

Table 1: MS/MS identification of PARP-1 and Mitofilin in PARP-1 immunoprecipitated sample.

The peptide list resulting from MS analysis of PARP-1 immunoprecipitation are reported.

Protein Name	Accession No. (P09874)	Protein Score	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %	Protein MW	rotein PI	Pep. Count	MS Ion Intensity
Poly [ADP-ribose] polymerase-1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)) ADP-ribosyltransferase	PPOL_HUMAN	242	100	100	203	100	113679,6	8,99	20	6538193
Peptide Information										
Calc. Mass	Obsrv. Mass	± da ± ppm	Start Seq.	End Sequence Seq.		Ion Score	C. I. %	Modification		
823,4645	823,4717	0,0072	9	852	857 QLHNRR					
829,489	829,4863	-0,0027	-3	131	137 IEKGQVR					
868,4788	868,4811	0,0023	3	858	864 LLWHGSR					
868,4788	868,4811	0,0023	3	858	864 LLWHGSR	32	99,589			
897,4828	897,4891	0,0063	7	629	635 NFKYPK					
1024,5798	1024,5881	0,0083	8	857	864 RLLWHGSR					
1066,5891	1066,6002	0,0111	10	486	495 AEPVEVVAPR					
1066,5891	1066,6002	0,0111	10	486	495 AEPVEVVAPR	52	99,996			
1146,5499	1146,5647	0,0148	13	893	902 GIYFADMVSK			Oxidation (M)[7]		
1184,631	1184,6501	0,0191	16	337	345 EFREISYLK					
1185,5786	1185,608	0,0294	25	108	118 TLGDFAAEYAK					
1193,556	1193,5782	0,0222	19	156	164 WYHPGCFVK			Carbamidomethyl (C)[6]		
1259,6011	1259,6216	0,0205	16	674	683 MIFDVESMKK			Oxidation (M)[1,8]		
1291,6311	1291,657	0,0259	20	23	33 CSESIPKDSLRL			Carbamidomethyl (C)[1]		
1361,8038	1361,8291	0,0253	19	551	563 VFSATLGLVDIVK					
1365,8464	1365,8768	0,0304	22	662	673 SKLPKPVQDLIK					
1372,7067	1372,7366	0,0299	22	571	581 LQLEDDKENR					
1377,7485	1377,7858	0,0373	27	865	877 TTNFAGILSQGLR					
1377,7485	1377,7858	0,0373	27	865	877 TTNFAGILSQGLR	118	100			
1399,7175	1399,751	0,0335	24	269	281 QQVPSGESAILDR					
1499,7125	1499,7551	0,0426	28	65	77 HPDVEVDGFSELR					
1530,7758	1530,8193	0,0435	28	802	814 VVDRDSEAEIIR					
2138,1643	2138,1956	0,0313	15	467	485 SLQELFLAHLSPWGAEVK					

Protein Name	Accession No. (Q16891)	Protein Score	Protein Score C. I. %	Total Ion Score	Total Ion C. I. %	Protein MW	Protein PI	Pep. Count	MS Ion Intensity
Mitochondrial inner membrane protein (Mitofilin) (p87/89)	IMMT_HUMAN	390	100	290	100	84025,5	6,08	27	6476540,5

Peptide Information

Calc. Mass	Obsrv. Mass	\pm da \pm ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
847,3845	847,3862	0,0017	2	67	72 WDSHFR			
914,5166	914,5187	0,0021	2	411	417 RIDQLNR			
964,521	964,521	0	0	443	451 RAFDSAVAK			
982,5468	982,5515	0,0047	5	633	640 ARFYAVQK			
1002,5577	1002,5546	-0,0031	-3	276	284 TVEGALKER			
1015,5683	1015,5664	-0,0019	-2	719	726 RVAQDWLK			
1053,5211	1053,5193	-0,0018	-2	624	632 GVYSEETLR			
1053,5211	1053,5193	-0,0018	-2	624	632 GVYSEETLR	30	98,425	
1119,5654	1119,5627	-0,0027	-2	486	495 QAAAHTDHLR			
1149,5898	1149,5837	-0,0061	-5	517	525 LSEQELQFR			
1153,5959	1153,5881	-0,0078	-7	196	205 ERPPEEVAAR			
1177,6323	1177,6254	-0,0069	-6	709	718 FVNQLKGESR			
1177,6323	1177,6254	-0,0069	-6	709	718 FVNQLKGESR	27	96,785	
1235,5573	1235,5266	-0,0307	-25	258	269 AAMDNSEIAGEK			
1305,6909	1305,6836	-0,0073	-6	517	526 LSEQELQFR			
1323,6825	1323,6802	-0,0023	-2	111	122 ISSVSEVMKESK			
1419,6652	1419,6583	-0,0069	-5	67	77 WDSHFRESVEK			
1456,7754	1456,762	-0,0134	-9	412	423 IDQLNRELAEQK			
1522,874	1522,8658	-0,0082	-5	565	577 KAHQLWLSVEALK			
1525,8043	1525,8114	0,0071	5	331	343 LHNMIVDLDNVVK			Oxidation (M)[4]
1527,8278	1527,8171	-0,0107	-7	354	366 VVSQYHELVVQAR			
1527,8278	1527,8171	-0,0107	-7	354	366 VVSQYHELVVQAR	62	99,999	Phospho (ST)[8]
1602,8403	1602,8326	-0,0077	-5	565	577 KAHQLWLSVEALK			
1823,8882	1823,8767	-0,0115	-6	548	564 GIEQAVQSHAVAEER			
1871,996	1871,9846	-0,0114	-6	582	600 TSSAETPTIPLGSAVEAIK			
2065,0083	2065,0051	-0,0032	-2	500	516 VQEQLKSEFEQNLSEK			
2093,0732	2093,061	-0,0122	-6	546	564 LRGIEQAVQSHAVAEER			
2198,0723	2198,0654	-0,0069	-3	527	545 LSQEVDNFTLDINTAYAR	112	100	
2198,0723	2198,0654	-0,0069	-3	527	545 LSQEVDNFTLDINTAYAR			
2341,1306	2341,1362	0,0056	2	507	525 SEFEQNLSEKLSEQLQFR			
2354,1736	2354,175	0,0014	1	526	545 RLSQEVDNFTLDINTAYAR			
2506,1877	2506,187	-0,0007	0	601	623 ANCSDNFTQALTAAPPELSTR	58	99,998	Carbamidomethyl (C)[3]
2506,1877	2506,187	-0,0007	0	601	623 ANCSDNFTQALTAAPPELSTR			Carbamidomethyl (C)[3]

Protein Name	Accession No. (Q16891)	Protein Score	Protein Score	Total Ion Score	Total Ion C. I. %	Protein MW	Protein pI	Pep. Count	MS Ion Intensity
Mitochondrial inner membrane protein (Mitofilin) (p87/89)	IMMT_HUMAN	177	100	142	100	84025,5	6,08	17	9437753

Peptide Information

Calc. Mass	Obsrv. Mass	\pm da	\pm ppm	Start Seq.	End Sequence Seq.	Ion Score	C. I. %	Modification
847,3845	847,3863	0,0018	2	67	72 WDSHFR			
914,5166	914,5225	0,0059	6	411	417 RIDQLNR			
1015,5683	1015,5664	-0,0019	-2	719	726 RVAQDWLK			
1037,5391	1037,5355	-0,0036	-3	102	110 KSIQSGPLK			Phospho (ST)[2]
1053,5211	1053,5197	-0,0014	-1	624	632 GYSEETLR			
1149,5898	1149,5867	-0,0031	-3	517	525 LSEQELQFR			
1149,5898	1149,5867	-0,0031	-3	517	525 LSEQELQFR	14	52,759	
1153,5959	1153,588	-0,0079	-7	196	205 ERPPEEVAAR			
1177,6323	1177,6283	-0,004	-3	709	718 FVNQLKGESR			
1305,6909	1305,6879	-0,003	-2	517	526 LSEQELQFRR			
1527,8278	1527,8231	-0,0047	-3	354	366 VVSQYHELVVQAR	67	100	
1527,8278	1527,8231	-0,0047	-3	354	366 VVSQYHELVVQAR			
1602,8403	1602,8368	-0,0035	-2	565	577 KAHQLWLSVEALK			Phospho (ST)[8]
1823,8882	1823,8872	-0,001	-1	548	564 GIEQAVQSHAVAEER			
1871,996	1871,9915	-0,0045	-2	582	600 TSSAETPTIPLGSAVEAIK			
2093,0732	2093,0774	0,0042	2	546	564 LRGIEQAVQSHAVAEER			
2198,0723	2198,0808	0,0085	4	527	545 LSQEQVDNFTLDINTAYAR			
2198,0723	2198,0808	0,0085	4	527	545 LSQEQVDNFTLDINTAYAR	61	99,999	
2354,1736	2354,1721	-0,0015	-1	526	545 RLSQEQVDNFTLDINTAYAR			
2506,1877	2506,1926	0,0049	2	601	623 ANCDNFTQALTAAPPELTR			Carbamidomethyl (C)[3]