

MASCOT Search Results

Protein View: ADT2_HUMAN

ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7

Database: SwissProt
Score: 296
Monoisotopic mass (M_r): 33059
Calculated pI: 9.71
Taxonomy: [Homo sapiens](#)

Sequence similarity is available as [an NCBI BLAST search of ADT2_HUMAN against nr.](#)

Search parameters

MS data file: A2018042404.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: [Carbamidomethyl \(C\)](#)
Variable modifications: [Deamidated \(NQ\)](#), [Oxidation \(M\)](#)

Protein sequence coverage: 29%

Matched peptides shown in **bold red**.

1 MTDAAVSFAK **DFLAGGVAAA** **ISK**TAVAPIE RVKLLQVQH ASKQITADEQ
51 YKGIIDCVVR **IPKEQGVLSF** **WRGNLANVIR** YFPTQALNFA FDKYKQIFL
101 GGVDKRTQFW LYFAGNLASG GAAGATSLCF VYPLDFARTR **LAADVKGAGA**
151 **ERFRGLGDC** LVKIYKSDGI KGLYQGFNVV VQGIIYRAA YFGIYDTAKG
201 MLFDPKNTTHI VISWMIAQTV TAVAGLTSYP FDTVRRRMM QSGRK**GT**DTIM
251 **YGT**GLDCWRK IARDEGGKAF **FG**AWSNVLR GMGGAFLVL YDEIKKYT

Unformatted sequence string: [298 residues](#) (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
12204	11 - 23	610.3377	1218.6607	1218.6608	-0.066	0	38	0.0019	1	U	K.DFLAGGVAAAISK.T
9768	24 - 31	428.7494	855.4843	855.4814	3.38	0	31	0.0068	1		K.TAVAPIER.V
13621	61 - 72	487.2721	1458.7944	1458.7983	-2.72	1	58	1.6e-005	1	U	R.IPKEQGVLSFWR.G
9769	73 - 80	428.7534	855.4923	855.4926	-0.33	0	47	0.0001	1		R.GNLANVIR.Y
8547	141 - 147	673.3874	672.3801	672.3806	-0.77	0	42	0.00068	1		R.LAADVGK.A
8548	141 - 147	673.3879	672.3806	672.3806	-0.039	0	46	0.00029	1		R.LAADVGK.A
11852	141 - 152	386.5461	1156.6164	1156.6200	-3.11	1	38	0.0024	1	U	R.LAADVGKAGAEER.E
11853	141 - 152	579.3182	1156.6219	1156.6200	1.66	1	42	0.00057	1	U	R.LAADVGKAGAEER.E
12622	153 - 163	431.8909	1292.6509	1292.6547	-2.97	1	31	0.014	1	U	R.EFRGLGDCLVK.I
15634	245 - 259	606.2825	1815.8258	1815.8284	-1.45	1	63	5.4e-006	1	U	R.KGTDTIMYTGTLDCWR.K
15161	246 - 259	852.8666	1703.7186	1703.7284	-5.73	0	38	0.00056	1	U	K.GTDTIMYTGTLDCWR.K + Oxidation (M)
9873	273 - 280	451.7442	901.4738	901.4770	-3.49	0	45	0.00053	1		K.GAWSNVLR.G

