

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI					
46402201	Jim Morris Clemson [human]	1410.56	66.67	1	25	25	428	471	51.4	8.82					
A3	Sequence	# PSMs	# Proteins	# Protein Groups	Protein Group Accessions	Modifications	ΔCn	XCorr	Charge	MH+ [Da]	ΔM [ppm]	RT [min]	# Missed Cleavages		
High	AAQLSASfcaAPLVK	6	1	1	1.46402201	C9(Cys->Dha); C10(Dioxidation)	0.0000	4.22	2	1506.74455	-11.69	95.13	0		
High	ATAIDGSVFEK	9	1	1	1.46402201		0.0000	3.74	2	1250.66338	0.49	86.86	0		
High	DSGIGGAIFISAMVNDK	29	1	1	1.46402201		0.0000	4.71	2	1751.86418	0.46	110.36	0		
High	DVAMAALNQFTMSVESMR	42	1	1	1.46402201	M13(Oxidation)	0.0000	4.92	2	2117.96904	1.18	112.52	0		
High	DVAMAALNQFTMSVESMR	16	1	1	1.46402201		0.0000	6.01	3	2101.97129	-0.16	114.69	0		
High	EGAVVDSSTSAFK	17	1	1	1.46402201		0.0000	3.57	2	1297.62651	-0.45	67.85	0		
High	FAGmISADR	25	1	1	1.46402201	M4(Oxidation)	0.0000	3.07	2	983.46153	-0.02	62.05	0		
High	FAGmISADR	10	1	1	1.46402201		0.0000	3.21	2	967.46733	0.71	72.73	0		
High	FAGmISADRmPGLQFTR	3	1	1	1.46402201	M4(Oxidation); M10(Oxidation)	0.0000	2.65	3	1929.93106	-0.01	80.60	1		
High	FDLIDDDASLNK	3	1	1	1.46402201		0.0000	4.32	2	1365.65398	0.48	90.81	0		
High	FDLIDDDASLNKGGQALEK	7	1	1	1.46402201		0.0000	3.58	3	2120.05332	1.23	89.82	1		
High	FVLPPTKFDLIDDDASLNK	3	1	1	1.46402201		0.0000	4.19	3	2152.11600	-0.62	102.44	1		
High	FVLPPTKFDLIDDDASLNKGGQALEK	4	1	1	1.46402201		0.0000	3.76	4	2906.51723	0.86	99.23	2		
High	GSALTPINmESGNFDSK	24	1	1	1.46402201	M9(Oxidation)	0.0000	4.13	2	1783.81731	0.29	76.85	0		
High	GSALTPINmESGNFDSK	13	1	1	1.46402201		0.0000	3.78	2	1767.82317	0.73	84.77	0		
High	GVQGNVDVIALQLAAAFGR	34	1	1	1.46402201		0.0000	5.47	2	1728.94109	1.07	128.11	0		
High	LNNILEHISIQGNDGETVR	7	1	1	1.46402201		0.0000	6.03	3	2122.09018	0.65	90.88	0		
High	mISGmYLGEIAR	8	1	1	1.46402201	M1(Oxidation); M5(Oxidation)	0.0000	3.71	2	1372.66057	0.41	82.17	0		
High	MISGmYLGEIAR	29	1	1	1.46402201	M5(Oxidation)	0.0000	2.51	2	1356.66594	0.62	87.38	0		
High	MISGmYLGEIAR	9	1	1	1.46402201		0.0000	4.38	2	1340.67046	0.21	95.02	0		
High	mLPSVYK	2	1	1	1.46402201	M1(Oxidation)	0.0000	2.03	2	1016.51354	1.36	74.98	0		
High	mPGLQFTR	2	1	1	1.46402201	M1(Oxidation)	0.0000	2.13	2	965.48888	1.57	75.00	0		
High	mPGLQFTR	10	1	1	1.46402201		0.0000	2.51	2	949.49248	0.03	82.66	0		
High	QIMTYLLEMVEGLEGR	18	1	1	1.46402201	M3(Oxidation)	0.0000	4.75	2	2061.00786	2.25	126.91	0		
High	QIMTYLLEMVEGLEGR	10	1	1	1.46402201		0.0000	5.54	2	2045.00774	-0.28	141.93	0		
High	RLNILEHISIQGNDGETVR	15	1	1	1.46402201		0.0000	5.21	3	2278.19126	0.58	88.65	0		
High	RVLQDNINR	2	1	1	1.46402201		0.0000	3.59	2	1127.63030	2.01	56.69	1		
High	TVPLGFTSFPEVQTK	26	1	1	1.46402201		0.0000	3.87	2	1797.94231	0.04	110.76	0		
High	VACKEGAVDSSSTSAFK	3	1	1	1.46402201	C3(Cys->Dha)	0.0000	3.06	3	1664.84983	0.45	69.10	1		
High	VACKEGAVDSSSTSAFK	2	1	1	1.46402201	C3(Dioxidation)	0.0000	2.74	3	1730.82566	-0.56	72.61	1		
High	VACKEGAVDSSSTSAFK	2	1	1	1.46402201	C3(Delta-S(-1)Se(1))	0.0000	4.44	2	1746.82109	22.81	73.50	1		
High	VACKEGAVDSSSTSAFK	2	1	1	1.46402201	C3(Trioxidation)	0.0000	4.44	2	1746.82109	-0.26	73.50	1		
High	VNVVALNDVTGLTSLHYFKDPEVQVG	1	1	1	1.46402201	C7(Dioxidation); C37(Cys->Dha)	0.0000	3.00	5	5608.83222	0.92	124.02	2		
High	VNVVALNDVTGLTSLHYFKDPEVQVG	2	1	1	1.46402201		0.0000	3.31	4	5610.82436	-0.11	125.12	2		
High	YALEGNATLDFDIASNVK	20	1	1	1.46402201		0.0000	5.68	2	2088.02983	0.64	123.53	0		
High	YALEGNATLDFDIASNVK	13	1	1	1.46402201		0.0000	4.48	3	2216.12766	1.89	117.03	1		