

**Mascot Search Results**

**Protein View**

Match to: [gi|576695773](#) Score: **92** Expect: **0.012**  
Actin [*Echinococcus granulosus*]  
  
Nominal mass (M<sub>r</sub>): **43780**; Calculated pI value: **5.31**  
NCBI BLAST search of [gi|576695773](#) against nr  
Unformatted [sequence string](#) for pasting into other applications  
  
Taxonomy: [Echinococcus granulosus](#)  
  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications: Oxidation (M)  
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P  
Sequence Coverage: **34%**

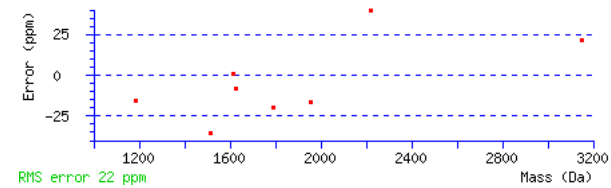
Matched peptides shown in **Bold Red**

1 MANPLPSIDN LSPSR**L**AMGD EEVQALVV**D**N GSGMCKAGFA GDDAPRAVFP  
51 SIVGRPR**HQ**G VMVGM**GQ**KDS YVGDEA**Q**SKR GILTLKYPIE HGIVTNWDDM  
101 EK**I**WHHTFY**N** ELRVAPE**E**HP VLLTEAP**L**NP KANREKMTQI MFETFNT**P**AM  
151 YVG**I**QAVLSL YASGR**TT**GIV LD**S**GDGV**T**HS VPIYEGY**A**LP HAILR**L**DLAG  
201 RDLTDYLMKI LTERGYS**F**TT TAEREIV**R**DI KEKLCY**V**ALD FEQEMATAAS  
251 SSSLEK**S**YEL PDGQV**I**TIG**N** ERFRCPES**L**F QPSFLG**M**ESA GIHSTF**N**AI  
301 MKCDVD**I**RKD LYANTVLS**G**G TTMYPGI**A**DR MQKEITS**L**AP STMKIKIV**A**P  
351 PERKYSV**W**IG GSILAS**L**STF QQMWISK**Q**EY DESGP**G**IVHR KCF

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
1 - 15	1627.7979	1626.7906	1626.8035	-8	0	-MANPLPSIDN <b>L</b> SPSR.L Oxidation (M) ( <a href="#">No match</a> )
16 - 36	2223.0964	2222.0891	2222.0017	39	0	R.LAMGDEEVQALVV <b>D</b> NGSGMCK.A ( <a href="#">No match</a> )
58 - 68	1187.5472	1186.5399	1186.5587	-16	0	R.HQGV <b>M</b> VMG <b>GQ</b> K.D Oxidation (M) ( <a href="#">No match</a> )
103 - 113	1515.6952	1514.6879	1514.7419	-36	0	K.IWHHTFY <b>N</b> ELR.V ( <a href="#">No match</a> )
114 - 131	1954.0328	1953.0255	1953.0571	-16	0	R.VAPEEHPVLLTEAP <b>L</b> NP <b>K</b> .A ( <a href="#">No match</a> )
166 - 195	3151.7104	3150.7031	3150.6350	22	0	R.TTGIVLD <b>S</b> GDGV <b>T</b> HSVPIYEGY <b>A</b> LP <b>H</b> AILR.L ( <a href="#">No match</a> )
257 - 272	1790.8569	1789.8496	1789.8846	-20	0	K.SYELPDGQV <b>I</b> TIG <b>N</b> ER.F ( <a href="#">No match</a> )
257 - 272	1790.8569	1789.8496	1789.8846	-20	0	K.SYELPDGQV <b>I</b> TIG <b>N</b> ER.F ( <a href="#">Ions score 38</a> )
378 - 391	1614.7885	1613.7812	1613.7798	1	1	K.QEYDESGPGIVHR <b>K</b> .C ( <a href="#">No match</a> )



Mascot: <http://www.matrixscience.com/>