

<http://www.matrixscience.com>

Mascot es un motor de búsqueda que usa datos de espectrometría de masas para identificar proteínas en Bases de Datos

Mascot

HOME : WHAT'S NEW : MASCOT : HELP : PRODUCTS : SUPPORT : TRAINING : CONTACT

Search

Mascot Search

- **Peptide Mass Fingerprint:** The experimental data are a list of peptide mass values from an enzymatic digest of a protein.
 - [Example of results report](#)
 - [More information](#)
- **Sequence Query:** One or more peptide mass values associated with information such as partial or ambiguous sequence strings, amino acid composition information, MS/MS fragment ion masses, etc. A super-set of a sequence tag query.
 - [Example of results report](#)
 - [More information](#)
- **MS/MS Ion Search:** Identification based on raw MS/MS data from one or more peptides.
 - [Example of results report](#)
 - [More information](#)

Search Form Defaults: [Follow this link to save your preferred search form defaults as a browser cookie.](#)

Mascot Help

- Mascot Overview
- Search parameter reference
- Data file format
- Scoring algorithm
- Results format
- Results Interpretation
- Error tolerant search
- Decoy database search
- Quantitation
- User Meeting Presentations
- 2008
- More Help
- Help Topic Index
- Unimod
- Useful Links

Entrada de datos

MASCOT Peptide Mass Fingerprint

Your name	<input type="text"/>	Email	<input type="text"/>
Search title	<input type="text"/>		
Database	MSDB <input type="button" value="v"/>		
Taxonomy	All entries <input type="button" value="v"/>		
Enzyme	Trypsin <input type="button" value="v"/>	Allow up to	1 <input type="button" value="v"/> missed cleavages
Fixed modifications	<input type="text" value="Acetyl (K)"/> Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term) <input type="button" value="v"/>	Variable modifications	<input type="text" value="Acetyl (K)"/> Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term) <input type="button" value="v"/>
Protein mass	<input type="text"/> kDa	Peptide tol. ±	1.2 <input type="text"/> Da <input type="button" value="v"/>
Mass values	<input checked="" type="radio"/> MH ⁺ <input type="radio"/> M _r <input type="radio"/> M-H ⁻	Monoisotopic	<input checked="" type="radio"/> Average <input type="radio"/>
Data file	<input type="text"/>	<input type="button" value="Examinar..."/>	
Query	<input type="text"/>		
NB Contents of this field are ignored if a data file is specified.			
Decoy	<input type="checkbox"/>	Report top	AUTO <input type="button" value="v"/> hits
<input type="button" value="Start Search ..."/>		<input type="button" value="Reset Form"/>	

Parámetros de búsqueda

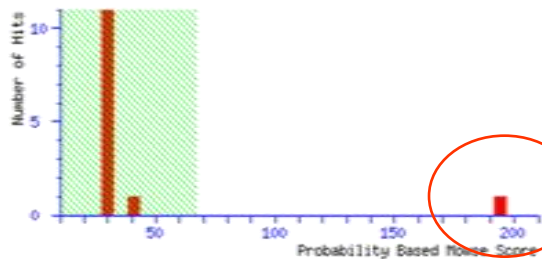
Salida de resultados

Mascot Search Results

User :
Email :
Search title : Peptide Mass Fingerprint Example
Database : SwissProt 51.6 (257964 sequences; 93947433 residues)
Timestamp : 19 Feb 2007 at 14:08:10 GMT
Top Score : 194 for **PML_HUMAN**, Probable transcription factor PML (Tripartite motif-containing protein 19) (RING finger protein 71)

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 67 are significant ($p < 0.05$).



Proteína
correctamente
identificada

Concise Protein Summary Report

Format As [Help](#)
Significance threshold p < Max. number of hits

1.	PML_HUMAN	Mass: 97455	Score: 194	Expect: 1e-14	Queries matched: 15
	Probable transcription factor PML (Tripartite motif-containing protein 19) (RING finger protein 71)				
	MURC_IDILO	Mass: 52994	Score: 51	Expect: 2	Queries matched: 5
	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase) - I				
	DPOL_RICHE	Mass: 104386	Score: 50	Expect: 2.8	Queries matched: 6
	DNA polymerase I (EC 2.7.7.7) (POL I) - Rickettsia helvetica				
	THIO_POMPY	Mass: 11877	Score: 41	Expect: 20	Queries matched: 3
	Thioredoxin (Trx) - Pongo pygmaeus (Orangutan)				
	BBL2_BROS4	Mass: 50569	Score: 40	Expect: 28	Queries matched: 4

Nº de coincidencias con \geq Score que son esperados que ocurran por azar. Cuánto más próximo a 0, más significativo es el score.

Protein View

Match to: PML_HUMAN Score: 194 Expect: 1e-14
 Probable transcription factor PML (Tripartite motif-containing protein 19) (RING finger protein 71)

Nominal mass (M₂): 97455; Calculated pI value: 5.88
 NCBI BLAST search of PML_HUMAN against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Cleavage by Trypsin: cuts C-term side of **K** unless next residue is P
 Number of mass values searched: 18
 Number of mass values matched: 15
 Sequence Coverage: 22%

Matched peptides shown in **Bold Red**

```

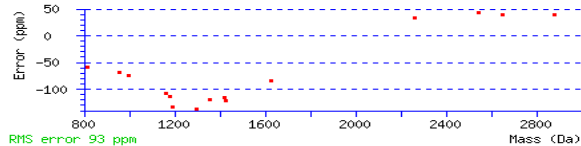
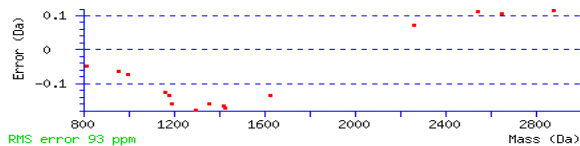
1 MEPAPARSPR PQQDPARPQE PTMPPPETPS EGRQPSPS PTERAPASEE
51 EFQFLRCQQC QAEAKCPKLL PCLHTLCSGC LEASGMQCPI CQAFWPLGAD
101 TPALDNVFFE SLQRRLSVYR QIVDAQAVCT RCKESADFWC FECEQLLCAK
151 CFEAHQWFLK HEARPLAELR NQSVRFLDG TRKTNIFCS NFNHRTPTLI
201 SIYCRGSKP LCCSCALLDS SHSELKCDIS AEIQQRQEEL DAMTQALQEQ
251 DSAFGAVHAQ MHAVGQLGR ARATEELIR ERVRQVVAVHV RAQERELLEA
301 VDARYQRDYE EMASRLRLD AVLQRIRTGS ALVQRMKCYA SDQEVLDMHG
351 FLRQALRLR QEEPQSLQAA VRTDGFDEFK VRLQDLSSCI TQGKDAVSK
401 KASFEAASTF RDPIDVDLPE EAERVKAQVQ ALGLAEAQPM AVVQSVPGAH
451 PVVVAFSIK GFSYGEDVSN TTAQRRKCS QTQCPRKVIK MESEEGKEAR
501 LARSSPEQRPR PSTSKAVSPP HLDGPPSPRS PVIGSEVFLP NSNHVASGAG
551 EABERVVVIS SSEDSDAENS SSRELDDSSS ESSDLQLEGP STLRVLDENL
601 ADPQAEDRPL VFFDLKIDNE TQKISQLAAV NRESKFRVVI QPEALFSIYS
651 KAVSLEVGLQ HFLSFLSSMR RPILACYKLW GPGLPNFFRA LEDINRLWEF
701 QEAISGFLAA LPLIRERVPG ASSFKLKNLA QTYLARNMSE RSMAAVLAM
751 RDLCRLEVS PGPQLAHVY PFSSLQCFAS LQPLVQAVL PRAEARLLAL
801 HNVSFMELLS AHRRDRQGGL KKYSRYLSLQ TTTLPPAQPA FNLQALGTYF
851 EGLLEGPALA RAEGVSTPLA GRGLAERASQ QS
    
```

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

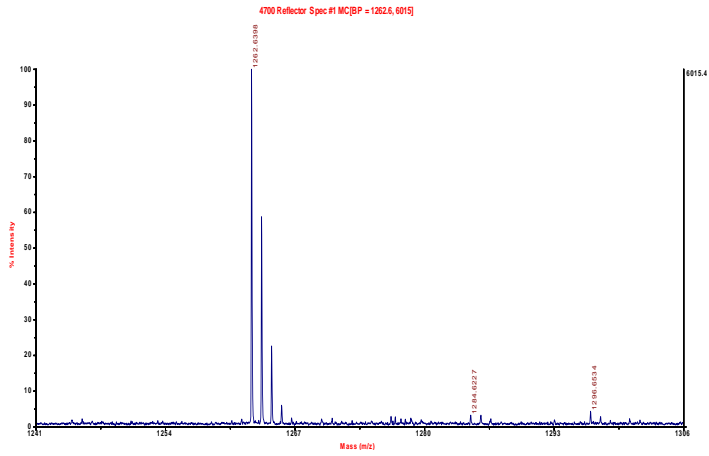
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
8 - 33	2882.5000	2881.4927	2881.3777	0.1150	0	R.SPR Q QDPAR PQE PTMP PPETPS EGR.Q
34 - 44	1182.4400	1181.4327	1181.5677	-0.1349	0	R.Q PS PS P TER.A
45 - 56	1423.5200	1422.5127	1422.6779	-0.1652	0	R.AP A SE E EQ F LR.C
161 - 170	1191.5000	1190.4927	1190.6520	-0.1592	0	K.HEAR P LA E LR.N
308 - 315	1000.3300	999.3227	999.3967	-0.0740	0	R.D Y E M AS.R.L
319 - 325	814.4300	813.4227	813.4708	-0.0481	0	R.LD A V L Q R .I
359 - 372	1624.7400	1623.7327	1623.8692	-0.1365	1	R.LR Q EE P Q S L Q AA V R.T
361 - 372	1355.5300	1354.5227	1354.6841	-0.1613	0	R.Q EE P Q SL Q AA V R.T
373 - 380	958.3500	957.3427	957.4080	-0.0653	0	R.T D GF D E F K.V
491 - 500	1165.3900	1164.3827	1164.5081	-0.1253	1	K.M E SE E G K EAR.L
504 - 515	1300.4700	1299.4627	1299.6419	-0.1792	0	R.S S PE Q RP R ST S K.A
516 - 529	1426.5700	1425.5627	1425.7365	-0.1737	0	K.A V SP P HL D PP S PR.S
530 - 555	2653.3900	2652.3827	2652.2780	0.1048	0	R.S P VIG S EV F L P NS N H V AS G AG E A E ER.V
574 - 594	2265.1100	2264.1027	2264.0292	0.0735	0	R.E L DD S SE S SD L Q L E G P S T L R.V
595 - 616	2544.4100	2543.4027	2543.2908	0.1120	0	R.V L D E N L AD P Q A ED R PL V FF D L K .I

No match to: 1320.4000, 1348.4100, 2550.3000



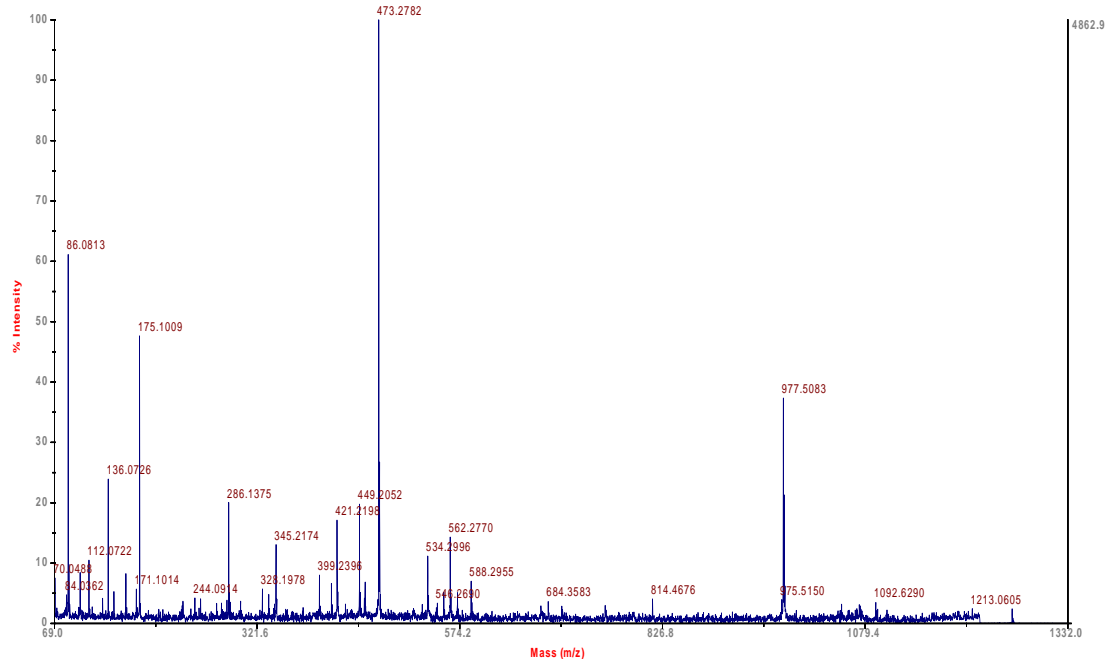
AC P29590; P29591; P29592; P29593; Q00755; Q96541;
 DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
 DT 30-MAY-2000, sequence version 2.
 DT 02-SEP-2008, entry version 112.
 DE RecName: Full=Probable transcription factor PML;
 DE AltName: Full=Tripartite motif-containing protein 19;
 DE AltName: Full=RING finger protein 71;
 GN Name=PML; Synonyms=MYL, RNF71, TRIM19;

Selección de péptidos precursores

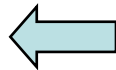


MSMS1262.67

4700 MS/MS Precursor 1262.67 Spec #1 [BP = 473.3, 4863]



Ion peak list



Datos MSMS (ion peak list)

MASCOT Sequence Query

Your name	<input type="text"/>	Email	<input type="text"/>
Search title	<input type="text"/>		
Database	MSDB		
Taxonomy	All entries		
Enzyme	Trypsin	Allow up to	1 missed cleavages
Fixed modifications	Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term)	Variable modifications	Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term)
Quantitation	None		
Peptide tol. ±	1.2 Da	MS/MS tol. ±	0.6 Da
Peptide charge	Mr	Monoisotopic	<input checked="" type="radio"/> Average <input type="radio"/>
Query	<input type="text"/>		
Instrument	Default		
Decoy	<input type="checkbox"/>	Report top	AUTO hits
<input type="button" value="Start Search ..."/>		<input type="button" value="Reset Form"/>	

MASCOT MS/MS Ions Search

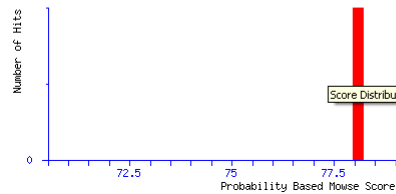
Your name	<input type="text"/>	Email	<input type="text"/>
Search title	<input type="text"/>		
Database	MSDB		
Taxonomy	All entries		
Enzyme	Trypsin	Allow up to	1 missed cleavages
Fixed modifications	Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term)	Variable modifications	Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term)
Quantitation	None		
Peptide tol. ±	1.2 Da # ¹³ C 0	MS/MS tol. ±	0.6 Da
Peptide charge	2+	Monoisotopic	<input checked="" type="radio"/> Average <input type="radio"/>
Data file	<input type="text"/>	Examiner...	
Data format	Mascot generic	Precursor	<input type="text"/> m/z
Instrument	Default	Error tolerant	<input type="checkbox"/>
Decoy	<input type="checkbox"/>	Report top	AUTO hits
<input type="button" value="Start Search ..."/>		<input type="button" value="Reset Form"/>	

Salida de resultados de Sequence Query (MSMS Spectra)

Email :
 Search title : Sequence Query Example (error tolerant tag)
 Database : SwissProt 51.6 (257964 sequences; 93947433 residues)
 Timestamp : 19 Feb 2007 at 14:11:21 GMT
 Protein hits : [CASB_BOVIN](#) Beta-casein precursor - Bos taurus (Bovine)
 [IF3X_DICDI](#) Putative eukaryotic translation initiation factor 3 subunit (eIF-3) - Dictyostelium discoideum (Sli

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 33 indicate identity or extensive homology ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As: Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits: AUTO

Standard scoring: MudPIT scoring Ions score or expect cut-off: 0 Show sub-sets: 0

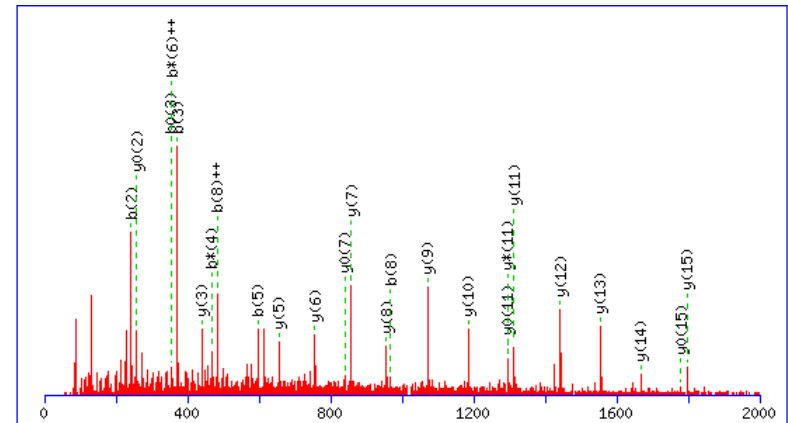
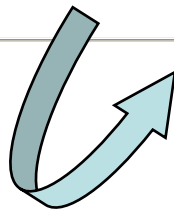
Show pop-ups: Suppress pop-ups Sort unassigned: Decreasing Score Require bold red:

Select All Select None Search Selected

1. [CASB_BOVIN](#) Mass: 25091 Score: 78 Queries matched: 1
 Beta-casein precursor - Bos taurus (Bovine)
 Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 1	1031.4000	2060.7854	1980.8548	79.9306	0	78	1.7e-06	1 K.FQSEQQQTEDELQDK.I

Proteins matching the same set of peptides:



MS/MS Fragmentation of [FQSEQQQTEDELQDK](#)
 Found in [CASB_BOVIN](#), Beta-casein precursor - Bos taurus (Bovine)
 Match to Query 1: 2060.785448 from(1031.400000,2+) etag(977.4,[QK][QK][QK]EE,1619.7)
 Monoisotopic mass of neutral peptide Mr(calc): 1980.8548
 Unsuspected modification: 79.9306 Da, located in the region N-term to S3
 Ions Score: 78 Expect: 1.7e-06

#	b	b ⁺⁺	b ⁺	b ⁰	b ⁰	b ⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁰	y ⁰	y ⁺⁺	#
1	148.0757	74.5415					F							16
2	276.1343	138.5708	259.1077	130.0575			Q	1834.7937	917.9005	1817.7672	909.3872	1816.7832	908.8952	15
3	363.1663	182.0868	346.1397	173.5735	345.1557	173.0815	S	1706.7351	853.8712	1689.7086	845.3579	1688.7246	844.8659	14
4	492.2089	246.6081	475.1823	238.0948	474.1983	237.6028	E	1619.7031	810.3552	1602.6766	801.8419	1601.6926	801.3499	13
5	621.2515	311.1294	604.2249	302.6161	603.2409	302.1241	E	1490.6605	745.8339	1473.6340	737.3206	1472.6500	736.8286	12
6	749.3101	375.1587	732.2835	366.6454	731.2995	366.1534	Q	1361.6179	681.3126	1344.5914	672.7993	1343.6074	672.3073	11
7	877.3686	439.1880	860.3421	430.6747	859.3581	430.1827	Q	1233.5594	617.2833	1216.5328	608.7700	1215.5488	608.2780	10
8	1005.4272	503.2172	988.4007	494.7040	987.4167	494.2120	Q	1105.5008	553.2540	1088.4742	544.7408	1087.4902	544.2487	9
9	1106.4749	553.7411	1089.4483	545.2278	1088.4643	544.7358	T	977.4422	489.2247	960.4156	480.7115	959.4316	480.2195	8
10	1235.5175	618.2624	1218.4909	609.7491	1217.5069	609.2571	E	876.3945	438.7009	859.3680	430.1876	858.3840	429.6956	7
11	1350.5444	675.7759	1333.5179	667.2626	1332.5339	666.7706	D	747.3519	374.1796	730.3254	365.6663	729.3414	365.1743	6
12	1479.5870	740.2972	1462.5605	731.7839	1461.5765	731.2919	E	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	5
13	1592.6711	796.8392	1575.6445	788.3259	1574.6605	787.8339	L	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	4
14	1720.7297	860.8685	1703.7031	852.3552	1702.7191	851.8632	Q	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3

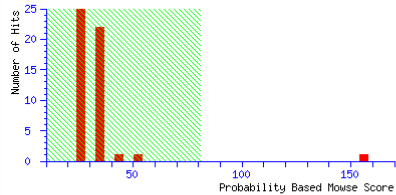
Salida de resultados de Sequence Query (Búsqueda combinada de PMF y PFF)

(MATRIX) Mascot Search Results

User :
 Email :
 Search title : SampleSetID: 14, AnalysisID: 181, MaldiWellID: 2723, SpectrumID: 3884, Path=\\08T
 Database : NCBIInr 080626 (6640940 sequences; 2276975120 residues)
 Timestamp : 24 Sep 2008 at 17:21:33 GMT
 Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search
 Top Score : 156 for [gi|159113013](#), Glucokinase [Giardia lamblia ATCC 50803]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 81 are significant ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As: Protein Summary (deprecated) [Help](#)

Significance threshold $p < 0.05$ Max. number of hits 20

Standard scoring: MudPIT scoring Ions score cut-off 0 Show sub-sets

Show pop-ups: Suppress pop-ups Sort unassigned: Decreasing Score Require bold red

Re-Search All Search Unmatched



Protein View

Match to: [gi|159113013](#) Score: 156 Expect: 1.7e-009
 Glucokinase [Giardia lamblia ATCC 50803]

Nominal mass (M_r): 38259; Calculated pI value: 5.69

NCBI BLAST search of [gi|159113013](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Giardia lamblia ATCC 50803](#)
 Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|16630861](#) from [Giardia intestinalis](#)
[gi|157434833](#) from [Giardia lamblia ATCC 50803](#)

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Sequence Coverage: 14%

Matched peptides shown in **Bold Red**

```

1 MPYSLSGDLG GTKCFIAIHD LDVLKTDPPRA APLLEHELLC KDYQSTGDLI
51 NDFLKRWDRE TPIVGLGVA GPVTNGRWCI TMLDWNSEEE ELQNTTGVGK
101 MKLINDFAAI GYGLLAIRPD DYLDPDFDARG SVSTPTVVPD NSTGIVSYAG
151 AGTGFVGVFV ADGWAYAAEG GHTTFSPEEA EDHALAQFIK EKYNTDHVSF
201 ERVVSLGLRL MMHDFFWKL SGLASPVLRE HVLSRDHDID HGFLAKCAET
251 GDRYALKIFK KFFYYGYFYL GNICVLFPRK DYFIAGGILAKD KDLNLVCGPC
301 REDFCRGLYT KGRNSHLPNG VSFHVVTNQK LGIVGAAYFC TKM
  
```

Show predicted peptides also

Sort Peptides By: Residue Number Increasing Mass Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
193	- 202	1267.5710	1266.5637	1266.5629	0.0008	0	K.YNTDHSFER.V (No match)
211	- 218	1140.4900	1139.4827	1139.4858	-0.0031	0	R.NMHDFFWK.N Oxidation (M) (Ions score 10)
211	- 218	1140.4900	1139.4827	1139.4858	-0.0031	0	R.NMHDFFWK.N Oxidation (M) (No match)
211	- 218	1140.4900	1139.4827	1139.4858	-0.0031	0	R.NMHDFFWK.N Oxidation (M) (No match)
219	- 229	1126.6561	1125.6488	1125.6506	-0.0017	0	K.MLSGLASPVLR.E (No match)
236	- 246	1261.5846	1260.5773	1260.5808	-0.0035	0	R.DHDIDMGFLAK.C (No match)
236	- 246	1277.5812	1276.5739	1276.5758	-0.0018	0	R.DHDIDMGFLAK.C Oxidation (M) (Ions score 73)
236	- 246	1277.5812	1276.5739	1276.5758	-0.0018	0	R.DHDIDMGFLAK.C Oxidation (M) (No match)
281	- 291	1167.6392	1166.6319	1166.6335	-0.0016	0	K.DYFIAGGILAK.D (Ions score 49)
281	- 291	1167.6392	1166.6319	1166.6335	-0.0016	0	K.DYFIAGGILAK.D (No match)

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Results List

1. [gi|159113013](#) Mass: 38259 Score: 156 Expect: 1.7e-009 Queries matched: 9

Glucokinase [Giardia lamblia ATCC 50803]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1126.6561	1125.6488	1125.6506	-0.0017	219	- 229	0	---	K.NLSGLASPVLR.E
1140.4900	1139.4827	1139.4858	-0.0031	211	- 218	0	10	R.NMHDFFWK.N + Oxidation (M)
1140.4900	1139.4827	1139.4858	-0.0031	211	- 218	0	---	R.NMHDFFWK.N + Oxidation (M)
1167.6392	1166.6319	1166.6335	-0.0016	281	- 291	0	49	K.DYFIAGGILAK.D
1167.6392	1166.6319	1166.6335	-0.0016	281	- 291	0	---	K.DYFIAGGILAK.D
1261.5846	1260.5773	1260.5808	-0.0035	236	- 246	0	---	R.DHDIDMGFLAK.C
1267.5710	1266.5637	1266.5629	0.0008	193	- 202	0	---	K.YNTDHSFER.V
1277.5812	1276.5739	1276.5758	-0.0018	236	- 246	0	73	R.DHDIDMGFLAK.C + Oxidation (M)
1277.5812	1276.5739	1276.5758	-0.0018	236	- 246	0	---	R.DHDIDMGFLAK.C + Oxidation (M)

No match to: 850.2542, 850.4948, 853.3255, 856.2545, 857.2662, 858.2584, 859.2527, 860.2634, 861.2578, 862.3109, 863.3129, 867.3217, 869.4474, 874.2842, 875.3333, 878.2533, 880.2489, 882.2752, 884.2811, 886.3156, 887.2660, 888.2822, 890.3176, 892.3212, 895.2640, 896.3218, 898.2856, 900.2611, 902.2969, 904.2787, 911.3513, 914.3533, 918.2825, 920.3241, 924.3392, 925.3494, 928.3502, 932.3561, 938.3030, 939.3422, 942.2662, 944.3466, 945.3507, 948.3356, 952.2762, 954.3179, 957.3728, 965.3690, 970.3492, 980.3402, 1010.3970, 1204.5529, 1229.5800, 1268.5671, 1293.5649, 1339.5016, 1525.6986, 1911.8318, 2224.9812