	Q181T8|PGK_CLOD6
EVVFAADDNVVGENAK	76	838.8	2		Phosphoglycerate kinase OS=Clostridium difficile (s	Q181T8|PGK_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
ELASLAEIFVNDAFGTAHR	50	688.0	3		Phosphoglycerate kinase OS=Clostridium difficile (s	Q181T8|PGK_CLOD6
FLGEAVANPVRPFTAILGGAK	60	710.0	3		Phosphoglycerate kinase OS=Clostridium difficile (s	Q181T8|PGK_CLOD6
AM*AELTDATTVIGGGDSAAAVNQLGFGDK	36	933.0	3	Oxidation (M)	Phosphoglycerate kinase OS=Clostridium difficile (s	Q181T8|PGK_CLOD6
LTEELINEGYAR	47	704.2	2		Isoleucyl-tRNA synthetase OS=Clostridium difficile (	Q182V2|Q182V2_CLOD6
M*NLFVGALSK	41	548.2	2	Oxidation (M)	Isoleucyl-tRNA synthetase OS=Clostridium difficile (	Q182V2|Q182V2_CLOD6
SVTVETFGIDYSDVEKN	77	951.8	2		Peptidyl-prolyl cis-trans isomerase OS=Clostridium	Q18D70|Q18D70_CLOD6
TDSADKPQTPQVM*K	33	521.2	3	Oxidation (M)	Peptidyl-prolyl cis-trans isomerase OS=Clostridium	Q18D70|Q18D70_CLOD6
VIEGM*DTVDEIASVR	75	825.3	2	Oxidation (M)	Peptidyl-prolyl cis-trans isomerase OS=Clostridium	Q18D70|Q18D70_CLOD6
NSDAIEIK	53	445.2	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
VANFLNVSLEELKTFAR	79	976.1	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
AIAM*GADAVAIASSALM*AAACQQYR	50	848.5	3	2 Oxidation (M)	Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
VTEEIAKVR	63	522.8	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
DATSIPTIFALYR	33	734.5	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
LVDELREVSEGRPIGVK	31	632.7	3		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
YIFEYVPNKYSVTEENLK	42	746.4	3		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
LLKDATSIPTIFALYR	42	911.5	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
AIAM*GADAVAIASSALMAAACQQYR	35	843.1	3	Oxidation (M)	Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
VANFLNVSLEELK	83	738.4	2		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
ISGHKDIHDLSVDDLYTVNSEISNYTNIQHV	48	1176.2	3		Putative oxidative stress protein OS=Clostridium diff	Q18A21|Q18A21_CLOD6
SIAELFSEGEDIFR	75	806.8	2		Shikimate kinase OS=Clostridium difficile (strain 63	Q187E9|Q187E9_CLOD6
ILEDININSRPLLK	30	546.6	3		Shikimate kinase OS=Clostridium difficile (strain 63	Q187E9|Q187E9_CLOD6
AQAEGKFDEEIVPVVIK	50	936.5	2		Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
TGLATLCIGGGM*GTTLIVKR	50	679.0	3	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
IM*GYGPVPATK	35	575.2	2	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
EKAEELGIEPLATIVSYGTAGVDPK	72	863.4	3		Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
ALEAANM*TIEDIDLVEANEAFAAQSVAVIR	43	1064.5	3	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
TAVGSFGGAFK	41	521.2	2		Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
ANITPDMIDESLLGGVLTAGLGQNIAR	61	913.8	3		Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
DGTVTAGNASGINDGAAM*LVVM*AK	51	766.0	3	2 Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
ANITPDM*IDESLLGGVLTAGLGQNIAR	57	919.5	3	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
M*REVVIASAAR	31	609.8	2	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
SVSAVELGVTAAK	67	616.3	2		Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
QIALGAGIPVEKPAM*TINIVCGSGLR	46	894.8	3	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
KDGTVTAGNASGINDGAAM*LVVM*AK	34	808.3	3	2 Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6
ILTTLLYEM*K	49	620.8	2	Oxidation (M)	Acetyl-CoA acetyltransferase OS=Clostridium difficil	Q18AR0|THLA_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
ITSSDESIIVAK	87	631.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AFVDDYNALM*DKVYGLVTTK	75	1140.0	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
NLEADVTDDQGRVTHISK	57	666.9	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
LVSVTDTEEATK	72	646.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
IVFEYSGSSASK	68	637.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ASYSEM*TGELIISR	63	786.9	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
KLGISEHENYNK	41	716.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
GSAGAEKINYQFAVSQMAEPAK	31	766.4	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
KAGM*ENSSSASQNVYSK	63	902.4	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ALAGYSSNYDDK	55	652.3	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
LVSVTDTEEATKNM*K	58	841.4	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
VIGNDSLAGQIASDNGITFTTDASGTK	72	1327.5	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
LGISEHENYNK	53	652.3	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AGM*ENSSSASQNVYSK	76	838.3	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
KIVFEYSGSSASK	66	701.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ALIDDSDKVYK	54	633.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
GSAGAEKINYQFAVSQM*AEPAK	42	771.7	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
YSSQMNYFSQAQGN	31	812.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
YSALESLLNK	56	569.3	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AFVEDIQSM*FFGDADTIIALRK	90	835.5	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
EGILRNDDELR	36	665.3	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
EQNSFKIDNIDYNVNSK	40	1015.0	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INSLCADNDIRASYSEM*TGELIISR	31	949.1	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INSLCADNDIR	60	645.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
GQISFNADTFSK	71	657.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
YSSQM*NYFSQAQGN	42	820.8	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INYQFAVSQM*AEPAKVTIK	48	718.7	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ALAGYSSNYDDKGM*FEK	55	638.3	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ALAGYSSNYDDKGMFEK	61	948.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AFVEDIQSM*FFGDADTIIALR	68	792.7	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ITSSDESIIVAKGSAGAEK	89	931.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
GSAKLVSVTDTEEATK	67	818.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INYQFAVSQMAEPAK	74	849.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AFVDDYNALMDKVYGLVTTK	51	755.4	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
QTGSSSDIDLK	56	575.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
AGMENSSSASQNVYSK	84	830.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
NDDELRAFVEDIQSMFFGDADTIIALR	53	1034.9	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
NDDELRAFVEDIQSM*FFGDADTIIALR	72	1040.1	3	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
ASYSEMTGELIISR	75	778.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INYQFAVSQMAEPAKVTIK	52	713.7	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
INSLCADNDIRASYSEMTGELIISR	59	943.7	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
LVSVTDTEEATKNMK	86	833.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
IDNIDYNVNSK	79	647.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
INYQFAVSQM*AEPAK	74	856.9	2	Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
VTGLSGNFDM*EGIIEASM*IR	41	725.0	3	2 Oxidation (M)	Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
IDNIDYNVNSKGSAK	43	819.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
NLEADVTDDQGR	80	666.8	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
KAGMENSSSASQNVYSK	72	894.4	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
IVFEYSGSSASKLTK	84	808.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
KGQISFNADTFSK	85	721.9	2		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
QIAEQERNISR	32	448.6	3		Flagellar cap protein OS=Clostridium difficile (strain	Q18CX9|Q18CX9_CLOD6
M*GLLLDM*SPR	33	582.7	2	2 Oxidation (M)	DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
VEELFEAR	41	496.7	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
FATSDLNDLYR	31	657.7	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
TLLQNIDLEQQSK	36	765.3	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
LVDVSQDVIVR	67	621.7	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
LLELGAPDIIVR	39	654.8	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
LGIQAFEPILVEGK	34	757.4	2		DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
FLM*LSVNNILAPK	35	738.3	2	Oxidation (M)	DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
M*LQEAVDALIDNGRR	32	572.9	3	Oxidation (M)	DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
QGQM*LEAGDPLTQGFINPHDIVR	38	851.3	3	Oxidation (M)	DNA-directed RNA polymerase subunit beta' OS=Cl	Q18CF3|RPOC_CLOD6
TLGYFAQLAK	54	556.3	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VVSWYDNEMSYTSQLIR	72	1046.0	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
AIGLVIPSLK	50	505.8	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VVSWYDNEM*SYTSQLIR	70	1054.5	2	Oxidation (M)	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
M*M*EQQDKFEVVAINDLTDAK	65	786.7	3	2 Oxidation (M)	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VAINGFGR	33	417.2	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
AIGLVIPSLKGK	31	598.4	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VM*EVDGKQLVK	48	631.4	2	Oxidation (M)	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VPVVTGSITELVCTLGK	93	887.0	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VLNDKYGIEK	41	589.9	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
ARAAAGNIVPNTTGAAK	38	792.0	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
VVISAPATGDLK	34	585.9	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
GLM*TTIHAYTNDQNTLDGPHPK	52	814.0	3	Oxidation (M)	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
KVVISAPATGDLK	58	649.9	2		Glyceraldehyde-3-phosphate dehydrogenase 2 OS=	Q181T9|Q181T9_CLOD6
NIVVGANKTEYHIK	33	793.4	2		Prolyl-tRNA synthetase 1 OS=Clostridium difficile (s	Q18CD2|SYP1_CLOD6
GVEVGHIFK	44	493.3	2		Prolyl-tRNA synthetase 1 OS=Clostridium difficile (s	Q18CD2|SYP1_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
EIPADAEITSHQLM*VR	42	913.5	2	Oxidation (M)	Prolyl-tRNA synthetase 1 OS=Clostridium difficile (s	Q18CD2|SYP1_CLOD6
VQGEVEVVDNEQKEK	57	865.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N2|Q183N2_CLOD6
SEALEYLLNNIR	72	717.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N2|Q183N2_CLOD6
TVDYENISSDEGLIFTLINESEVKPIGGTGSS	36	1167.8	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183N2|Q183N2_CLOD6
SIQTISHNISNLDTDGYSR	60	1061.4	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
QINDVYNSSAGITVR	69	819.3	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
NSFYDYQFR	33	620.3	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
KIINNVDNSR	56	586.8	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
DFFITSNVAGEDIIK	85	834.8	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
AFAESVGLDSQK	63	626.3	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
GQLGTGVHVTDVTR	88	720.3	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
VSTISDHYK	40	525.2	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
SLVVENASNLATLISESYKK	49	722.7	3		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
SLVVENASNLATLISESYK	116	1019.4	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
IDIGVAGGK	35	415.2	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
MSVSGVSLDEEMTELM*K	36	951.4	2	Oxidation (M)	Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
SIDIISGSGSTPNDLLDERDR	91	754.0	3		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
SNSNELKLTTEEASK	62	825.9	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
SDLKDVSDGLAK	42	624.3	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
AFAESVGLDSQKVNQDEVNQR	98	778.9	3		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
AGLFSILNTANSGMNAHQK	68	659.0	3		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
IINNVDNSR	40	522.8	2		Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
AGLFSILNTANSGM*NAHQK	49	664.0	3	Oxidation (M)	Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
TGISGTLQGLFEM*HGK	48	564.5	3	Oxidation (M)	Putative flagellar hook-associated protein OS=Clost	Q18CW5|Q18CW5_CLOD6
TVYIIGSESTISKNVENQLLSK	59	808.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
GLQLTDALAASTIAK	79	737.0	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
NSKEFYLSK	37	558.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
TVYIIGSESTISK	86	699.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
NAPVVLVENGSNK	73	670.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
SYALGSSEIISDELVK	94	855.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
SYALGSSEIISDELVKSTNSIR	32	790.7	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
YLDWSEIKPGYIAVQGENIIK	45	813.2	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
DADDIGNFIFNEWK	80	842.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
DGVPIILTDGNSVGFDTTGLK	93	1060.0	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183N5|Q183N5_CLOD6
KYNVDANLIK	42	589.3	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
GVESISDLYK	52	555.7	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
SRGVESISDLYK	34	677.3	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
FIEVDTKDK	37	365.5	3		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
AIIKVESDFNPNTVSSAGAK	55	1024.4	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
YNVDANLIK	45	525.2	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
VESDFNPNTVSSAGAK	53	811.8	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
DLGVTNPFNIEQNIDAGTR	68	1037.8	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
LFNELDSVANNTVGK	58	810.8	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
SRIENAVEQASK	32	666.3	2		Putative transglycosylase OS=Clostridium difficile (s	Q18CX0|Q18CX0_CLOD6
VLFAVDELTGLIGAAAIMRPSK	40	758.0	3		Putative uncharacterized protein OS=Clostridium dif	Q189C2|Q189C2_CLOD6
VLFAVDELTGLIGAAAIM*RPSK	60	763.7	3	Oxidation (M)	Putative uncharacterized protein OS=Clostridium dif	Q189C2|Q189C2_CLOD6
LVGPAGEVEMKEGVIVASR	42	647.6	3		Putative propanediol utilization protein OS=Clostridiu	Q183B8|Q183B8_CLOD6
APIKESGDIAGTPGVK	60	770.3	2		Putative propanediol utilization protein OS=Clostridiu	Q183B8|Q183B8_CLOD6
LVGPAGEVEM*KEGVIVASR	59	978.9	2	Oxidation (M)	Putative propanediol utilization protein OS=Clostridiu	Q183B8|Q183B8_CLOD6
ALVFENVLVR	47	580.2	2		Putative propanediol utilization protein OS=Clostridiu	Q183B8|Q183B8_CLOD6
AFTNAQFETR	36	592.7	2		Subunit of oxygen-sensitive 2-hydroxyisocaproyl-Co	Q188I1|Q188I1_CLOD6
VVINDLLAEQYANAFK	87	904.4	2		Subunit of oxygen-sensitive 2-hydroxyisocaproyl-Co	Q188I1|Q188I1_CLOD6
IQGLVEVM*EER	44	659.8	2	Oxidation (M)	Subunit of oxygen-sensitive 2-hydroxyisocaproyl-Co	Q188I1|Q188I1_CLOD6
ENVNTLLR	32	479.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
QGLIDYVVPQLYWPIGLK	35	701.7	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
LKSPVVM*LGNSVTSAQK	92	888.0	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SVGINTAVVQVRPK	90	734.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SIKPNVVFGVSPAGIWR	48	609.7	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SNQLVDALTSGPLAAK	72	792.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
NKSSDPTGSDTSGNESYVGTYADTR	55	870.6	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
DIANSTSIQKDLK	41	716.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
LYITSGTGEADSLSIASK	123	906.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
QGQSSYGGQNIAK	31	669.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SLYSSSEEPVTPPSNVK	35	910.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
DAYFIGGNLSISDSVINKLDK	33	757.3	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
DNVSDEVYNWISDLK	38	898.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
TNPVEKLYITSGTGEADSLSIASK	66	827.7	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
DIANSTSIQK	47	538.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
ITM*ADESIDKLPANHPAK	52	656.2	3	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SLYSSSEEPVTPPSNVKVEK	70	726.3	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
AAWISTVYNLDWPK	69	832.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SSDPTGSDTSGNESYVGTYADTR	60	789.9	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
SPVVM*LGNSVTSAQK	61	767.4	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
VGGSDRYSTSLM*IAK	33	534.1	3	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
TTLVYEAGDGINQNTLNTFLNLVK	36	880.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
QGQSSYGGQNIAKEIVQQVTLNR	37	840.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
FYPNAEYSSM*FVSK	54	843.2	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
EIVQQVTLNR	56	600.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
SSDPTGSDTSGNESYVGTYADTRAWIK	82	956.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
KTTLVYEAGDGINQNTLNTFLNLVK	69	923.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
GTNVDLYIGQGIYK	58	770.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183K2|Q183K2_CLOD6
VKDGETEGYVK	39	612.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
YVDISEGVGYTNADK	65	815.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
DKSESSEVIEELEK	88	811.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
VKVEDGEGWLATR	71	730.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
GSSLLVLEDNGDWLK	50	823.4	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
VEDGEGWLATR	61	616.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
IREEGQVQNIAYSGDEFTVLGTQGEWVK	55	1052.1	3		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
TVSVTSINSSYYTAR	76	824.9	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
YVDISEGVGYTNADKVNLR	43	704.9	3		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
NAVGKNIPR	52	484.9	2		Putative cell wall hydrolase OS=Clostridium difficile	Q18CS3|Q18CS3_CLOD6
GVVVEAELGVLAGTEDDVTSDVHK	106	813.6	3		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
AASDEIGVDVALHLDHGPNM*DAIK	42	835.3	3	Oxidation (M)	Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
DAIQAVVESKIDDVLGSANSIN	79	1129.9	2		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
TGVDSLAIAIGTSHGAFK	80	582.2	3		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
IDDVLGSANSIN	63	609.2	2		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
DAIQAVVESK	47	530.2	2		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
AYEGGFAIGAFNISDLEQLQGVLK	62	848.0	3		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
LRFDILEEIQSK	58	745.8	2		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
LAM*TAAIR	32	431.7	2	Oxidation (M)	Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
YTQPAEAVEFVER	87	769.8	2		Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
INM*DTDLR	38	497.2	2	Oxidation (M)	Putative fructose-bisphosphate aldolase OS=Clostri	Q188J1|Q188J1_CLOD6
TM*GTQIGIGIEDTVK	64	789.9	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TAETVYQIGDGM*KDSVINSIASSLSK	45	911.2	3	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
VLNKEDLESM*GLNLK	68	859.8	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
LNPSDVIIIGDDGSVSQKAVSQIK	72	828.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TMGTQIGIGIEDTVK	72	782.0	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
KYTLNTALATTEYLR	113	879.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
LAGATRFETAVEISK	81	796.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
LNPSDVIIIGDDGSVSQK	78	929.0	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
LKAPILITPK	32	547.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
AVSQIKSAVNVNVTR	33	793.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
GINVVM*TR	32	453.2	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
VKTM*GTQIGIGIEDTVK	79	903.5	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TLDNGKDYLYVLR	74	785.5	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
DSVINSIASSLSK	58	660.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
SAVNVNVTR	47	480.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TFYPDKELSAM*LVAK	32	865.0	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
SDIIVDSITAGPLAAK	72	786.0	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
VLNKEDLESMGLNLK	32	568.2	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
YTLNTALATTEYLR	82	815.6	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TYVSAYHSTNLSEK	64	800.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
IGGVDRHETSLLIAK	55	537.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
APILITPK	51	426.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
VSGADRHETNANVIK	44	537.6	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
AGEDQQPIILANK	53	698.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
IIDQISK	31	408.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
RLNPSDVIIIGDDGSVSQK	57	671.8	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TVVIDPGHGGSDSGATSGLNGGAQEK	38	804.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
SKGINVVM*TR	48	560.8	2	Oxidation (M)	Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
TAASNILKR	57	487.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183L9|Q183L9_CLOD6
IAGLDVKR	34	436.3	2		Chaperone protein dnaK OS=Clostridium difficile (st	Q182E8|DNAK_CLOD6
SQIFSTAADNQTAVDIHVLQGER	46	834.4	3		Chaperone protein dnaK OS=Clostridium difficile (st	Q182E8|DNAK_CLOD6
SMAYDNTTLGR	47	614.8	2		Chaperone protein dnaK OS=Clostridium difficile (st	Q182E8|DNAK_CLOD6
TTPSVVAFTKDGER	55	754.4	2		Chaperone protein dnaK OS=Clostridium difficile (st	Q182E8|DNAK_CLOD6
LISSTVIPNR	37	550.2	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
GETELTAEER	56	567.6	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
STGPYSLVTQQPLGGK	38	816.8	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
SVGELLQNQVR	42	621.8	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
LGPEEITR	47	457.7	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
EAPIIGTGIEYR	41	659.8	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
LSALGPGGLSR	30	514.2	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
ISAEDIINPETGEVFVK	44	930.9	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
IGAEVDSGDILVGK	64	686.8	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
INEFGFIESPYR	70	736.3	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6
VLTDEDQEIEVR	46	723.3	2		DNA-directed RNA polymerase subunit beta OS=Cl	Q18CF1|RPOB_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
ILITGSPIGGISEK	52	692.9	2		Putative 2-hydroxyacyl-CoA dehydratase OS=Clostr	Q186V7|Q186V7_CLOD6
SLGVTITEEDIR	40	666.8	2		Putative 2-hydroxyacyl-CoA dehydratase OS=Clostr	Q186V7|Q186V7_CLOD6
SNDLLVDEEIEDVYDALTQK	41	770.4	3		Putative 2-hydroxyacyl-CoA dehydratase OS=Clostr	Q186V7|Q186V7_CLOD6
QFDSFNEAR	36	557.2	2		Putative 2-hydroxyacyl-CoA dehydratase OS=Clostr	Q186V7|Q186V7_CLOD6
TGDIENVGITAR	56	623.2	2		Alanyl-tRNA synthetase OS=Clostridium difficile (str	Q18BE7|SYA_CLOD6
ILSEGGVAAGVR	57	564.7	2		Alanyl-tRNA synthetase OS=Clostridium difficile (str	Q18BE7|SYA_CLOD6
EVLDSRGNPTVEVEVVLEDGAM*GR	47	863.4	3	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
AGYTAVISHR	33	537.8	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
M*GAEVFHSLKK	47	632.3	2	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
LGANAILGVSM*AVAR	59	730.0	2	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
GNPTVEVEVVLEDGAM*GR	77	944.4	2	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
AIVPSGASTGAFEAVELR	77	888.0	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
EVLDSRGNPTVEVEVVLEDGAMGR	41	857.8	3		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
VNQIGTITETLDAIEM*AK	106	982.0	2	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
VNQIGTITETLDAIEMAKR	32	701.8	3		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
VNQIGTITETLDAIEM*AKR	36	707.1	3	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
RAGYTAVISHR	35	410.9	3		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
GIENGVANSILVK	44	657.4	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
SVIELVYAR	57	525.3	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
YNQLLRIEEM*VGEQAR	31	656.0	3	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
VNQIGTITETLDAIEMAK	103	974.0	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
IEEM*VGEQAR	62	589.3	2	Oxidation (M)	Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
LQLVGDDLFVTNTERLEK	49	1046.1	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
AAADEIGLPLFQYLGGVNAK	44	683.4	3		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
SGETEDSTIADLAVAVNAGQIK	70	1095.5	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
EALELIVEAITK	60	664.9	2		Enolase OS=Clostridium difficile (strain 630) GN=en	Q181T5|ENO_CLOD6
AVFTEWLDSR	44	612.2	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
VDVMPANTVK	30	537.3	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
DFILAQVR	34	481.1	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
EPGSTGEPLYLDVR	44	766.8	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
YAQAYFDYDSK	52	685.7	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
AVFTEWLDSRNDGEASK	46	642.5	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
TVFDNLVSEQPK	60	688.8	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
SGGITM*SHLR	40	358.9	3	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
HFLDAM*PSTVER	36	709.8	2	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
IVNM*NYAAVDAGINALVK	78	946.4	2	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
QSYVYQYDLLK	55	710.3	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
NKIVDAM*TELVSM*DICEDAK	31	771.9	3	2 Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
DTTPSDIKTVFDNLVSEQPK	60	1117.4	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
DVFYGKENAPM*IIGGR	64	891.8	2	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
GTAQNPDIYFQTR	64	755.8	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
NDIKFYTVNAVK	34	471.2	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
NGFTVGIVDDVTNTSLTPSEPIKIASK	68	935.4	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
NGFTVGIVDDVTNTSLTPSEPIK	58	1202.9	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
VDVM*PANTVK	43	545.2	2	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
TKEPGSTGEPLYLDVR	72	881.4	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
ALASQALSIFGDHQDVM*AAR	81	706.6	3	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
INM*IMQSAFFK	59	673.2	2	Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
VAGELLPGVFHVSAR	54	517.8	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
INM*IM*QSAFFK	56	681.2	2	2 Oxidation (M)	Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
LGQEIGLGNR	46	528.7	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
YYQNIVGIVEK	54	663.3	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
YGLGSKDTTPSDIK	36	741.3	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
QFPEEADGLFAK	32	676.2	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
YAQAYFDYDSKK	45	500.2	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
DNALSPNHPVAR	43	430.9	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
IVNMNYAAVDAGINALVK	59	938.4	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
FWGLGSDGTVGANK	58	704.8	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
ALASQALSIFGDHQDVMAAR	75	701.2	3		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
VVTQLYGDR	49	525.8	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
FGDTPIR	39	403.2	2		Pyruvate-flavodoxin oxidoreductase OS=Clostridium	Q183B6|Q183B6_CLOD6
SNLGSDAETLMLDSVAR	96	889.8	2		Putative exported protein OS=Clostridium difficile (st	Q181S4|Q181S4_CLOD6
DIDGVKTGILDVSSDFTK	68	955.4	2		Putative exported protein OS=Clostridium difficile (st	Q181S4|Q181S4_CLOD6
TGILDVSSDFTK	50	641.7	2		Putative exported protein OS=Clostridium difficile (st	Q181S4|Q181S4_CLOD6
SNLGSDAETLM*LDSVAR	85	897.8	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q181S4|Q181S4_CLOD6
VSGM*SFTNFLDK	72	681.3	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
FEVTYQDEVNASALTGTDRYETSIK	94	946.7	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
ATLALSDETPGYIVNTK	89	896.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*PSSLKENSGLYASSNMIK	37	691.6	3	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*FTTTAVM*K	53	531.1	2	2 Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IMDENNSNAFIEIPGVIGR	56	697.2	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
FEVTYQDEVNASALTGTDR	64	1058.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NTILLADNDSYGHDNFLK	74	1025.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NLNKDNMYSIASISK	61	849.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NGKDYYLVDEK	53	672.2	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
ENSGLYASSNM*IK	48	715.2	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
VDVNDNGTLTVSSPYIENGPEDK	47	822.0	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
EKIQTLLSK	38	530.3	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IEISGNGGVYSK	52	612.3	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IM*DENNSNAFIEIPGVIGR	61	1053.4	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
YTSQSYM*FGSVK	60	707.3	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
AKPGAFSVYCNDGFTLAEILVER	32	853.0	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MFTTTAVMK	42	515.2	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MFTTTAVM*K	48	523.2	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
LNLDTPVVK	47	499.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*PSSLKENSGLYASSNM*IK	34	697.2	3	2 Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
DNMYSIASISK	57	614.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
KIEVNLPQNSSFAVYDDK	49	690.0	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*FTTTAVMK	57	523.2	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
VDVNDNGTLTVSSPYIENGPEDKYVYIGQD	37	1153.5	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
YGAVSAQYALIDNGK	71	785.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
YTSQSYMFGSVK	62	699.3	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
TPENSFDSSK	51	556.2	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*LLNHSSGLM*GSSFK	62	547.5	3	2 Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IGDDIANK	44	423.1	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
TPENSFDSSKLAK	62	475.2	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IDDNNISNSVK	91	609.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
VSGM*SFTNFLDKYINNPLNLQNTK	53	925.7	3	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IQTLLSK	35	401.7	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
YQSSDIELHDYSK	31	528.8	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NLNKDNM*YSIASISK	59	857.4	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NSNGILSPASVK	52	593.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MPSSLKENSGLYASSNMIK	44	1029.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
GGVIVFLGSPNAR	47	643.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IDDNNISNSVKEAWK	47	578.5	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
LVDDGKLNLDTPVVK	65	813.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NTILLADNDSYGHDNFLKELQK	80	850.1	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
VSGMSFTNFLDK	66	673.4	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IEVNLPQNSSFAVYDDKGVPVNYSLVTK	34	1033.1	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
DNM*YSIASISK	57	622.7	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
NNITYLNM*SSYDDVPGLGQTASLYYVAQK	55	1081.4	3	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MPSSLKENSGLYASSNM*IK	34	691.6	3	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
IEVNLPQNSSFAVYDDK	77	969.8	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
M*LLNHSSGLMGSSFK	57	812.8	2	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MLLNHSSGLMGSSFK	56	536.9	3		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
DYYLVDEK	33	522.7	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
MLLNHSSGLM*GSSFK	70	542.3	3	Oxidation (M)	Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
YINNPLNLQNTK	66	716.3	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
SFTCELESNGYAK	96	753.3	2		Cell surface protein (Putative penicillin-binding prote	Q18BY9|Q18BY9_CLOD6
ALCEELLAM*PVVAGQK	39	873.5	2	Oxidation (M)	Prolyl-tRNA synthetase 2 OS=Clostridium difficile (s	Q18CD7|SYP2_CLOD6
IKEETGATIR	40	559.3	2		Prolyl-tRNA synthetase 2 OS=Clostridium difficile (s	Q18CD7|SYP2_CLOD6
VAPIQVVIVPIAAK	48	709.5	2		Prolyl-tRNA synthetase 2 OS=Clostridium difficile (s	Q18CD7|SYP2_CLOD6
LIGGLIM*THSDNR	32	721.8	2	Oxidation (M)	Prolyl-tRNA synthetase 2 OS=Clostridium difficile (s	Q18CD7|SYP2_CLOD6
IAPVVIELLGEGR	30	683.4	2		Electron transfer flavoprotein alpha-subunit OS=Clos	Q188I8|Q188I8_CLOD6
LADKLGGVVGSSR	31	420.2	3		Electron transfer flavoprotein alpha-subunit OS=Clos	Q188I8|Q188I8_CLOD6
IVNYSSATLK	30	548.1	2		Probable amino-acid ABC transporter,substrate-bind	Q185W5|Q185W5_CLOD6
VGVGTGAVANEILK	46	664.3	2		Probable amino-acid ABC transporter,substrate-bind	Q185W5|Q185W5_CLOD6
GNYQDLEM*GRLDAVVAQDVEALIAIK	30	950.0	3	Oxidation (M)	Probable amino-acid ABC transporter,substrate-bind	Q185W5|Q185W5_CLOD6
GFEVDFWDEFAK	63	745.2	2		Probable amino-acid ABC transporter,substrate-bind	Q185W5|Q185W5_CLOD6
SESAVLVNDNSIADALSATPFAK	41	774.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
ISNNSSSTIIR	90	596.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
QLNAENINFER	49	674.6	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
TINNSFSIETKK	34	691.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
NGCYVEAVEVNTSTKEVSR	54	715.0	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
ADANDIIK	31	430.1	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
FNNYAEIEGGVK	65	670.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
NKNDLIDSLAVGVLAAK	119	870.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
NSGNIDTVTGK	42	553.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
LDTTQKDVLNTK	47	459.3	3		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
NGCYVEAVEVNTSTK	93	836.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
TINNSFSIETK	42	627.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
NSSPIVLAGNK	53	550.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
TVTIELDGR	46	502.3	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
AKDAPILLTQSNK	46	699.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
RADANDIIK	34	508.2	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
SYVIGGTYSISNSVER	85	866.4	2		Cell surface protein OS=Clostridium difficile (strain 6	Q183M7|Q183M7_CLOD6
GTPVIAIATQEK	45	614.3	2		Glucosamine--fructose-6-phosphate aminotransferas	Q18CK9|Q18CK9_CLOD6
TVVSSEHAFYLGR	85	733.4	2		Glucosamine--fructose-6-phosphate aminotransferas	Q18CK9|Q18CK9_CLOD6
DSPLVVGVGEGENFIASDIPALLK	30	1221.1	2		Glucosamine--fructose-6-phosphate aminotransferas	Q18CK9|Q18CK9_CLOD6
LSVLAEDLEKNPIDGNLGIGHTR	41	821.4	3		Glucosamine--fructose-6-phosphate aminotransferas	Q18CK9|Q18CK9_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
ILSITNVVGSSIAR	60	715.4	2		Glucosamine--fructose-6-phosphate aminotransfera	Q18CK9|Q18CK9_CLOD6
GAYVVAIAQSHNKDVEK	72	915.0	2		Glucosamine--fructose-6-phosphate aminotransfera	Q18CK9|Q18CK9_CLOD6
M*NYTTQM*DAAR	40	667.3	2	2 Oxidation (M)	Phosphomethylpyrimidine synthase OS=Clostridium	Q186R0|THIC_CLOD6
VAIDM*KAEAIM*DLSNYGK	43	667.6	3	2 Oxidation (M)	Phosphomethylpyrimidine synthase OS=Clostridium	Q186R0|THIC_CLOD6
NNTTYVDWNAVEGANTAYTLVTKK	46	891.7	3		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
ILVAYNHIK	52	357.5	3		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
VGAIVQTVKPEQTQKPAPPGK	32	725.0	3		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
HVMYEGVR	41	495.7	2		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
SYVTGTNSVYGPK	70	686.7	2		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
SLSHPLPFDKTAYPK	45	567.6	3		Putative exported protein OS=Clostridium difficile (st	Q184N0|Q184N0_CLOD6
EGVEVNPIDGTELTVLGLVGDTSKIDAK	47	957.5	3		Putative chorismate biosynthesis-related protein [inc	Q187E1|Q187E1_CLOD6
TIASAVGREI	39	508.7	2		Putative chorismate biosynthesis-related protein [inc	Q187E1|Q187E1_CLOD6
SWM*VDSLSK	37	534.7	2	Oxidation (M)	Putative chorismate biosynthesis-related protein [inc	Q187E1|Q187E1_CLOD6
NTLDLSAILAVK	80	629.4	2		Putative chorismate biosynthesis-related protein [inc	Q187E1|Q187E1_CLOD6
WIAELLGTEVR	60	643.8	2		(R)-2-hydroxyisocaproate dehydrogenase OS=Clost	Q188H7|Q188H7_CLOD6
AAALDTFETEGLFLNKK	44	623.3	3		(R)-2-hydroxyisocaproate dehydrogenase OS=Clost	Q188H7|Q188H7_CLOD6
AAALDTFETEGLFLNK	80	870.5	2		(R)-2-hydroxyisocaproate dehydrogenase OS=Clost	Q188H7|Q188H7_CLOD6
YGIATALAGTQGNYR	71	778.3	2		Putative basal-body rod modification protein OS=Clo	Q18CZ5|Q18CZ5_CLOD6
IGEVDENSGEENDSSEQESPEEA	41	1240.2	2		Putative basal-body rod modification protein OS=Clo	Q18CZ5|Q18CZ5_CLOD6
SNNLSQLER	61	530.7	2		Putative basal-body rod modification protein OS=Clo	Q18CZ5|Q18CZ5_CLOD6
NINDIANKQVR	49	642.8	2		Putative basal-body rod modification protein OS=Clo	Q18CZ5|Q18CZ5_CLOD6
GPQAANVVRL	60	512.7	2		Putative cold shock protein OS=Clostridium difficile	Q18BL9|Q18BL9_CLOD6
TLEEGQSVEFEVVDGAK	80	918.8	2		Putative cold shock protein OS=Clostridium difficile	Q18BL9|Q18BL9_CLOD6
TATAEDANDVISYIR	95	819.8	2		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
GAFTGEVSPLM*LK	60	683.3	2	Oxidation (M)	Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
GLYGELANEVR	63	611.2	2		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
TATAEDANDVISYIREVIK	42	703.6	3		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
IGAQNM*HFEEK	43	660.2	2	Oxidation (M)	Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
ALENVLKDDLAK	45	664.8	2		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
ALEVGIDPILCVGETLEQR	81	704.9	3		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
GAFTGEVSPLMLK	65	675.2	2		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6
VVVAYEPIWAIGTGK	64	801.9	2		Triosephosphate isomerase OS=Clostridium difficile	Q181T6|Q181T6_CLOD6

Sequence	**Score**	**m/z**	**z**	**Modification**	**Protein_Name**	**Protein_ID**
YGTYVNR	33	436.6	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
VSYGNQTGYVSSQYLAEK	65	997.3	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
TITGNAVNFR	58	546.7	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
KVTISNINSSYYSSR	114	859.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
YLGTSVNDSTNENAENSSNDLVK	56	1235.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
KSVGVSIPR	46	471.7	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
VTISNINSSYYSSR	76	795.8	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
SVGVSIPR	39	407.6	2		Putative cell wall hydrolase OS=Clostridium difficile	Q181Y8|Q181Y8_CLOD6
IDVFDSDEFGK	39	636.2	2		Spermidine synthase OS=Clostridium difficile (strain	Q18A85|SPEE_CLOD6
VLVIGGGDGGTVR	37	600.2	2		Spermidine synthase OS=Clostridium difficile (strain	Q18A85|SPEE_CLOD6
FYEYDSIEDDVR	71	775.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ATLTDVTTVNQEINKLGK	31	648.9	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TYIGTTESMDAPTTPNYR	33	1009.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
FDVSDKTINDFEVR	59	562.3	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ILNENIASM*AK	68	610.2	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ILTSTAVGNEK	57	566.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ILGYEIIR	43	488.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
FVSDTMYVPVGAK	37	707.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
GPIITFDK	38	445.7	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
YAEDTPSGGDIK	66	626.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
VSASFSDGIQSGSLVK	93	791.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
FTDNISPLNNR	67	645.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TVGFVDAKGNSK	36	611.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
IEGLKDNTTYEVR	52	769.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TGVLNTTDIESDKVTLNVPATAVYQGISK	55	1012.4	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
GNADLNTQVDR	89	601.7	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SYTM*DTFMATPR	49	718.8	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TENDSHGPLQNPEIDNIKDNDASTTYK	31	1006.4	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SYTM*DTFM*ATPR	53	726.7	2	2 Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
NTSTTYNPLTNYK	39	758.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
VVAYDYHLNPTEEFEVGTVK	62	770.9	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TINDFEVR	38	497.2	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SGEINLNTGK	52	516.7	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SYTMDTFM*ATPR	57	718.8	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
LGEKDSGTVNVGTDNIEYTIK	56	752.0	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SDGNYLDGENGTQVK	59	798.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TKFTDNISPLNNR	50	760.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ATLTDVTTVNQEINK	70	823.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
TQDLDGNGTVDDNEFNLTKNDM*APK	53	923.7	3	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
MTATNHLGTSGMSK	59	718.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TYIGTTESM*DAPTTPNYR	42	1017.3	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
AGDEITVYVGSK	61	619.7	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
YAEDTPSGGDIKVR	40	503.2	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
KILNENIASMAK	66	666.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
IQVSVCSSYSYK	53	710.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
LAQDLYNDR	71	554.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
FVSDTM*YVPVGAK	49	715.2	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
KIQYVNDEAR	58	618.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ALSSSDPINSLPK	71	664.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ILNENIASMAK	63	602.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SNISELKFYEYDSIEDDVR	38	775.0	3		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
AWGVEITPELNSIM*DSK	54	953.8	2	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
NNSDADLSNDTFYAK	94	837.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
VSIQSLNGDWSSGYK	57	821.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
SYTMDTFMATPR	56	710.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
DIEAYGLYR	52	550.2	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
TQDLDGNGTVDDNEFNLTK	65	1048.9	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
YNDLQGDTPVGQR	59	731.8	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
LIYTQYYGESGAYK	100	828.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
GEPYYPGTNVGNSYGYSEK	41	1041.4	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
ETLPIVGLK	41	485.3	2		Putative exported protein OS=Clostridium difficile (st	Q183N3|Q183N3_CLOD6
LLENLNEGKIFK	36	709.3	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
TEKNLM*AGFAGESEAR	52	863.8	2	Oxidation (M)	Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
IAYLFEAVGK	48	555.7	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
NLMAGFAGESEAR	78	676.7	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
NKYTYYASK	32	569.1	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
NLM*AGFAGESEAR	84	684.6	2	Oxidation (M)	Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
KEGYNQIAAIFEETANNEK	49	723.6	3		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
LLHDGM*PSTEENLK	38	800.3	2	Oxidation (M)	Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
EEGFDKIAYLFEAVGK	61	908.4	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
LLENLNEGK	46	515.2	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
EGYNQIAAIFEETANNEKEHAK	34	835.9	3		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
LLHDGM*PSTEENLKDAAAGENYEWTDM*Y	50	1145.0	3	2 Oxidation (M)	Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
DAAAGENYEWTDMYAK	73	917.7	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
AYFNIKAENY	54	616.7	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
TEKNLMAGFAGESEAR	62	855.8	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
YLKLLENLNEGK	44	717.3	2		Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
DAAAGENYEWTDM*YAK	60	925.8	2	Oxidation (M)	Rubrerythrin OS=Clostridium difficile (strain 630) GN	Q18A24|Q18A24_CLOD6
ELLSIGNLNLK	39	607.3	2		Putative penicillin-binding protein repressor OS=Clos	Q183K0|Q183K0_CLOD6
TNM*NPNEIISLGKELLSIGNLNLK	52	881.0	3	Oxidation (M)	Putative penicillin-binding protein repressor OS=Clos	Q183K0|Q183K0_CLOD6
TNM*NPNEIISLGK	59	723.7	2	Oxidation (M)	Putative penicillin-binding protein repressor OS=Clos	Q183K0|Q183K0_CLOD6
VIETYYGK	34	486.8	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
IYIVGGESAVSNTAK	96	754.9	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
LAGDDRHTTSVAVAK	40	770.9	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
YTGGSQVGQPIYEIK	36	820.4	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
GEADAMSIAAK	76	532.2	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
TIYVGIGDEK	41	547.7	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
NIDDVQLAEITIK	90	736.4	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
NSDLNTVSPQDLYDGYRLTVK	46	800.4	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
IYIVGGESAVSNTAKK	65	818.9	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
IITNIDELEK	41	594.3	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
ATELTVESTNEK	66	661.3	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
LVDGLAATPLAQSK	44	692.3	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
KAPILLASDNEIPK	44	503.6	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
NSDLNTVSPQDLYDGYR	36	978.9	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
YENSADLSAEANSITEK	73	921.4	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
GHITNSANEVVAEATEK	48	590.6	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
TDITDSQKNALSK	40	474.2	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
AAELKAPIIVNGWNDLSADAIK	40	770.5	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
VIETYYGKLDK	45	664.9	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
LVNALGENK	32	479.2	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
QLESVTKNIER	38	439.6	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
ATELTVESTNEKDLK	49	559.9	3		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
DAFVVGAK	31	403.7	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
YTDNIVIVNSNK	60	690.4	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
APIIVNGWNDLSADAIK	38	899.0	2		Cell surface protein (Putative S-layer protein) OS=C	Q183M5|Q183M5_CLOD6
NKDIDEITQVGGGYNQK	63	939.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
TYELEISAFDGR	37	700.9	2		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
TRYETAVEVSK	47	428.2	3		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
LGVDNVYIVDSGNSISSKVENEIK	42	860.4	3		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
SIMLDKVPGGK	44	572.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
INNVFVAK	50	452.8	2		Cell surface protein OS=Clostridium difficile (strain 6	Q181V6|Q181V6_CLOD6
LANQGFLAK	37	481.2	2		Valyl-tRNA synthetase OS=Clostridium difficile (stra	Q180A1|Q180A1_CLOD6

Sequence	Score	m/z	z	Modification	Protein_Name	Protein_ID
FVFM*NIDEDIIKNM*TR	36	673.2	3	2 Oxidation (M)	Valyl-tRNA synthetase OS=Clostridium difficile (stra	Q180A1|Q180A1_CLOD6
FSAVGAGFEGGLEALCR	60	870.8	2		Tellurium resistance protein OS=Clostridium difficile	Q186J1|Q186J1_CLOD6
VLNSENDEEILR	49	716.3	2		Tellurium resistance protein OS=Clostridium difficile	Q186J1|Q186J1_CLOD6
SACPQTYSFLQNLAK	68	864.3	2		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
LTDEKEYAYLK	63	686.8	2		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
TWDDVPGLGGSTVALR	56	548.8	3		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
SAQFKQIFAK	43	584.2	2		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
YLNALKQNNLK	40	659.8	2		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
GWEGTGKTWDDVPGLGGSTVALR	62	1180.5	2		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
DTLSQIVVFPTGNYDKNEANAMVNR	32	933.0	3		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
LKSACPQTYSFLQNLAK	39	656.9	3		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
LANIDGKYLNALK	45	478.2	3		Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
DTLSQIVVFPTGNYDKNEANAM*VNR	56	938.3	3	Oxidation (M)	Putative exported protein OS=Clostridium difficile (st	Q183R7|Q183R7_CLOD6
KLVSEGDDVPAN	35	622.2	2		Putative NUDIX-family hydrolase OS=Clostridium di	Q189Y6|Q189Y6_CLOD6
ILGGGLPYESAVQR	33	730.3	2		Putative NUDIX-family hydrolase OS=Clostridium di	Q189Y6|Q189Y6_CLOD6